

Gene Ontology: tool for the unification of biology

Nature Genetics

25, 25-29

DOI: [10.1038/75556](https://doi.org/10.1038/75556)

Citation Report

#	ARTICLE	IF	CITATIONS
1	New approaches to antiviral drug discovery (genomics/proteomics). , 2007, , 1211-1218.		1
7	Being Positive about Selection. , 2006, 4, e87.		0
13	Protein Identification and Analysis Tools in the ExPASy Server. , 1999, 112, 531-552.		1,932
14	Integrative database analysis in structural genomics. , 2000, 7, 960-963.		45
15	Ets target genes: past, present and future. Oncogene, 2000, 19, 6533-6548.	2.6	335
16	Differential gene expression technologies for identifying surrogate markers of drug efficacy and toxicity. Drug Discovery Today, 2000, 5, 560-568.	3.2	37
17	The current excitement in bioinformaticsâ€™ analysis of whole-genome expression data: how does it relate to protein structure and function?. Current Opinion in Structural Biology, 2000, 10, 574-584.	2.6	73
18	Transcription, genomes, function. Trends in Genetics, 2000, 16, 409-415.	2.9	125
19	Ontology-based knowledge representation for bioinformatics. Briefings in Bioinformatics, 2000, 1, 398-414.	3.2	272
20	Measuring Shifts in Function and Evolutionary Opportunity Using Variability Profiles: A Case Study of the Globins. Journal of Molecular Evolution, 2000, 51, 223-233.	0.8	32
21	Analysis of molecular profile data using generative and discriminative methods. Physiological Genomics, 2000, 4, 109-126.	1.0	92
22	Bioinformatics. American Journal of Respiratory Cell and Molecular Biology, 2000, 23, 705-711.	1.4	28
23	Supporting Web based biology with ontologies. , 0, , .		4
24	MultiFun, a Multifunctional Classification Scheme for<i>Escherichia coli</i>K-12 Gene Products. Microbial & Comparative Genomics, 2000, 5, 205-222.	0.6	131
25	Representing and Analysing Molecular and Cellular Function Using the Computer. Biological Chemistry, 2000, 381, 921-35.	1.2	77
26	MultiFun, a Multifunctional Classification Scheme for<i>Escherichia coli</i>K-12 Gene Products. Microbial & Comparative Genomics, 2000, 5, 205-222.	0.6	45
27	The Drosophila genome. Current Opinion in Genetics and Development, 2000, 10, 612-616.	1.5	18
28	Recent developments and future directions in computational genomics. FEBS Letters, 2000, 480, 42-48.	1.3	49

#	ARTICLE	IF	CITATIONS
29	GENOMICS: The Babel of Bioinformatics. <i>Science</i> , 2000, 290, 471-473.	6.0	63
30	Mouse genome informatics in a new age of biological inquiry. , 0, , .		11
31	Transparent access to multiple bioinformatics information sources. <i>IBM Systems Journal</i> , 2001, 40, 532-551.	3.1	147
32	A functional update of the <i>Escherichia coli</i> K-12 genome. <i>Genome Biology</i> , 2001, 2, research0035.1.	13.9	111
33	Genome cartography through domain annotation. <i>Genome Biology</i> , 2001, 2, comment2006.1.	13.9	9
34	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690.	13.7	653
35	BIND--The Biomolecular Interaction Network Database. <i>Nucleic Acids Research</i> , 2001, 29, 242-245.	6.5	842
36	PicSNP: A Browsable Catalog of Nonsynonymous Single Nucleotide Polymorphisms in the Human Genome. <i>Biochemical and Biophysical Research Communications</i> , 2001, 287, 288-291.	1.0	19
37	PROGRAM DESCRIPTION. <i>Genomics</i> , 2001, 74, 121-128.	1.3	47
38	Fold Predictions for Bacterial Genomes. <i>Journal of Structural Biology</i> , 2001, 134, 219-231.	1.3	25
39	Review: What Can Structural Classifications Reveal about Protein Evolution?. <i>Journal of Structural Biology</i> , 2001, 134, 145-165.	1.3	47
40	Spotting the target: microarrays for disease gene discovery. <i>Current Opinion in Genetics and Development</i> , 2001, 11, 258-263.	1.5	51
41	Systematic approaches to mouse mutagenesis. <i>Current Opinion in Genetics and Development</i> , 2001, 11, 268-273.	1.5	106
42	Challenges for intelligent systems in biology. <i>IEEE Intelligent Systems</i> , 2001, 16, 14-18.	4.0	23
43	Information Technology Tools for Efficient SNP Studies. <i>Molecular Diagnosis and Therapy</i> , 2001, 1, 303-314.	3.3	3
44	Gene classification using expression profiles: a feasibility study. , 2001, , .		24
45	An algebra for semantic interoperability of information sources. , 2001, , .		23
46	Creating the Gene Ontology Resource: Design and Implementation. <i>Genome Research</i> , 2001, 11, 1425-1433.	2.4	881

#	ARTICLE	IF	CITATIONS
47	Analysis of Expression Patterns: The Scope of the Problem, the Problem of Scope. Disease Markers, 2001, 17, 59-65.	0.6	8
48	Candidate Genes and Single Nucleotide Polymorphisms (SNPs) in the Study of Human Disease. Disease Markers, 2001, 17, 89-98.	0.6	96
49	PRECIS: an automated pipeline for producing concise reports about proteins. , 2001, , .		1
50	Identification and Classification of Differentially Expressed Genes in Renal Cell Carcinoma by Expression Profiling on a Global Human 31,500-Element cDNA Array. Genome Research, 2001, 11, 1861-1870.	2.4	184
51	<title>Storage, data management, and retrieval in bioinformatics</title>. , 2001, 4676, 248.		0
52	Which craft is best in bioinformatics?. Computers & Chemistry, 2001, 25, 329-339.	1.2	17
53	Genome comparisons highlight similarity and diversity within the eukaryotic kingdoms. Current Opinion in Chemical Biology, 2001, 5, 86-89.	2.8	19
54	Analysing gene expression data from DNA microarrays to identify candidate genes. Journal of Pathology, 2001, 195, 53-65.	2.1	122
55	Issues in the design of medical ontologies used for knowledge sharing. Journal of Medical Systems, 2001, 25, 95-108.	2.2	13
56	Community watch. Nature Genetics, 2001, 28, 1-2.	9.4	6
57	Verification and initial annotation of the NIA mouse 15K cDNA clone set. Nature Genetics, 2001, 28, 17-18.	9.4	100
58	A literature network of human genes for high-throughput analysis of gene expression. Nature Genetics, 2001, 28, 21-28.	9.4	655
59	Human disease genes. Nature, 2001, 409, 853-855.	13.7	346
60	Bioinformatics beyond sequence: mapping gene function in the embryo. Nature Reviews Genetics, 2001, 2, 409-417.	7.7	59
61	Biology's name game. Nature, 2001, 411, 631-632.	13.7	54
62	Genome annotation: from sequence to biology. Nature Reviews Genetics, 2001, 2, 493-503.	7.7	324
63	A tour of structural genomics. Nature Reviews Genetics, 2001, 2, 801-809.	7.7	152
64	Profiling the malaria genome: a gene survey of three species of malaria parasite with comparison to other apicomplexan species. Molecular and Biochemical Parasitology, 2001, 118, 201-210.	0.5	40

#	ARTICLE	IF	CITATIONS
65	A status report on the sequencing and annotation of the <i>P. falciparum</i> genome. <i>Molecular and Biochemical Parasitology</i> , 2001, 118, 133-138.	0.5	11
66	The human proteomics initiative (HPI). <i>Trends in Biotechnology</i> , 2001, 19, 178-181.	4.9	87
68	Gene expression microarrays and the integration of biological knowledge. <i>Trends in Biotechnology</i> , 2001, 19, 412-415.	4.9	79
71	Mouse genomics: Making sense of the sequence. <i>Current Biology</i> , 2001, 11, R311-R314.	1.8	5
72	Novel computational methods in anti-microbial target identification. <i>Drug Discovery Today</i> , 2001, 6, 72-80.	3.2	21
73	Clustering and analysis of protein families. <i>Current Opinion in Structural Biology</i> , 2001, 11, 334-339.	2.6	48
74	Whole-genome analysis: annotations and updates. <i>Current Opinion in Structural Biology</i> , 2001, 11, 377-381.	2.6	35
76	DIAN: A Novel Algorithm for Genome Ontological Classification. <i>Genome Research</i> , 2001, 11, 1766-1779.	2.4	13
77	WormBase: network access to the genome and biology of <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2001, 29, 82-86.	6.5	290
78	The Mouse Genome Database (MGD): integration nexus for the laboratory mouse. <i>Nucleic Acids Research</i> , 2001, 29, 91-94.	6.5	70
79	The Mouse Gene Expression Database (GXD). <i>Nucleic Acids Research</i> , 2001, 29, 98-101.	6.5	70
80	Changes in global gene expression patterns during development and maturation of the rat kidney. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 5649-5654.	3.3	168
81	Amygdala-enriched genes identified by microarray technology are restricted to specific amygdaloid subnuclei. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 5270-5275.	3.3	155
82	Microarray probe selection strategies. <i>Briefings in Bioinformatics</i> , 2001, 2, 329-340.	3.2	56
83	Proteome Analysis Database: online application of InterPro and CluSTr for the functional classification of proteins in whole genomes. <i>Nucleic Acids Research</i> , 2001, 29, 44-48.	6.5	84
84	PartsList: a web-based system for dynamically ranking protein folds based on disparate attributes, including whole-genome expression and interaction information. <i>Nucleic Acids Research</i> , 2001, 29, 1750-1764.	6.5	45
85	Recent advances in computational genomics. <i>Pharmacogenomics</i> , 2001, 2, 361-372.	0.6	6
86	Title is missing!. <i>Nature Genetics</i> , 2001, 28, 21-28.	9.4	482

#	ARTICLE	IF	CITATIONS
87	Mining the bibliome. <i>Pharmacogenomics Journal</i> , 2001, 1, 88-89.	0.9	14
88	Detection of cis -element clusters in higher eukaryotic DNA. <i>Bioinformatics</i> , 2001, 17, 878-889.	1.8	225
89	Interrelating Different Types of Genomic Data, from Proteome to Secretome: 'Oming in on Function. <i>Genome Research</i> , 2001, 11, 1463-1468.	2.4	155
90	The use of animal models in expression pharmacogenomic analyses. <i>Pharmacogenomics Journal</i> , 2001, 1, 48-58.	0.9	12
91	Chapter 20. Bioinformatics in the drug discovery process. <i>Annual Reports in Medicinal Chemistry</i> , 2001, 36, 201-210.	0.5	1
92	Agent interaction for bioinformatics data management. <i>Applied Artificial Intelligence</i> , 2001, 15, 917-947.	2.0	16
93	Altered Cellular mRNA Levels in Human Cytomegalovirus-Infected Fibroblasts: Viral Block to the Accumulation of Antiviral mRNAs. <i>Journal of Virology</i> , 2001, 75, 12319-12330.	1.5	265
94	GENIES: a natural-language processing system for the extraction of molecular pathways from journal articles. <i>Bioinformatics</i> , 2001, 17, S74-S82.	1.8	410
95	Functional Versatility and Molecular Diversity of the Metabolic Map of Escherichia coli. <i>Genome Research</i> , 2001, 11, 1503-1510.	2.4	29
96	From molecular activities and processes to biological function. <i>Briefings in Bioinformatics</i> , 2001, 2, 81-93.	3.2	31
97	Protein function from the perspective of molecular interactions and genetic networks. <i>Briefings in Bioinformatics</i> , 2001, 2, 38-50.	3.2	21
98	Evaluating Mutant Mice: Anatomic Pathology. <i>Veterinary Pathology</i> , 2001, 38, 1-19.	0.8	78
99	Automatic rule generation for protein annotation with the C4.5 data mining algorithm applied on SWISS-PROT. <i>Bioinformatics</i> , 2001, 17, 920-926.	1.8	113
100	Large-scale identification of mammalian proteins localized to nuclear sub-compartments. <i>Human Molecular Genetics</i> , 2001, 10, 1995-2011.	1.4	108
101	PlasmoDB: An integrative database of the Plasmodium falciparum genome. Tools for accessing and analyzing finished and unfinished sequence data. <i>Nucleic Acids Research</i> , 2001, 29, 66-69.	6.5	94
102	A multi-agent system for automated genomic annotation. , 2001, , .		18
103	Title is missing!. <i>Nature Genetics</i> , 2001, 28, 1-2.	9.4	147
104	Title is missing!. <i>Nature Genetics</i> , 2001, 28, 17-18.	9.4	45

#	ARTICLE	IF	CITATIONS
105	Prediction of higher order functional networks from genomic data. <i>Pharmacogenomics</i> , 2001, 2, 373-385.	0.6	11
106	XML, bioinformatics and data integration. <i>Bioinformatics</i> , 2001, 17, 115-125.	1.8	231
107	Tagging gene and protein names in full text articles. , 2002, , .		26
108	Comparative Genome and Proteome Analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 298, 149-159.	6.0	531
109	Protein-based analysis of alternative splicing in the human genome. , 0, , .		7
110	euGenes: a eukaryote genome information system. <i>Nucleic Acids Research</i> , 2002, 30, 145-148.	6.5	39
111	Ontologies in the life sciences. <i>Knowledge Engineering Review</i> , 2002, 17, 77-80.	2.1	2
112	FANTOM DB: database of Functional Annotation of RIKEN Mouse cDNA Clones. <i>Nucleic Acids Research</i> , 2002, 30, 116-118.	6.5	55
113	Saccharomyces Genome Database (SGD) provides secondary gene annotation using the Gene Ontology (GO). <i>Nucleic Acids Research</i> , 2002, 30, 69-72.	6.5	322
114	Proteome Map of the Chloroplast Lumen of <i>Arabidopsis thaliana</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 8354-8365.	1.6	388
115	Saccharomyces genome database. <i>Methods in Enzymology</i> , 2002, 350, 329-346.	0.4	188
117	Assembly, Verification, and Initial Annotation of the NIA Mouse 7.4K cDNA Clone Set. <i>Genome Research</i> , 2002, 12, 1999-2003.	2.4	49
118	Cross-Referencing Eukaryotic Genomes: TIGR Orthologous Gene Alignments (TOGA). <i>Genome Research</i> , 2002, 12, 493-502.	2.4	134
119	Influence of the period-dependent circadian clock on diurnal, circadian, and aperiodic gene expression in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9562-9567.	3.3	167
120	BioMAS: A MULTI-AGENT SYSTEM FOR GENOMIC ANNOTATION. <i>International Journal of Cooperative Information Systems</i> , 2002, 11, 265-292.	0.6	22
121	Molecular characterization of lymphatic endothelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16069-16074.	3.3	436
122	Extension and Integration of the Gene Ontology (GO): Combining GO Vocabularies With External Vocabularies. <i>Genome Research</i> , 2002, 12, 1982-1991.	2.4	81
123	Large-Scale Protein Annotation through Gene Ontology. <i>Genome Research</i> , 2002, 12, 785-794.	2.4	96

#	ARTICLE	IF	CITATIONS
124	Rat Genome Database (RGD): mapping disease onto the genome. <i>Nucleic Acids Research</i> , 2002, 30, 125-128.	6.5	96
125	ARROGANT: an application to manipulate large gene collections. <i>Bioinformatics</i> , 2002, 18, 1410-1417.	1.8	10
126	Molecular Fossils in the Human Genome: Identification and Analysis of the Pseudogenes in Chromosomes 21 and 22. <i>Genome Research</i> , 2002, 12, 272-280.	2.4	167
127	Progress in bioinformatics and the importance of being earnest. <i>Biotechnology Annual Review</i> , 2002, 8, 1-54.	2.1	10
128	Extracting functional information from microarrays: A challenge for functional genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12509-12511.	3.3	21
129	Genome-wide Transcriptional Orchestration of Circadian Rhythms in <i>Drosophila</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 14048-14052.	1.6	236
130	Fly Factory. <i>Genome Research</i> , 2002, 12, 1017-1018.	2.4	2
132	The Use of Phylogenetic Profiles for Gene Predictions. <i>Current Genomics</i> , 2002, 3, 131-137.	0.7	28
133	GENERATION OF EXPRESSED SEQUENCE TAGS FROM A NORMALIZED PORCINE SKELETAL MUSCLE cDNA LIBRARY. <i>Animal Biotechnology</i> , 2002, 13, 211-222.	0.7	33
134	Information management systems for pharmacogenomics. <i>Pharmacogenomics</i> , 2002, 3, 651-667.	0.6	7
135	On the efficient evaluation of relaxed queries in biological databases. , 2002, , .		9
136	Identification of Genes Periodically Expressed in the Human Cell Cycle and Their Expression in Tumors. <i>Molecular Biology of the Cell</i> , 2002, 13, 1977-2000.	0.9	1,352
137	Genomics for Applied Microbiology. <i>Advances in Applied Microbiology</i> , 2002, 51, 201-248e.	1.3	14
138	Conserved codon composition of ribosomal protein coding genes in <i>Escherichia coli</i> , <i>Mycobacterium tuberculosis</i> and <i>Saccharomyces cerevisiae</i> : lessons from supervised machine learning in functional genomics. <i>Nucleic Acids Research</i> , 2002, 30, 2599-2607.	6.5	60
139	Association of nucleotide patterns with gene function classes: application to human 3' untranslated sequences. <i>Bioinformatics</i> , 2002, 18, 182-189.	1.8	56
140	Associating Genes with Gene Ontology Codes Using a Maximum Entropy Analysis of Biomedical Literature. <i>Genome Research</i> , 2002, 12, 203-214.	2.4	161
142	An efficient algorithm for large-scale detection of protein families. <i>Nucleic Acids Research</i> , 2002, 30, 1575-1584.	6.5	3,173
143	Annotating the human proteome: the Human Proteome Survey Database (HumanPSDTM) and an in-depth target database for G protein-coupled receptors (GPCR-PDTM) from Incyte Genomics. <i>Nucleic Acids Research</i> , 2002, 30, 137-141.	6.5	65

#	ARTICLE	IF	CITATIONS
144	Transitive functional annotation by shortest-path analysis of gene expression data. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12783-12788.	3.3	295
145	The Celera Discovery System™. Nucleic Acids Research, 2002, 30, 129-136.	6.5	55
146	Using Text Analysis to Identify Functionally Coherent Gene Groups. Genome Research, 2002, 12, 1582-1590.	2.4	63
147	Dissection of Transient Oxidative Stress Response in <i>Saccharomyces cerevisiae</i> by Using DNA Microarrays. Molecular Biology of the Cell, 2002, 13, 2783-2794.	0.9	103
148	MitoNuc: a database of nuclear genes coding for mitochondrial proteins. Update 2002. Nucleic Acids Research, 2002, 30, 172-173.	6.5	12
149	READ: RIKEN Expression Array Database. Nucleic Acids Research, 2002, 30, 211-213.	6.5	37
150	PipeOnline 2.0: automated EST processing and functional data sorting. Nucleic Acids Research, 2002, 30, 4761-4769.	6.5	49
151	Profiling Patterned Transcripts in <i>Drosophila</i> Embryos. Genome Research, 2002, 12, 1040-1047.	2.4	21
152	GenomeHistory: a software tool and its application to fully sequenced genomes. Nucleic Acids Research, 2002, 30, 3378-3386.	6.5	69
153	Predicting Protein Cellular Localization Using a Domain Projection Method. Genome Research, 2002, 12, 1168-1174.	2.4	97
154	Impact of the Presence of Paralogs on Sequence Divergence in a Set of Mouse-Human Orthologs. Genome Research, 2002, 12, 1370-1376.	2.4	59
155	Relating Whole-Genome Expression Data with Protein-Protein Interactions. Genome Research, 2002, 12, 37-46.	2.4	605
156	Judging the Quality of Gene Expression-Based Clustering Methods Using Gene Annotation. Genome Research, 2002, 12, 1574-1581.	2.4	259
157	PROTEOMICS: Enhanced: Integrating Interactomes. Science, 2002, 295, 284-287.	6.0	77
158	Functional Genomics of the Endocrine Pancreas: The Pancreas Clone Set and PancChip, New Resources for Diabetes Research. Diabetes, 2002, 51, 1997-2004.	0.3	77
159	Annotation of microbial genomes. Methods in Microbiology, 2002, 33, 3-26.	0.4	5
160	Biology-driven Clustering of Microarray Data. , 2002, , 65-79.		3
161	From genes to disease. Genome Biology, 2002, 3, spotlight-20020515-01.	13.9	0

#	ARTICLE	IF	CITATIONS
162	Asymmetric Functional Divergence of Duplicate Genes in Yeast. <i>Molecular Biology and Evolution</i> , 2002, 19, 1760-1768.	3.5	118
163	An Ontology for Pharmaceutical Ligands and Its Application for in Silico Screening and Library Design. <i>Journal of Chemical Information and Computer Sciences</i> , 2002, 42, 947-955.	2.8	104
164	Profiling Gene Expression Using Onto-Express. <i>Genomics</i> , 2002, 79, 266-270.	1.3	429
165	Computational Analysis of Alternative Splicing Using EST Tissue Information. <i>Genomics</i> , 2002, 80, 326-330.	1.3	44
166	Global Analysis of Gene Expression Patterns in Developing Mouse Neocortex Using Serial Analysis of Gene Expression. <i>Molecular and Cellular Neurosciences</i> , 2002, 19, 560-573.	1.0	26
167	Genomics Applications That Facilitate the Understanding of Drug Action and Toxicity. , 0, , 83-125.		2
168	Discovering statistically significant biclusters in gene expression data. <i>Bioinformatics</i> , 2002, 18, S136-S144.	1.8	717
169	Dietary effects of arachidonate-rich fungal oil and fish oil on murine hepatic and hippocampal gene expression. <i>Lipids in Health and Disease</i> , 2002, 1, 2.	1.2	80
170	Microarray analysis of orthologous genes: conservation of the translational machinery across species at the sequence and expression level. <i>Genome Biology</i> , 2002, 4, R4.	13.9	19
171	The GRID: The General Repository for Interaction Datasets. <i>Genome Biology</i> , 2002, 3, preprint0013.1.	13.9	0
172	Osprey: A Network Visualization System. <i>Genome Biology</i> , 2002, 3, preprint0012.1.	13.9	4
173	An integrated computational pipeline and database to support whole-genome sequence annotation. <i>Genome Biology</i> , 2002, 3, research0081.1.	13.9	44
174	Systematic determination of patterns of gene expression during <i>Drosophila</i> embryogenesis. <i>Genome Biology</i> , 2002, 3, research0088.1.	13.9	600
175	Evolutionary conservation of otd/Otx2 transcription factor action: a genome-wide microarray analysis in <i>Drosophila</i> . <i>Genome Biology</i> , 2002, 3, research0015.1.	13.9	23
177	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0
178	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. indica). <i>Science</i> , 2002, 296, 79-92.	6.0	3,146
179	Interrogating a High-Density SNP Map for Signatures of Natural Selection. <i>Genome Research</i> , 2002, 12, 1805-1814.	2.4	852
180	Modelling biological processes using workflow and Petri Net models. <i>Bioinformatics</i> , 2002, 18, 825-837.	1.8	124

#	ARTICLE	IF	CITATIONS
181	Spontaneous oxidative stress and liver tumors in mice lacking methionine adenosyltransferase 1A. <i>FASEB Journal</i> , 2002, 16, 1292-1294.	0.2	259
182	Evaluation of computational metabolic-pathway predictions for <i>Helicobacter pylori</i> . <i>Bioinformatics</i> , 2002, 18, 715-724.	1.8	88
183	MIPS Arabidopsisthaliana Database (MAtdB): an integrated biological knowledge resource based on the first complete plant genome. <i>Nucleic Acids Research</i> , 2002, 30, 91-93.	6.5	159
184	Perspective: Microarray Technology, Seeing More Than Spots. <i>Endocrinology</i> , 2002, 143, 1983-1989.	1.4	49
185	Metabolic pathway analysis in trypanosomes and malaria parasites. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2002, 357, 101-107.	1.8	25
186	Studying Genomes Through the Aeons: Protein Families, Pseudogenes and Proteome Evolution. <i>Journal of Molecular Biology</i> , 2002, 318, 1155-1174.	2.0	174
187	Prediction of Human Protein Function from Post-translational Modifications and Localization Features. <i>Journal of Molecular Biology</i> , 2002, 319, 1257-1265.	2.0	312
188	Toward a systematic definition of protein function that scales to the genome level: defining function in terms of interactions. <i>Proceedings of the IEEE</i> , 2002, 90, 1848-1858.	16.4	8
189	Gene Expression During the Life Cycle of <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 297, 2270-2275.	6.0	843
190	Gene Expression Phenotype in Heterozygous Carriers of Ataxia Telangiectasia. <i>American Journal of Human Genetics</i> , 2002, 71, 791-800.	2.6	50
191	The value of microarray techniques for quantitative gene profiling in molecular diagnostics. <i>Trends in Molecular Medicine</i> , 2002, 8, 269-272.	3.5	40
192	The systemic paradigm and its relevance to the modelling of biological functions. <i>Comptes Rendus - Biologies</i> , 2002, 325, 419-430.	0.1	4
193	Expression profiling in stably regenerating skeletal muscle of dystrophin-deficient mdx mice. <i>Neuromuscular Disorders</i> , 2002, 12, S118-S124.	0.3	34
194	Functional genomics of immune responses. <i>Immunology and Allergy Clinics of North America</i> , 2002, 22, 891-910.	0.7	2
195	Medical Informatics: Searching for Underlying Components. <i>Methods of Information in Medicine</i> , 2002, 41, 12-19.	0.7	48
196	Gene expression profiling reveals role for EGF-family ligands in mesangial cell proliferation. <i>American Journal of Physiology - Renal Physiology</i> , 2002, 283, F1151-F1159.	1.3	34
197	Expression profiling of human renal carcinomas with functional taxonomic analysis. <i>BMC Bioinformatics</i> , 2002, 3, 26.	1.2	48
198	Olling the way to machine understandable bioinformatics resources. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2002, 6, 129-134.	3.6	21

#	ARTICLE	IF	CITATIONS
199	AvGI, an index of genes transcribed in the salivary glands of the ixodid tick <i>Amblyomma variegatum</i> . <i>International Journal for Parasitology</i> , 2002, 32, 1447-1456.	1.3	78
200	Electronic tools to manage gene expression data. <i>Trends in Genetics</i> , 2002, 18, 108-110.	2.9	7
201	The FLEXGene Repository. <i>Archives of Medical Research</i> , 2002, 33, 318-324.	1.5	41
202	Conservation and diversification of gene function in plant development. <i>Current Opinion in Plant Biology</i> , 2002, 5, 56-61.	3.5	10
203	Introducing GeneDB: a generic database. <i>Trends in Parasitology</i> , 2002, 18, 465-467.	1.5	4
204	Comparative genomics approaches to study organism similarities and differences. <i>Journal of Biomedical Informatics</i> , 2002, 35, 142-150.	2.5	68
205	Two biomedical sublanguages: a description based on the theories of Zellig Harris. <i>Journal of Biomedical Informatics</i> , 2002, 35, 222-235.	2.5	164
206	Genome-Wide Transcript Profiles in Aging and Calorically Restricted <i>Drosophila melanogaster</i> . <i>Current Biology</i> , 2002, 12, 712-723.	1.8	528
207	A Comprehensive Collection of Chicken cDNAs. <i>Current Biology</i> , 2002, 12, 1965-1969.	1.8	305
208	Text-based knowledge discovery: search and mining of life-sciences documents. <i>Drug Discovery Today</i> , 2002, 7, S89-S98.	3.2	44
209	Genome annotation techniques: new approaches and challenges. <i>Drug Discovery Today</i> , 2002, 7, S70-S76.	3.2	33
210	Functional transcriptomes: comparative analysis of biological pathways and processes in eukaryotes to infer genetic networks among transcripts. <i>Current Opinion in Structural Biology</i> , 2002, 12, 355-361.	2.6	16
211	Bioinformatics: Using the Molecular Biology Data. , 0, , 265-284.		0
212	TEMBLOR – Perspectives of EBI Database Services. <i>Comparative and Functional Genomics</i> , 2002, 3, 47-50.	2.0	3
213	Ontology Based Document Enrichment in Bioinformatics. <i>Comparative and Functional Genomics</i> , 2002, 3, 42-46.	2.0	5
214	The Plant Ontology Consortium and Plant Ontologies. <i>Comparative and Functional Genomics</i> , 2002, 3, 137-142.	2.0	91
215	Website Review: How to Get the Best From Fission Yeast Genome Data. <i>Comparative and Functional Genomics</i> , 2002, 3, 282-288.	2.0	10
216	A Computational Strategy for Protein Function Assignment which Addresses the Multidomain Problem. <i>Comparative and Functional Genomics</i> , 2002, 3, 423-440.	2.0	12

#	ARTICLE	IF	CITATIONS
217	Functional Genomics: High-Throughput mRNA, Protein, and Metabolite Analyses. <i>Metabolic Engineering</i> , 2002, 4, 98-106.	3.6	97
218	A framework for integrating the songbird brain. <i>Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology</i> , 2002, 188, 961-980.	0.7	31
219	Expression profiling in mouse fetal thymus reveals clusters of coordinately expressed genes that mark individual stages of T-cell ontogeny. <i>Immunogenetics</i> , 2002, 54, 469-478.	1.2	4
220	The genomics of yeast responses to environmental stress and starvation. <i>Functional and Integrative Genomics</i> , 2002, 2, 181-192.	1.4	363
221	Yeast genomic databases and the challenge of the post-genomic era. <i>Functional and Integrative Genomics</i> , 2002, 2, 212-237.	1.4	19
222	Towards patient-specific tumor antigen selection for vaccination. <i>Immunological Reviews</i> , 2002, 188, 164-176.	2.8	73
223	Functional genomics: tools of the trade. <i>New Phytologist</i> , 2002, 153, 27-36.	3.5	47
224	Evidence for large domains of similarly expressed genes in the <i>Drosophila</i> genome. , 2002, 1, 5.		422
225	The need for a standard nomenclature for gene classification (a Nucleotide Function Code) and an automated data-based tool to assist in understanding the molecular associations in cell signalling in plant-pathogen interactions. <i>Molecular Plant Pathology</i> , 2002, 3, 103-109.	2.0	1
226	Gene expression profile of Vitamin D3 treated HL60 cells shows an incomplete molecular phenotypic conversion to monocytes. <i>Cell Death and Differentiation</i> , 2002, 9, 1185-1195.	5.0	12
227	Sequence and analysis of chromosome 2 of <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2002, 418, 79-85.	13.7	176
228	Sequence of <i>Plasmodium falciparum</i> chromosomes 2, 10, 11 and 14. <i>Nature</i> , 2002, 419, 531-534.	13.7	167
229	Sequence of <i>Plasmodium falciparum</i> chromosomes 1, 3 and 9 and 13. <i>Nature</i> , 2002, 419, 527-531.	13.7	156
230	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881
231	Sequence of <i>Plasmodium falciparum</i> chromosome 12. <i>Nature</i> , 2002, 419, 534-537.	13.7	58
232	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	13.7	1,548
233	Extensive and divergent circadian gene expression in liver and heart. <i>Nature</i> , 2002, 417, 78-83.	13.7	1,391
234	Analyzing yeast protein-protein interaction data obtained from different sources. <i>Nature Biotechnology</i> , 2002, 20, 991-997.	9.4	508

#	ARTICLE	IF	CITATIONS
235	GenMAPP, a new tool for viewing and analyzing microarray data on biological pathways. Nature Genetics, 2002, 31, 19-20.	9.4	895
236	Saving sulfur. Nature Genetics, 2002, 31, 228-230.	9.4	14
237	Reversing Babel with GO. Nature Genetics, 2002, 31, 230-230.	9.4	1
238	Microarray databases: standards and ontologies. Nature Genetics, 2002, 32, 469-473.	9.4	133
239	Options available“from start to finish”for obtaining data from DNA microarrays II. Nature Genetics, 2002, 32, 481-489.	9.4	240
240	Association of genes to genetically inherited diseases using data mining. Nature Genetics, 2002, 31, 316-319.	9.4	330
241	Large-scale prediction of Saccharomyces cerevisiae gene function using overlapping transcriptional clusters. Nature Genetics, 2002, 31, 255-265.	9.4	313
242	The use and analysis of microarray data. Nature Reviews Drug Discovery, 2002, 1, 951-960.	21.5	407
243	Genomics and natural language processing. Nature Reviews Genetics, 2002, 3, 601-610.	7.7	126
244	SCOR: a Structural Classification of RNA database. Nucleic Acids Research, 2002, 30, 392-394.	6.5	103
245	Title is missing!. Plant Molecular Biology, 2002, 48, 59-74.	2.0	14
246	Microarray data quality analysis: lessons from the AFGC project. Arabidopsis Functional Genomics Consortium. Plant Molecular Biology, 2002, 48, 119-132.	2.0	76
247	Gramene: a resource for comparative grass genomics. Nucleic Acids Research, 2002, 30, 103-105.	6.5	213
248	Gramene, a Tool for Grass Genomics. Plant Physiology, 2002, 130, 1606-1613.	2.3	177
249	EST Sequencing, Annotation and Macroarray Transcriptome Analysis Identify Preferentially Root-Expressed Genes in Sugar Beet. Plant Biology, 2002, 4, 700-710.	1.8	23
250	Mining the bibliome: searching for a needle in a haystack?. EMBO Reports, 2002, 3, 200-203.	2.0	51
251	Search and retrieve. EMBO Reports, 2002, 3, 396-400.	2.0	22
252	A Guide to Building Image-Centric Databases. Neuroinformatics, 2003, 1, 359-378.	1.5	8

#	ARTICLE	IF	CITATIONS
253	The Cell-Centered Database: A Database for Multiscale Structural and Protein Localization Data from Light and Electron Microscopy. <i>Neuroinformatics</i> , 2003, 1, 379-396.	1.5	105
254	A Protein Interaction Map of <i>Drosophila melanogaster</i> . <i>Science</i> , 2003, 302, 1727-1736.	6.0	2,151
255	Title is missing!. <i>Machine Learning</i> , 2003, 52, 119-145.	3.4	6
256	Computational approaches to protein-protein interaction. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 245-255.	1.2	11
257	Structural genomics: Computational methods for structure analysis. <i>Protein Science</i> , 2003, 12, 1813-1821.	3.1	104
258	Bioinformatics and Medical Informatics: Collaborations on the Road to Genomic Medicine?. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2003, 10, 515-522.	2.2	76
259	Target Selection and Determination of Function in Structural Genomics. <i>IUBMB Life</i> , 2003, 55, 249-255.	1.5	22
260	Development of a Chemical Structure Comparison Method for Integrated Analysis of Chemical and Genomic Information in the Metabolic Pathways. <i>Journal of the American Chemical Society</i> , 2003, 125, 11853-11865.	6.6	423
261	Revamp a model?status and prospects of the <i>Dictyostelium</i> genome project. <i>Current Genetics</i> , 2003, 44, 59-72.	0.8	14
262	Automatic prediction of protein function. <i>Cellular and Molecular Life Sciences</i> , 2003, 60, 2637-2650.	2.4	225
263	Functional genomics and proteomics: charting a multidimensional map of the yeast cell. <i>Trends in Cell Biology</i> , 2003, 13, 344-356.	3.6	126
264	Malaria parasite and vector genomes: partners in crime. <i>Trends in Parasitology</i> , 2003, 19, 356-362.	1.5	8
265	Target validation through high throughput proteomics analysis. <i>Targets</i> , 2003, 2, 217-223.	0.3	3
266	Beyond similarity-based methods to associate genes for the inference of function. <i>Biosilico</i> , 2003, 1, 89-96.	0.5	0
267	Binformatics: not just for sequences anymore. <i>Biosilico</i> , 2003, 1, 103-111.	0.5	2
268	Designing databases to store biological information. <i>Biosilico</i> , 2003, 1, 134-142.	0.5	10
269	A shallow parser based on closed-class words to capture relations in biomedical text. <i>Journal of Biomedical Informatics</i> , 2003, 36, 145-158.	2.5	85
270	Plans for HDBase—a research community website for Huntington's Disease. <i>Clinical Neuroscience Research</i> , 2003, 3, 197-217.	0.8	6

#	ARTICLE	IF	CITATIONS
271	Reading the fine print of the human genome. IEEE Engineering in Medicine and Biology Magazine, 2003, 22, 105-108.	1.1	0
272	Organelle proteomics: looking at less to see more. Trends in Cell Biology, 2003, 13, 629-638.	3.6	161
273	An automated method for finding molecular complexes in large protein interaction networks. BMC Bioinformatics, 2003, 4, 2.	1.2	4,773
274	cDNA2Genome: a tool for mapping and annotating cDNAs. BMC Bioinformatics, 2003, 4, 39.	1.2	12
275	PubMatrix: a tool for multiplex literature mining. BMC Bioinformatics, 2003, 4, 61.	1.2	180
276	Differential representation of sunflower ESTs in enriched organ-specific cDNA libraries in a small scale sequencing project. BMC Genomics, 2003, 4, 40.	1.2	38
277	Genomic characterization of a repetitive motif strongly associated with developmental genes in Drosophila. BMC Genomics, 2003, 4, 52.	1.2	4
278	Helminth vaccines: from mining genomic information for vaccine targets to systems used for protein expression. International Journal for Parasitology, 2003, 33, 621-640.	1.3	88
279	Predicting gene function by conserved co-expression. Trends in Genetics, 2003, 19, 238-242.	2.9	175
280	Molecular basis of inherited diseases: a structural perspective. Trends in Genetics, 2003, 19, 505-513.	2.9	92
281	Scaling laws in the functional content of genomes. Trends in Genetics, 2003, 19, 479-484.	2.9	267
282	Model systems in drug discovery: chemical genetics meets genomics. , 2003, 99, 183-220.		43
283	From biological databases to platforms for biomedical discovery. Trends in Biotechnology, 2003, 21, 263-268.	4.9	25
284	Molecular characterization of acute leukemias by use of microarray technology. Genes Chromosomes and Cancer, 2003, 37, 396-405.	1.5	133
285	Phenotype discovery by gene expression profiling: Mapping of biological processes linked to BMP-2-mediated osteoblast differentiation. Journal of Cellular Biochemistry, 2003, 89, 401-426.	1.2	164
286	Dynamic visualization of expressed gene networks. Journal of Cellular Physiology, 2003, 196, 419-429.	2.0	11
287	Building Ontologies in DAML + OIL. Comparative and Functional Genomics, 2003, 4, 133-141.	2.0	17
288	An Approach to Inferring Transcriptional Regulation Among Genes From Large-Scale Expression Data. Comparative and Functional Genomics, 2003, 4, 148-154.	2.0	10

#	ARTICLE	IF	CITATIONS
289	Automatic Classification of Protein Functions from the Literature. Comparative and Functional Genomics, 2003, 4, 75-79.	2.0	1
290	Developing a Protein-Interactions Ontology. Comparative and Functional Genomics, 2003, 4, 85-89.	2.0	13
291	Standards and Ontologies for Functional Genomics: Towards Unified Ontologies for Biology and Biomedicine. Comparative and Functional Genomics, 2003, 4, 116-120.	2.0	4
292	Bringing Ontology to the Gene Ontology. Comparative and Functional Genomics, 2003, 4, 90-93.	2.0	15
293	ISMB 2003 Text Mining SIG Meeting Report. Comparative and Functional Genomics, 2003, 4, 667-673.	2.0	2
294	Ontology Recapitulates Physiology. Chemistry and Biology, 2003, 10, 784-786.	6.2	0
295	Genomic data modeling. Information Systems, 2003, 28, 287-310.	2.4	21
296	Ontologies for proteomics: towards a systematic definition of structure and function that scales to the genome level. Current Opinion in Chemical Biology, 2003, 7, 44-54.	2.8	51
297	Gene profiling of hippocampal neuronal culture. Journal of Neurochemistry, 2003, 85, 1279-1288.	2.1	36
298	An ontology of human developmental anatomy. Journal of Anatomy, 2003, 203, 347-355.	0.9	36
299	Automatic annotation of protein function based on family identification. Proteins: Structure, Function and Bioinformatics, 2003, 53, 683-692.	1.5	51
300	Better prediction of sub-cellular localization by combining evolutionary and structural information. Proteins: Structure, Function and Bioinformatics, 2003, 53, 917-930.	1.5	80
301	The Make 2D-DB II package: Conversion of federated two-dimensional gel electrophoresis databases into a relational format and interconnection of distributed databases. Proteomics, 2003, 3, 1441-1444.	1.3	34
302	GIMS: an integrated data storage and analysis environment for genomic and functional data. Yeast, 2003, 20, 1291-1306.	0.8	39
303	From genomics to proteomics. Nature, 2003, 422, 193-197.	13.7	886
304	Biomedical informatics for proteomics. Nature, 2003, 422, 233-237.	13.7	181
305	Righting the wrongs. EMBO Reports, 2003, 4, 829-831.	2.0	10
306	Pancreatic cancer escape variants that evade immunogene therapy through loss of sensitivity to IFN γ -induced apoptosis. Gene Therapy, 2003, 10, 1067-1078.	2.3	35

#	ARTICLE	IF	CITATIONS
307	Making sense of microarray data to classify cancer. <i>Pharmacogenomics Journal</i> , 2003, 3, 308-311.	0.9	7
308	Genomics of the Periinfarction Cortex after Focal Cerebral Ischemia. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2003, 23, 786-810.	2.4	166
309	A universal legal framework as a prerequisite for database interoperability. <i>Nature Biotechnology</i> , 2003, 21, 979-982.	9.4	11
310	An integrated functional genomics screening program reveals a role for BMP-9 in glucose homeostasis. <i>Nature Biotechnology</i> , 2003, 21, 294-301.	9.4	171
311	Evolution of gene expression in the <i>Drosophila melanogaster</i> subgroup. <i>Nature Genetics</i> , 2003, 33, 138-144.	9.4	324
312	Natural variation in human gene expression assessed in lymphoblastoid cells. <i>Nature Genetics</i> , 2003, 33, 422-425.	9.4	533
313	Bioinformatics in the post-sequence era. <i>Nature Genetics</i> , 2003, 33, 305-310.	9.4	174
314	Treatment-specific changes in gene expression discriminate in vivo drug response in human leukemia cells. <i>Nature Genetics</i> , 2003, 34, 85-90.	9.4	239
315	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. <i>Nature Genetics</i> , 2003, 34, 166-176.	9.4	1,543
316	Trans-acting regulatory variation in <i>Saccharomyces cerevisiae</i> and the role of transcription factors. <i>Nature Genetics</i> , 2003, 35, 57-64.	9.4	583
317	Evolutionary and biomedical implications of a <i>Schistosoma japonicum</i> complementary DNA resource. <i>Nature Genetics</i> , 2003, 35, 139-147.	9.4	281
318	Integrating biological databases. <i>Nature Reviews Genetics</i> , 2003, 4, 337-345.	7.7	275
319	Classification schemes for protein structure and function. <i>Nature Reviews Genetics</i> , 2003, 4, 508-519.	7.7	101
320	The chicken as a model for large-scale analysis of vertebrate gene function. <i>Nature Reviews Genetics</i> , 2003, 4, 87-98.	7.7	154
321	Prediction of human protein function according to Gene Ontology categories. <i>Bioinformatics</i> , 2003, 19, 635-642.	1.8	233
322	Predicting Gene Ontology Biological Process From Temporal Gene Expression Patterns. <i>Genome Research</i> , 2003, 13, 965-979.	2.4	88
323	Amino Acid Properties and Consequences of Substitutions. , 0, , 289-316.		327
324	Application of Microarray Technology in Environmental and Comparative Physiology. <i>Annual Review of Physiology</i> , 2003, 65, 231-259.	5.6	153

#	ARTICLE	IF	CITATIONS
325	Genetic disorders and renal cell carcinoma. <i>Urologic Clinics of North America</i> , 2003, 30, 133-141.	0.8	18
326	A Gene-Coexpression Network for Global Discovery of Conserved Genetic Modules. <i>Science</i> , 2003, 302, 249-255.	6.0	2,034
327	Prediction of protein function from protein sequence and structure. <i>Quarterly Reviews of Biophysics</i> , 2003, 36, 307-340.	2.4	376
328	Modeling Biology Using Relational Databases. <i>Current Protocols in Bioinformatics</i> , 2003, 00, Unit9.3.	25.8	0
329	Sequence analysis of a rainbow trout cDNA library and creation of a gene index. <i>Cytogenetic and Genome Research</i> , 2003, 102, 347-354.	0.6	97
330	MicroRNA targets in <i>Drosophila</i> . <i>Genome Biology</i> , 2003, 5, R1.	13.9	3,023
331	The construction of an EST database for <i>Bombyx mori</i> and its application. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 14121-14126.	3.3	245
332	Identification of pseudogenes in the <i>Drosophila melanogaster</i> genome. <i>Nucleic Acids Research</i> , 2003, 31, 1033-1037.	6.5	87
333	Initial large-scale exploration of protein-protein interactions in human brain. , 0, , .		6
334	EMDep: a web-based system for the deposition and validation of high-resolution electron microscopy macromolecular structural information. <i>Journal of Structural Biology</i> , 2003, 144, 228-237.	1.3	49
335	<i>Zea mays</i> ontology – a database of international terms. <i>Trends in Plant Science</i> , 2003, 8, 517-520.	4.3	29
336	Comparative genomics of <i>Physcomitrella patens</i> gametophytic transcriptome and <i>Arabidopsis thaliana</i> : Implication for land plant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8007-8012.	3.3	341
337	Application of eVOC: controlled vocabularies for unifying gene expression data. <i>Comptes Rendus - Biologies</i> , 2003, 326, 1089-1096.	0.1	8
338	A new hybrid approach to predict subcellular localization of proteins by incorporating gene ontology. <i>Biochemical and Biophysical Research Communications</i> , 2003, 311, 743-747.	1.0	133
339	OrthoMCL: Identification of Ortholog Groups for Eukaryotic Genomes. <i>Genome Research</i> , 2003, 13, 2178-2189.	2.4	5,497
340	Functional Fingerprints of Folds: Evidence for Correlated Structure–Function Evolution. <i>Journal of Molecular Biology</i> , 2003, 326, 1-9.	2.0	50
341	Inferring Functional Relationships of Proteins from Local Sequence and Spatial Surface Patterns. <i>Journal of Molecular Biology</i> , 2003, 332, 505-526.	2.0	151
342	Gene expression patterns define pathways correlated with loss of differentiation in lung adenocarcinomas. <i>FEBS Letters</i> , 2003, 540, 167-170.	1.3	18

#	ARTICLE	IF	CITATIONS
343	Gene expression profiling as a tool for the diagnosis of acute leukemias. <i>Seminars in Hematology</i> , 2003, 40, 281-295.	1.8	36
344	Use of microarrays for investigating the subtoxic effects of snake venoms: insights into venom-induced apoptosis in human umbilical vein endothelial cells. <i>Toxicon</i> , 2003, 41, 429-440.	0.8	38
345	Building a BRIDGE for the integration of heterogeneous data from functional genomics into a platform for systems biology. <i>Journal of Biotechnology</i> , 2003, 106, 157-167.	1.9	22
346	EMMA: a platform for consistent storage and efficient analysis of microarray data. <i>Journal of Biotechnology</i> , 2003, 106, 135-146.	1.9	100
347	Exploring the immunogenome with bioinformatics. <i>Seminars in Immunology</i> , 2003, 15, 233-238.	2.7	1
348	ESTs from the basidiomycete <i>Schizophyllum commune</i> grown on nitrogen-replete and nitrogen-limited media. <i>Fungal Genetics and Biology</i> , 2003, 39, 191-198.	0.9	17
349	Differential gene expression analysis in fish exposed to endocrine disrupting compounds. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2003, 136, 149-161.	0.7	49
350	Global functional profiling of gene expression†This work was funded in part by a Sun Microsystems grant awarded to S.D., NIH Grant HD36512 to S.A.K., a Wayne State University SOM Dean's Post-Doctoral Fellowship, and an NICHD Contraception and Infertility Loan to G.C.O. Support from the WSU MCBI mode is gratefully appreciated.. <i>Genomics</i> , 2003, 81, 98-104.	1.3	544
351	Exploring the salivary gland transcriptome and proteome of the <i>Anopheles stephensi</i> mosquito. <i>Insect Biochemistry and Molecular Biology</i> , 2003, 33, 717-732.	1.2	181
352	A catalogue of <i>Anopheles gambiae</i> transcripts significantly more or less expressed following a blood meal. <i>Insect Biochemistry and Molecular Biology</i> , 2003, 33, 865-882.	1.2	70
353	Bioinformatics: Organisms from Venus, Technology from Jupiter, Algorithms from Mars. <i>European Journal of Control</i> , 2003, 9, 237-278.	1.6	10
354	<i>Leishmania major</i> chromosome 3 contains two long convergent polycistronic gene clusters separated by a tRNA gene. <i>Nucleic Acids Research</i> , 2003, 31, 4201-4210.	6.5	65
355	A Bayesian Networks Approach for Predicting Protein-Protein Interactions from Genomic Data. <i>Science</i> , 2003, 302, 449-453.	6.0	1,183
356	PANTHER: a browsable database of gene products organized by biological function, using curated protein family and subfamily classification. <i>Nucleic Acids Research</i> , 2003, 31, 334-341.	6.5	578
357	The environmental stress response: a common yeast response to diverse environmental stresses. , 2003, , 11-70.		96
358	Primer on Medical Genomics Part V: Bioinformatics. <i>Mayo Clinic Proceedings</i> , 2003, 78, 57-64.	1.4	24
359	Pilot survey of expressed sequence tags (ESTs) from the asexual blood stages of <i>Plasmodium vivax</i> in human patients. <i>Malaria Journal</i> , 2003, 2, 21.	0.8	7
360	Challenges Faced in the Integration of Biological Information. , 2003, , 11-34.		4

#	ARTICLE	IF	CITATIONS
361	Functional classification of proteins for the prediction of cellular function from a protein-protein interaction network. <i>Genome Biology</i> , 2003, 5, R6.	13.9	252
362	New methods for finding disease-susceptibility genes: impact and potential. <i>Genome Biology</i> , 2003, 4, 119.	13.9	37
363	Identifying biological themes within lists of genes with EASE. <i>Genome Biology</i> , 2003, 4, R70.	3.8	1,664
364	DAVID: Database for Annotation, Visualization, and Integrated Discovery. <i>Genome Biology</i> , 2003, 4, 1.	3.8	1,411
365	A comparative proteomics resource: proteins of <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2003, 4, R51.	13.9	25
366	Profiling of pathway-specific changes in gene expression following growth of human cancer cell lines transplanted into mice. <i>Genome Biology</i> , 2003, 4, R46.	13.9	42
367	A method to assess compositional bias in biological sequences and its application to prion-like glutamine/asparagine-rich domains in eukaryotic proteomes. <i>Genome Biology</i> , 2003, 4, R40.	13.9	135
368	GeneHopper: a web-based search engine to link gene-expression platforms through GenBank accession numbers. <i>Genome Biology</i> , 2003, 4, R35.	13.9	12
369	Clustering gene-expression data with repeated measurements. <i>Genome Biology</i> , 2003, 4, R34.	13.9	168
370	Analysis and functional classification of transcripts from the nematode <i>Meloidogyne incognita</i> . <i>Genome Biology</i> , 2003, 4, R26.	13.9	133
371	GoMiner: a resource for biological interpretation of genomic and proteomic data. <i>Genome Biology</i> , 2003, 4, R28.	13.9	1,038
372	The GRID: the General Repository for Interaction Datasets. <i>Genome Biology</i> , 2003, 4, R23.	13.9	238
373	Osprey: a network visualization system. <i>Genome Biology</i> , 2003, 4, R22.	13.9	391
374	Exploiting microarrays to reveal differential gene expression in the nervous system. <i>Genome Biology</i> , 2003, 4, 105.	13.9	18
375	Integrating computationally assembled mouse transcript sequences with the Mouse Genome Informatics (MGI) database. <i>Genome Biology</i> , 2003, 4, R16.	3.8	16
376	MAPPFinder: using Gene Ontology and GenMAPP to create a global gene-expression profile from microarray data. <i>Genome Biology</i> , 2003, 4, R7.	13.9	776
377	PAINT: A Promoter Analysis and Interaction Network Generation Tool for Gene Regulatory Network Identification. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 235-252.	1.0	119
378	Using gene ontology on genome-scale studies to find significant associations of biologically relevant terms to groups of genes. , 0, , .		1

#	ARTICLE	IF	CITATIONS
379	Refining the extraction of relevant documents from biomedical literature to create a corpus for pathway text mining. , 0, , .		2
380	A contradiction-based framework for testing gene regulation hypotheses. , 0, , .		3
381	PANTHER: A Library of Protein Families and Subfamilies Indexed by Function. <i>Genome Research</i> , 2003, 13, 2129-2141.	2.4	2,703
382	The Nuclear Protein Database (NPD): sub-nuclear localisation and functional annotation of the nuclear proteome. <i>Nucleic Acids Research</i> , 2003, 31, 328-330.	6.5	85
383	Towards automated derivation of biological pathways using high-throughput biological data. , 0, , .		0
384	Tomato expression database (TED) - an interactive management tool for tomato expression profiling data. , 0, , .		1
385	Linking technological change to business needs. <i>IEEE Engineering Management Review</i> , 2003, 31, 49-49.	1.0	21
386	Genome-wide identification of in vivo <i>Drosophila</i> Engrailed-binding DNA fragments and related target genes. <i>Development (Cambridge)</i> , 2003, 130, 1243-1254.	1.2	42
387	The TIGRFAMs database of protein families. <i>Nucleic Acids Research</i> , 2003, 31, 371-373.	6.5	821
388	The sequence and analysis of <i>Trypanosoma brucei</i> chromosome II. <i>Nucleic Acids Research</i> , 2003, 31, 4856-4863.	6.5	59
389	Endoplasmic Reticulum Stress Is a Determinant of Retrovirus-Induced Spongiform Neurodegeneration. <i>Journal of Virology</i> , 2003, 77, 12617-12629.	1.5	75
390	Predicting Gene Function From Patterns of Annotation. <i>Genome Research</i> , 2003, 13, 896-904.	2.4	121
391	Annotation of the Arabidopsis Genome. <i>Plant Physiology</i> , 2003, 132, 461-468.	2.3	137
392	A literature-based method for assessing the functional coherence of a gene group. <i>Bioinformatics</i> , 2003, 19, 396-401.	1.8	49
393	The phylogenetic diversity of eukaryotic transcription. <i>Nucleic Acids Research</i> , 2003, 31, 653-660.	6.5	39
394	Genome-wide discovery of transcriptional modules from DNA sequence and gene expression. <i>Bioinformatics</i> , 2003, 19, i273-i282.	1.8	211
395	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. <i>Nucleic Acids Research</i> , 2003, 31, 365-370.	6.5	3,096
397	Assessment of Genome-Wide Protein Function Classification for <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2003, 13, 2118-2128.	2.4	40

#	ARTICLE	IF	CITATIONS
398	OntoBlast function: from sequence similarities directly to potential functional annotations by ontology terms. <i>Nucleic Acids Research</i> , 2003, 31, 3799-3803.	6.5	96
399	The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. <i>Nucleic Acids Research</i> , 2003, 31, 414-417.	6.5	64
400	Automated Gene Ontology annotation for anonymous sequence data. <i>Nucleic Acids Research</i> , 2003, 31, 3712-3715.	6.5	77
401	From Gene Networks to Gene Function. <i>Genome Research</i> , 2003, 13, 2568-2576.	2.4	142
402	GPCRDB information system for G protein-coupled receptors. <i>Nucleic Acids Research</i> , 2003, 31, 294-297.	6.5	299
403	Genome evolution reveals biochemical networks and functional modules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15428-15433.	3.3	140
404	Public services from the European Bioinformatics Institute. <i>Briefings in Bioinformatics</i> , 2003, 4, 332-340.	3.2	10
405	Viewing and annotating sequence data with Artemis. <i>Briefings in Bioinformatics</i> , 2003, 4, 124-132.	3.2	136
406	Comparing Bacterial Genomes Through Conservation Profiles. <i>Genome Research</i> , 2003, 13, 991-998.	2.4	26
407	The DNA sequence of chromosome I of an African trypanosome: gene content, chromosome organisation, recombination and polymorphism. <i>Nucleic Acids Research</i> , 2003, 31, 4864-4873.	6.5	56
408	Inferring Higher Functional Information for RIKEN Mouse Full-Length cDNA Clones With FACTS. <i>Genome Research</i> , 2003, 13, 1520-1533.	2.4	14
409	Predictive Metabolic Engineering: A Goal for Systems Biology. <i>Plant Physiology</i> , 2003, 132, 420-425.	2.3	141
410	INCLUSive: a web portal and service registry for microarray and regulatory sequence analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3468-3470.	6.5	46
411	Exploring Alternative Transcript Structure in the Human Genome Using BLOCKS and InterPro. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 289-306.	0.3	10
412	GoFish finds genes with combinations of Gene Ontology attributes. <i>Bioinformatics</i> , 2003, 19, 788-789.	1.8	14
413	GATA-1-Mediated Proliferation Arrest during Erythroid Maturation. <i>Molecular and Cellular Biology</i> , 2003, 23, 5031-5042.	1.1	186
414	Transcriptional Response of Lymphoblastoid Cells to Ionizing Radiation. <i>Genome Research</i> , 2003, 13, 2092-2100.	2.4	132
415	Connecting Sequence and Biology in the Laboratory Mouse. <i>Genome Research</i> , 2003, 13, 1505-1519.	2.4	18

#	ARTICLE	IF	CITATIONS
416	Cryptococcus neoformans Gene Expression during Experimental Cryptococcal Meningitis. Eukaryotic Cell, 2003, 2, 1336-1349.	3.4	129
417	Systemic and cell type-specific gene expression patterns in scleroderma skin. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12319-12324.	3.3	385
418	SOURCE: a unified genomic resource of functional annotations, ontologies, and gene expression data. Nucleic Acids Research, 2003, 31, 219-223.	6.5	376
419	NetAffx: Affymetrix probesets and annotations. Nucleic Acids Research, 2003, 31, 82-86.	6.5	438
420	Target Explorer: an automated tool for the identification of new target genes for a specified set of transcription factors. Nucleic Acids Research, 2003, 31, 3589-3592.	6.5	86
421	GenePublisher: automated analysis of DNA microarray data. Nucleic Acids Research, 2003, 31, 3471-3476.	6.5	30
422	The computational analysis of scientific literature to define and recognize gene expression clusters. Nucleic Acids Research, 2003, 31, 4553-4560.	6.5	47
423	Advances in spotted microarray resources for expression profiling. Briefings in Functional Genomics & Proteomics, 2003, 2, 21-30.	3.8	15
424	Gene expression data preprocessing. Bioinformatics, 2003, 19, 655-656.	1.8	84
425	Predicting protein function from protein/protein interaction data: a probabilistic approach. Bioinformatics, 2003, 19, i197-i204.	1.8	317
426	CREME: a framework for identifying cis-regulatory modules in human-mouse conserved segments. Bioinformatics, 2003, 19, i283-i291.	1.8	94
427	UniqueProt: creating representative protein sequence sets. Nucleic Acids Research, 2003, 31, 3789-3791.	6.5	108
428	Sequence " Evolution " Function. , 2003, , .		124
429	The European Bioinformatics Institute's data resources. Nucleic Acids Research, 2003, 31, 43-50.	6.5	56
430	Handbook on Enterprise Architecture. , 2003, , .		99
431	The Drosophila phenotype gap -- and how to close it. Briefings in Functional Genomics & Proteomics, 2003, 2, 121-127.	3.8	11
432	GeneMerge--post-genomic analysis, data mining, and hypothesis testing. Bioinformatics, 2003, 19, 891-892.	1.8	261
433	G Protein-Coupled Receptor Genes in the FANTOM2 Database. Genome Research, 2003, 13, 1466-1477.	2.4	32

#	ARTICLE	IF	CITATIONS
434	New Evidence for Genome-Wide Duplications at the Origin of Vertebrates Using an Amphioxus Gene Set and Completed Animal Genomes. <i>Genome Research</i> , 2003, 13, 1056-1066.	2.4	157
435	In silico tools for signal transduction research. <i>Briefings in Bioinformatics</i> , 2003, 4, 315-324.	3.2	3
436	THE SCHISTOSOMA MANSONI GENE INDEX: GENE DISCOVERY AND BIOLOGY BY RECONSTRUCTION AND ANALYSIS OF EXPRESSED GENE SEQUENCES. <i>Journal of Parasitology</i> , 2003, 89, 261-269.	0.3	28
437	ELM server: a new resource for investigating short functional sites in modular eukaryotic proteins. <i>Nucleic Acids Research</i> , 2003, 31, 3625-3630.	6.5	555
438	Genome-Wide Survey of Human Alternative Pre-mRNA Splicing with Exon Junction Microarrays. <i>Science</i> , 2003, 302, 2141-2144.	6.0	1,297
439	Identifying underlying factors in breast cancer using independent component analysis. , 0, , .		8
440	Proteomics and Bioinformatics. <i>Advances in Protein Chemistry</i> , 2003, 65, 353-369.	4.4	4
441	Statistical and visual morph movie analysis of crystallographic mutant selection bias in protein mutation resource data. , 0, , .		1
442	Ensembl 2002: accommodating comparative genomics. <i>Nucleic Acids Research</i> , 2003, 31, 38-42.	6.5	216
443	Large-scale delineation of secreted protein biomarkers overexpressed in cancer tissue and serum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3410-3415.	3.3	425
444	A Bayesian framework for combining heterogeneous data sources for gene function prediction (in <i>Saccharomyces cerevisiae</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8348-8353.	3.3	491
445	eVOC: A Controlled Vocabulary for Unifying Gene Expression Data. <i>Genome Research</i> , 2003, 13, 1222-1230.	2.4	144
446	Microarray Data Analysis and Mining. , 2004, 94, 67-90.		9
447	Whither Biological Database Research?. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 61-65.	1.0	0
448	Millions of Years of Evolution Preserved: A Comprehensive Catalog of the Processed Pseudogenes in the Human Genome. <i>Genome Research</i> , 2003, 13, 2541-2558.	2.4	376
449	Common Objects: Think Global, Act Local. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 103-104.	1.0	0
450	Transcriptional network controlled by the trithorax-group gene <i>ash2</i> in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3293-3298.	3.3	21
451	PRISM, a Generic Large Scale Proteomic Investigation Strategy for Mammals*S. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 96-106.	2.5	145

#	ARTICLE	IF	CITATIONS
452	Genomic binding by the Drosophila Myc, Max, Mad/Mnt transcription factor network. <i>Genes and Development</i> , 2003, 17, 1101-1114.	2.7	352
453	GEPAS: a web-based resource for microarray gene expression data analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3461-3467.	6.5	161
454	WormBase: a cross-species database for comparative genomics. <i>Nucleic Acids Research</i> , 2003, 31, 133-137.	6.5	107
455	Mining the Biomedical Literature in the Genomic Era: An Overview. <i>Journal of Computational Biology</i> , 2003, 10, 821-855.	0.8	203
456	Genetic Expression Profiling of Six Odontogenic Tumors. <i>Journal of Dental Research</i> , 2003, 82, 551-557.	2.5	26
457	Saccharomyces Genome Database (SGD) provides biochemical and structural information for budding yeast proteins. <i>Nucleic Acids Research</i> , 2003, 31, 216-218.	6.5	57
458	Integrated Mapping, Chromosomal Sequencing and Sequence Analysis of <i>Cryptosporidium parvum</i> . <i>Genome Research</i> , 2003, 13, 1787-99.	2.4	60
459	A SUITE OF DAML+OIL ONTOLOGIES TO DESCRIBE BIOINFORMATICS WEB SERVICES AND DATA. <i>International Journal of Cooperative Information Systems</i> , 2003, 12, 197-224.	0.6	126
460	Honor thy symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10452-10459.	3.3	795
462	GENEANNOTATION: PREDICTION AND TESTING. <i>Annual Review of Genomics and Human Genetics</i> , 2003, 4, 69-88.	2.5	56
463	The Digital Human: Towards a Unified Ontology. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 421-424.	1.0	2
464	Genome-Wide In Silico Identification of Transcriptional Regulators Controlling the Cell Cycle in Human Cells. <i>Genome Research</i> , 2003, 13, 773-780.	2.4	275
465	Long-term global gene expression patterns in irradiated human lymphocytes. <i>Carcinogenesis</i> , 2003, 24, 1837-1845.	1.3	47
466	Specific differences in gene expression profile revealed by cDNA microarray analysis of glutathione S-transferase placental form (GST-P) immunohistochemically positive rat liver foci and surrounding tissue. <i>Carcinogenesis</i> , 2003, 25, 439-443.	1.3	53
467	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , 2003, 19, 717-726.	1.8	65
468	CLICK and EXPANDER: a system for clustering and visualizing gene expression data. <i>Bioinformatics</i> , 2003, 19, 1787-1799.	1.8	327
469	Differentiation of stress, metabolism, communication, and defense responses following transplantation. <i>Journal of Leukocyte Biology</i> , 2003, 73, 379-390.	1.5	12
470	ChipInfo: software for extracting gene annotation and gene ontology information for microarray analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3483-3486.	6.5	84

#	ARTICLE	IF	CITATIONS
471	caCORE: A common infrastructure for cancer informatics. <i>Bioinformatics</i> , 2003, 19, 2404-2412.	1.8	140
472	Discovering molecular pathways from protein interaction and gene expression data. <i>Bioinformatics</i> , 2003, 19, i264-i272.	1.8	237
473	Kernel hierarchical gene clustering from microarray expression data. <i>Bioinformatics</i> , 2003, 19, 2097-2104.	1.8	53
474	Gene function, metabolic pathways and comparative genomics in yeast. , 0, , .		1
475	ILP for Mathematical Discovery. <i>Lecture Notes in Computer Science</i> , 2003, , 93-111.	1.0	9
476	Managing core resources for genomics and proteomics. <i>Pharmacogenomics</i> , 2003, 4, 343-350.	0.6	4
477	Serial Analysis of Gene Expression. , 2003, 226, 271-284.		0
478	Analysis of Expression Data: An Overview. <i>Current Protocols in Human Genetics</i> , 2003, 38, 11.4.1.	3.5	1
479	Global Predictions and Tests of Erythroid Regulatory Regions. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003, 68, 335-344.	2.0	7
480	Web-based exchange of biochemical information. <i>Bioinformatics</i> , 2003, 19, 1730-1731.	1.8	3
481	Induction of Enzyme Classes from Biological Databases. <i>Lecture Notes in Computer Science</i> , 2003, , 269-280.	1.0	4
482	Global Functional Profiling of Gene Expression Data. , 2003, , 306-325.		6
483	Graphical modeling based gene interaction analysis for microarray data. <i>SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining</i> , 2003, 5, 91-100.	3.2	4
484	Gene Identification and Expression Analysis of 86,136 Expressed Sequence Tags (EST) from the Rice Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 26-42.	3.0	18
485	EST Pipeline System: Detailed and Automated EST Data Processing and Mining. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 236-242.	3.0	12
486	Analysis of Expression Data: An Overview. <i>Current Protocols in Bioinformatics</i> , 2003, 3, 7.1.1.	25.8	0
487	The Gene Ontology (GO) Project: Structured Vocabularies for Molecular Biology and Their Application to Genome and Expression Analysis. <i>Current Protocols in Bioinformatics</i> , 2003, 00, Unit 7.2.	25.8	23
488	DAVID: Database for Annotation, Visualization, and Integrated Discovery. <i>Genome Biology</i> , 2003, 4, 1.	3.8	7,168

#	ARTICLE	IF	CITATIONS
489	The graft response to transplantation: a gene expression profile analysis. <i>Physiological Genomics</i> , 2003, 15, 52-64.	1.0	12
491	Bovine mammary gene expression profiling using a cDNA microarray enhanced for mammary-specific transcripts. <i>Physiological Genomics</i> , 2003, 16, 8-18.	1.0	66
492	Gene Expression Profiling of Renal Cell Carcinoma and Its Implications in Diagnosis, Prognosis, and Therapeutics. <i>Advances in Cancer Research</i> , 2003, 89, 157-181.	1.9	31
493	Using the TIGR Gene Index Databases for Biological Discovery. <i>Current Protocols in Bioinformatics</i> , 2003, 3, Unit 1.6.	25.8	4
494	Linking Technological Change to Business Needs. <i>Research Technology Management</i> , 2003, 46, 47-52.	0.6	32
495	Integrating functional genomics data. <i>Biochemical Society Transactions</i> , 2003, 31, 1484-1487.	1.6	14
496	Mouse and Rat Genome Informatics. , 0, , 119-142.		0
497	Functional Relationship and Gene Ontology Classification of Breast Cancer Biomarkers. <i>International Journal of Biological Markers</i> , 2003, 18, 241-272.	0.7	18
498	The Universal Medical Language System and the Gene Ontology: Some Critical Reflections. <i>Lecture Notes in Computer Science</i> , 2003, , 135-148.	1.0	19
499	Integr8: Enhanced Inter-Operability of European Molecular Biology Databases. <i>Methods of Information in Medicine</i> , 2003, 42, 154-160.	0.7	9
500	Gene expression profile of endothelin-1-induced growth in glomerular mesangial cells. <i>American Journal of Physiology - Cell Physiology</i> , 2003, 285, C1109-C1115.	2.1	18
501	Selecting text features for gene name classification. , 2003, , .		14
505	Genome Projects and Gene Therapy: Gateways to Next Generation Biological Weapons. <i>Military Medicine</i> , 2003, 168, 864-871.	0.4	14
506	Bioinformatics Resources for In Silico Proteome Analysis. <i>Journal of Biomedicine and Biotechnology</i> , 2003, 2003, 231-236.	3.0	11
507	Transcriptome Analysis of Mouse Stem Cells and Early Embryos. <i>PLoS Biology</i> , 2003, 1, e74.	2.6	156
508	ArrayTrack—supporting toxicogenomic research at the U.S. Food and Drug Administration National Center for Toxicological Research.. <i>Environmental Health Perspectives</i> , 2003, 111, 1819-1826.	2.8	197
509	Expression Profiler. <i>Statistics in the Health Sciences</i> , 2003, , 142-162.	0.2	5
510	Software Packages for Quantitative Microarray-Based Gene Expression Analysis. <i>Current Pharmaceutical Biotechnology</i> , 2003, 4, 417-437.	0.9	19

#	ARTICLE	IF	CITATIONS
511	Open Source Software for the Analysis of Microarray Data. <i>BioTechniques</i> , 2003, 34, S45-S51.	0.8	223
512	Gene Expression Databases and Data Mining. <i>BioTechniques</i> , 2003, 34, S36-S44.	0.8	29
514	Integrating Genomic and Proteomic Data: The Integr8 Project. <i>Journal of Integrative Bioinformatics</i> , 2004, 1, 108-115.	1.0	1
515	Tools für die Proteom-Analyse in silico. <i>IT - Information Technology</i> , 2004, 46, 20-25.	0.6	0
516	Transcriptional profiling of in vitro smooth muscle cell differentiation identifies specific patterns of gene and pathway activation. <i>Physiological Genomics</i> , 2004, 19, 292-302.	1.0	26
517	Using Support Vector Machines for Classifying Large Sets of Multi-Represented Objects. , 2004, , .		13
518	Annotation and cross-indexing of array elements on multiple platforms.. <i>Environmental Health Perspectives</i> , 2004, 112, 506-510.	2.8	19
519	A comprehensive nonredundant expressed sequence tag collection for the developing <i>Rattus norvegicus</i> heart. <i>Physiological Genomics</i> , 2004, 17, 245-252.	1.0	7
520	Database development in toxicogenomics: issues and efforts.. <i>Environmental Health Perspectives</i> , 2004, 112, 495-505.	2.8	112
521	Joint analysis of multiple cDNA microarray studies via multivariate mixed models applied to genetic improvement of beef cattle1. <i>Journal of Animal Science</i> , 2004, 82, 3430-3439.	0.2	40
523	Experimental Systems: A Life of Their Own?. , 2004, , 127-153.		0
526	Reductionism and the Nature of Explanations. , 2004, , 18-50.		0
527	Discovery: Solving Biological Problems. , 2004, , 51-87.		0
528	Scientific Inference: Testing Hypotheses. , 2004, , 88-126.		0
529	Model Organisms: Of Flies and Elephants. , 2004, , 154-187.		1
530	Reference and Conceptual Change: Out of Mendel's Garden?. , 2004, , 188-228.		0
531	Developmental Biology and the Genetic Program: Explaining Ontogeny. , 2004, , 229-265.		0
532	Scientific Realism: In Search of the Truth. , 2004, , 266-296.		0

#	ARTICLE	IF	CITATIONS
535	Computational Ontologies and Information Systems I: Foundations. Communications of the Association for Information Systems, 2004, 14, .	0.7	43
536	Protein Variations: Resources and Tools. , 2004, , 389-422.		0
539	Ontology-Assisted Database Integration to Support Natural Language Processing and Biomedical Data-mining. Journal of Integrative Bioinformatics, 2004, 1, 1-10.	1.0	14
540	Evaluation of the host transcriptional response to human cytomegalovirus infection. Physiological Genomics, 2004, 18, 51-62.	1.0	35
541	Bioinformatics: Towards New Directions for Public Health. Methods of Information in Medicine, 2004, 43, 208-214.	0.7	26
542	Ischemic but not pharmacological preconditioning elicits a gene expression profile similar to unprotected myocardium. Physiological Genomics, 2004, 20, 117-130.	1.0	40
543	Identification of Gene Expression Changes Associated with the Progression of Retinal Degeneration in the rd1 Mouse. , 2004, 45, 2929.		88
544	Interaction Networks in Yeast Define and Enumerate the Signaling Steps of the Vertebrate Aryl Hydrocarbon Receptor. PLoS Biology, 2004, 2, e65.	2.6	28
545	Public Health Implications of Bioinformatics. Yearbook of Medical Informatics, 2004, 13, 137-143.	0.8	0
546	Gene Expression Profile in Thyroid of Transgenic Mice Overexpressing the Adenosine Receptor 2a. Molecular Endocrinology, 2004, 18, 194-213.	3.7	9
547	Proteomic Informatics. International Review of Neurobiology, 2004, 61, 127-157.	0.9	10
548	THEA: ontology-driven analysis of microarray data. Bioinformatics, 2004, 20, 2636-2643.	1.8	28
549	Conservation and Coevolution in the Scale-Free Human Gene Coexpression Network. Molecular Biology and Evolution, 2004, 21, 2058-2070.	3.5	192
550	Identification of Cathepsin B as a Mediator of Neuronal Death Induced by A β ² -activated Microglial Cells Using a Functional Genomics Approach. Journal of Biological Chemistry, 2004, 279, 5565-5572.	1.6	117
551	YETI: Yeast Exploration Tool Integrator. Bioinformatics, 2004, 20, 284-285.	1.8	3
552	3did: interacting protein domains of known three-dimensional structure. Nucleic Acids Research, 2004, 33, D413-D417.	6.5	160
553	Cytoskeletal Activation and Altered Gene Expression in Endothelial Barrier Regulation by Simvastatin. American Journal of Respiratory Cell and Molecular Biology, 2004, 30, 662-670.	1.4	144
554	Proteomics: current techniques and potential applications to lung disease. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2004, 287, L1-L23.	1.3	99

#	ARTICLE	IF	CITATIONS
555	Highly conserved upstream sequences for transcription factor genes and implications for the regulatory network. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17156-17161.	3.3	37
556	An ontology for collaborative construction and analysis of cellular pathways. Bioinformatics, 2004, 20, 349-356.	1.8	47
557	A discriminative model for identifying spatial cis-regulatory modules. , 2004, , .		5
558	Probabilistic discovery of overlapping cellular processes and their regulation. , 2004, , .		14
559	Statistically rigorous automated protein annotation. Bioinformatics, 2004, 20, 1066-1073.	1.8	10
560	Learning to cluster using local neighborhood structure. , 2004, , .		3
561	The Functional Genomic Distribution of Protein Divergence in Two Animal Phyla: Coevolution, Genomic Conflict, and Constraint. Genome Research, 2004, 14, 802-811.	2.4	77
562	Gender-Specific Gene Expression in Post-Mortem Human Brain: Localization to Sex Chromosomes. Neuropsychopharmacology, 2004, 29, 373-384.	2.8	206
563	GFINDER: Genome Function INtegrated Discoverer through dynamic annotation, statistical analysis, and mining. Nucleic Acids Research, 2004, 32, W293-W300.	6.5	72
564	Prediction of Protein Function in the Absence of Significant Sequence Similarity. Current Medicinal Chemistry, 2004, 11, 2135-2142.	1.2	57
565	Phylogenomic inference of protein molecular function: advances and challenges. Bioinformatics, 2004, 20, 170-179.	1.8	184
566	Gene Expression Profiles Predict Survival and Progression of Pleural Mesothelioma. Clinical Cancer Research, 2004, 10, 849-859.	3.2	121
568	Integrative Biological Analysis of the APOE*3-Leiden Transgenic Mouse. OMICS A Journal of Integrative Biology, 2004, 8, 3-13.	1.0	108
569	Large-scale meta-analysis of cancer microarray data identifies common transcriptional profiles of neoplastic transformation and progression. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9309-9314.	3.3	874
570	Probing microRNAs with microarrays: Tissue specificity and functional inference. Rna, 2004, 10, 1813-1819.	1.6	342
571	GO::TermFinder--open source software for accessing Gene Ontology information and finding significantly enriched Gene Ontology terms associated with a list of genes. Bioinformatics, 2004, 20, 3710-3715.	1.8	1,782
572	siRNA-mediated gene silencing: a global genome view. Nucleic Acids Research, 2004, 32, 3836-3845.	6.5	65
573	SCA db: spinocerebellar ataxia candidate gene database. Bioinformatics, 2004, 20, 2656-2661.	1.8	3

#	ARTICLE	IF	CITATIONS
574	A mouse model for Finnish variant late infantile neuronal ceroid lipofuscinosis, CLN5, reveals neuropathology associated with early aging. <i>Human Molecular Genetics</i> , 2004, 13, 2893-2906.	1.4	75
575	The initiative role of XPC protein in cisplatin DNA damaging treatment-mediated cell cycle regulation. <i>Nucleic Acids Research</i> , 2004, 32, 2231-2240.	6.5	53
576	Semantic Search among Heterogeneous Biological Databases Based on Gene Ontology. <i>Acta Biochimica Et Biophysica Sinica</i> , 2004, 36, 365-370.	0.9	19
577	Gene-Ontology analysis reveals association of tissue-specific 5' CpG-island genes with development and embryogenesis. <i>Human Molecular Genetics</i> , 2004, 13, 1969-1978.	1.4	31
578	Systematic changes in gene expression in postmortem human brains associated with tissue pH and terminal medical conditions. <i>Human Molecular Genetics</i> , 2004, 13, 609-616.	1.4	237
579	Genolevures: comparative genomics and molecular evolution of hemiascomycetous yeasts. <i>Nucleic Acids Research</i> , 2004, 32, 315D-318.	6.5	71
580	Annotation Transfer Between Genomes: Protein-Protein Interologs and Protein-DNA Regulogs. <i>Genome Research</i> , 2004, 14, 1107-1118.	2.4	516
581	Broadly Altered Gene Expression in Blood Leukocytes in Essential Hypertension Is Absent During Treatment. <i>Hypertension</i> , 2004, 43, 947-951.	1.3	73
582	Host Cell Gene Expression during Human Immunodeficiency Virus Type 1 Latency and Reactivation and Effects of Targeting Genes That Are Differentially Expressed in Viral Latency. <i>Journal of Virology</i> , 2004, 78, 9458-9473.	1.5	106
583	Different Gene Expression Patterns in Invasive Lobular and Ductal Carcinomas of the Breast. <i>Molecular Biology of the Cell</i> , 2004, 15, 2523-2536.	0.9	540
584	Global protein function annotation through mining genome-scale data in yeast <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2004, 32, 6414-6424.	6.5	104
585	FatiGO: a web tool for finding significant associations of Gene Ontology terms with groups of genes. <i>Bioinformatics</i> , 2004, 20, 578-580.	1.8	1,024
586	PeerGAD: a peer-review-based and community-centric web application for viewing and annotating prokaryotic genome sequences. <i>Nucleic Acids Research</i> , 2004, 32, 3124-3135.	6.5	15
587	Arginine methyltransferase affects interactions and recruitment of mRNA processing and export factors. <i>Genes and Development</i> , 2004, 18, 2024-2035.	2.7	119
588	Gostat: find statistically overrepresented Gene Ontologies within a group of genes. <i>Bioinformatics</i> , 2004, 20, 1464-1465.	1.8	1,125
589	Discovery Science. <i>Lecture Notes in Computer Science</i> , 2004, , .	1.0	3
590	An ORFeome-based Analysis of Human Transcription Factor Genes and the Construction of a Microarray to Interrogate Their Expression. <i>Genome Research</i> , 2004, 14, 2041-2047.	2.4	130
591	HyBrow: a prototype system for computer-aided hypothesis evaluation. <i>Bioinformatics</i> , 2004, 20, i257-i264.	1.8	47

#	ARTICLE	IF	CITATIONS
592	Nutritional Homeostasis in Batch and Steady-State Culture of Yeast. <i>Molecular Biology of the Cell</i> , 2004, 15, 4089-4104.	0.9	179
593	GermOnline, a cross-species community knowledgebase on germ cell differentiation. <i>Nucleic Acids Research</i> , 2004, 32, 560D-567.	6.5	26
595	ClutrFree: cluster tree visualization and interpretation. <i>Bioinformatics</i> , 2004, 20, 2869-2871.	1.8	30
596	Bayesian integrated functional analysis of microarray data. <i>Bioinformatics</i> , 2004, 20, 2943-2953.	1.8	20
597	Large-scale assessment of the utility of low-resolution protein structures for biochemical function assignment. <i>Bioinformatics</i> , 2004, 20, 1087-1096.	1.8	51
598	Identification of the Substrates and Interaction Proteins of Aurora Kinases from a Protein-Protein Interaction Model. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 93-104.	2.5	35
599	Mouse Chromosome 17A3.3 Contains 13 Genes That Encode Functional Tryptic-like Serine Proteases with Distinct Tissue and Cell Expression Patterns. <i>Journal of Biological Chemistry</i> , 2004, 279, 2438-2452.	1.6	64
600	Ontologizing gene-expression microarray data: characterizing clusters with Gene Ontology. <i>Bioinformatics</i> , 2004, 20, 979-981.	1.8	81
601	A genomic view of estrogen actions in human breast cancer cells by expression profiling of the hormone-responsive transcriptome. <i>Journal of Molecular Endocrinology</i> , 2004, 32, 719-775.	1.1	80
602	The FunCat, a functional annotation scheme for systematic classification of proteins from whole genomes. <i>Nucleic Acids Research</i> , 2004, 32, 5539-5545.	6.5	988
603	Data mining techniques to study the disulfide-bonding state in proteins: signal peptide is a strong descriptor. <i>Bioinformatics</i> , 2004, 20, 2509-2512.	1.8	7
604	Large-Scale Generation and Analysis of Expressed Sequence Tags from Porcine Ovary1. <i>Biology of Reproduction</i> , 2004, 71, 1991-2002.	1.2	19
605	Transcriptional Transitions during Dictyostelium Spore Germination. <i>Eukaryotic Cell</i> , 2004, 3, 1101-1110.	3.4	24
606	Identification of a Gene Expression Signature Associated with Recurrent Disease in Squamous Cell Carcinoma of the Head and Neck. <i>Cancer Research</i> , 2004, 64, 55-63.	0.4	373
607	Coordinated Genetic Regulation of Growth and Lignin Revealed by Quantitative Trait Locus Analysis of cDNA Microarray Data in an Interspecific Backcross of Eucalyptus. <i>Plant Physiology</i> , 2004, 135, 2368-2378.	2.3	205
608	Expression Profiling of t(12;22) Positive Clear Cell Sarcoma of Soft Tissue Cell Lines Reveals Characteristic Up-Regulation of Potential New Marker Genes Including ERBB3. <i>Cancer Research</i> , 2004, 64, 3395-3405.	0.4	73
609	Pattern of genes influenced by conditional expression of the transcription factors HNF6, HNF4 and HNF1 in a pancreatic β -cell line. <i>Nucleic Acids Research</i> , 2004, 32, e150-e150.	6.5	52
610	Weight loss regulates inflammation-related genes in white adipose tissue of obese subjects. <i>FASEB Journal</i> , 2004, 18, 1657-1669.	0.2	569

#	ARTICLE	IF	CITATIONS
611	Comparative Analysis of Protein Domain Organization. <i>Genome Research</i> , 2004, 14, 343-353.	2.4	80
612	Developmental Expression of 2489 Gene Clusters During Pig Embryogenesis: An Expressed Sequence Tag Project1. <i>Biology of Reproduction</i> , 2004, 71, 1230-1243.	1.2	53
613	The Human Plasma Proteome. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 311-326.	2.5	801
614	BioMap. , 2004, , .		11
615	Predicting subcellular localization of proteins in a hybridization space. <i>Bioinformatics</i> , 2004, 20, 1151-1156.	1.8	88
616	Pathbase: a database of mutant mouse pathology. <i>Nucleic Acids Research</i> , 2004, 32, 512D-515.	6.5	49
617	Shared relationship analysis: ranking set cohesion and commonalities within a literature-derived relationship network. <i>Bioinformatics</i> , 2004, 20, 191-198.	1.8	103
618	Evolutionary Expressed Sequence Tag Analysis of Drosophila Female Reproductive Tracts Identifies Genes Subjected to Positive Selection. <i>Genetics</i> , 2004, 168, 1457-1465.	1.2	199
619	ASD: the Alternative Splicing Database. <i>Nucleic Acids Research</i> , 2004, 32, 64D-69.	6.5	176
620	Expression Profiling of T-Cell Lymphomas Differentiates Peripheral and Lymphoblastic Lymphomas and Defines Survival Related Genes. <i>Clinical Cancer Research</i> , 2004, 10, 4971-4982.	3.2	88
621	SPrCY: comparison of structural predictions in the <i>Saccharomyces cerevisiae</i> genome. <i>Bioinformatics</i> , 2004, 20, 2312-2314.	1.8	14
622	Data exploration tools for the Gene Ontology database. <i>Bioinformatics</i> , 2004, 20, 3442-3454.	1.8	17
623	Global Survey of Chromatin Accessibility Using DNA Microarrays. <i>Genome Research</i> , 2004, 14, 1374-1381.	2.4	28
624	The Ensembl Core Software Libraries. <i>Genome Research</i> , 2004, 14, 929-933.	2.4	116
625	Control of Yeast Filamentous-Form Growth by Modules in an Integrated Molecular Network. <i>Genome Research</i> , 2004, 14, 380-390.	2.4	78
626	Comparative Genomics of Transcriptional Control in the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2004, 14, 1548-1554.	2.4	221
627	The Gene Ontology Annotation (GOA) Database: sharing knowledge in Uniprot with Gene Ontology. <i>Nucleic Acids Research</i> , 2004, 32, 262D-266.	6.5	780
628	SMART 4.0: towards genomic data integration. <i>Nucleic Acids Research</i> , 2004, 32, 142D-144.	6.5	892

#	ARTICLE	IF	CITATIONS
629	DBSubLoc: database of protein subcellular localization. <i>Nucleic Acids Research</i> , 2004, 32, 122D-124.	6.5	43
630	RNAiDB and PhenoBlast: web tools for genome-wide phenotypic mapping projects. <i>Nucleic Acids Research</i> , 2004, 32, 406D-410.	6.5	62
631	ArrayXPath: mapping and visualizing microarray gene-expression data with integrated biological pathway resources using Scalable Vector Graphics. <i>Nucleic Acids Research</i> , 2004, 32, W460-W464.	6.5	57
632	Transcription factor binding element detection using functional clustering of mutant expression data. <i>Nucleic Acids Research</i> , 2004, 32, 2362-2371.	6.5	13
633	The effect of stress withdrawal on gene expression and certain biochemical and cell biological properties of peroxide-conditioned cell lines. <i>FASEB Journal</i> , 2004, 18, 480-488.	0.2	37
634	An orderly retreat: Dedifferentiation is a regulated process. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7005-7010.	3.3	46
635	Incipient Alzheimer's disease: Microarray correlation analyses reveal major transcriptional and tumor suppressor responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2173-2178.	3.3	988
636	Shared Transcriptional Signature in <i>Caenorhabditis elegans</i> Dauer Larvae and Long-lived <i>daf-2</i> Mutants Implicates Detoxification System in Longevity Assurance. <i>Journal of Biological Chemistry</i> , 2004, 279, 44533-44543.	1.6	347
637	MitoP2, an integrated database on mitochondrial proteins in yeast and man. <i>Nucleic Acids Research</i> , 2004, 32, 459D-462.	6.5	75
638	Gene expression profiles of transcripts in amyloid precursor protein transgenic mice: up-regulation of mitochondrial metabolism and apoptotic genes is an early cellular change in Alzheimer's disease. <i>Human Molecular Genetics</i> , 2004, 13, 1225-1240.	1.4	309
639	Computational inference of transcriptional regulatory networks from expression profiling and transcription factor binding site identification. <i>Nucleic Acids Research</i> , 2004, 32, 179-188.	6.5	99
640	yMGV: a cross-species expression data mining tool. <i>Nucleic Acids Research</i> , 2004, 32, 323D-325.	6.5	6
641	Gene annotation from scientific literature using mappings between keyword systems. <i>Bioinformatics</i> , 2004, 20, 2084-2091.	1.8	46
642	CLENCH: a program for calculating Cluster ENriCHment using the Gene Ontology. <i>Bioinformatics</i> , 2004, 20, 1196-1197.	1.8	59
643	SeqExpress: desktop analysis and visualization tool for gene expression experiments. <i>Bioinformatics</i> , 2004, 20, 1649-1650.	1.8	9
644	Genomic and Proteomic Determinants of Outcome in Patients Undergoing Thoracoabdominal Aortic Aneurysm Repair. <i>Journal of Immunology</i> , 2004, 172, 7103-7109.	0.4	61
645	A graph-theoretic modeling on GO space for biological interpretation of gene clusters. <i>Bioinformatics</i> , 2004, 20, 381-388.	1.8	65
646	WILMA-automated annotation of protein sequences. <i>Bioinformatics</i> , 2004, 20, 127-128.	1.8	9

#	ARTICLE	IF	CITATIONS
647	Identification of Candidate Disease Genes by EST Alignments, Synteny, and Expression and Verification of Ensembl Genes on Rat Chromosome 1q43-54. <i>Genome Research</i> , 2004, 14, 640-650.	2.4	17
648	The Gene Ontology Categorizer. <i>Bioinformatics</i> , 2004, 20, i169-i177.	1.8	64
649	Genome-Wide Analysis of mRNA Stability Using Transcription Inhibitors and Microarrays Reveals Posttranscriptional Control of Ribosome Biogenesis Factors. <i>Molecular and Cellular Biology</i> , 2004, 24, 5534-5547.	1.1	310
650	Handbook on Ontologies. , 2004, , .		375
652	Comparative Genomics of Gene Expression in the Parasitic and Free-Living Nematodes <i>Strongyloides stercoralis</i> and <i>Caenorhabditis elegans</i> . <i>Genome Research</i> , 2004, 14, 209-220.	2.4	87
653	CARRIE web service: automated transcriptional regulatory network inference and interactive analysis. <i>Nucleic Acids Research</i> , 2004, 32, W213-W216.	6.5	30
654	A graph-theoretic approach to testing associations between disparate sources of functional genomics data. <i>Bioinformatics</i> , 2004, 20, 3353-3362.	1.8	42
655	GOblet: a platform for Gene Ontology annotation of anonymous sequence data. <i>Nucleic Acids Research</i> , 2004, 32, W313-W317.	6.5	79
656	Onto-Tools: an ensemble of web-accessible, ontology-based tools for the functional design and interpretation of high-throughput gene expression experiments. <i>Nucleic Acids Research</i> , 2004, 32, W449-W456.	6.5	139
657	New challenges in gene expression data analysis and the extended GEPAS. <i>Nucleic Acids Research</i> , 2004, 32, W485-W491.	6.5	47
658	Calculating the statistical significance of physical clusters of co-regulated genes in the genome: the role of chromatin in domain-wide gene regulation. <i>Nucleic Acids Research</i> , 2004, 32, 1798-1807.	6.5	27
659	The <i>Candida</i> Genome Database (CGD), a community resource for <i>Candida albicans</i> gene and protein information. <i>Nucleic Acids Research</i> , 2004, 33, D358-D363.	6.5	95
660	PFD: a database for the investigation of protein folding kinetics and stability. <i>Nucleic Acids Research</i> , 2004, 33, D279-D283.	6.5	21
661	SIEGE: Smoking Induced Epithelial Gene Expression Database. <i>Nucleic Acids Research</i> , 2004, 33, D573-D579.	6.5	24
662	The Yeast Resource Center Public Data Repository. <i>Nucleic Acids Research</i> , 2004, 33, D378-D382.	6.5	25
663	The PANTHER database of protein families, subfamilies, functions and pathways. <i>Nucleic Acids Research</i> , 2004, 33, D284-D288.	6.5	686
664	PartiGeneDB--collating partial genomes. <i>Nucleic Acids Research</i> , 2004, 33, D303-D307.	6.5	8
665	The Legume Information System (LIS): an integrated information resource for comparative legume biology. <i>Nucleic Acids Research</i> , 2004, 33, D660-D665.	6.5	104

#	ARTICLE	IF	CITATIONS
666	Positioning Arabidopsis in Plant Biology. A Key Step Toward Unification of Plant Research. <i>Plant Physiology</i> , 2004, 135, 602-606.	2.3	8
667	Sfp1 is a stress- and nutrient-sensitive regulator of ribosomal protein gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14315-14322.	3.3	335
668	A method for finding communities of related genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5241-5248.	3.3	205
669	Early Target Genes of IL-12 and STAT4 Signaling in Th Cells. <i>Journal of Immunology</i> , 2004, 172, 6775-6782.	0.4	80
670	BRENDA, the enzyme database: updates and major new developments. <i>Nucleic Acids Research</i> , 2004, 32, 431D-433.	6.5	679
671	The Cell Wall Navigator Database. A Systems-Based Approach to Organism-Unrestricted Mining of Protein Families Involved in Cell Wall Metabolism. <i>Plant Physiology</i> , 2004, 136, 3003-3008.	2.3	64
672	Proteomic Analysis of the Intestinal Epithelial Cell Response to Enteropathogenic <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 20127-20136.	1.6	76
673	<i>Saccharomyces</i> genome database: Underlying principles and organisation. <i>Briefings in Bioinformatics</i> , 2004, 5, 9-22.	3.2	83
674	CYGD: the Comprehensive Yeast Genome Database. <i>Nucleic Acids Research</i> , 2004, 33, D364-D368.	6.5	288
675	Swiss-Prot: Juggling between evolution and stability. <i>Briefings in Bioinformatics</i> , 2004, 5, 39-55.	3.2	338
676	IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , 2004, 32, 452D-455.	6.5	864
677	Identification of Differentially Expressed Genes in Scrapie-Infected Mouse Brains by Using Global Gene Expression Technology. <i>Journal of Virology</i> , 2004, 78, 11051-11060.	1.5	129
678	The Diatom EST Database. <i>Nucleic Acids Research</i> , 2004, 33, D344-D347.	6.5	75
679	BIOIE: RETARGETABLE INFORMATION EXTRACTION AND ONTOLOGICAL ANNOTATION OF BIOLOGICAL INTERACTIONS FROM THE LITERATURE. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 551-568.	0.3	23
680	PupaSNP Finder: a web tool for finding SNPs with putative effect at transcriptional level. <i>Nucleic Acids Research</i> , 2004, 32, W242-W248.	6.5	86
681	Coexpression Analysis of Human Genes Across Many Microarray Data Sets. <i>Genome Research</i> , 2004, 14, 1085-1094.	2.4	688
682	Functional Divergence of Duplicated Genes Formed by Polyploidy during Arabidopsis Evolution[W]. <i>Plant Cell</i> , 2004, 16, 1679-1691.	3.1	996
683	STATISTICAL AND VISUAL MORPH MOVIE ANALYSIS OF CRYSTALLOGRAPHIC MUTANT SELECTION BIAS IN PROTEIN MUTATION RESOURCE DATA. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 61-75.	0.3	2

#	ARTICLE	IF	CITATIONS
684	Protein Databases on the Internet. <i>Current Protocols in Molecular Biology</i> , 2004, 68, Unit 19.4.	2.9	11
685	Protein Interaction Networks. <i>Expert Review of Proteomics</i> , 2004, 1, 239-249.	1.3	79
686	Cellular responses to ErbB-2 overexpression in human mammary luminal epithelial cells: comparison of mRNA and protein expression. <i>British Journal of Cancer</i> , 2004, 90, 173-181.	2.9	43
687	QA/QC: challenges and pitfalls facing the microarray community and regulatory agencies. <i>Expert Review of Molecular Diagnostics</i> , 2004, 4, 761-777.	1.5	99
688	Integrated Analysis of Microarray Data and Gene Function Information. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 106-117.	1.0	12
689	Knowledge discovery in a microarray data warehouse. , 2004, , .		0
690	Disease ontology based grid middleware for human disease research study. , 0, , .		5
691	Natural Language Processing and Systems Biology. , 2004, , 147-173.		36
692	The Binding Sites for the Chromatin Insulator Protein CTCF Map to DNA Methylation-Free Domains Genome-Wide. <i>Genome Research</i> , 2004, 14, 1594-1602.	2.4	121
693	RULEMINER: A KNOWLEDGE SYSTEM FOR SUPPORTING HIGH-THROUGHPUT PROTEIN FUNCTION ANNOTATIONS. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 595-617.	0.3	17
694	Coping with cold: An integrative, multitissue analysis of the transcriptome of a poikilothermic vertebrate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16970-16975.	3.3	410
695	Sperm-Induced Modification of the Oviductal Gene Expression Profile After Natural Insemination in Mice. <i>Biology of Reproduction</i> , 2004, 71, 60-65.	1.2	147
696	GENERATION OF A LARGE GENE/PROTEIN LEXICON BY MORPHOLOGICAL PATTERN ANALYSIS. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 01, 611-626.	0.3	19
697	ACID: a database for microarray clone information. <i>Bioinformatics</i> , 2004, 20, 2305-2306.	1.8	18
698	ORFDB: an information resource linking scientific content to a high-quality Open Reading Frame (ORF) collection. <i>Nucleic Acids Research</i> , 2004, 32, 595D-599.	6.5	18
699	Functional Bias and Spatial Organization of Genes in Mutational Hot and Cold Regions in the Human Genome. <i>PLoS Biology</i> , 2004, 2, e29.	2.6	88
700	Gene expression in juvenile arthritis and spondyloarthritis: pro-angiogenic ELR+ chemokine genes relate to course of arthritis. <i>Rheumatology</i> , 2004, 43, 973-979.	0.9	81
701	Textpresso: An Ontology-Based Information Retrieval and Extraction System for Biological Literature. <i>PLoS Biology</i> , 2004, 2, e309.	2.6	504

#	ARTICLE	IF	CITATIONS
702	Genomic data visualization on the Web. <i>Bioinformatics</i> , 2004, 20, 1804-1805.	1.8	12
703	Molecular Signatures of Proliferation and Quiescence in Hematopoietic Stem Cells. <i>PLoS Biology</i> , 2004, 2, e301.	2.6	309
704	Pathbase: a new reference resource and database for laboratory mouse pathology. <i>Radiation Protection Dosimetry</i> , 2004, 112, 525-528.	0.4	21
705	Distinct Genomic Integration of MLV and SIV Vectors in Primate Hematopoietic Stem and Progenitor Cells. <i>PLoS Biology</i> , 2004, 2, e423.	2.6	243
706	Highly Conserved Non-Coding Sequences Are Associated with Vertebrate Development. <i>PLoS Biology</i> , 2004, 3, e7.	2.6	833
707	Human T lymphotropic virus type-1 p30II alters cellular gene expression to selectively enhance signaling pathways that activate T lymphocytes. <i>Retrovirology</i> , 2004, 1, 39.	0.9	36
708	ArchDB: automated protein loop classification as a tool for structural genomics. <i>Nucleic Acids Research</i> , 2004, 32, 185D-188.	6.5	61
709	NetAffx Gene Ontology Mining Tool: a visual approach for microarray data analysis. <i>Bioinformatics</i> , 2004, 20, 1462-1463.	1.8	75
710	Distinctive Features of Plant Organs Characterized by Global Analysis of Gene Expression in Arabidopsis. <i>DNA Research</i> , 2004, 11, 11-25.	1.5	27
711	Functional Evolution of the Yeast Protein Interaction Network. <i>Molecular Biology and Evolution</i> , 2004, 21, 1171-1176.	3.5	66
712	Genexpressionsanalysen bei akuten Leukämien: Diagnostik der Zukunft? / Gene expression profiling in acute leukemia: diagnostics of the future?. <i>Laboratoriums Medizin</i> , 2004, 28, 225-232.	0.1	0
713	The Unified Medical Language System (UMLS): integrating biomedical terminology. <i>Nucleic Acids Research</i> , 2004, 32, 267D-270.	6.5	2,858
714	Gene expression profiling in human insulinoma tissue: genes involved in the insulin secretion pathway and cloning of novel full-length cDNAs.. <i>Endocrine-Related Cancer</i> , 2004, 11, 295-303.	1.6	30
715	Over 20% of human transcripts might form sense-antisense pairs. <i>Nucleic Acids Research</i> , 2004, 32, 4812-4820.	6.5	287
716	GO-Mapper: functional analysis of gene expression data using the expression level as a score to evaluate Gene Ontology terms. <i>Bioinformatics</i> , 2004, 20, 2618-2625.	1.8	45
718	Tailored gene array databases: applications in mechanistic toxicology. <i>Bioinformatics</i> , 2004, 20, 507-517.	1.8	19
719	Ontologies for Behavior. <i>Bioinformatics</i> , 2004, 20, 3700-3701.	1.8	13
720	Bayesian mixture model based clustering of replicated microarray data. <i>Bioinformatics</i> , 2004, 20, 1222-1232.	1.8	184

#	ARTICLE	IF	CITATIONS
721	The distribution and query systems of the RCSB Protein Data Bank. <i>Nucleic Acids Research</i> , 2004, 32, 223D-225.	6.5	108
722	Comparative Analysis of Amino Acid Repeats in Rodents and Humans. <i>Genome Research</i> , 2004, 14, 549-554.	2.4	149
723	VirGen: a comprehensive viral genome resource. <i>Nucleic Acids Research</i> , 2004, 32, 289D-292.	6.5	16
724	A Gene Expression Map for the Euchromatic Genome of <i>Drosophila melanogaster</i> . <i>Science</i> , 2004, 306, 655-660.	6.0	275
725	Differential Gene Expression of Blood-Derived Cell Lines in Familial Combined Hyperlipidemia. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2004, 24, 2149-2154.	1.1	31
726	An update of the HLA genomic region, locus information and disease associations: 2004. <i>Tissue Antigens</i> , 2004, 64, 631-649.	1.0	352
727	Development and evaluation of an <i>Arabidopsis</i> whole genome Affymetrix probe array. <i>Plant Journal</i> , 2004, 38, 545-561.	2.8	223
728	The transcriptome of adult female <i>Anopheles darlingi</i> salivary glands. <i>Insect Molecular Biology</i> , 2004, 13, 73-88.	1.0	94
729	Iron-regulated transcription and capsule formation in the fungal pathogen <i>Cryptococcus neoformans</i> . <i>Molecular Microbiology</i> , 2004, 55, 1452-1472.	1.2	90
730	Regulation of gene expression by dietary Ca ²⁺ in kidneys of 25-hydroxyvitamin D ₃ -1 α -hydroxylase knockout mice. <i>Kidney International</i> , 2004, 65, 531-539.	2.6	59
731	Brain-derived neurotrophic factor signaling modifies hippocampal gene expression during epileptogenesis in transgenic mice. <i>European Journal of Neuroscience</i> , 2004, 19, 3245-3254.	1.2	29
732	Targeted cellular process profiling approach for uterine leiomyoma using cDNA microarray, proteomics and gene ontology analysis. <i>International Journal of Experimental Pathology</i> , 2004, 84, 267-279.	0.6	46
733	AnoXcel: an <i>Anopheles gambiae</i> protein database. <i>Insect Molecular Biology</i> , 2004, 13, 449-457.	1.0	45
734	The major histocompatibility complex origin. <i>Immunological Reviews</i> , 2004, 198, 216-232.	2.8	54
735	Integration of chemical-genetic and genetic interaction data links bioactive compounds to cellular target pathways. <i>Nature Biotechnology</i> , 2004, 22, 62-69.	9.4	584
736	Comparing genomic expression patterns across species identifies shared transcriptional profile in aging. <i>Nature Genetics</i> , 2004, 36, 197-204.	9.4	434
737	Familial combined hyperlipidemia is associated with upstream transcription factor 1 (USF1). <i>Nature Genetics</i> , 2004, 36, 371-376.	9.4	295
738	A probabilistic view of gene function. <i>Nature Genetics</i> , 2004, 36, 559-564.	9.4	120

#	ARTICLE	IF	CITATIONS
739	Integrated global profiling of cancer. <i>Nature Reviews Cancer</i> , 2004, 4, 638-644.	12.8	132
740	Chemogenomics: an emerging strategy for rapid target and drug discovery. <i>Nature Reviews Genetics</i> , 2004, 5, 262-275.	7.7	340
741	Human brain evolution: insights from microarrays. <i>Nature Reviews Genetics</i> , 2004, 5, 850-860.	7.7	185
742	Biological robustness. <i>Nature Reviews Genetics</i> , 2004, 5, 826-837.	7.7	1,937
743	The involvement of XPC protein in the cisplatin DNA damaging treatment-mediated cellular response. <i>Cell Research</i> , 2004, 14, 303-314.	5.7	31
744	TEAM: a tool for the integration of expression, and linkage and association maps. <i>European Journal of Human Genetics</i> , 2004, 12, 633-638.	1.4	22
745	From microarray data to results. <i>EMBO Reports</i> , 2004, 5, 459-463.	2.0	4
746	Mitochondrial dysfunction in schizophrenia: evidence for compromised brain metabolism and oxidative stress. <i>Molecular Psychiatry</i> , 2004, 9, 684-697.	4.1	810
747	Independent component analysis of microarray data in the study of endometrial cancer. <i>Oncogene</i> , 2004, 23, 6677-6683.	2.6	97
748	Evolutionary changes in cis and trans gene regulation. <i>Nature</i> , 2004, 430, 85-88.	13.7	771
749	Comparative analysis of processed pseudogenes in the mouse and human genomes. <i>Trends in Genetics</i> , 2004, 20, 62-67.	2.9	201
750	Transcripts of aging. <i>Trends in Genetics</i> , 2004, 20, 221-224.	2.9	26
751	A common framework for understanding the origin of genetic dominance and evolutionary fates of gene duplications. <i>Trends in Genetics</i> , 2004, 20, 287-290.	2.9	186
752	Genome duplication led to highly selective expansion of the <i>Arabidopsis thaliana</i> proteome. <i>Trends in Genetics</i> , 2004, 20, 461-464.	2.9	259
753	Protein domains enriched in mammalian tissue-specific or widely expressed genes. <i>Trends in Genetics</i> , 2004, 20, 468-472.	2.9	33
754	Gene discovery in the adenophorean nematode <i>Trichinella spiralis</i> : an analysis of transcription from three life cycle stages. <i>Molecular and Biochemical Parasitology</i> , 2004, 137, 277-291.	0.5	56
755	The <i>Schistosoma mansoni</i> soluble proteome: a comparison across four life-cycle stages. <i>Molecular and Biochemical Parasitology</i> , 2004, 138, 57-66.	0.5	142
756	Development of public toxicogenomics software for microarray data management and analysis. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2004, 549, 241-253.	0.4	98

#	ARTICLE	IF	CITATIONS
757	The emerging in-silico scientist: how text-based bioinformatics is bridging biology and artificial intelligence. IEEE Engineering in Medicine and Biology Magazine, 2004, 23, 87-93.	1.1	16
758	Herpesvirus of turkeys: microarray analysis of host gene responses to infection. Virology, 2004, 318, 102-111.	1.1	32
759	Searching for pathogenic gene functions to cervical cancer. Gynecologic Oncology, 2004, 93, 41-48.	0.6	43
760	Applying Support Vector Machines for Gene Ontology based gene function prediction. BMC Bioinformatics, 2004, 5, 116.	1.2	60
761	Handling multiple testing while interpreting microarrays with the Gene Ontology Database. BMC Bioinformatics, 2004, 5, 124.	1.2	28
762	Extending the mutual information measure to rank inferred literature relationships. BMC Bioinformatics, 2004, 5, 145.	1.2	95
763	Information assessment on predicting protein-protein interactions. BMC Bioinformatics, 2004, 5, 154.	1.2	136
764	PASBio: predicate-argument structures for event extraction in molecular biology. BMC Bioinformatics, 2004, 5, 155.	1.2	60
765	GOTree Machine (GOTM): a web-based platform for interpreting sets of interesting genes using Gene Ontology hierarchies. BMC Bioinformatics, 2004, 5, 16.	1.2	388
766	Implications for domain fusion protein-protein interactions based on structural information. BMC Bioinformatics, 2004, 5, 161.	1.2	12
767	VisANT: an online visualization and analysis tool for biological interaction data. BMC Bioinformatics, 2004, 5, 17.	1.2	220
768	GOTcha: a new method for prediction of protein function assessed by the annotation of seven genomes. BMC Bioinformatics, 2004, 5, 178.	1.2	205
769	CLOE: identification of putative functional relationships among genes by comparison of expression profiles between two species. BMC Bioinformatics, 2004, 5, 179.	1.2	21
770	Quantifying the relationship between co-expression, co-regulation and gene function. BMC Bioinformatics, 2004, 5, 18.	1.2	313
771	Optimal cDNA microarray design using expressed sequence tags for organisms with limited genomic information. BMC Bioinformatics, 2004, 5, 191.	1.2	21
772	Comparing functional annotation analyses with Catmap. BMC Bioinformatics, 2004, 5, 193.	1.2	77
773	MiCoViTo: a tool for gene-centric comparison and visualization of yeast transcriptome states. BMC Bioinformatics, 2004, 5, 20.	1.2	4
774	Defining transcriptional networks through integrative modeling of mRNA expression and transcription factor binding data. BMC Bioinformatics, 2004, 5, 31.	1.2	212

#	ARTICLE	IF	CITATIONS
775	Computational identification of transcription factor binding sites by functional analysis of sets of genes sharing overrepresented upstream motifs. <i>BMC Bioinformatics</i> , 2004, 5, 57.	1.2	30
776	A molecular 'signature' of primary breast cancer cultures; patterns resembling tumor tissue. <i>BMC Genomics</i> , 2004, 5, 47.	1.2	51
777	Protein kinases of the human malaria parasite <i>Plasmodium falciparum</i> : the kinome of a divergent eukaryote. <i>BMC Genomics</i> , 2004, 5, 79.	1.2	440
778	FunnyBase: a systems level functional annotation of <i>Fundulus</i> ESTs for the analysis of gene expression. <i>BMC Genomics</i> , 2004, 5, 96.	1.2	30
779	Technological advances and genomics in metazoan parasites. <i>International Journal for Parasitology</i> , 2004, 34, 139-152.	1.3	18
780	GeneWays: a system for extracting, analyzing, visualizing, and integrating molecular pathway data. <i>Journal of Biomedical Informatics</i> , 2004, 37, 43-53.	2.5	230
781	Bioinformatics integration and agent technology. <i>Journal of Biomedical Informatics</i> , 2004, 37, 205-219.	2.5	60
782	High Coding Density on the Largest <i>Paramecium tetraurelia</i> Somatic Chromosome. <i>Current Biology</i> , 2004, 14, 1397-1404.	1.8	52
783	Proteomic analysis of post-mitochondrial fractions of young and old rat kidney. <i>Experimental Gerontology</i> , 2004, 39, 1155-1168.	1.2	17
784	Gene Expression Profiles of Mouse Aorta and Cultured Vascular Smooth Muscle Cells Differ Widely, Yet Show Common Responses to Dioxin Exposure. <i>Cardiovascular Toxicology</i> , 2004, 4, 385-404.	1.1	21
785	Ultraconserved Elements in the Human Genome. <i>Science</i> , 2004, 304, 1321-1325.	6.0	1,496
786	Expression profiling of the developing testis in wild-type and <i>Dazl</i> knockout mice. <i>Molecular Reproduction and Development</i> , 2004, 67, 26-54.	1.0	45
787	Taverna: a tool for the composition and enactment of bioinformatics workflows. <i>Bioinformatics</i> , 2004, 20, 3045-3054.	1.8	1,303
788	Gene expression profiling of individual cases reveals consistent transcriptional changes in alcoholic human brain. <i>Journal of Neurochemistry</i> , 2004, 90, 1050-1058.	2.1	120
789	Exploring the Portability of Informatics Capabilities from a Clinical Application to a Bioscience Application. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2004, 11, 294-299.	2.2	1
790	Design of Genetics Home Reference: A New NLM Consumer Health Resource. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2004, 11, 439-447.	2.2	28
791	Automated Encoding of Clinical Documents Based on Natural Language Processing. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2004, 11, 392-402.	2.2	430
792	Muscle Plasticity and High Throughput Gene Expression Studies. <i>Journal of Muscle Research and Cell Motility</i> , 2004, 25, 231-234.	0.9	3

#	ARTICLE	IF	CITATIONS
793	Using the Gene Ontology for Microarray Data Mining: A Comparison of Methods and Application to Age Effects in Human Prefrontal Cortex. <i>Neurochemical Research</i> , 2004, 29, 1213-1222.	1.6	202
794	SCOR: Structural Classification of RNA, version 2.0. <i>Nucleic Acids Research</i> , 2004, 32, 182D-184.	6.5	98
795	Altered Hippocampal Transcript Profile Accompanies an Age-Related Spatial Memory Deficit in Mice. <i>Learning and Memory</i> , 2004, 11, 253-260.	0.5	148
796	Global Mapping of the Yeast Genetic Interaction Network. <i>Science</i> , 2004, 303, 808-813.	6.0	1,908
797	Bioinformatics Strategies for Translating Genome-Wide Expression Analyses into Clinically Useful Cancer Markers. <i>Annals of the New York Academy of Sciences</i> , 2004, 1020, 32-40.	1.8	53
798	Bayesian Decomposition: Analyzing Microarray Data within a Biological Context. <i>Annals of the New York Academy of Sciences</i> , 2004, 1020, 212-226.	1.8	11
799	A survey of SL1-spliced transcripts from the root-lesion nematode <i>Pratylenchus penetrans</i> . <i>Molecular Genetics and Genomics</i> , 2004, 272, 138-148.	1.0	33
800	Ontologies for Knowledge Management: An Information Systems Perspective. <i>Knowledge and Information Systems</i> , 2004, 6, 380-401.	2.1	155
801	Visualizing the Laboratory Mouse: Capturing Phenotype Information. <i>Genetica</i> , 2004, 122, 89-97.	0.5	18
802	A unigene catalogue of 5700 expressed genes in cassava. <i>Plant Molecular Biology</i> , 2004, 56, 541-554.	2.0	53
803	Functional genomics of cell elongation in developing cotton fibers. <i>Plant Molecular Biology</i> , 2004, 54, 911-929.	2.0	237
804	Functional annotation of mouse mutations in embryonic stem cells by use of expression profiling. <i>Mammalian Genome</i> , 2004, 15, 1-13.	1.0	11
805	Global gene expression in human myocardium?oligonucleotide microarray analysis of regional diversity and transcriptional regulation in heart failure. <i>Journal of Molecular Medicine</i> , 2004, 82, 308-316.	1.7	80
806	An expression profile of human pancreatic islet mRNAs by Serial Analysis of Gene Expression (SAGE). <i>Diabetologia</i> , 2004, 47, 284-299.	2.9	41
807	The T _i ½bingen approach: identification, selection, and validation of tumor-associated HLA peptides for cancer therapy. <i>Cancer Immunology, Immunotherapy</i> , 2004, 53, 187-195.	2.0	132
808	Molecular Evolution in Large Genetic Networks: Does Connectivity Equal Constraint?. <i>Journal of Molecular Evolution</i> , 2004, 58, 203-211.	0.8	138
809	Characterization of the protein processing and secretion pathways in a comprehensive set of expressed sequence tags from <i>Trichoderma reesei</i> . <i>FEMS Microbiology Letters</i> , 2004, 230, 275-282.	0.7	20
810	Classification of common functional loops of kinase super-families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 539-555.	1.5	23

#	ARTICLE	IF	CITATIONS
811	A unified representation of multiprotein complex data for modeling interaction networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 99-108.	1.5	26
812	Intregrated analysis of the human cardiac transcriptome, proteome and phosphoproteome. <i>Proteomics</i> , 2004, 4, 1505-1516.	1.3	31
813	A method of knowledge modeling and its application to gene function analysis. <i>Systems and Computers in Japan</i> , 2004, 35, 21-30.	0.2	0
814	Microarray gene expression profiling and analysis in renal cell carcinoma. <i>BMC Urology</i> , 2004, 4, 9.	0.6	51
815	Title is missing!. <i>Cancer Cell International</i> , 2004, 4, S58.	1.8	0
816	All systems GO for understanding mouse gene function. <i>Journal of Biology</i> , 2004, 3, 20.	2.7	4
817	Use of mass spectrometry to identify protein biomarkers of disease severity in the synovial fluid and serum of patients with rheumatoid arthritis. <i>Arthritis and Rheumatism</i> , 2004, 50, 3792-3803.	6.7	259
818	Short tandem repeats are associated with diverse mRNAs encoding membrane-targeted proteins. <i>BioEssays</i> , 2004, 26, 434-444.	1.2	12
819	Shared components of protein complexes?versatile building blocks or biochemical artefacts?. <i>BioEssays</i> , 2004, 26, 1333-1343.	1.2	40
820	Altered gene expression in acute systemic inflammation detected by complete coverage of the human liver transcriptome. <i>Hepatology</i> , 2004, 39, 353-364.	3.6	30
821	Identification of discriminators of hepatoma by gene expression profiling using a minimal dataset approach. <i>Hepatology</i> , 2004, 39, 944-953.	3.6	98
822	Downregulation of tissue factor by RNA interference in human melanoma LOX-L cells reduces pulmonary metastasis in nude mice. <i>International Journal of Cancer</i> , 2004, 112, 994-1002.	2.3	39
823	Screening for control genes in rat global cerebral ischemia using high-density oligonucleotide array. <i>Journal of Neuroscience Research</i> , 2004, 76, 512-518.	1.3	19
824	Molecular evolution in the yeast transcriptional regulation network. <i>The Journal of Experimental Zoology</i> , 2004, 302B, 392-411.	1.4	38
825	The PlaNet Consortium: A Network of European Plant Databases Connecting Plant Genome Data in an Integrated Biological Knowledge Resource. <i>Comparative and Functional Genomics</i> , 2004, 5, 184-189.	2.0	6
826	Shaping Biological Knowledge: Applications in Proteomics. <i>Comparative and Functional Genomics</i> , 2004, 5, 190-195.	2.0	5
827	New Computational Tools for Brassica Genome Research. <i>Comparative and Functional Genomics</i> , 2004, 5, 276-280.	2.0	25
828	Mapping the Gene Ontology Into the Unified Medical Language System. <i>Comparative and Functional Genomics</i> , 2004, 5, 354-361.	2.0	35

#	ARTICLE	IF	CITATIONS
829	A critical and Integrated View of the Yeast Interactome. <i>Comparative and Functional Genomics</i> , 2004, 5, 382-402.	2.0	17
830	Comparative Analysis of the Testis and Ovary Transcriptomes in Zebrafish by Combining Experimental and Computational Tools. <i>Comparative and Functional Genomics</i> , 2004, 5, 403-418.	2.0	48
831	Biomedical Informatics and Granularity. <i>Comparative and Functional Genomics</i> , 2004, 5, 501-508.	2.0	29
832	Ontologies for the Description of Mouse Phenotypes. <i>Comparative and Functional Genomics</i> , 2004, 5, 545-551.	2.0	31
833	Obol: Integrating Language and Meaning in Bio-Ontologies. <i>Comparative and Functional Genomics</i> , 2004, 5, 509-520.	2.0	82
834	Ontology for Genome Comparison and Genomic Rearrangements. <i>Comparative and Functional Genomics</i> , 2004, 5, 537-544.	2.0	4
835	The Montagues and the Capulets. <i>Comparative and Functional Genomics</i> , 2004, 5, 623-632.	2.0	9
836	A short study on the success of the Gene Ontology. <i>Web Semantics</i> , 2004, 1, 235-240.	2.2	61
837	BioAmbients: an abstraction for biological compartments. <i>Theoretical Computer Science</i> , 2004, 325, 141-167.	0.5	354
838	Ontology concepts and tools for statistical genomics. <i>Journal of Multivariate Analysis</i> , 2004, 90, 213-228.	0.5	7
839	A strategy for identifying putative causes of gene expression variation in human cancers. <i>Journal of the Franklin Institute</i> , 2004, 341, 77-88.	1.9	21
840	Identification of related gene/protein names based on an HMM of name variations. <i>Computational Biology and Chemistry</i> , 2004, 28, 97-107.	1.1	17
841	INBIOMED: a platform for the integration and sharing of genetic, clinical and epidemiological data oriented to biomedical research. , 0, , .		2
842	Functional Proteomics Mapping of a Human Signaling Pathway. <i>Genome Research</i> , 2004, 14, 1324-1332.	2.4	278
843	A High-throughput Approach for Subcellular Proteome. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 441-455.	2.5	71
844	Comparative analysis of gene sets in the gene ontology space under the multiple hypothesis testing framework. , 2004, , 425-35.		21
845	Generation of Attribute Value Taxonomies from Data for Data-Driven Construction of Accurate and Compact Classifiers. , 0, , .		10
846	UniProt: the Universal Protein knowledgebase. <i>Nucleic Acids Research</i> , 2004, 32, 115D-119.	6.5	2,994

#	ARTICLE	IF	CITATIONS
847	EGOMiner: a comprehensive genomics and proteomics data analysis and biological function interpretation system. , 2004, 2004, 2809-12.		0
848	Linking molecular function and biological process terms in the ontology for gene expression data analysis. , 2004, 2004, 2984-6.		2
849	The 14-3-3 proteins in the teleost fish rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Journal of Experimental Biology</i> , 2004, 207, 3361-3368.	0.8	26
850	Genome-Scale Gene Function Prediction Using Multiple Sources of High-Throughput Data in Yeast <i>Saccharomyces cerevisiae</i> . <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 322-333.	1.0	51
851	Cluster analysis of the p53 genetic regulatory network: topology and biology. , 0, , .		6
852	Biomedical ontologies in post-genomic information systems. , 0, , .		2
853	AVT-NBL: An Algorithm for Learning Compact and Accurate Naïve Bayes Classifiers from Attribute Value Taxonomies and Data. , 0, , .		9
854	Cellular function prediction and biological pathway discovery in <i>Arabidopsis thaliana</i> using microarray data. , 2004, 2004, 2881-4.		6
855	In Vivo Epinephrine-Mediated Regulation of Gene Expression in Human Skeletal Muscle. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2004, 89, 2000-2014.	1.8	55
856	Gene Expression Profiling as a Diagnostic Tool in Acute Myeloid Leukemia. <i>Molecular Diagnosis and Therapy</i> , 2004, 4, 225-237.	3.3	6
857	Biomedical Literature Mining. <i>Molecular Diagnosis and Therapy</i> , 2004, 4, 383-393.	3.3	33
858	Comparative Analysis of Gene Expression for Convergent Evolution of Camera Eye Between Octopus and Human. <i>Genome Research</i> , 2004, 14, 1555-1561.	2.4	78
859	hMiDas and hMitChip: new opportunities in mitochondrial bioinformatics and genomic medicine. , 0, , .		3
860	A Knowledge-Based Clustering Algorithm Driven by Gene Ontology. <i>Journal of Biopharmaceutical Statistics</i> , 2004, 14, 687-700.	0.4	99
861	Inferring Cellular Networks Using Probabilistic Graphical Models. <i>Science</i> , 2004, 303, 799-805.	6.0	1,003
862	Assigning gene ontology categories (GO) to yeast genes using text-based supervised learning methods. , 0, , .		1
864	Comprehensive Proteomic Analysis of Human Pancreatic Juice. <i>Journal of Proteome Research</i> , 2004, 3, 1042-1055.	1.8	194
865	GENEVESTIGATOR. <i>Arabidopsis Microarray Database and Analysis Toolbox</i> . <i>Plant Physiology</i> , 2004, 136, 2621-2632.	2.3	2,232

#	ARTICLE	IF	CITATIONS
866	Identifying gene ontology concepts in natural-language text. , 2004, 2004, 2821-3.		3
867	Proteomic analysis of post-mitochondrial fractions of young and old rat kidney. <i>Experimental Gerontology</i> , 2004, 39, 1155-1155.	1.2	0
868	The Gene Ontology (GO) database and informatics resource. <i>Nucleic Acids Research</i> , 2004, 32, 258D-261.	6.5	3,462
869	<i>Schistosoma mansoni</i> genome project: an update. <i>Parasitology International</i> , 2004, 53, 183-192.	0.6	56
870	HIV-associated dementia, Alzheimer's disease, multiple sclerosis, and schizophrenia: gene expression review. <i>Journal of the Neurological Sciences</i> , 2004, 224, 3-17.	0.3	18
871	Large-scale isolation of ESTs from medaka embryos and its application to medaka developmental genetics. <i>Mechanisms of Development</i> , 2004, 121, 915-932.	1.7	93
872	Text analytics for life science using the Unstructured Information Management Architecture. <i>IBM Systems Journal</i> , 2004, 43, 490-515.	3.1	48
873	Alterations in the expression of DEAD-box and other RNA binding proteins during HIV-1 replication. <i>Retrovirology</i> , 2004, 1, 42.	0.9	47
874	Phenotype Characterisation Using Integrated Gene Transcript, Protein and Metabolite Profiling. <i>Applied Bioinformatics</i> , 2004, 3, 205-217.	1.7	60
875	GoSurfer. <i>Applied Bioinformatics</i> , 2004, 3, 261-264.	1.7	101
876	GeneDB: a resource for prokaryotic and eukaryotic organisms. <i>Nucleic Acids Research</i> , 2004, 32, 339D-343.	6.5	199
877	Structure-Based Partitioning of Large Concept Hierarchies. <i>Lecture Notes in Computer Science</i> , 2004, , 289-303.	1.0	108
878	Gene expression profile of omental adipose tissue in human obesity. <i>FASEB Journal</i> , 2004, 18, 215-217.	0.2	155
879	Towards ubiquitous bio-information computing: data protocols, middleware, and Web services for heterogeneous biological information integration and retrieval. , 0, , .		1
880	Evolving views of involution. <i>Breast Cancer Research</i> , 2004, 6, 89-92.	2.2	8
881	Gene expression profiling of mammary gland development reveals putative roles for death receptors and immune mediators in post-lactational regression. <i>Breast Cancer Research</i> , 2004, 6, R92.	2.2	295
882	Using ontologies to describe mouse phenotypes. <i>Genome Biology</i> , 2004, 6, R8.	13.9	191
883	The Mammalian Phenotype Ontology as a tool for annotating, analyzing and comparing phenotypic information. <i>Genome Biology</i> , 2004, 6, R7.	13.9	343

#	ARTICLE	IF	CITATIONS
884	A Drosophila protein-interaction map centered on cell-cycle regulators. <i>Genome Biology</i> , 2004, 5, R96.	3.8	172
885	GOToolBox: functional analysis of gene datasets based on Gene Ontology. <i>Genome Biology</i> , 2004, 5, R101.	13.9	319
886	A scale of functional divergence for yeast duplicated genes revealed from analysis of the protein-protein interaction network. <i>Genome Biology</i> , 2004, 5, R76.	13.9	36
887	Genome-wide mutagenesis of <i>Zea mays</i> L. using RescueMu transposons. <i>Genome Biology</i> , 2004, 5, R82.	13.9	66
888	An <i>Ambystoma mexicanum</i> EST sequencing project: analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema cDNA libraries. <i>Genome Biology</i> , 2004, 5, R67.	13.9	67
889	Function-informed transcriptome analysis of <i>Drosophila</i> renal tubule. <i>Genome Biology</i> , 2004, 5, R69.	13.9	192
890	A first-draft human protein-interaction map. <i>Genome Biology</i> , 2004, 5, r63.	13.9	188
891	Cross-species comparison of genome-wide expression patterns. <i>Genome Biology</i> , 2004, 5, 232.	13.9	42
892	Evolutionary conservation and selection of human disease gene orthologs in the rat and mouse genomes. <i>Genome Biology</i> , 2004, 5, R47.	13.9	116
893	A survey of ovary-, testis-, and soma-biased gene expression in <i>Drosophila melanogaster</i> adults. <i>Genome Biology</i> , 2004, 5, R40.	13.9	273
894	TXTGate: profiling gene groups with text-based information. <i>Genome Biology</i> , 2004, 5, R43.	13.9	59
895	The regulatory content of intergenic DNA shapes genome architecture. <i>Genome Biology</i> , 2004, 5, R25.	13.9	115
896	Defining a Molecular Atlas of the Hippocampus Using DNA Microarrays and High-Throughput In Situ Hybridization. <i>Journal of Neuroscience</i> , 2004, 24, 3879-3889.	1.7	255
897	ONCOMINE: A Cancer Microarray Database and Integrated Data-Mining Platform. <i>Neoplasia</i> , 2004, 6, 1-6.	2.3	3,212
898	Effect of linoleic acid on proliferation and gene expression in the breast cancer cell line T47D. <i>Cancer Letters</i> , 2004, 209, 25-35.	3.2	47
899	Cluster analysis of genes with significant change in expression in cells conditioned to survive TBOOH. <i>Experimental Eye Research</i> , 2004, 78, 301-308.	1.2	8
900	Bioinformatics and Systems Biology, rapidly evolving tools for interpreting plant response to global change. <i>Field Crops Research</i> , 2004, 90, 117-131.	2.3	11
901	Learning module networks from genome-wide location and expression data. <i>FEBS Letters</i> , 2004, 578, 297-304.	1.3	48

#	ARTICLE	IF	CITATIONS
902	Insight into <i>Trichoderma reesei</i> 's genome content, organization and evolution revealed through BAC library characterization. <i>Fungal Genetics and Biology</i> , 2004, 41, 1077-1087.	0.9	22
903	Response of rainbow trout transcriptome to model chemical contaminants. <i>Biochemical and Biophysical Research Communications</i> , 2004, 320, 745-753.	1.0	120
904	Prediction of protein subcellular locations by GO's PseAA predictor. <i>Biochemical and Biophysical Research Communications</i> , 2004, 320, 1236-1239.	1.0	165
905	A genome-wide and nonredundant mouse transcription factor database. <i>Biochemical and Biophysical Research Communications</i> , 2004, 322, 787-793.	1.0	137
906	Predicting 22 protein localizations in budding yeast. <i>Biochemical and Biophysical Research Communications</i> , 2004, 323, 425-428.	1.0	46
907	T lymphocyte activation gene identification by coregulated expression on DNA microarrays. <i>Genomics</i> , 2004, 83, 989-999.	1.3	73
908	Learnability-based further prediction of gene functions in Gene Ontology. <i>Genomics</i> , 2004, 84, 922-928.	1.3	21
909	Textmining in support of knowledge discovery for vaccine development. <i>Methods</i> , 2004, 34, 488-495.	1.9	8
910	Microarray analysis of the effect of diesel exhaust particles on in vitro cultured macrophages. <i>Toxicology in Vitro</i> , 2004, 18, 377-391.	1.1	35
911	The effect of the phytoestrogen coumestrol on the NZB/W F1 murine model of systemic lupus. <i>Journal of Autoimmunity</i> , 2004, 23, 323-332.	3.0	19
912	The promise of functional genomics: completing the encyclopedia of a cell. <i>Current Opinion in Microbiology</i> , 2004, 7, 546-554.	2.3	44
913	From wild wolf to domestic dog: gene expression changes in the brain. <i>Molecular Brain Research</i> , 2004, 126, 198-206.	2.5	128
914	Schistosome transcriptomes: new insights into the parasite and schistosomiasis. <i>Trends in Molecular Medicine</i> , 2004, 10, 217-225.	3.5	63
915	Exploring the sialome of the blood-sucking bug <i>Rhodnius prolixus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2004, 34, 61-79.	1.2	133
916	Genes transcribed in the salivary glands of female <i>Rhipicephalus appendiculatus</i> ticks infected with <i>Theileria parva</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2004, 34, 1117-1128.	1.2	98
917	Prediction and Functional Analysis of Native Disorder in Proteins from the Three Kingdoms of Life. <i>Journal of Molecular Biology</i> , 2004, 337, 635-645.	2.0	1,828
918	Quantifying Structure-Function Uncertainty: A Graph Theoretical Exploration into the Origins and Limitations of Protein Annotation. <i>Journal of Molecular Biology</i> , 2004, 337, 933-949.	2.0	14
919	A Description Scheme of Biological Processes Based on Elementary Bricks of Action. <i>Journal of Molecular Biology</i> , 2004, 339, 77-88.	2.0	9

#	ARTICLE	IF	CITATIONS
920	COMPARATIVE GENOMICS. Annual Review of Genomics and Human Genetics, 2004, 5, 15-56.	2.5	156
921	Studying dna microarray data using independent component analysis. , 0, , .		8
922	Genome-wide germline-enriched and sex-biased expression profiles in Caenorhabditis elegans. Development (Cambridge), 2004, 131, 311-323.	1.2	414
923	Methods in Comparative Genomics: Genome Correspondence, Gene Identification and Regulatory Motif Discovery. Journal of Computational Biology, 2004, 11, 319-355.	0.8	88
924	Annotating and mining the ligand-target chemogenomics knowledge space. Drug Discovery Today Biosilico, 2004, 2, 190-200.	0.7	25
925	Codifying bioinformatics processes without programming. Drug Discovery Today Biosilico, 2004, 2, 164-169.	0.7	2
926	PRISM: a new strategy to analyze the mammalian proteome. Drug Discovery Today: TARGETS, 2004, 3, 37-42.	0.5	0
927	Sister grouping of chimpanzees and humans as revealed by genome-wide phylogenetic analysis of brain gene expression profiles. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2957-2962.	3.3	213
928	Global regulation of erythroid gene expression by transcription factor GATA-1. Blood, 2004, 104, 3136-3147.	0.6	372
929	Regional Patterns of Gene Expression in Human and Chimpanzee Brains. Genome Research, 2004, 14, 1462-1473.	2.4	311
930	A module map showing conditional activity of expression modules in cancer. Nature Genetics, 2004, 36, 1090-1098.	9.4	622
931	Gene and Protein Profiling of the Response of MAâ€10 Leydig Tumor Cells to Human Chorionic Gonadotropin. Journal of Andrology, 2004, 25, 900-913.	2.0	26
932	Annotation of Parasite Genomes. , 2004, 270, 017-044.		8
933	ACLAME: A CLAssification of Mobile genetic Elements. Nucleic Acids Research, 2004, 32, 45D-49.	6.5	173
934	Extracting human protein interactions from MEDLINE using a full-sentence parser. Bioinformatics, 2004, 20, 604-611.	1.8	195
935	Comparative Genomic Analysis Identifies an ADP-Ribosylation Factorâ€like Gene as the Cause of Bardet-Biedl Syndrome (BBS3). American Journal of Human Genetics, 2004, 75, 475-484.	2.6	220
936	Genetic Variation in Radiation-Induced Expression Phenotypes. American Journal of Human Genetics, 2004, 75, 885-890.	2.6	57
937	A Methodology for Biologically Relevant Pattern Discovery from Gene Expression Data. Lecture Notes in Computer Science, 2004, , 230-241.	1.0	19

#	ARTICLE	IF	CITATIONS
938	Genomics and Proteomics: Design and Sources of Annotation. , 0, , 113-130.		0
939	Columba: Multidimensional Data Integration of Protein Annotations. Lecture Notes in Computer Science, 2004, , 156-171.	1.0	6
940	LinkSuiteTM: Formally Robust Ontology-Based Data and Information Integration. Lecture Notes in Computer Science, 2004, , 124-139.	1.0	5
941	Challenges in Genome-Wide Transcription Analysis when Using Microarrays for Non-Model Bacteria. Complexus, 2004, 2, 71-78.	0.7	0
942	Extracting and Explaining Biological Knowledge in Microarray Data. Lecture Notes in Computer Science, 2004, , 699-703.	1.0	6
943	Using Gen MAPP and MAPPFinder to View Microarray Data on Biological Pathways and Identify Global Trends in the Data. Current Protocols in Bioinformatics, 2004, 5, Unit 7.5.	25.8	10
944	Genomics of Preconditioning. Stroke, 2004, 35, 2683-2686.	1.0	84
945	Transcript Signatures in Experimental Asthma: Identification of STAT6-Dependent and -Independent Pathways. Journal of Immunology, 2004, 172, 1815-1824.	0.4	117
946	Using reasoning to guide annotation with gene ontology terms in GOAT. SIGMOD Record, 2004, 33, 27-32.	0.7	20
947	A three-layer multidatabase system for functional statistical analyses of microarray experiment results. , 2004, 2004, 2805-8.		0
948	The Use of Go Terms to Understand the Biological Significance of Microarray Differential Gene Expression Data. , 2004, , 233-247.		4
949	The RCSB Protein Data Bank: a redesigned query system and relational database based on the mmCIF schema. Nucleic Acids Research, 2004, 33, D233-D237.	6.5	303
950	KARMA: a web server application for comparing and annotating heterogeneous microarray platforms. Nucleic Acids Research, 2004, 32, W441-W444.	6.5	15
951	GOAL: automated Gene Ontology analysis of expression profiles. Nucleic Acids Research, 2004, 32, W492-W499.	6.5	40
952	Clustering Multi-represented Objects with Noise. Lecture Notes in Computer Science, 2004, , 394-403.	1.0	46
953	PSORTdb: a protein subcellular localization database for bacteria. Nucleic Acids Research, 2004, 33, D164-D168.	6.5	117
954	Data mining parasite genomes. Parasitology, 2004, 128, S23-S31.	0.7	5
955	RANDOM FOREST SIMILARITY FOR PROTEIN-PROTEIN INTERACTION PREDICTION FROM MULTIPLE SOURCES. , 2004, , .		78

#	ARTICLE	IF	CITATIONS
956	Gene expression profiling of normal and malignant CD34-derived megakaryocytic cells. <i>Blood</i> , 2004, 104, 3126-3135.	0.6	71
957	Analyzing Networks with VisANT. <i>Current Protocols in Bioinformatics</i> , 2004, 8, Unit 8.8.	25.8	13
959	Gene Discovery and Gene Expression in the Rice Blast Fungus, <i>Magnaporthe grisea</i> : Analysis of Expressed Sequence Tags. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 1337-1347.	1.4	83
960	Gene expression profile analysis of 4-phenylbutyrate treatment of IB3-1 bronchial epithelial cell line demonstrates a major influence on heat-shock proteins. <i>Physiological Genomics</i> , 2004, 16, 204-211.	1.0	75
961	DNA microarray analysis of neonatal mouse lung connects regulation of KDR with dexamethasone-induced inhibition of alveolar formation. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2004, 286, L411-L419.	1.3	43
962	EST-based Analysis of Gene Expression in the Porcine Brain. <i>Genomics, Proteomics and Bioinformatics</i> , 2004, 2, 237-244.	3.0	7
963	Searching the Mouse Genome Informatics (MGI) Resources for Information on Mouse Biology from Genotype to Phenotype. <i>Current Protocols in Bioinformatics</i> , 2004, 5, Unit 1.7.	25.8	10
964	Integrating Whole-Genome Expression Results into Metabolic Networks with Pathway Processor. <i>Current Protocols in Bioinformatics</i> , 2004, 5, Unit 7.6.	25.8	1
965	Impact of commensal microbiota on murine gastrointestinal tract gene ontologies. <i>Physiological Genomics</i> , 2004, 19, 22-31.	1.0	32
967	Bioinformatics: harvesting information for plant and crop science. <i>Seminars in Cell and Developmental Biology</i> , 2004, 15, 721-731.	2.3	4
968	Bayesian Decomposition Classification of the Project Normal Data Set. , 2004, , 211-231.		2
970	Design of KEGG and GO. , 2005, , .		0
972	Transcriptional Profile of NeuroD1 Expression in a Human Fetal Astroglial Cell Line. <i>Gene Expression</i> , 2005, 12, 123-136.	0.5	7
973	A semantic grid-based data access and integration service for bioinformatics. , 2005, , .		2
974	ConsDiff: an algorithm for the detection of conserved differences between protein sequences. <i>Data and Knowledge Engineering</i> , 2005, 53, 31-43.	2.1	0
975	Microarray analysis of gene expression following preparation of sterile intestinal loops in calves. <i>Canadian Journal of Animal Science</i> , 2005, 85, 13-22.	0.7	10
976	Gene expression profiling of muscle tissue in Brahman steers during nutritional restriction1. <i>Journal of Animal Science</i> , 2005, 83, 1-12.	0.2	109
978	Genes Associated with Prognosis in Adenocarcinoma Across Studies at Multiple Institutions. , 2005, , 239-253.		3

#	ARTICLE	IF	CITATIONS
979	Transcriptome Analysis of Human Colon Caco-2 Cells Exposed to Sulforaphane. <i>Journal of Nutrition</i> , 2005, 135, 1865-1872.	1.3	116
980	Unsupervised Machine Learning to Support Functional Characterization of Genes: Emphasis on Cluster Description and Class Discovery. , 2005, , 175-192.		0
981	Protein Interaction Prediction by Integrating Genomic Features and Protein Interaction Network Analysis. , 2005, , 61-81.		3
982	Ontologies and Functional Genomics. , 2005, , 99-112.		6
984	Interoperability of bioinformatics resources. <i>VINE: the Journal of Information and Knowledge Management Systems</i> , 2005, 35, 132-139.	1.0	2
985	Medical ontologies to support human disease research and control. <i>International Journal of Web and Grid Services</i> , 2005, 1, 139.	0.4	22
986	Automating Literature-Based Lead Discovery. <i>Frontiers in Medicinal Chemistry</i> , 2005, 1, 267-286.	0.2	0
988	Systems Biology: Applications in Drug Discovery. , 2005, , 123-183.		15
989	Using the Tools and Resources of the RCSB Protein Data Bank. <i>Current Protocols in Bioinformatics</i> , 2005, 9, 1.9.1.	25.8	1
990	A brief Perl tutorial for bioinformatics. , 2005, , .		0
991	EVALUATION OF LEXICAL METHODS FOR DETECTING RELATIONSHIPS BETWEEN CONCEPTS FROM MULTIPLE ONTOLOGIES. , 2005, , .		23
992	FINDING GENERIFS VIA GENE ONTOLOGY ANNOTATIONS. , 2005, , .		14
993	PHENOGO: ASSIGNING PHENOTYPIC CONTEXT TO GENE ONTOLOGY ANNOTATIONS WITH NATURAL LANGUAGE PROCESSING. , 2005, , .		24
994	PREDICTING GENE FUNCTIONS FROM TEXT USING A CROSS-SPECIES APPROACH. , 2005, , .		5
995	FAST, CHEAP AND OUT OF CONTROL: A ZERO CURATION MODEL FOR ONTOLOGY DEVELOPMENT. , 2005, , .		14
996	PUTTING SEMANTICS INTO THE SEMANTIC WEB: HOW WELL CAN IT CAPTURE BIOLOGY?. , 2005, , .		3
997	DISCOVERING REGULATED NETWORKS DURING HIV-1 LATENCY AND REACTIVATION. , 2005, , .		4
998	Proteomic Analysis and Extensive Protein Identification from Dry, Germinating Arabidopsis Seeds and Young Seedlings. <i>BMB Reports</i> , 2005, 38, 650-660.	1.1	35

#	ARTICLE	IF	CITATIONS
1001	Gene expression profiling of ovine skin and wool follicle development using a combined ovine - bovine skin cDNA microarray. <i>Australian Journal of Experimental Agriculture</i> , 2005, 45, 867.	1.0	16
1002	The Gene Ontology project. , 2005, , .		10
1003	Identification of Biological Relationships from Text Documents. , 2005, , 449-489.		7
1006	EXPLORING IMPORTANT ISSUES IN THE IMPLEMENTATION OF GENE SET ENRICHMENT ANALYSIS. , 2005, , .		0
1007	PROTEIN SUBCELLULAR LOCALIZATION PREDICTION WITH WOLF PSORT. , 2005, , .		84
1008	Leaky ribosomal scanning in mammalian genomes: significance of histone H4 alternative translation in vivo. <i>Nucleic Acids Research</i> , 2005, 33, 1298-1308.	6.5	31
1009	Grid Services Complemented by Domain Ontology Supporting Biomedical Community. <i>Lecture Notes in Computer Science</i> , 2005, , 86-98.	1.0	2
1010	Epistatic and Environmental Control of Genome-Wide Gene Expression. <i>Twin Research and Human Genetics</i> , 2005, 8, 5-15.	0.3	14
1011	Bioinformatics Challenges and Opportunities. , 2005, , 63-94.		1
1012	Weaning induces NOS-2 expression through NF- κ B modulation in the lactating mammary gland: importance of GSH. <i>Biochemical Journal</i> , 2005, 391, 581-588.	1.7	24
1013	Protein domains. , 2005, , .		0
1014	Predicting enzyme family classes by hybridizing gene product composition and pseudo-amino acid composition. <i>Journal of Theoretical Biology</i> , 2005, 234, 145-149.	0.8	90
1015	Contribution of the transcriptional regulator Leu3p to physiology and gene expression in nitrogen- and carbon-limited chemostat cultures. <i>FEMS Yeast Research</i> , 2005, 5, 885-897.	1.1	45
1016	Expressed sequence tags from life cycle stages of <i>Trichinella spiralis</i> : Application to biology and parasite control. <i>Veterinary Parasitology</i> , 2005, 132, 13-17.	0.7	21
1017	Molecular responses to xenoestrogens: Mechanistic insights from toxicogenomics. <i>Toxicology</i> , 2005, 213, 177-193.	2.0	55
1018	Tri-nucleotide repeats and their association with genes in rice genome. <i>BioSystems</i> , 2005, 82, 248-256.	0.9	5
1019	Diagonal reverse-phase chromatography applications in peptide-centric proteomics: Ahead of catalogue-omics?. <i>Analytical Biochemistry</i> , 2005, 345, 18-29.	1.1	70
1020	The transcriptional regulator pool of the marine bacterium <i>Rhodospirillum rubrum</i> revealed by whole genome comparisons. <i>FEMS Microbiology Letters</i> , 2005, 242, 137-145.	0.7	15

#	ARTICLE	IF	CITATIONS
1021	Unconventional systems analysis problems in molecular biology: a case study in gene regulatory network modeling. <i>Computers and Chemical Engineering</i> , 2005, 29, 547-563.	2.0	14
1022	Gene Expression in Stem Cell-Supporting Stromal Cell Lines. <i>Annals of the New York Academy of Sciences</i> , 2005, 1044, 159-167.	1.8	31
1023	Complete reannotation of the Arabidopsis genome: methods, tools, protocols and the final release. <i>BMC Biology</i> , 2005, 3, 7.	1.7	149
1024	Isolation and annotation of 10828 putative full length cDNAs from indica rice. <i>Science in China Series C: Life Sciences</i> , 2005, 48, 445.	1.3	17
1025	â€œBeijing Regionâ€ (3pter-D3S3397) of the Human Genome: Complete sequence and analysis. <i>Science in China Series C: Life Sciences</i> , 2005, 48, 311.	1.3	1
1026	Growing Applications and Advancements in Microarray Technology and Analysis Tools. <i>Cell Biochemistry and Biophysics</i> , 2005, 43, 149-166.	0.9	24
1027	Storage and Retrieval of Microarray Data and Open Source Microarray Database Software. <i>Molecular Biotechnology</i> , 2005, 30, 239-252.	1.3	11
1028	The Impact of the NIH Public Access Policy on Literature Informatics: What Role Can the Neuroinformaticists Play?. <i>Neuroinformatics</i> , 2005, 3, 081-092.	1.5	4
1029	Representation and Highâ€Quality Annotation of the <i>Physcomitrella patens</i> Transcriptome Demonstrates a High Proportion of Proteins Involved in Metabolism in Mosses. <i>Plant Biology</i> , 2005, 7, 238-250.	1.8	96
1030	The Search for Candidate Genes of Alcoholism: Evidence from Expression Profiling Studies. <i>Addiction Biology</i> , 2005, 10, 71-79.	1.4	29
1031	Transcriptional profiling using a novel cDNA array identifies differential gene expression during porcine embryo elongation. <i>Molecular Reproduction and Development</i> , 2005, 71, 129-139.	1.0	19
1032	Molecular Classification of Renal Tumors by Gene Expression Profiling. <i>Journal of Molecular Diagnostics</i> , 2005, 7, 206-218.	1.2	130
1033	Primary Differentiation in the Human Blastocyst: Comparative Molecular Portraits of Inner Cell Mass and Trophectoderm Cells. <i>Stem Cells</i> , 2005, 23, 1514-1525.	1.4	197
1034	Functional genomics databases on the web. <i>Cellular Microbiology</i> , 2005, 7, 1053-1059.	1.1	4
1035	Global transcript profiling of potato tuber using LongSAGE. <i>Plant Biotechnology Journal</i> , 2005, 3, 175-185.	4.1	24
1036	Dynamic changes in developmental gene expression in the basal chordate <i>Ciona intestinalis</i> . <i>Development Growth and Differentiation</i> , 2005, 47, 187-199.	0.6	16
1037	Screening for rapidly evolving genes in the ectomycorrhizal fungus <i>Paxillus involutus</i> using cDNA microarrays. <i>Molecular Ecology</i> , 2005, 15, 535-550.	2.0	33
1038	The search for genotype/phenotype associations and the phenome scan. <i>Paediatric and Perinatal Epidemiology</i> , 2005, 19, 264-275.	0.8	36

#	ARTICLE	IF	CITATIONS
1039	Gene expression profile identifies a rare epithelioid variant case of pleomorphic liposarcoma carrying FUS-CHOP transcript. <i>Histopathology</i> , 2005, 46, 334-341.	1.6	21
1040	Midgut and salivary gland transcriptomes of the arbovirus vector <i>Culicoides sonorensis</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overloc 81	1.0	81
1041	AnoBase: a genetic and biological database of anophelines. <i>Insect Molecular Biology</i> , 2005, 14, 591-597.	1.0	9
1042	Identification of hemoglobin-alpha and -beta subunits as potential serum biomarkers for the diagnosis and prognosis of ovarian cancer. <i>Cancer Science</i> , 2005, 96, 197-201.	1.7	71
1043	Highly conserved gene expression profiles in humans with allergic rhinitis altered by immunotherapy. <i>Clinical and Experimental Allergy</i> , 2005, 35, 1581-1590.	1.4	10
1044	Exploring functional relationships between components of the gene expression machinery. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 175-182.	3.6	89
1045	Gene expression profiling of noninvasive primary urothelial tumours using microarrays. <i>British Journal of Cancer</i> , 2005, 93, 1182-1190.	2.9	54
1046	Reverse engineering gene regulatory networks. <i>Nature Biotechnology</i> , 2005, 23, 554-555.	9.4	141
1047	Functional annotation and network reconstruction through cross-platform integration of microarray data. <i>Nature Biotechnology</i> , 2005, 23, 238-243.	9.4	137
1048	Minimum information requested in the annotation of biochemical models (MIRIAM). <i>Nature Biotechnology</i> , 2005, 23, 1509-1515.	9.4	553
1049	Mutation accumulation of the transcriptome. <i>Nature Genetics</i> , 2005, 37, 458-460.	9.4	9
1050	Epigenetics of hypertension in pregnancy. <i>Nature Genetics</i> , 2005, 37, 460-461.	9.4	18
1051	Complex trait analysis of gene expression uncovers polygenic and pleiotropic networks that modulate nervous system function. <i>Nature Genetics</i> , 2005, 37, 233-242.	9.4	695
1052	The transcriptional consequences of mutation and natural selection in <i>Caenorhabditis elegans</i> . <i>Nature Genetics</i> , 2005, 37, 544-548.	9.4	242
1053	A function for interleukin 2 in Foxp3-expressing regulatory T cells. <i>Nature Immunology</i> , 2005, 6, 1142-1151.	7.0	1,577
1054	Expression profiling reveals a distinct transcription signature in follicular thyroid carcinomas with a PAX8-PPAR γ fusion oncogene. <i>Oncogene</i> , 2005, 24, 1467-1476.	2.6	68
1055	Altered expression of cell cycle genes distinguishes aggressive neuroblastoma. <i>Oncogene</i> , 2005, 24, 1533-1541.	2.6	65
1056	G1/S transcriptional networks modulated by the HOX11/TLX1 oncogene of T-cell acute lymphoblastic leukemia. <i>Oncogene</i> , 2005, 24, 5561-5575.	2.6	45

#	ARTICLE	IF	CITATIONS
1057	7q deletion mapping and expression profiling in uterine fibroids. <i>Oncogene</i> , 2005, 24, 6545-6554.	2.6	33
1058	Two subclasses of lung squamous cell carcinoma with different gene expression profiles and prognosis identified by hierarchical clustering and non-negative matrix factorization. <i>Oncogene</i> , 2005, 24, 7105-7113.	2.6	90
1059	Expression Profiling in Alcoholism Research. <i>Alcoholism: Clinical and Experimental Research</i> , 2005, 29, 1066-1073.	1.4	6
1060	Cerebellar Gene Expression Profiling and eQTL Analysis in Inbred Mouse Strains Selected for Ethanol Sensitivity. <i>Alcoholism: Clinical and Experimental Research</i> , 2005, 29, 1568-1579.	1.4	22
1061	Comparative transcriptome analysis reveals significant differences in gene expression and signalling pathways between developmental and dark/starvation-induced senescence in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2005, 42, 567-585.	2.8	924
1062	Comparative gene expression profile of mouse carotid body and adrenal medulla under physiological hypoxia. <i>Journal of Physiology</i> , 2005, 566, 491-503.	1.3	37
1063	Patient-based cross-platform comparison of oligonucleotide microarray expression profiles. <i>Laboratory Investigation</i> , 2005, 85, 1024-1039.	1.7	56
1064	Highly coupled ATP synthesis by F1-ATPase single molecules. <i>Nature</i> , 2005, 433, 773-777.	13.7	380
1065	Microarray analysis shows that some microRNAs downregulate large numbers of target mRNAs. <i>Nature</i> , 2005, 433, 769-773.	13.7	4,435
1066	Predictive models of molecular machines involved in <i>Caenorhabditis elegans</i> early embryogenesis. <i>Nature</i> , 2005, 436, 861-865.	13.7	260
1067	Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005, 437, 69-87.	13.7	2,222
1068	A protein interaction network of the malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2005, 438, 103-107.	13.7	480
1069	The <i>Plasmodium</i> protein network diverges from those of other eukaryotes. <i>Nature</i> , 2005, 438, 108-112.	13.7	128
1070	A haplotype map of the human genome. <i>Nature</i> , 2005, 437, 1299-1320.	13.7	5,440
1071	High-throughput two-hybrid analysis. The promise and the peril. <i>FEBS Journal</i> , 2005, 272, 5391-5399.	2.2	163
1072	RATES OF DIVERGENCE IN GENE EXPRESSION PROFILES OF PRIMATES, MICE, AND FLIES: STABILIZING SELECTION AND VARIABILITY AMONG FUNCTIONAL CATEGORIES. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 126-137.	1.1	131
1073	EVOLUTION OF INSECT METAMORPHOSIS: A MICROARRAY-BASED STUDY OF LARVAL AND ADULT GENE EXPRESSION IN THE ANT <i>CAMPONOTUS FESTINATUS</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 858-870.	1.1	30
1074	Cellular process classification of human papillomavirus-16-positive SiHa cervical carcinoma cell using Gene Ontology. <i>International Journal of Gynecological Cancer</i> , 2005, 15, 94-106.	1.2	3

#	ARTICLE	IF	CITATIONS
1075	Gene expression of energy and protein metabolism in hearts of hypertensive nitric oxide- or GSH-depleted mice. <i>European Journal of Pharmacology</i> , 2005, 513, 21-33.	1.7	8
1076	Integration of tools and resources for display and analysis of genomic data for protozoan parasites. <i>International Journal for Parasitology</i> , 2005, 35, 481-493.	1.3	8
1077	Protozoan genomes: gene identification and annotation. <i>International Journal for Parasitology</i> , 2005, 35, 495-512.	1.3	13
1078	Identification of Transcriptional Regulatory Elements in Chemosensory Receptor Genes by Probabilistic Segmentation. <i>Current Biology</i> , 2005, 15, 347-352.	1.8	42
1079	Knowledge-assisted recognition of cluster boundaries in gene expression data. <i>Artificial Intelligence in Medicine</i> , 2005, 35, 171-183.	3.8	16
1080	Computational intelligence in solving bioinformatics problems. <i>Artificial Intelligence in Medicine</i> , 2005, 35, 1-8.	3.8	26
1081	Characterization of primitive marrow CD34+ cells that persist after a sublethal dose of total body irradiation. <i>Experimental Hematology</i> , 2005, 33, 1388-1401.	0.2	9
1082	Text-mining approaches in molecular biology and biomedicine. <i>Drug Discovery Today</i> , 2005, 10, 439-445.	3.2	121
1083	Biological networks and analysis of experimental data in drug discovery. <i>Drug Discovery Today</i> , 2005, 10, 653-662.	3.2	108
1084	PAX of mind for pathway researchers. <i>Drug Discovery Today</i> , 2005, 10, 937-942.	3.2	102
1085	Beyond annotation transfer by homology: novel protein-function prediction methods to assist drug discovery. <i>Drug Discovery Today</i> , 2005, 10, 1475-1482.	3.2	84
1086	Gene Expression Profiling in Murine Obliterative Airway Disease. <i>American Journal of Transplantation</i> , 2005, 5, 2170-2184.	2.6	16
1087	From worm to human: bioinformatics approaches to identify FOXO target genes. <i>Mechanisms of Ageing and Development</i> , 2005, 126, 209-215.	2.2	51
1088	Text-based analysis of genes, proteins, aging, and cancer. <i>Mechanisms of Ageing and Development</i> , 2005, 126, 193-208.	2.2	5
1089	Gene expression profiling in mouse lung following polymeric hexamethylene diisocyanate exposure. <i>Toxicology and Applied Pharmacology</i> , 2005, 205, 53-64.	1.3	17
1090	Clues to function in gene deserts. <i>Trends in Biotechnology</i> , 2005, 23, 269-271.	4.9	15
1091	Plant conserved non-coding sequences and paralogue evolution. <i>Trends in Genetics</i> , 2005, 21, 60-65.	2.9	147
1092	Enhancer sequence conservation between vertebrates is favoured in developmental regulator genes. <i>Trends in Genetics</i> , 2005, 21, 207-210.	2.9	59

#	ARTICLE	IF	CITATIONS
1093	Transcriptional analysis of in vivo <i>Plasmodium yoelii</i> liver stage gene expression. <i>Molecular and Biochemical Parasitology</i> , 2005, 142, 177-183.	0.5	41
1094	Restraint stress alters lung gene expression in an experimental influenza A viral infection. <i>Journal of Neuroimmunology</i> , 2005, 162, 103-111.	1.1	15
1095	Microarray analysis of differential gene expression in temporomandibular joint condylar cartilage after experimentally induced osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2005, 13, 1115-1125.	0.6	66
1096	Ontogeny of transcription profiles during mouse early craniofacial development. <i>Reproductive Toxicology</i> , 2005, 19, 339-352.	1.3	6
1097	Mapping molecular responses to xenoestrogens through Gene Ontology and pathway analysis of toxicogenomic data. <i>Reproductive Toxicology</i> , 2005, 20, 433-440.	1.3	31
1098	Predicting protein function from sequence and structural data. <i>Current Opinion in Structural Biology</i> , 2005, 15, 275-284.	2.6	280
1099	The study of metabolic pathways in tumors based on the transcriptome. <i>Seminars in Cancer Biology</i> , 2005, 15, 290-299.	4.3	12
1100	Ab initio identification of putative human transcription factor binding sites by comparative genomics. <i>BMC Bioinformatics</i> , 2005, 6, 110.	1.2	31
1101	AVID: an integrative framework for discovering functional relationships among proteins. <i>BMC Bioinformatics</i> , 2005, 6, 136.	1.2	34
1102	Satelloq: a database for the identification and prioritization of satellite repeats in disease association studies. <i>BMC Bioinformatics</i> , 2005, 6, 145.	1.2	16
1103	Alkahest NuclearBLAST : a user-friendly BLAST management and analysis system. <i>BMC Bioinformatics</i> , 2005, 6, 147.	1.2	7
1104	pSLIP: SVM based protein subcellular localization prediction using multiple physicochemical properties. <i>BMC Bioinformatics</i> , 2005, 6, 152.	1.2	74
1105	Tools enabling the elucidation of molecular pathways active in human disease: application to Hepatitis C virus infection. <i>BMC Bioinformatics</i> , 2005, 6, 154.	1.2	14
1106	Theme discovery from gene lists for identification and viewing of multiple functional groups. <i>BMC Bioinformatics</i> , 2005, 6, 162.	1.2	46
1107	Dissecting systems-wide data using mixture models: application to identify affected cellular processes. <i>BMC Bioinformatics</i> , 2005, 6, 177.	1.2	2
1108	FIGENIX: intelligent automation of genomic annotation: expertise integration in a new software platform. <i>BMC Bioinformatics</i> , 2005, 6, 198.	1.2	109
1109	stam—a Bioconductor compliant R package for structured analysis of microarray data. <i>BMC Bioinformatics</i> , 2005, 6, 211.	1.2	3
1110	Dynamic covariation between gene expression and proteome characteristics. <i>BMC Bioinformatics</i> , 2005, 6, 215.	1.2	9

#	ARTICLE	IF	CITATIONS
1111	Pathway level analysis of gene expression using singular value decomposition. BMC Bioinformatics, 2005, 6, 225.	1.2	332
1112	Systematic survey reveals general applicability of "guilt-by-association" within gene coexpression networks. BMC Bioinformatics, 2005, 6, 227.	1.2	370
1113	EXPANDER--an integrative program suite for microarray data analysis. BMC Bioinformatics, 2005, 6, 232.	1.2	283
1114	Alternative splicing and protein function. BMC Bioinformatics, 2005, 6, 266.	1.2	41
1115	ErmineJ: tool for functional analysis of gene expression data sets. BMC Bioinformatics, 2005, 6, 269.	1.2	233
1116	Commensurate distances and similar motifs in genetic congruence and protein interaction networks in yeast. BMC Bioinformatics, 2005, 6, 270.	1.2	20
1117	Automated methods of predicting the function of biological sequences using GO and BLAST. BMC Bioinformatics, 2005, 6, 272.	1.2	39
1118	Probabilistic annotation of protein sequences based on functional classifications. BMC Bioinformatics, 2005, 6, 302.	1.2	24
1119	Atlas - a data warehouse for integrative bioinformatics. BMC Bioinformatics, 2005, 6, 34.	1.2	110
1120	The use of edge-betweenness clustering to investigate biological function in protein interaction networks. BMC Bioinformatics, 2005, 6, 39.	1.2	166
1121	Towards precise classification of cancers based on robust gene functional expression profiles. BMC Bioinformatics, 2005, 6, 58.	1.2	146
1122	Statistical Viewer: a tool to upload and integrate linkage and association data as plots displayed within the Ensembl genome browser. BMC Bioinformatics, 2005, 6, 95.	1.2	11
1124	Learning Statistical Models for Annotating Proteins with Function Information using Biomedical Text. BMC Bioinformatics, 2005, 6, S18.	1.2	32
1125	Protein annotation as term categorization in the gene ontology using word proximity networks. BMC Bioinformatics, 2005, 6, S20.	1.2	31
1126	Data-poor categorization and passage retrieval for Gene Ontology Annotation in Swiss-Prot. BMC Bioinformatics, 2005, 6, S23.	1.2	27
1127	Automating Genomic Data Mining via a Sequence-based Matrix Format and Associative Rule Set. BMC Bioinformatics, 2005, 6, S2.	1.2	10
1128	ESTree db: a Tool for Peach Functional Genomics. BMC Bioinformatics, 2005, 6, S16.	1.2	38
1129	ParPEST: a pipeline for EST data analysis based on parallel computing. BMC Bioinformatics, 2005, 6, S9.	1.2	32

#	ARTICLE	IF	CITATIONS
1130	Transcribed Tc1-like transposons in salmonid fish. BMC Genomics, 2005, 6, 107.	1.2	42
1131	Laterally transferred elements and high pressure adaptation in <i>Photobacterium profundum</i> strains. BMC Genomics, 2005, 6, 122.	1.2	91
1132	XenDB: Full length cDNA prediction and cross species mapping in <i>Xenopus laevis</i> . BMC Genomics, 2005, 6, 123.	1.2	5
1133	Comparative analyses of six solanaceous transcriptomes reveal a high degree of sequence conservation and species-specific transcripts. BMC Genomics, 2005, 6, 124.	1.2	77
1134	GeneSeer: A sage for gene names and genomic resources. BMC Genomics, 2005, 6, 134.	1.2	7
1135	Genes involved in complex adaptive processes tend to have highly conserved upstream regions in mammalian genomes. BMC Genomics, 2005, 6, 168.	1.2	26
1136	An EST-based approach for identifying genes expressed in the intestine and gills of pre-smolt Atlantic salmon (<i>Salmo salar</i>). BMC Genomics, 2005, 6, 171.	1.2	22
1137	Gene expression in the brain and kidney of rainbow trout in response to handling stress. BMC Genomics, 2005, 6, 3.	1.2	130
1138	Gene expression signature of estrogen receptor α status in breast cancer. BMC Genomics, 2005, 6, 37.	1.2	126
1139	Comprehensive in silico functional specification of mouse retina transcripts. BMC Genomics, 2005, 6, 40.	1.2	14
1140	Investigating hookworm genomes by comparative analysis of two <i>Ancylostoma</i> species. BMC Genomics, 2005, 6, 58.	1.2	47
1141	Comparison of array-based comparative genomic hybridization with gene expression-based regional expression biases to identify genetic abnormalities in hepatocellular carcinoma. BMC Genomics, 2005, 6, 67.	1.2	34
1142	Expression profile of immune response genes in patients with Severe Acute Respiratory Syndrome. BMC Immunology, 2005, 6, 2.	0.9	263
1143	Expressed sequence tags from the oomycete fish pathogen <i>Saprolegnia parasitica</i> reveal putative virulence factors. BMC Microbiology, 2005, 5, 46.	1.3	90
1144	Floral gene resources from basal angiosperms for comparative genomics research. BMC Plant Biology, 2005, 5, 5.	1.6	100
1145	Differences in gene expression in prostate cancer, normal appearing prostate tissue adjacent to cancer and prostate tissue from cancer free organ donors. BMC Cancer, 2005, 5, 45.	1.1	126
1146	Response rate of fibrosarcoma cells to cytotoxic drugs on the expression level correlates to the therapeutic response rate of fibrosarcomas and is mediated by regulation of apoptotic pathways. BMC Cancer, 2005, 5, 74.	1.1	14
1147	Integrating biological research through Web services. Computer, 2005, 38, 26-31.	1.2	13

#	ARTICLE	IF	CITATIONS
1148	Data mining in protein interactomics. IEEE Engineering in Medicine and Biology Magazine, 2005, 24, 95-102.	1.1	10
1149	Indicative oligodendrocyte dysfunction in spinal cords of human fetuses suffering from a lethal motoneuron disease. Journal of Neurobiology, 2005, 65, 269-281.	3.7	8
1150	Activation of an energy providing response in human keratinocytes after \hat{I}^3 irradiation. Journal of Cellular Biochemistry, 2005, 95, 620-631.	1.2	19
1151	Molecular profile of catabolic versus anabolic treatment regimens of parathyroid hormone (PTH) in rat bone: An analysis by DNA microarray. Journal of Cellular Biochemistry, 2005, 95, 403-418.	1.2	92
1152	AML M3 and AML M3 variant each have a distinct gene expression signature but also share patterns different from other genetically defined AML subtypes. Genes Chromosomes and Cancer, 2005, 43, 113-127.	1.5	42
1153	Identification of genes involved in the initiation of human Th1 or Th2 cell commitment. European Journal of Immunology, 2005, 35, 3307-3319.	1.6	66
1154	Genome-wide response of the human Hep3B hepatoma cell to proinflammatory cytokines, from transcription to translation. Hepatology, 2005, 42, 946-955.	3.6	15
1155	Microarray-based gene expression profiling of benign, atypical and anaplastic meningiomas identifies novel genes associated with meningioma progression. International Journal of Cancer, 2005, 114, 249-256.	2.3	129
1156	Identification and validation of novel ERBB2 (HER2, NEU) targets including genes involved in angiogenesis. International Journal of Cancer, 2005, 114, 590-597.	2.3	53
1157	Gene expression differences over a critical period of afferent-dependent neuron survival in the mouse auditory brainstem. Journal of Comparative Neurology, 2005, 493, 460-474.	0.9	37
1158	Distributed robustness versus redundancy as causes of mutational robustness. BioEssays, 2005, 27, 176-188.	1.2	258
1159	Genescene: An ontology-enhanced integration of linguistic and co-occurrence based relations in biomedical texts. Journal of the Association for Information Science and Technology, 2005, 56, 457-468.	2.6	37
1160	Integrated bioinformatics application for automated target discovery. Journal of the Association for Information Science and Technology, 2005, 56, 483-492.	2.6	1
1161	Computational Analysis of Modular Protein Architectures. , 2005, , 439-476.		2
1162	Cerebral gene expression profiles in sporadic Creutzfeldt-Jakob disease. Annals of Neurology, 2005, 58, 242-257.	2.8	51
1163	Genome Sequencing and Analysis. , 2005, , 43-73.		5
1164	Differential gene expression in epidermis of mice sensitive and resistant to phorbol ester skin tumor promotion. Molecular Carcinogenesis, 2005, 44, 122-136.	1.3	29
1165	Towards a Semantic Lexicon for Biological Language Processing. Comparative and Functional Genomics, 2005, 6, 61-66.	2.0	11

#	ARTICLE	IF	CITATIONS
1166	The 8th Annual Bio-Ontologies Meeting. <i>Comparative and Functional Genomics</i> , 2005, 6, 370-372.	2.0	0
1167	Protein Evolution in the Context of <i>Drosophila</i> Development. <i>Journal of Molecular Evolution</i> , 2005, 60, 774-785.	0.8	54
1168	EST Sequencing from Embryogenic <i>Cyclamen persicum</i> Cell Cultures Identifies a High Proportion of Transcripts Homologous to Plant Genes Involved in Somatic Embryogenesis. <i>Journal of Plant Growth Regulation</i> , 2005, 24, 102-115.	2.8	37
1169	Bioinformatics and Proteomics Approaches for Aging Research. <i>Biogerontology</i> , 2005, 6, 227-232.	2.0	10
1170	Functional profiling of human atrial and ventricular gene expression. <i>Pflügers Archiv European Journal of Physiology</i> , 2005, 450, 201-208.	1.3	85
1171	Cycloheximide treatment of cotton ovules alters the abundance of specific classes of mRNAs and generates novel ESTs for microarray expression profiling. <i>Molecular Genetics and Genomics</i> , 2005, 274, 477-493.	1.0	21
1172	The effect of replicate number and image analysis method on sweetpotato [<i>Ipomoea batatas</i> (L.) Lam.] cDNA microarray results. <i>Plant Molecular Biology Reporter</i> , 2005, 23, 367-381.	1.0	1
1173	CandiVF – Candida albicans Virulence Factor Database. <i>International Journal of Peptide Research and Therapeutics</i> , 2005, 11, 271-277.	0.9	8
1174	Expression of copper-responsive genes in HepG2 cells. <i>Molecular and Cellular Biochemistry</i> , 2005, 279, 141-147.	1.4	27
1175	Towards Unraveling Ethanol-specific Neuro-metabolomics Based on Ethanol Responsive Genes In vivo. <i>Neurochemical Research</i> , 2005, 30, 1179-1190.	1.6	7
1176	Exercise responsive genes measured in peripheral blood of women with chronic fatigue syndrome and matched control subjects. <i>BMC Physiology</i> , 2005, 5, 5.	3.6	57
1177	Genome-wide characterization of gene expression variations and DNA copy number changes in prostate cancer cell lines. <i>Prostate</i> , 2005, 63, 187-197.	1.2	62
1178	Genome analysis and gene expression profiling of neuroblastoma and ganglioneuroblastoma reveal differences between neuroblastic and Schwannian stromal cells. <i>Journal of Pathology</i> , 2005, 207, 346-357.	2.1	36
1179	Identification and distribution of protein families in 120 completed genomes using Gene3D. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 603-615.	1.5	38
1180	A graph spectral analysis of the structural similarity network of protein chains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 152-163.	1.5	21
1181	Correspondence of function and phylogeny of ABC proteins based on an automated analysis of 20 model protein data sets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 888-899.	1.5	23
1182	Edge-count probabilities for the identification of local protein communities and their organization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 800-818.	1.5	31
1183	Computational reconstruction of the human skeletal muscle secretome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 776-792.	1.5	111

#	ARTICLE	IF	CITATIONS
1184	Proteomic analysis of plasma membrane vesicles isolated from the rat renal cortex. <i>Proteomics</i> , 2005, 5, 101-112.	1.3	61
1185	Proteome analysis of early somatic embryogenesis in <i>Picea glauca</i> . <i>Proteomics</i> , 2005, 5, 461-473.	1.3	166
1186	Changes in the proteomic profile during differentiation and maturation of human monocyte-derived dendritic cells stimulated with granulocyte macrophage colony stimulating factor/interleukin-4 and lipopolysaccharide. <i>Proteomics</i> , 2005, 5, 1186-1198.	1.3	74
1187	The human platelet proteome mapped by peptide-centric proteomics: A functional protein profile. <i>Proteomics</i> , 2005, 5, 3193-3204.	1.3	126
1188	A proteomic analysis of cold stress responses in rice seedlings. <i>Proteomics</i> , 2005, 5, 3162-3172.	1.3	302
1189	A proteomic analysis of salivary glands of female <i>Anopheles gambiae</i> mosquito. <i>Proteomics</i> , 2005, 5, 3765-3777.	1.3	63
1190	Plasma Proteome Database as a resource for proteomics research. <i>Proteomics</i> , 2005, 5, 3531-3536.	1.3	135
1191	A functional annotation of subproteomes in human plasma. <i>Proteomics</i> , 2005, 5, 3506-3519.	1.3	82
1192	Data management and preliminary data analysis in the pilot phase of the HUPO Plasma Proteome Project. <i>Proteomics</i> , 2005, 5, 3246-3261.	1.3	53
1193	Changes in adipose tissue gene expression with energy-restricted diets in obese women ¹⁴ . <i>American Journal of Clinical Nutrition</i> , 2005, 81, 1275-1285.	2.2	142
1194	microRNA Target Predictions across Seven <i>Drosophila</i> Species and Comparison to Mammalian Targets. <i>PLoS Computational Biology</i> , 2005, 1, e13.	1.5	393
1195	Coherent Expression Chromosome Cluster Analysis Reveals Differential Regulatory Functions of Amino-Terminal and Distal Parathyroid Hormone-Related Protein Domains in Prostate Carcinoma. <i>Journal of Biomedicine and Biotechnology</i> , 2005, 2005, 353-363.	3.0	5
1196	Functional genomics in <i>Saccharomyces cerevisiae</i> . , 2005, , .		0
1197	Functional inference from probabilistic protein interaction networks. , 2005, , .		0
1198	Microarray Annotation and Biological Information on Function. <i>Methods of Information in Medicine</i> , 2005, 44, 468-472.	0.7	5
1199	MEGO: gene functional module expression based on gene ontology. <i>BioTechniques</i> , 2005, 38, 277-283.	0.8	13
1200	Computational, Integrative, and Comparative Methods for the Elucidation of Genetic Coexpression Networks. <i>Journal of Biomedicine and Biotechnology</i> , 2005, 2005, 172-180.	3.0	29
1201	A Limited Autoimmunity to p185 ^{neu} Elicited by DNA and Allogeneic Cell Vaccine Hampers the Progression of Preneoplastic Lesions in HER-2/NEU Transgenic Mice. <i>International Journal of Immunopathology and Pharmacology</i> , 2005, 18, 351-363.	1.0	8

#	ARTICLE	IF	CITATIONS
1202	Hepatic Gene Expression Profiles Are Altered by Genistein Supplementation in Mice with Diet-Induced Obesity. <i>Journal of Nutrition</i> , 2005, 135, 33-41.	1.3	87
1203	Optimization and Applications. <i>Oberwolfach Reports</i> , 2005, 2, 69-133.	0.0	2
1205	Gene expression and phenotypic characterization of mouse heart after chronic constant or intermittent hypoxia. <i>Physiological Genomics</i> , 2005, 22, 292-307.	1.0	75
1206	Cellular process classification of human papillomavirus-16-positive SiHa cervical carcinoma cell using Gene Ontology. <i>International Journal of Gynecological Cancer</i> , 2005, 15, 94-106.	1.2	2
1209	Large-scale protein annotation. , 2005, , .		1
1210	Introduction to ontologies in biomedicine: from powertools to assistants. , 2005, , .		0
1212	Functional classification of proteins based on protein interaction data. , 2005, , .		0
1213	A Knowledge Integration Framework for Information Visualization. <i>Lecture Notes in Computer Science</i> , 2005, , 207-220.	1.0	7
1214	Identify lymphatic metastasis-associated genes in mouse hepatocarcinoma cell lines using gene chip. <i>World Journal of Gastroenterology</i> , 2005, 11, 1463.	1.4	43
1215	Tools and strategies for physiological genomics: the Rat Genome Database. <i>Physiological Genomics</i> , 2005, 23, 246-256.	1.0	25
1216	Androgen Control of Gene Expression in the Mouse Meibomian Gland. , 2005, 46, 3666.		80
1218	Differentially transcribed genes in skeletal muscle of Duroc and Taoyuan pigs1. <i>Journal of Animal Science</i> , 2005, 83, 2075-2086.	0.2	59
1219	Applications of Text Mining in Molecular Biology, from Name Recognition to Protein Interaction Maps. , 2005, , 41-59.		0
1220	Genomic Resources for Cancer Biologists. , 2005, , 3-17.		1
1221	Multi-represented kNN-Classification for Large Class Sets. <i>Lecture Notes in Computer Science</i> , 2005, , 511-522.	1.0	6
1222	A latent variable model for chemogenomic profiling. <i>Bioinformatics</i> , 2005, 21, 3286-3293.	1.8	53
1223	Information Extraction in the Life Sciences: Perspectives for Medicinal Chemistry, Pharmacology and Toxicology. <i>Current Topics in Medicinal Chemistry</i> , 2005, 5, 785-796.	1.0	16
1224	Differential Expression of Novel Potential Regulators in Hematopoietic Stem Cells. <i>PLoS Genetics</i> , 2005, 1, e28.	1.5	245

#	ARTICLE	IF	CITATIONS
1225	Improving the Precision of the Structureâ€“Function Relationship by Considering Phylogenetic Context. PLoS Computational Biology, 2005, 1, e9.	1.5	15
1226	Automatic extraction of gene/protein biological functions from biomedical text. Bioinformatics, 2005, 21, 1227-1236.	1.8	69
1227	Visualizing information across multidimensional post-genomic structured and textual databases. Bioinformatics, 2005, 21, 1659-1667.	1.8	14
1228	Steady-state effects of temperature acclimation on the transcriptome of the rainbow trout heart. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2005, 289, R1177-R1184.	0.9	114
1229	Network structures and algorithms in Bioconductor. Bioinformatics, 2005, 21, 135-136.	1.8	74
1230	Inference of transcriptional regulatory network by two-stage constrained space factor analysis. Bioinformatics, 2005, 21, 4033-4038.	1.8	62
1231	BarleyExpress: a web-based submission tool for enriched microarray database annotations. Bioinformatics, 2005, 21, 399-401.	1.8	9
1232	GOAnno: GO annotation based on multiple alignment. Bioinformatics, 2005, 21, 2095-2096.	1.8	36
1233	Co-occurrence based meta-analysis of scientific texts: retrieving biological relationships between genes. Bioinformatics, 2005, 21, 2049-2058.	1.8	56
1234	Microarray Data Analysis Using Neural Network Classifiers and Gene Selection Methods. , 2005, , 207-222.		5
1235	YeastHub: a semantic web use case for integrating data in the life sciences domain. Bioinformatics, 2005, 21, i85-i96.	1.8	88
1236	Balancing protein similarity and gene co-expression reveals new links between genetic conservation and developmental diversity in invertebrates. Bioinformatics, 2005, 21, 1550-1558.	1.8	15
1237	GandrKBâ€“ontological microarray annotation and visualization. Bioinformatics, 2005, 21, 2785-2786.	1.8	1
1238	TAMO: a flexible, object-oriented framework for analyzing transcriptional regulation using DNA-sequence motifs. Bioinformatics, 2005, 21, 3164-3165.	1.8	81
1239	MeSHer: identifying biological concepts in microarray assays based on PubMed references and MeSH terms. Bioinformatics, 2005, 21, 3324-3326.	1.8	18
1240	Butylhydroquinone Protects Cells Genetically Deficient in Glutathione Biosynthesis from Arsenite-Induced Apoptosis Without Significantly Changing Their Prooxidant Status. Toxicological Sciences, 2005, 87, 365-384.	1.4	50
1241	Study of coordinative gene expression at the biological process level. Bioinformatics, 2005, 21, 3651-3657.	1.8	11
1242	Gene Ontology Mapping as an Unbiased Method for Identifying Molecular Pathways and Processes Affected by Toxicant Exposure: Application to Acute Effects Caused by the Rodent Non-Genotoxic Carcinogen Diethylhexylphthalate. Toxicological Sciences, 2005, 86, 453-469.	1.4	62

#	ARTICLE	IF	CITATIONS
1243	Database of mRNA gene expression profiles of multiple human organs. <i>Genome Research</i> , 2005, 15, 443-450.	2.4	110
1244	BioMOBY Successfully Integrates Distributed Heterogeneous Bioinformatics Web Services. The PlaNet Exemplar Case. <i>Plant Physiology</i> , 2005, 138, 5-17.	2.3	84
1245	Cytoskeletal Rearrangements in Synovial Fibroblasts as a Novel Pathophysiological Determinant of Modeled Rheumatoid Arthritis. <i>PLoS Genetics</i> , 2005, 1, e48.	1.5	49
1246	Reduced-order modelling of biochemical networks: application to the GTPase-cycle signalling module. <i>IET Systems Biology</i> , 2005, 152, 229.	2.0	38
1247	Computational Modeling of Biological Processes with Petri Net-Based Architecture. , 2005, , 179-242.		6
1248	Time to Organize the Bioinformatics Resourceome. <i>PLoS Computational Biology</i> , 2005, 1, e76.	1.5	70
1249	Genome-Wide Requirements for Resistance to Functionally Distinct DNA-Damaging Agents. <i>PLoS Genetics</i> , 2005, 1, e24.	1.5	144
1250	Genes Induced by Reovirus Infection Have a Distinct Modular Cis- Regulatory Architecture. <i>Current Genomics</i> , 2005, 6, 501-513.	0.7	1
1251	Protein Molecular Function Prediction by Bayesian Phylogenomics. <i>PLoS Computational Biology</i> , 2005, 1, e45.	1.5	162
1252	Comparative Gene Expression Analysis by a Differential Clustering Approach: Application to the <i>Candida albicans</i> Transcription Program. <i>PLoS Genetics</i> , 2005, 1, e39.	1.5	124
1253	Functional Coverage of the Human Genome by Existing Structures, Structural Genomics Targets, and Homology Models. <i>PLoS Computational Biology</i> , 2005, 1, e31.	1.5	63
1254	Discovering molecular functions significantly related to phenotypes by combining gene expression data and biological information. <i>Bioinformatics</i> , 2005, 21, 2988-2993.	1.8	103
1255	Integration of GO annotations in Correspondence Analysis: facilitating the interpretation of microarray data. <i>Bioinformatics</i> , 2005, 21, 2424-2429.	1.8	30
1256	Formalizing concepts of species, sex and developmental stage in anatomical ontologies. <i>Bioinformatics</i> , 2005, 21, 2773-2779.	1.8	13
1257	Proteome Dynamics during C2C12 Myoblast Differentiation. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 887-901.	2.5	118
1258	Significance analysis of functional categories in gene expression studies: a structured permutation approach. <i>Bioinformatics</i> , 2005, 21, 1943-1949.	1.8	314
1259	On the quality of tree-based protein classification. <i>Bioinformatics</i> , 2005, 21, 1876-1890.	1.8	18
1260	Predicting protein localization in budding Yeast. <i>Bioinformatics</i> , 2005, 21, 944-950.	1.8	103

#	ARTICLE	IF	CITATIONS
1261	Evidence of a Large-Scale Functional Organization of Mammalian Chromosomes. <i>PLoS Genetics</i> , 2005, 1, e33.	1.5	88
1262	Functional Genomics of Blood Pressure Determination: Dissecting and Assembling a Polygenic Trait by Experimental Genetics. <i>Current Hypertension Reviews</i> , 2005, 1, 35-50.	0.5	14
1263	DPDB: a database for the storage, representation and analysis of polymorphism in the <i>Drosophila</i> genus. <i>Bioinformatics</i> , 2005, 21, ii26-ii30.	1.8	14
1264	GOChase: correcting errors from Gene Ontology-based annotations for gene products. <i>Bioinformatics</i> , 2005, 21, 829-831.	1.8	16
1265	Aberrant expression of neutrophil and macrophage-related genes in a murine model for human neutrophil-specific granule deficiency. <i>Journal of Leukocyte Biology</i> , 2005, 78, 1153-1165.	1.5	33
1266	Comparing the human and chimpanzee genomes: Searching for needles in a haystack. <i>Genome Research</i> , 2005, 15, 1746-1758.	2.4	265
1267	There's more to a model than code. , 2005, , .		0
1268	CRAVE: a database, middleware and visualization system for phenotype ontologies. <i>Bioinformatics</i> , 2005, 21, 1257-1262.	1.8	11
1269	Clusters of Co-expressed Genes in Mammalian Genomes Are Conserved by Natural Selection. <i>Molecular Biology and Evolution</i> , 2005, 22, 767-775.	3.5	154
1270	It's All GO for Plant Scientists. <i>Plant Physiology</i> , 2005, 138, 1268-1279.	2.3	35
1271	Genetical Genomics Analysis of a Yeast Segregant Population for Transcription Network Inference. <i>Genetics</i> , 2005, 170, 533-542.	1.2	90
1272	Munich Information Center for Protein Sequences Plant Genome Resources. A Framework for Integrative and Comparative Analyses. <i>Plant Physiology</i> , 2005, 138, 1301-1309.	2.3	13
1273	Gene-Expression Omnibus integration and clustering Tools in SeqExpress. <i>Bioinformatics</i> , 2005, 21, 2550-2551.	1.8	22
1274	DNA Microarray Analysis of Nitrogen Fixation and Fe(III) Reduction in <i>Geobacter sulfurreducens</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 2530-2538.	1.4	86
1275	The Arabidopsis genome: A foundation for plant research. <i>Genome Research</i> , 2005, 15, 1632-1642.	2.4	110
1276	The Spatial Organization of Lipid Synthesis in the Yeast <i>Saccharomyces cerevisiae</i> Derived from Large Scale Green Fluorescent Protein Tagging and High Resolution Microscopy. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 662-672.	2.5	150
1277	Mammalian male germ cells are fertile ground for expression profiling of sexual reproduction. <i>Reproduction</i> , 2005, 129, 1-7.	1.1	57
1278	The bioinformatics resource for oral pathogens. <i>Nucleic Acids Research</i> , 2005, 33, W734-W740.	6.5	36

#	ARTICLE	IF	CITATIONS
1279	Plant Protein Annotation in the UniProt Knowledgebase. <i>Plant Physiology</i> , 2005, 138, 59-66.	2.3	42
1280	RATES OF DIVERGENCE IN GENE EXPRESSION PROFILES OF PRIMATES, MICE, AND FLIES: STABILIZING SELECTION AND VARIABILITY AMONG FUNCTIONAL CATEGORIES. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 126.	1.1	33
1281	A network of transcriptionally coordinated functional modules in <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , 2005, 15, 1298-1306.	2.4	29
1282	Defining the mammalian CARome. <i>Genome Research</i> , 2005, 16, 197-207.	2.4	255
1283	Gene expression profiling of gilthead sea bream during early development and detection of stress-related genes by the application of cDNA microarray technology. <i>Physiological Genomics</i> , 2005, 23, 182-191.	1.0	71
1284	Binding sites for metabolic disease related transcription factors inferred at base pair resolution by chromatin immunoprecipitation and genomic microarrays. <i>Human Molecular Genetics</i> , 2005, 14, 3435-3447.	1.4	71
1285	Rates of Protein Evolution Are Positively Correlated with Developmental Timing of Expression During Mouse Spermatogenesis. <i>Molecular Biology and Evolution</i> , 2005, 22, 1044-1052.	3.5	94
1286	Influence of Androgens on Gene Expression in the BALB/c Mouse Submandibular Gland. <i>Journal of Dental Research</i> , 2005, 84, 1187-1192.	2.5	24
1287	EVOLUTION OF INSECT METAMORPHOSIS: A MICROARRAY-BASED STUDY OF LARVAL AND ADULT GENE EXPRESSION IN THE ANT <i>CAMPONOTUS FESTINATUS</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 858.	1.1	7
1288	Inverse Relationship Between Evolutionary Rate and Age of Mammalian Genes. <i>Molecular Biology and Evolution</i> , 2005, 22, 598-606.	3.5	152
1289	Gene Expression Profile Studies of Human Keratoconus Cornea for NEIBank: A Novel Cornea-Expressed Gene and the Absence of Transcripts for Aquaporin 5. , 2005, 46, 1239.		95
1290	Inferring gene transcriptional modulatory relations: a genetical genomics approach. <i>Human Molecular Genetics</i> , 2005, 14, 1119-1125.	1.4	76
1291	Identification of Transcriptional Networks during Liver Regeneration. <i>Journal of Biological Chemistry</i> , 2005, 280, 3715-3722.	1.6	107
1292	Molecular decomposition of complex clinical phenotypes using biologically structured analysis of microarray data. <i>Bioinformatics</i> , 2005, 21, 1971-1978.	1.8	38
1293	Differential Proteomic Analysis of Bronchoalveolar Lavage Fluid in Asthmatics following Segmental Antigen Challenge. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1251-1264.	2.5	150
1294	Genome Cluster Database. A Sequence Family Analysis Platform for Arabidopsis and Rice. <i>Plant Physiology</i> , 2005, 138, 47-54.	2.3	45
1295	Kernel methods for predicting protein-protein interactions. <i>Bioinformatics</i> , 2005, 21, i38-i46.	1.8	447
1296	Large-scale identification of yeast integral membrane protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12123-12128.	3.3	260

#	ARTICLE	IF	CITATIONS
1297	Novel specificities emerge by stepwise duplication of functional modules. <i>Genome Research</i> , 2005, 15, 552-559.	2.4	78
1298	Proton NMR spectroscopy shows lipids accumulate in skeletal muscle in response to burn trauma-induced apoptosis. <i>FASEB Journal</i> , 2005, 19, 1431-1440.	0.2	31
1299	Genome-wide regulatory complexity in yeast promoters: Separation of functionally conserved and neutral sequence. <i>Genome Research</i> , 2005, 15, 205-213.	2.4	43
1300	Discovering regulatory binding-site modules using rule-based learning. <i>Genome Research</i> , 2005, 15, 856-866.	2.4	41
1301	Transcriptome Profiles of Host Gene Expression in a Monkey Model of Human Malaria. <i>Journal of Infectious Diseases</i> , 2005, 191, 400-409.	1.9	26
1302	Calcineurin Triggers Reactive/Inflammatory Processes in Astrocytes and Is Upregulated in Aging and Alzheimer's Models. <i>Journal of Neuroscience</i> , 2005, 25, 4649-4658.	1.7	200
1303	Incorporating Biological Information as a Prior in an Empirical Bayes Approach to Analyzing Microarray Data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2005, 4, Article12.	0.2	19
1304	A semantic analysis of the annotations of the human genome. <i>Bioinformatics</i> , 2005, 21, 3416-3421.	1.8	61
1305	Object-oriented biological system integration: a SARS coronavirus example. <i>Bioinformatics</i> , 2005, 21, 2502-2509.	1.8	11
1306	BioLingua: a programmable knowledge environment for biologists. <i>Bioinformatics</i> , 2005, 21, 199-207.	1.8	37
1307	Comparison of Non-Human Primate and Human Whole Blood Tissue Gene Expression Profiles. <i>Toxicological Sciences</i> , 2005, 87, 306-314.	1.4	27
1308	The planarian <i>Schmidtea mediterranea</i> as a model for epigenetic germ cell specification: Analysis of ESTs from the hermaphroditic strain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18491-18496.	3.3	140
1309	GENE CLASSIFICATION USING EXPRESSION PROFILES: A FEASIBILITY STUDY. <i>International Journal on Artificial Intelligence Tools</i> , 2005, 14, 641-660.	0.7	30
1311	Mapping cis-regulatory domains in the human genome using multi-species conservation of synteny. <i>Human Molecular Genetics</i> , 2005, 14, 3057-3063.	1.4	70
1312	TO-GO: a Java-based Gene Ontology navigation environment. <i>Bioinformatics</i> , 2005, 21, 3580-3581.	1.8	5
1313	Widespread Correlations Between Dominance and Homozygous Effects of Mutations: Implications for Theories of Dominance. <i>Genetics</i> , 2005, 171, 385-392.	1.2	91
1314	Analysis of ARD1 Function in Hypoxia Response Using Retroviral RNA Interference*. <i>Journal of Biological Chemistry</i> , 2005, 280, 17749-17757.	1.6	84
1315	A Regulatory Network Analysis of Phenotypic Plasticity in Yeast. <i>American Naturalist</i> , 2005, 165, 515-523.	1.0	40

#	ARTICLE	IF	CITATIONS
1316	PACdb: PolyA Cleavage Site and 3'-UTR Database. <i>Bioinformatics</i> , 2005, 21, 3691-3693.	1.8	53
1317	AnoEST: Toward <i>A. gambiae</i> functional genomics. <i>Genome Research</i> , 2005, 15, 893-899.	2.4	19
1318	Identifying subtle interrelated changes in functional gene categories using continuous measures of gene expression. <i>Bioinformatics</i> , 2005, 21, 1129-1137.	1.8	61
1319	Learning computer programs with the bayesian optimization algorithm. , 2005, , .		26
1320	Construction of gene interaction and regulatory networks in bovine skeletal muscle from expression data. <i>Australian Journal of Experimental Agriculture</i> , 2005, 45, 821.	1.0	12
1321	Recent additions and improvements to the Onto-Tools. <i>Nucleic Acids Research</i> , 2005, 33, W762-W765.	6.5	106
1322	Large-scale databases in toxicogenomics. <i>Pharmacogenomics</i> , 2005, 6, 749-754.	0.6	12
1323	An information-driven approach to pharmacogenomics. <i>Pharmacogenomics</i> , 2005, 6, 473-480.	0.6	5
1324	Genomics of Basal Metazoans. <i>Integrative and Comparative Biology</i> , 2005, 45, 639-648.	0.9	8
1325	A criticality-based framework for task composition in multi-agent bioinformatics integration systems. <i>Bioinformatics</i> , 2005, 21, 3155-3163.	1.8	13
1326	Computational characterization of proteins. <i>Expert Review of Proteomics</i> , 2005, 2, 129-138.	1.3	1
1327	A Unique Role of Monocyte Chemoattractant Protein 1 among Chemokines in Adipose Tissue of Obese Subjects. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2005, 90, 5834-5840.	1.8	183
1328	Post-Genomic Design of Bioactive Molecules. <i>Current Computer-Aided Drug Design</i> , 2005, 1, 147-162.	0.8	0
1329	Regulation of Gene Expression in Magnocellular Neurons in Rat Supraoptic Nucleus during Sustained Hypoosmolality. <i>Endocrinology</i> , 2005, 146, 1254-1267.	1.4	27
1330	Comparative gene expression analysis of blood and brain provides concurrent validation of SELENBP1 up-regulation in schizophrenia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15533-15538.	3.3	306
1331	Research in Computational Molecular Biology. <i>Lecture Notes in Computer Science</i> , 2005, , .	1.0	2
1332	The next generation of literature analysis: Integration of genomic analysis into text mining. <i>Briefings in Bioinformatics</i> , 2005, 6, 287-297.	3.2	95
1333	An Integrated Cancer Biomarker Information System. , 2005, 2005, 2851-4.		2

#	ARTICLE	IF	CITATIONS
1334	Development of a Laboratory Information System for Cancer Collaboration Projects. , 2005, 2005, 2859-62.		20
1335	Functional specificity of shuttling hnRNPs revealed by genome-wide analysis of their RNA binding profiles. Rna, 2005, 11, 383-393.	1.6	88
1336	Response of the Lung to Pulmonary Insulin Dosing in the Rat Model and Effects of Changes in Formulation. Diabetes Technology and Therapeutics, 2005, 7, 516-524.	2.4	4
1337	Differential coexpression analysis using microarray data and its application to human cancer. Bioinformatics, 2005, 21, 4348-4355.	1.8	233
1338	Towards a SemanticWeb for Bioinformatics using Ontology-based Annotation. , 0, , .		16
1340	Functional Modularity in a Large-Scale Mammalian Molecular Interaction Network. , 0, , .		0
1341	Intrinsic Disorder and Prote in Modifications: Building an SVM Predictor for Methylation. , 2005, , .		28
1343	Protein structure and evolutionary history determine sequence space topology. Genome Research, 2005, 15, 385-392.	2.4	82
1344	Algorithms and Software for Collaborative Discovery from Autonomous, Semantically Heterogeneous, Distributed Information Sources. Lecture Notes in Computer Science, 2005, , 13-44.	1.0	14
1345	Clusters of Adjacent and Similarly Expressed Genes across Normal Human Tissues Complicate Comparative Transcriptomic Discovery. OMICS A Journal of Integrative Biology, 2005, 9, 351-363.	1.0	6
1346	A Novel Bioinformatics Technique For Predicting Condition-Specific Transcription Factor Binding Sites. , 2005, , .		0
1347	Gene Ontology Automatic Annotation Using a Domain Based Gene Product Similarity Measure. , 0, , .		5
1348	Characterizing the Grape Transcriptome. Analysis of Expressed Sequence Tags from Multiple Vitis Species and Development of a Compendium of Gene Expression during Berry Development. Plant Physiology, 2005, 139, 574-597.	2.3	159
1349	Bio-ontology construction using object-oriented paradigm. , 2005, , .		1
1350	A Discriminative Model for Identifying Spatial cis-Regulatory Modules. Journal of Computational Biology, 2005, 12, 822-834.	0.8	27
1351	Automated genome annotation and pathway identification using the KEGG Orthology (KO) as a controlled vocabulary. Bioinformatics, 2005, 21, 3787-3793.	1.8	3,124
1352	Modeling gene and genome duplications in eukaryotes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5454-5459.	3.3	850
1353	UTILIZING EVOLUTIONARY INFORMATION AND GENE EXPRESSION DATA FOR ESTIMATING GENE NETWORKS WITH BAYESIAN NETWORK MODELS. Journal of Bioinformatics and Computational Biology, 2005, 03, 1295-1313.	0.3	51

#	ARTICLE	IF	CITATIONS
1354	The Relationship Between Protein Sequence, Structure and Function. , 2005, , 15-29.		4
1355	Transcriptional Response of <i>Saccharomyces cerevisiae</i> to the Plasma Membrane-Perturbing Compound Chitosan. <i>Eukaryotic Cell</i> , 2005, 4, 703-715.	3.4	144
1356	Structure, function, and evolution of transient and obligate protein-protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10930-10935.	3.3	335
1357	Phenotypical Enrichment Strategies for Microarray Data Analysis Applied in a Type II Diabetes Study. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 251-265.	1.0	11
1358	Comparative Plant Genomics Resources at PlantGDB. <i>Plant Physiology</i> , 2005, 139, 610-618.	2.3	95
1359	Pathogenomics Analysis of <i>Leishmania</i> spp.: Flagellar Gene Families of Putative Virulence Factors. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 173-193.	1.0	9
1360	A mouse atlas of gene expression: Large-scale digital gene-expression profiles from precisely defined developing C57BL/6J mouse tissues and cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18485-18490.	3.3	112
1362	Gene Expression Profiling Reveals Multiple Protective Influences of the Peptide Î±-Melanocyte-Stimulating Hormone in Experimental Heart Transplantation. <i>Journal of Immunology</i> , 2005, 175, 3391-3401.	0.4	23
1363	Information-based clustering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18297-18302.	3.3	177
1365	Simvastatin attenuates vascular leak and inflammation in murine inflammatory lung injury. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2005, 288, L1026-L1032.	1.3	246
1366	<i>Drosophila melanogaster</i> : A case study of a model genomic sequence and its consequences. <i>Genome Research</i> , 2005, 15, 1661-1667.	2.4	69
1367	RNA expression profiling of normal and tumor cells following photodynamic therapy with 5-aminolevulinic acidâ€”induced protoporphyrin IX in vitro. <i>Molecular Cancer Therapeutics</i> , 2005, 4, 516-528.	1.9	42
1368	Expression Profiling of Rat Femur Revealed Suppression of Bone Formation Genes by Treatment with Alendronate and Estrogen but Not Raloxifene. <i>Molecular Pharmacology</i> , 2005, 68, 1225-1238.	1.0	24
1369	Elevated evolutionary rates in the laboratory strain of <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1092-1097.	3.3	90
1370	Molecular evidence for arterial repair in atherosclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16789-16794.	3.3	86
1371	Building a human kinase gene repository: Bioinformatics, molecular cloning, and functional validation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 8114-8119.	3.3	36
1373	Genes Regulated in Neurons Undergoing Transcription-dependent Apoptosis Belong to Signaling Pathways Rather than the Apoptotic Machinery. <i>Journal of Biological Chemistry</i> , 2005, 280, 5693-5702.	1.6	39
1374	Detecting clusters of different geometrical shapes in microarray gene expression data. <i>Bioinformatics</i> , 2005, 21, 1927-1934.	1.8	48

#	ARTICLE	IF	CITATIONS
1375	Accelerated Discovery of Novel Protein Function in Cultured Human Cells. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1319-1327.	2.5	24
1376	BABELOMICS: a suite of web tools for functional annotation and analysis of groups of genes in high-throughput experiments. <i>Nucleic Acids Research</i> , 2005, 33, W460-W464.	6.5	217
1377	GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data. <i>Nucleic Acids Research</i> , 2005, 33, W616-W620.	6.5	86
1378	Changing perspectives in yeast research nearly a decade after the genome sequence. <i>Genome Research</i> , 2005, 15, 1611-1619.	2.4	39
1379	A glimpse at the organization of the protein universe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5641-5642.	3.3	22
1380	Genome-wide analysis of cAMP-response element binding protein occupancy, phosphorylation, and target gene activation in human tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4459-4464.	3.3	878
1381	CLUSTERING AND RE-CLUSTERING FOR PATTERN DISCOVERY IN GENE EXPRESSION DATA. <i>Journal of Bioinformatics and Computational Biology</i> , 2005, 03, 281-301.	0.3	9
1382	An enhanced Java graph applet interface for visualizing interactomes. <i>Bioinformatics</i> , 2005, 21, 1741-1742.	1.8	7
1383	UBIC2 â€” TOWARDS UBIQUITOUS BIO-INFORMATION COMPUTING: DATA PROTOCOLS, MIDDLEWARE, AND WEB SERVICES FOR HETEROGENEOUS BIOLOGICAL INFORMATION INTEGRATION AND RETRIEVAL. <i>International Journal of Software Engineering and Knowledge Engineering</i> , 2005, 15, 475-485.	0.6	1
1384	Smart Graphics. <i>Lecture Notes in Computer Science</i> , 2005, , .	1.0	2
1385	Human T Lymphotropic Virus Type 1 Accessory Protein p12 Modulates Calcium-Mediated Cellular Gene Expression and Enhances p300 Expression in T Lymphocytes. <i>AIDS Research and Human Retroviruses</i> , 2005, 21, 273-284.	0.5	14
1386	Fractal Clustering and Knowledge-driven Validation Assessment for Gene Expression Profiling. , 2005, 2005, 4814-7.		0
1387	Improving Protein Function Prediction using the Hierarchical Structure of the Gene Ontology. , 2005, , .		54
1388	Ontology-Based Support for Human Disease Study. , 0, , .		23
1389	Pathway Analyst Automated Metabolic Pathway Prediction. , 2005, , .		6
1390	Knowledge-based computational search for genes associated with the metabolic syndrome. <i>Bioinformatics</i> , 2005, 21, 3146-3154.	1.8	17
1391	The promoters of human cell cycle genes integrate signals from two tumor suppressive pathways during cellular transformation. <i>Molecular Systems Biology</i> , 2005, 1, 2005.0022.	3.2	64
1393	Orthotopic Growth of Human Glioma Cells Quantitatively and Qualitatively Influences Radiation-Induced Changes in Gene Expression. <i>Cancer Research</i> , 2005, 65, 10389-10393.	0.4	47

#	ARTICLE	IF	CITATIONS
1394	In silico Analysis of 2085 Clones from a Normalized Rat Vestibular Periphery 3â€² cDNA Library. <i>Audiology and Neuro-Otology</i> , 2005, 10, 310-322.	0.6	8
1395	Structure and function of the human genome. <i>Genome Research</i> , 2005, 15, 1759-1766.	2.4	38
1396	DictyMOLD-a Dictyostelium discoideum genome browser database. <i>Bioinformatics</i> , 2005, 21, 696-697.	1.8	1
1397	Multi-way clustering of microarray data using probabilistic sparse matrix factorization. <i>Bioinformatics</i> , 2005, 21, i144-i151.	1.8	53
1398	Expression of cardiac myosin-binding protein-C (cMyBP-C) in <i>Drosophila</i> as a model for the study of human cardiomyopathies. <i>Human Molecular Genetics</i> , 2005, 14, 7-17.	1.4	12
1399	Assessing the limits of genomic data integration for predicting protein networks. <i>Genome Research</i> , 2005, 15, 945-953.	2.4	182
1400	Inferring combinatorial regulation of transcription in silico. <i>Nucleic Acids Research</i> , 2005, 33, 272-279.	6.5	51
1401	Development of Ewing's Sarcoma from Primary Bone Marrowâ€”Derived Mesenchymal Progenitor Cells. <i>Cancer Research</i> , 2005, 65, 11459-11468.	0.4	326
1402	The Predicted Impact of Coding Single Nucleotide Polymorphisms Database. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2005, 14, 2598-2604.	1.1	30
1403	Organ-Specific Expression of Arabidopsis Genome during Development. <i>Plant Physiology</i> , 2005, 138, 80-91.	2.3	164
1404	FPC Web Tools for Rice, Maize, and Distribution. <i>Plant Physiology</i> , 2005, 138, 116-126.	2.3	27
1405	Spliced-Leader trans-Splicing in Freshwater Planarians. <i>Molecular Biology and Evolution</i> , 2005, 22, 2048-2054.	3.5	36
1406	Gene function prediction from congruent synthetic lethal interactions in yeast. <i>Molecular Systems Biology</i> , 2005, 1, 2005.0026.	3.2	118
1407	In silico gene function prediction using ontology-based pattern identification. <i>Bioinformatics</i> , 2005, 21, 1237-1245.	1.8	74
1408	MEPD: a resource for medaka gene expression patterns. <i>Bioinformatics</i> , 2005, 21, 3195-3197.	1.8	24
1409	Transcriptional Profiling Reveals Complex Regulation of the Monocyte IL-1Î² System by IL-13. <i>Journal of Immunology</i> , 2005, 174, 834-845.	0.4	132
1410	Burn injury causes mitochondrial dysfunction in skeletal muscle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5368-5373.	3.3	93
1411	Effects of threshold choice on biological conclusions reached during analysis of gene expression by DNA microarrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 8961-8965.	3.3	98

#	ARTICLE	IF	CITATIONS
1412	Distinctions in the specificity of E2F function revealed by gene expression signatures. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15948-15953.	3.3	65
1413	Reduced Expression of the Insulin Receptor in Mouse Insulinoma (MIN6) Cells Reveals Multiple Roles of Insulin Signaling in Gene Expression, Proliferation, Insulin Content, and Secretion. Journal of Biological Chemistry, 2005, 280, 4992-5003.	1.6	86
1415	Gene clustering by Latent Semantic Indexing of MEDLINE abstracts. Bioinformatics, 2005, 21, 104-115.	1.8	150
1416	COBrA: a bio-ontology editor. Bioinformatics, 2005, 21, 825-826.	1.8	14
1417	Network constrained clustering for gene microarray data. Bioinformatics, 2005, 21, 4014-4020.	1.8	53
1418	The Institute for Genomic Research Osa1 Rice Genome Annotation Database. Plant Physiology, 2005, 138, 18-26.	2.3	201
1419	Conservation and Divergence of Light-Regulated Genome Expression Patterns during Seedling Development in Rice and Arabidopsis [W]. Plant Cell, 2005, 17, 3239-3256.	3.1	207
1420	Electronic Data Sources for Kinetic Models of Cell Signaling. Journal of Biochemistry, 2005, 137, 653-657.	0.9	8
1421	ArrayXPath II: mapping and visualizing microarray gene-expression data with biomedical ontologies and integrated biological pathway resources using Scalable Vector Graphics. Nucleic Acids Research, 2005, 33, W621-W626.	6.5	52
1422	Chlamydia trachomatis Variant with Nonfusing Inclusions: Growth Dynamic and Host-Cell Transcriptional Response. Journal of Infectious Diseases, 2005, 192, 1229-1236.	1.9	17
1423	Identification of differentially expressed proteins in oral squamous cell carcinoma using a global proteomic approach. International Journal of Oncology, 2005, 27, 59.	1.4	12
1424	Low-Dose Irradiation Alters the Transcript Profiles of Human Lymphoblastoid Cells Including Genes Associated with Cytogenetic Radioadaptive Response. Radiation Research, 2005, 164, 369-382.	0.7	125
1425	Resistance to Intestinal Entamoeba histolytica Infection Is Conferred by Innate Immunity and Gr-1 + Cells. Infection and Immunity, 2005, 73, 4522-4529.	1.0	83
1426	GenColors: accelerated comparative analysis and annotation of prokaryotic genomes at various stages of completeness. Bioinformatics, 2005, 21, 3669-3671.	1.8	16
1427	Fragnostic: walking through protein structure space. Nucleic Acids Research, 2005, 33, W249-W251.	6.5	22
1428	BRIGEP—the BRIDGE-based genome-transcriptome-proteome browser. Nucleic Acids Research, 2005, 33, W710-W716.	6.5	20
1429	GFINDER: genetic disease and phenotype location statistical analysis and mining of dynamically annotated gene lists. Nucleic Acids Research, 2005, 33, W717-W723.	6.5	61
1430	T-profiler: scoring the activity of predefined groups of genes using gene expression data. Nucleic Acids Research, 2005, 33, W592-W595.	6.5	190

#	ARTICLE	IF	CITATIONS
1431	Correlation between sequence conservation and the genomic context after gene duplication. <i>Nucleic Acids Research</i> , 2005, 33, 6164-6171.	6.5	38
1432	Nonsense-mediated mRNA decay factors act in concert to regulate common mRNA targets. <i>Rna</i> , 2005, 11, 1530-1544.	1.6	226
1433	Integrating protein annotation resources through the Distributed Annotation System. <i>Nucleic Acids Research</i> , 2005, 33, W468-W470.	6.5	20
1434	Identifying synonymous regulatory elements in vertebrate genomes. <i>Nucleic Acids Research</i> , 2005, 33, W403-W407.	6.5	20
1435	Analyzing the potato abiotic stress transcriptome using expressed sequence tags. <i>Genome</i> , 2005, 48, 598-605.	0.9	60
1436	BiNGO: a Cytoscape plugin to assess overrepresentation of Gene Ontology categories in Biological Networks. <i>Bioinformatics</i> , 2005, 21, 3448-3449.	1.8	3,901
1437	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , 2005, 15, 1034-1050.	2.4	3,517
1438	Genomic analysis of the response of mouse models to high-fat feeding shows a major role of nuclear receptors in the simultaneous regulation of lipid and inflammatory genes. <i>Atherosclerosis</i> , 2005, 182, 249-257.	0.4	34
1439	Identification of genes with a biocontrol function in <i>Trichoderma harzianum</i> mycelium using the expressed sequence tag approach. <i>Research in Microbiology</i> , 2005, 156, 416-423.	1.0	64
1440	The Proteomics Protocols Handbook. , 2005, , .		468
1441	Knowledge Management, Data Mining, and Text Mining in Medical Informatics. , 2005, , 3-33.		32
1444	Data Integration in the Life Sciences. <i>Lecture Notes in Computer Science</i> , 2005, , .	1.0	4
1445	Network constrained clustering for gene microarray data. , 0, , .		1
1446	Towards Interactive Exploration of Images, Meta-Data, and Analytic Results in the Open Microscopy Environment. , 0, , .		0
1447	A Novel Approach for Prediction of Multi-Labeled Protein Subcellular Localization for Prokaryotic Bacteria. , 0, , .		5
1448	Predicting Single Genes Related to Immune-Relevant Processes. , 2005, , .		0
1449	Hierarchy-Regularized Latent Semantic Indexing. , 0, , .		0
1450	Probabilistic Discovery of Overlapping Cellular Processes and Their Regulation. <i>Journal of Computational Biology</i> , 2005, 12, 909-927.	0.8	24

#	ARTICLE	IF	CITATIONS
1451	Correcting BLAST e-Values for Low-Complexity Segments. <i>Journal of Computational Biology</i> , 2005, 12, 980-1003.	0.8	10
1452	Abstracting Genes to Gene Ontology Terms Allows Comparison across Multiple Species. , 0, , .		1
1453	Cell intrinsic alterations underlie hematopoietic stem cell aging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 9194-9199.	3.3	972
1454	Clustering genes using gene expression and text literature data. , 2005, , 329-40.		6
1455	A Knowledge-Driven Method to Evaluate Multi-source Clustering. <i>Lecture Notes in Computer Science</i> , 2005, , 196-202.	1.0	1
1456	Combining Bayesian Networks and Decision Trees to Predict <i>Drosophila melanogaster</i> Protein-Protein Interactions. , 2005, , .		0
1457	Bayesian Decomposition Analysis of Bacterial Phylogenomic Profiles. <i>Molecular Diagnosis and Therapy</i> , 2005, 5, 63-70.	3.3	3
1458	Associative Clustering for Exploring Dependencies between Functional Genomics Data Sets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 203-216.	1.9	14
1459	The SOL Genomics Network. A Comparative Resource for Solanaceae Biology and Beyond. <i>Plant Physiology</i> , 2005, 138, 1310-1317.	2.3	398
1460	Direct Proteomic Mapping of <i>Streptomyces Luteogriseus</i> Strain 103 and <i>cnn1</i> and Insights into Antibiotic Biosynthesis. <i>Journal of Proteome Research</i> , 2005, 4, 1999-2006.	1.8	10
1461	The Subsystems Approach to Genome Annotation and its Use in the Project to Annotate 1000 Genomes. <i>Nucleic Acids Research</i> , 2005, 33, 5691-5702.	6.5	1,806
1462	CML tools and information flow in atomic scale simulations. <i>Molecular Simulation</i> , 2005, 31, 315-322.	0.9	9
1463	Functional ontologies for cognition: The systematic definition of structure and function. <i>Cognitive Neuropsychology</i> , 2005, 22, 262-275.	0.4	298
1464	Analyzing Gene Expression Time-Courses. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 179-193.	1.9	65
1465	Autophagy promotes MHC class II presentation of peptides from intracellular source proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7922-7927.	3.3	573
1466	WebGestalt: an integrated system for exploring gene sets in various biological contexts. <i>Nucleic Acids Research</i> , 2005, 33, W741-W748.	6.5	1,630
1467	Effective Pre-Processing Strategies for Functional Clustering of a Protein-Protein Interactions Network. , 0, , .		9
1468	Whole-proteome prediction of protein function via graph-theoretic analysis of interaction maps. <i>Bioinformatics</i> , 2005, 21, i302-i310.	1.8	421

#	ARTICLE	IF	CITATIONS
1469	Global Protein Shotgun Expression Profiling of Proliferating MCF-7 Breast Cancer Cells. <i>Journal of Proteome Research</i> , 2005, 4, 674-689.	1.8	33
1471	Advances in Toxicogenomics. <i>Chemical Research in Toxicology</i> , 2005, 18, 403-414.	1.7	59
1472	Phosphoproteome Analysis of HeLa Cells Using Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC). <i>Journal of Proteome Research</i> , 2005, 4, 1661-1671.	1.8	121
1473	Blast2GO: a universal tool for annotation, visualization and analysis in functional genomics research. <i>Bioinformatics</i> , 2005, 21, 3674-3676.	1.8	10,566
1474	Compositional Characterization of the Cytoskeleton of NK-Like Cells. <i>Journal of Proteome Research</i> , 2005, 4, 2081-2087.	1.8	23
1475	Analysis of differentially-regulated genes within a regulatory network by GPS genome navigation. <i>Bioinformatics</i> , 2005, 21, 4073-4083.	1.8	39
1476	Putting microarrays in a context: Integrated analysis of diverse biological data. <i>Briefings in Bioinformatics</i> , 2005, 6, 34-43.	3.2	60
1477	Global gene repression in hepatocellular carcinoma and fetal liver, and suppression of dudulin-2 mRNA as a possible marker for the cirrhosis-to-tumor transition. <i>Journal of Hepatology</i> , 2005, 42, 860-869.	1.8	29
1478	Genomic and functional characterization of stellate cells isolated from human cirrhotic livers. <i>Journal of Hepatology</i> , 2005, 43, 272-282.	1.8	78
1479	Mimicking Cellular Sorting Improves Prediction of Subcellular Localization. <i>Journal of Molecular Biology</i> , 2005, 348, 85-100.	2.0	273
1480	Mice with Ppt1 ^{ex4} mutation replicate the INCL phenotype and show an inflammation-associated loss of interneurons. <i>Neurobiology of Disease</i> , 2005, 18, 226-241.	2.1	73
1481	PABPN1 overexpression leads to upregulation of genes encoding nuclear proteins that are sequestered in oculopharyngeal muscular dystrophy nuclear inclusions. <i>Neurobiology of Disease</i> , 2005, 18, 551-567.	2.1	70
1482	Androgen regulation of gene expression in the mouse lacrimal gland. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2005, 96, 401-413.	1.2	29
1483	BmiGl: A database of cDNAs expressed in <i>Boophilus microplus</i> , the tropical/southern cattle tick. <i>Insect Biochemistry and Molecular Biology</i> , 2005, 35, 585-595.	1.2	72
1484	Transcriptional changes during neuronal death and replacement in the olfactory epithelium. <i>Molecular and Cellular Neurosciences</i> , 2005, 30, 90-107.	1.0	49
1485	Prediction of cis-regulatory elements using binding site matrices – the successes, the failures and the reasons for both. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 395-402.	1.5	57
1486	Simple sequence repeats in proteins and their significance for network evolution. <i>Gene</i> , 2005, 345, 113-118.	1.0	91
1487	The architecture of the protein domain universe. <i>Gene</i> , 2005, 347, 199-206.	1.0	19

#	ARTICLE	IF	CITATIONS
1488	Human genome-wide screen of haplotype-like blocks of reduced diversity. <i>Gene</i> , 2005, 349, 219-225.	1.0	43
1489	Broadly predicting specific gene functions with expression similarity and taxonomy similarity. <i>Gene</i> , 2005, 352, 75-81.	1.0	115
1490	List of lists-annotated (LOLA): A database for annotation and comparison of published microarray gene lists. <i>Gene</i> , 2005, 360, 78-82.	1.0	54
1491	A Human Protein-Protein Interaction Network: A Resource for Annotating the Proteome. <i>Cell</i> , 2005, 122, 957-968.	13.5	2,169
1492	Illuminating drug discovery with biological pathways. <i>FEBS Letters</i> , 2005, 579, 1872-1877.	1.3	100
1493	CO: A chemical ontology for identification of functional groups and semantic comparison of small molecules. <i>FEBS Letters</i> , 2005, 579, 4685-4691.	1.3	69
1494	2.45 GHz radiofrequency fields alter gene expression in cultured human cells. <i>FEBS Letters</i> , 2005, 579, 4829-4836.	1.3	79
1495	Comparative analysis of 87,000 expressed sequence tags from the fumonisin-producing fungus <i>Fusarium verticillioides</i> . <i>Fungal Genetics and Biology</i> , 2005, 42, 848-861.	0.9	91
1496	Analysis of Orthologous Gene Expression between Human Pulmonary Adenocarcinoma and a Carcinogen-Induced Murine Model. <i>American Journal of Pathology</i> , 2005, 167, 1763-1775.	1.9	269
1497	A 7872 cDNA microarray and its use in bovine functional genomics. <i>Veterinary Immunology and Immunopathology</i> , 2005, 105, 235-245.	0.5	52
1498	A robust hybrid between genetic algorithm and support vector machine for extracting an optimal feature gene subset. <i>Genomics</i> , 2005, 85, 16-23.	1.3	112
1499	Interpreting expression profiles of cancers by genome-wide survey of breadth of expression in normal tissues. <i>Genomics</i> , 2005, 86, 127-141.	1.3	230
1500	Nested genes in the human genome. <i>Genomics</i> , 2005, 86, 414-422.	1.3	71
1501	Assessment and integration of publicly available SAGE, cDNA microarray, and oligonucleotide microarray expression data for global coexpression analyses. <i>Genomics</i> , 2005, 86, 476-488.	1.3	44
1502	Studying phospholipid metabolism using yeast systematic and chemical genetics. <i>Methods</i> , 2005, 36, 102-108.	1.9	9
1503	Transcription factor gene expression profiling after acute intermittent nicotine treatment in the rat cerebral cortex. <i>Neuroscience</i> , 2005, 133, 787-796.	1.1	37
1504	Efficient Algorithms for Detecting Signaling Pathways in Protein Interaction Networks. <i>Lecture Notes in Computer Science</i> , 2005, , 1-13.	1.0	14
1505	Comparative analysis and characterization of expressed sequence tags in gilthead sea bream (<i>Sparus</i>) Tj ETQq1 1 0,784314 rgBT /Overl 1.7 84		

#	ARTICLE	IF	CITATIONS
1506	Transcriptome responses to carbon tetrachloride and pyrene in the kidney and liver of juvenile rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Aquatic Toxicology</i> , 2005, 74, 70-81.	1.9	71
1507	Nutrigenomics: The Impact of Biomics Technology on Nutrition Research. <i>Annals of Nutrition and Metabolism</i> , 2005, 49, 355-365.	1.0	98
1508	Evidence for a preferential targeting of 3'-UTRs by cis-encoded natural antisense transcripts. <i>Nucleic Acids Research</i> , 2005, 33, 5533-5543.	6.5	78
1509	Low-Dose Exposure to $\hat{1}^3$ Rays Induces Specific Gene Regulations in Normal Human Keratinocytes. <i>Radiation Research</i> , 2005, 163, 623-635.	0.7	96
1510	Molecular aging in human prefrontal cortex is selective and continuous throughout adult life. <i>Biological Psychiatry</i> , 2005, 57, 549-558.	0.7	202
1511	An atlas of differential gene expression during early <i>Xenopus</i> embryogenesis. <i>Mechanisms of Development</i> , 2005, 122, 365-439.	1.7	60
1512	Chapter 11 Protein bioinformatics. <i>Comprehensive Analytical Chemistry</i> , 2005, , 487-500.	0.7	0
1513	Protein Identification and Analysis Tools on the ExpASy Server. , 2005, , 571-607.		4,810
1514	The Arabidopsis Genome and Its Use in Cereal Genomics. , 2004, , 515-534.		0
1515	A global view of pleiotropy and phenotypically derived gene function in yeast. <i>Molecular Systems Biology</i> , 2005, 1, 2005.0001.	3.2	282
1516	ProFunc: a server for predicting protein function from 3D structure. <i>Nucleic Acids Research</i> , 2005, 33, W89-W93.	6.5	576
1517	Constructing and Analyzing a Large-Scale Gene-to-Gene Regulatory Network-Lasso-Constrained Inference and Biological Validation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 254-261.	1.9	74
1518	Data integration and visualization system for enabling conceptual biology. <i>Bioinformatics</i> , 2005, 21, i177-i185.	1.8	21
1519	Information Integration in Molecular Bioscience. <i>Applied Bioinformatics</i> , 2005, 4, 157-173.	1.7	8
1520	An Update on the Functional Molecular Immunology (FIMM) Database. <i>Applied Bioinformatics</i> , 2005, 4, 25-31.	1.7	15
1522	Sequence features in regions of weak and strong linkage disequilibrium. <i>Genome Research</i> , 2005, 15, 1519-1534.	2.4	89
1523	In Silico Reconstruction of the Metabolic Pathways of <i>Lactobacillus plantarum</i> : Comparing Predictions of Nutrient Requirements with Those from Growth Experiments. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7253-7262.	1.4	176
1524	Other Structure-Based Databases. <i>Methods of Biochemical Analysis</i> , 2005, , 217-236.	0.2	1

#	ARTICLE	IF	CITATIONS
1525	Reduction of Macrophage Infiltration and Chemoattractant Gene Expression Changes in White Adipose Tissue of Morbidly Obese Subjects After Surgery-Induced Weight Loss. <i>Diabetes</i> , 2005, 54, 2277-2286.	0.3	992
1527	Multidimensional protein identification technology: current status and future prospects. <i>Expert Review of Proteomics</i> , 2005, 2, 27-39.	1.3	35
1528	An Ontology-Driven Clustering Method for Supporting Gene Expression Analysis. , 0, , .		10
1530	Systematic analysis of gene expression in human brains before and after death. <i>Genome Biology</i> , 2005, 6, R112.	13.9	33
1531	Primary and secondary transcriptional effects in the developing human Down syndrome brain and heart. <i>Genome Biology</i> , 2005, 6, R107.	3.8	139
1532	Gene expression and metabolite profiling of <i>Populus euphratica</i> growing in the Negev desert. <i>Genome Biology</i> , 2005, 6, R101.	13.9	208
1533	Searching for differentially expressed gene combinations. <i>Genome Biology</i> , 2005, 6, R88.	13.9	57
1534	L2L: a simple tool for discovering the hidden significance in microarray expression data. <i>Genome Biology</i> , 2005, 6, R81.	13.9	111
1535	Tandem repeat copy-number variation in protein-coding regions of human genes. <i>Genome Biology</i> , 2005, 6, R69.	13.9	52
1536	Analysis of the <i>Macaca mulatta</i> transcriptome and the sequence divergence between <i>Macaca</i> and human. <i>Genome Biology</i> , 2005, 6, R60.	13.9	84
1537	Transcript copy number estimation using a mouse whole-genome oligonucleotide microarray. <i>Genome Biology</i> , 2005, 6, R61.	13.9	109
1538	Consolidating the set of known human protein-protein interactions in preparation for large-scale mapping of the human interactome. <i>Genome Biology</i> , 2005, 6, r40.	13.9	195
1539	Derivation of genetic interaction networks from quantitative phenotype data. <i>Genome Biology</i> , 2005, 6, R38.	13.9	114
1540	Pilot <i>Anopheles gambiae</i> full-length cDNA study: sequencing and initial characterization of 35,575 clones. <i>Genome Biology</i> , 2005, 6, R39.	13.9	21
1541	A DNA microarray survey of gene expression in normal human tissues. <i>Genome Biology</i> , 2005, 6, R22.	13.9	198
1542	Identifying genetic networks underlying myometrial transition to labor. <i>Genome Biology</i> , 2005, 6, R12.	13.9	65
1543	Genomic analysis of early murine mammary gland development using novel probe-level algorithms. <i>Genome Biology</i> , 2005, 6, R20.	13.9	17
1544	Fast and systematic genome-wide discovery of conserved regulatory elements using a non-alignment based approach. <i>Genome Biology</i> , 2005, 6, R18.	13.9	112

#	ARTICLE	IF	CITATIONS
1545	Gene expression profiling in murine autoimmune arthritis during the initiation and progression of joint inflammation. <i>Arthritis Research</i> , 2005, 7, R196.	2.0	34
1547	Pathway and gene-set activation measurement from mRNA expression data: the tissue distribution of human pathways. <i>Genome Biology</i> , 2006, 7, R93.	13.9	93
1548	PhyloFacts: an online structural phylogenomic encyclopedia for protein functional and structural classification. <i>Genome Biology</i> , 2006, 7, R83.	13.9	50
1549	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
1550	Shuffling of cis-regulatory elements is a pervasive feature of the vertebrate lineage. <i>Genome Biology</i> , 2006, 7, R56.	13.9	41
1551	Evolution of candidate transcriptional regulatory motifs since the human-chimpanzee divergence. <i>Genome Biology</i> , 2006, 7, R52.	13.9	16
1552	RNA editing of human microRNAs. <i>Genome Biology</i> , 2006, 7, R27.	13.9	295
1553	Comparative analysis of <i>Saccharomyces cerevisiae</i> WW domains and their interacting proteins. <i>Genome Biology</i> , 2006, 7, R30.	13.9	52
1554	Genes regulated by estrogen in breast tumor cells in vitro are similarly regulated in vivo in tumor xenografts and human breast tumors. <i>Genome Biology</i> , 2006, 7, R28.	13.9	108
1555	Deciphering cellular states of innate tumor drug responses. <i>Genome Biology</i> , 2006, 7, R19.	13.9	110
1556	Modulation of the transcription regulatory program in yeast cells committed to sporulation. <i>Genome Biology</i> , 2006, 7, R20.	13.9	63
1557	<i>Anopheles gambiae</i> genome reannotation through synthesis of ab initio and comparative gene prediction algorithms. <i>Genome Biology</i> , 2006, 7, R24.	13.9	18
1558	Effect of infliximab on mRNA expression profiles in synovial tissue of rheumatoid arthritis patients. <i>Arthritis Research and Therapy</i> , 2006, 8, R179.	1.6	72
1559	A model of anti-angiogenesis: differential transcriptosome profiling of microvascular endothelial cells from diffuse systemic sclerosis patients. <i>Arthritis Research and Therapy</i> , 2006, 8, R115.	1.6	56
1560	Variability in synovial inflammation in rheumatoid arthritis investigated by microarray technology. <i>Arthritis Research and Therapy</i> , 2006, 8, R47.	1.6	46
1561	A Survey of mRNA Sequences with a Non-AUG Start Codon in RefSeq Database. <i>Journal of Biomolecular Structure and Dynamics</i> , 2006, 24, 33-41.	2.0	37
1563	Concept of Sample in OMICS Technology. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 127-137.	1.0	44
1565	Ontology Annotation Treebrowser. <i>Applied Bioinformatics</i> , 2006, 5, 225-236.	1.7	12

#	ARTICLE	IF	CITATIONS
1567	Integration of a Two-Phase Partition Method into Proteomics Research on Rat Liver Plasma Membrane Proteins. <i>Journal of Proteome Research</i> , 2006, 5, 634-642.	1.8	83
1568	Molecular Profiling of Hepatocellular Carcinoma in Mice with a Chronic Deficiency of Hepatic S-Adenosylmethionine: A Relevance in Human Liver Diseases. <i>Journal of Proteome Research</i> , 2006, 5, 944-953.	1.8	18
1569	Hotspots for copy number variation in chimpanzees and humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8006-8011.	3.3	231
1570	Analyzing the Cardiac Muscle Proteome by Liquid Chromatography-Mass Spectrometry-Based Expression Proteomics. , 2007, 357, 15-32.		16
1571	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
1572	The dopamine D3 receptor plays an essential role in alcohol seeking and relapse. <i>FASEB Journal</i> , 2006, 20, 2223-2233.	0.2	105
1573	Functional genomics and proteomics in the clinical neurosciences: data mining and bioinformatics. <i>Progress in Brain Research</i> , 2006, 158, 83-108.	0.9	28
1575	Mining Gene Expression Profiles with Biological Prior Knowledge. , 2006, , .		1
1576	Gene Lethality Detection and Characterization via Topological Analysis of Regulatory Networks. <i>IEEE Transactions on Circuits and Systems Part 1: Regular Papers</i> , 2006, 53, 2438-2443.	0.1	3
1577	springScape: visualisation of microarray and contextual bioinformatic data using spring embedding and an 'information landscape'. <i>Bioinformatics</i> , 2006, 22, e99-e107.	1.8	22
1578	Heraclitus II: A Framework for Ontology Management and Evolution. , 2006, , .		13
1579	Biclustor Analysis of Genome-Wide Gene Expression. , 2006, , .		4
1580	Keeping Track of Changes in Database Schemas and Related Ontologies. , 0, , .		2
1581	Reconstruct feedback control of cell cycle-regulated networks of the yeast by neural network computing. , 2006, , .		0
1582	A Comparative Study on Feature Extraction from Protein Sequences for Subcellular Localization Prediction. , 2006, , .		8
1583	Semantic Model to Integrate Biological Resources. , 2006, , .		10
1584	Using Ontology Visualization to Coordinate Cross-species Functional Annotation for Human Disease Genes. , 2006, , .		2
1585	A Coevolution Approach for Database Schemas and Related Ontologies. , 2006, , .		12

#	ARTICLE	IF	CITATIONS
1586	Diffusion Kernel-Based Logistic Regression Models for Protein Function Prediction. OMICS A Journal of Integrative Biology, 2006, 10, 40-55.	1.0	90
1589	Scaling Laws in the Functional Content of Genomes. , 2006, , 236-253.		14
1592	Identifying Complex Biological Interactions based on Categorical Gene Expression Data. , 0, , .		4
1593	Efficient Algorithms for Detecting Signaling Pathways in Protein Interaction Networks. Journal of Computational Biology, 2006, 13, 133-144.	0.8	225
1594	Data Standards: A Call to Action. OMICS A Journal of Integrative Biology, 2006, 10, 94-99.	1.0	50
1595	A Special Issue on Data Standards. OMICS A Journal of Integrative Biology, 2006, 10, 84-93.	1.0	46
1596	Semantic Map of Services for Structural Bioinformatics. , 0, , .		9
1597	Biological network epitomes via topological compression. , 2006, , .		0
1598	A Language Modeling Text Mining Approach to the Annotation of Protein Community. , 2006, , .		2
1599	Advances in Protein Ontology Project. , 2006, , .		6
1600	Escherichia coli K-12: a cooperatively developed annotation snapshot--2005. Nucleic Acids Research, 2006, 34, 1-9.	6.5	606
1601	Brain-Gene Ontology: Integrating Bioinformatics and Neuroinformatics Data, Information and Knowledge to Enable Discoveries. , 2006, , .		2
1602	Fast and Accurate Method for Identifying High-Quality Protein-Interaction Modules by Clique Merging and Its Application to Yeast. Journal of Proteome Research, 2006, 5, 801-807.	1.8	22
1603	An Architecture for Visualisation and Interactive Analysis of Proteins. , 0, , .		5
1604	A Systematic Approach for Identifying Regulatory Interactions in Large Temporal Gene Expression Datasets from Peripheral Blood. , 2006, , .		0
1605	CAGE Basic/Analysis Databases: the CAGE resource for comprehensive promoter analysis. Nucleic Acids Research, 2006, 34, D632-D636.	6.5	78
1606	Gene function correlates with potential for G4 DNA formation in the human genome. Nucleic Acids Research, 2006, 34, 3887-3896.	6.5	452
1607	Visualization of complementary systems biology data with parallel heatmaps. IBM Journal of Research and Development, 2006, 50, 575-581.	3.2	6

#	ARTICLE	IF	CITATIONS
1608	A Computational Inference Framework for analyzing Gene Regulation Pathway using Microarray Data. , 2006, , .		0
1609	Graph data management for molecular and cell biology. IBM Journal of Research and Development, 2006, 50, 545-560.	3.2	32
1610	sgTarget: a target selection resource for structural genomics. Nucleic Acids Research, 2006, 34, W225-W230.	6.5	6
1611	Predicting Protein-Protein Interactions from Sequences in a Hybridization Space. Journal of Proteome Research, 2006, 5, 316-322.	1.8	158
1612	Topological Properties of Protein-Protein and Metabolic Interaction Networks of Drosophila melanogaster. Genomics, Proteomics and Bioinformatics, 2006, 4, 80-89.	3.0	6
1613	A Network Partition Algorithm for Mining Gene Functional Modules of Colon Cancer from DNA Microarray Data. Genomics, Proteomics and Bioinformatics, 2006, 4, 245-252.	3.0	7
1614	Seasonally hibernating phenotype assessed through transcript screening. Physiological Genomics, 2006, 24, 13-22.	1.0	138
1615	Novel β 1-Adrenergic Receptor Signaling Pathways: Secreted Factors and Interactions with the Extracellular Matrix. Molecular Pharmacology, 2006, 70, 129-142.	1.0	18
1616	The New Bioinformatics: Integrating Ecological Data from the Gene to the Biosphere. Annual Review of Ecology, Evolution, and Systematics, 2006, 37, 519-544.	3.8	164
1617	Jointly Analyzing Gene Expression and Copy Number Data in Breast Cancer Using Data Reduction Models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 2-16.	1.9	40
1618	Conservation and evolution of gene coexpression networks in human and chimpanzee brains. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17973-17978.	3.3	580
1619	Comparison and validation of community structures in complex networks. Physica A: Statistical Mechanics and Its Applications, 2006, 367, 559-576.	1.2	54
1620	Lymphoblastoid cell lines differing in p53 status show clear differences in basal gene expression with minor changes after irradiation. Radiotherapy and Oncology, 2006, 80, 236-249.	0.3	18
1621	Hepatic gene expression profile associated with non-alcoholic steatohepatitis protection by S-nitroso-N-acetylcysteine in ob/ob mice. Journal of Hepatology, 2006, 45, 725-733.	1.8	22
1622	Inhibition of Androgen-Independent Prostate Cancer by Estrogenic Compounds Is Associated with Increased Expression of Immune-Related Genes. Neoplasia, 2006, 8, 862-878.	2.3	28
1624	In vitro and in vivo effects of the PPAR-alpha agonists fenofibrate and retinoic acid in endometrial cancer. Molecular Cancer, 2006, 5, 13.	7.9	81
1625	Induction of the HIV-1 Tat co-factor cyclin T1 during monocyte differentiation is required for the regulated expression of a large portion of cellular mRNAs. Retrovirology, 2006, 3, 32.	0.9	25
1626	Transposable element derived DNaseI-hypersensitive sites in the human genome. Biology Direct, 2006, 1, 20.	1.9	33

#	ARTICLE	IF	CITATIONS
1627	Pathway Mapping Tools for Analysis of High Content Data. , 2007, 356, 319-350.		206
1628	[9] TM4 Microarray Software Suite. Methods in Enzymology, 2006, 411, 134-193.	0.4	1,767
1629	Counting the Zinc-Proteins Encoded in the Human Genome. Journal of Proteome Research, 2006, 5, 196-201.	1.8	887
1630	Schizosaccharomyces pombe comparative genomics; from sequence to systems. , 0, , 233-285.		21
1631	Metabolomic approaches to phenotype characterization and applications to complex diseases. Expert Review of Molecular Diagnostics, 2006, 6, 575-585.	1.5	84
1632	[22] Visualizing Networks. Methods in Enzymology, 2006, 411, 408-421.	0.4	20
1633	[21] Clustering Methods for Analyzing Large Data Sets: Gonad Development, A Study Case. Methods in Enzymology, 2006, 411, 387-407.	0.4	4
1634	Genome Wide Gene Expression Studies in Mood Disorders. OMICS A Journal of Integrative Biology, 2006, 10, 444-454.	1.0	53
1635	Zinc through the Three Domains of Life. Journal of Proteome Research, 2006, 5, 3173-3178.	1.8	544
1636	Identification of a Common Gene Expression Signature in Dilated Cardiomyopathy Across Independent Microarray Studies. Journal of the American College of Cardiology, 2006, 48, 1610-1617.	1.2	153
1637	Prediction and classification of protein functions. Drug Discovery Today: Technologies, 2006, 3, 145-151.	4.0	16
1638	Altered gene expression of transcriptional regulatory factors in tumor marker-positive cells during chemically induced hepatocarcinogenesis. Toxicology Letters, 2006, 167, 106-113.	0.4	16
1639	A Chick Retinal Proteome Database and Differential Retinal Protein Expressions during Early Ocular Development. Journal of Proteome Research, 2006, 5, 771-784.	1.8	35
1640	Large-Scale Predictions of Gram-Negative Bacterial Protein Subcellular Locations. Journal of Proteome Research, 2006, 5, 3420-3428.	1.8	153
1641	Four Stage Liquid Chromatographic Selection of Methionyl Peptides for Peptide-Centric Proteome Analysis:A The Proteome of Human Multipotent Adult Progenitor Cells. Journal of Proteome Research, 2006, 5, 1415-1428.	1.8	29
1642	Insulin-dependent Interactions of Proteins with GLUT4 Revealed through Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC)*. Journal of Proteome Research, 2006, 5, 64-75.	1.8	106
1643	Computational Proteomics Analysis System (CPAS):â€‰ An Extensible, Open-Source Analytic System for Evaluating and Publishing Proteomic Data and High Throughput Biological Experiments. Journal of Proteome Research, 2006, 5, 112-121.	1.8	204
1644	Molecular Phenotyping of Human Endometrium Distinguishes Menstrual Cycle Phases and Underlying Biological Processes in Normo-Ovulatory Women. Endocrinology, 2006, 147, 1097-1121.	1.4	532

#	ARTICLE	IF	CITATIONS
1645	Predicting Eukaryotic Protein Subcellular Location by Fusing Optimized Evidence-Theoretic K-Nearest Neighbor Classifiers. <i>Journal of Proteome Research</i> , 2006, 5, 1888-1897.	1.8	269
1646	Improving Functional Modularity in Protein-Protein Interactions Graphs Using Hub-Induced Subgraphs. <i>Lecture Notes in Computer Science</i> , 2006, , 371-382.	1.0	33
1647	Automated protein function prediction--the genomic challenge. <i>Briefings in Bioinformatics</i> , 2006, 7, 225-242.	3.2	307
1648	Leveraging Enzyme Structure~Function Relationships for Functional Inference and Experimental Design:~ The Structure~Function Linkage Database. <i>Biochemistry</i> , 2006, 45, 2545-2555.	1.2	157
1649	Gene Loss and Evolutionary Rates Following Whole-Genome Duplication in Teleost Fishes. <i>Molecular Biology and Evolution</i> , 2006, 23, 1808-1816.	3.5	352
1650	PIGOK:~ Linking Protein Identity to Gene Ontology and Function. <i>Journal of Proteome Research</i> , 2006, 5, 3429-3432.	1.8	10
1651	Influence of sex on gene expression in the mouse lacrimal gland. <i>Experimental Eye Research</i> , 2006, 82, 13-23.	1.2	38
1652	Identification of novel genes regulated in the developing human ventral mesencephalon. <i>Experimental Neurology</i> , 2006, 198, 427-437.	2.0	22
1653	Long-term gene expression changes in the cortex following cortical ischemia revealed by transcriptional profiling. <i>Experimental Neurology</i> , 2006, 200, 135-152.	2.0	16
1654	BIOREL: The benchmark resource to estimate the relevance of the gene networks. <i>FEBS Letters</i> , 2006, 580, 844-848.	1.3	5
1655	Identification of microRNAs from different tissues of chicken embryo and adult chicken. <i>FEBS Letters</i> , 2006, 580, 3610-3616.	1.3	59
1656	The non-random distribution of intronless human genes across molecular function categories. <i>FEBS Letters</i> , 2006, 580, 4303-4305.	1.3	11
1657	Global gene expression during nitrogen starvation in the rice blast fungus, <i>Magnaporthe grisea</i> . <i>Fungal Genetics and Biology</i> , 2006, 43, 605-617.	0.9	109
1658	A phylogenomic analysis of the Ascomycota. <i>Fungal Genetics and Biology</i> , 2006, 43, 715-725.	0.9	128
1659	Hum-PLoc: A novel ensemble classifier for predicting human protein subcellular localization. <i>Biochemical and Biophysical Research Communications</i> , 2006, 347, 150-157.	1.0	256
1660	A novel computational method to predict transcription factor DNA binding preference. <i>Biochemical and Biophysical Research Communications</i> , 2006, 348, 1034-1037.	1.0	55
1661	Computational analysis of microRNA targets in <i>Caenorhabditis elegans</i> . <i>Gene</i> , 2006, 365, 2-10.	1.0	41
1662	Heavy metal transporters in~Hemiascomycete yeasts. <i>Biochimie</i> , 2006, 88, 1639-1649.	1.3	17

#	ARTICLE	IF	CITATIONS
1663	Microarray analysis of gene expression during the inflammation and endochondral bone formation stages of rat femur fracture repair. <i>Bone</i> , 2006, 38, 521-529.	1.4	119
1664	Prospero Acts as a Binary Switch between Self-Renewal and Differentiation in <i>Drosophila</i> Neural Stem Cells. <i>Developmental Cell</i> , 2006, 11, 775-789.	3.1	348
1665	Graemlin: General and robust alignment of multiple large interaction networks. <i>Genome Research</i> , 2006, 16, 1169-1181.	2.4	274
1666	BIOINFORMATICS AND ITS APPLICATIONS IN PLANT BIOLOGY. <i>Annual Review of Plant Biology</i> , 2006, 57, 335-360.	8.6	100
1667	Transcriptome analyses of male germ cells with serial analysis of gene expression (SAGE). <i>Molecular and Cellular Endocrinology</i> , 2006, 250, 8-19.	1.6	30
1668	Integrated Prediction of the Helical Membrane Protein Interactome in Yeast. <i>Journal of Molecular Biology</i> , 2006, 357, 339-349.	2.0	25
1669	Complex Functionality of Gene Groups Identified from High-throughput Data. <i>Journal of Molecular Biology</i> , 2006, 363, 289-296.	2.0	19
1670	Towards a Comprehensive Analysis of the Protein Phosphatase 1 Interactome in <i>Drosophila</i> . <i>Journal of Molecular Biology</i> , 2006, 364, 196-212.	2.0	27
1671	Biomedical Language Processing: What's Beyond PubMed?. <i>Molecular Cell</i> , 2006, 21, 589-594.	4.5	244
1672	Genomic Association of the Proteasome Demonstrates Overlapping Gene Regulatory Activity with Transcription Factor Substrates. <i>Molecular Cell</i> , 2006, 21, 861-871.	4.5	104
1673	Cholera toxin induced novel genes in human lymphocytes and monocytes. <i>Molecular Immunology</i> , 2006, 43, 1267-1274.	1.0	9
1674	Transcriptional analysis of LPS-stimulated activation of trout (<i>Oncorhynchus mykiss</i>) monocyte/macrophage cells in primary culture treated with cortisol. <i>Molecular Immunology</i> , 2006, 43, 1340-1348.	1.0	135
1675	The sialotranscriptome of adult male <i>Anopheles gambiae</i> mosquitoes. <i>Insect Biochemistry and Molecular Biology</i> , 2006, 36, 570-575.	1.2	45
1676	Differentially expressed cortical genes contribute to perivascular deposition in transgenic mice with inducible neuron-specific expression of TGF β 1. <i>International Journal of Developmental Neuroscience</i> , 2006, 24, 177-186.	0.7	11
1677	Gene expression changes at metamorphosis induced by thyroid hormone in <i>Xenopus laevis</i> tadpoles. <i>Developmental Biology</i> , 2006, 291, 342-355.	0.9	120
1678	Hepatocyte iron loading capacity is associated with differentiation and repression of motility in the HepaRG cell line. <i>Genomics</i> , 2006, 87, 93-103.	1.3	26
1679	Detection and characterization of DNA variants in the promoter regions of hundreds of human disease candidate genes. <i>Genomics</i> , 2006, 87, 704-710.	1.3	26
1680	Application of transcriptional and biological network analyses in mouse germ-cell transcriptomes. <i>Genomics</i> , 2006, 88, 18-33.	1.3	26

#	ARTICLE	IF	CITATIONS
1681	Application of microarray technology in primate behavioral neuroscience research. <i>Methods</i> , 2006, 38, 227-234.	1.9	14
1682	Gene expression in the rat brain during sleep deprivation and recovery sleep: an Affymetrix GeneChip® study. <i>Neuroscience</i> , 2006, 137, 593-605.	1.1	128
1683	Differential gene expression in the rat cochlea after exposure to impulse noise. <i>Neuroscience</i> , 2006, 142, 425-435.	1.1	48
1684	Can cognitive processes be inferred from neuroimaging data?. <i>Trends in Cognitive Sciences</i> , 2006, 10, 59-63.	4.0	1,772
1685	The problem of neuronal cell types: a physiological genomics approach. <i>Trends in Neurosciences</i> , 2006, 29, 339-345.	4.2	145
1686	Current trends in molecular classification of adult renal tumors. <i>Urology</i> , 2006, 67, 873-880.	0.5	20
1687	Estrogen™s and Progesterone™s Impact on Gene Expression in the Mouse Lacrimal Gland. , 2006, 47, 158.		44
1688	The genome of the filamentous fungus <i>Ashbya gossypii</i> : annotation and evolutionary implications. , 0, , 197-232.		2
1689	Magellan: A Web Based System for the Integrated Analysis of Heterogeneous Biological Data and Annotations; Application to DNA Copy Number and Expression Data in Ovarian Cancer. <i>Cancer Informatics</i> , 2006, 2, 117693510600200.	0.9	4
1690	Abundantly expressed genes in pig adipose tissue: An expressed sequence tag approach1. <i>Journal of Animal Science</i> , 2006, 84, 2673-2683.	0.2	34
1691	Identification of novel transcriptional networks in response to treatment with the anticarcinogen 3H-1,2-dithiole-3-thione. <i>Physiological Genomics</i> , 2006, 24, 144-153.	1.0	25
1692	Detecting and profiling tissue-selective genes. <i>Physiological Genomics</i> , 2006, 26, 158-162.	1.0	54
1693	Integrative Analysis of Gene Expression Data Including an Assessment of Pathway Enrichment for Predicting Prostate Cancer. <i>Cancer Informatics</i> , 2006, 2, 117693510600200.	0.9	1
1694	A Mouse Stromal Response to Tumor Invasion Predicts Prostate and Breast Cancer Patient Survival. <i>PLoS ONE</i> , 2006, 1, e32.	1.1	50
1695	Bioinformatic Resources for in Silico Proteome Analysis. , 2006, , 469-475.		0
1696	Analysing Microarray Data using the Multi-functional Immune Ontologiser. <i>Journal of Integrative Bioinformatics</i> , 2006, 3, 14-36.	1.0	2
1697	Role of strain differences on host resistance and the transcriptional response of macrophages to infection with <i>Yersinia enterocolitica</i> . <i>Physiological Genomics</i> , 2006, 25, 75-84.	1.0	45
1698	The Practical Impact of Ontologies on Biomedical Informatics. <i>Yearbook of Medical Informatics</i> , 2006, 15, 124-135.	0.8	53

#	ARTICLE	IF	CITATIONS
1699	Being Positive about Selection. PLoS Biology, 2006, 4, e87.	2.6	35
1700	Definition of a web ontology for design-oriented material selection. Data Science Journal, 2006, 5, 52-63.	0.6	26
1701	Semantic Web Infrastructure for Fungal Enzyme Biotechnologists. SSRN Electronic Journal, 2006, , .	0.4	0
1702	Generation and analysis of expressed sequence tags from Botrytis cinerea. Biological Research, 2006, 39, 367-76.	1.5	14
1706	Bioinformatics as a Problem of Knowledge Representation: Applications to Some Aspects of Immunoregulation. , 2006, , 107-131.		0
1707	Functional annotation of the mouse genome: the challenge of phenotyping. , 2006, , .		0
1708	An information framework for systems-based design of biological nanotechnology. , 2006, , .		0
1709	The VANTED software system for transcriptomics, proteomics and metabolomics analysis. Journal of Pesticide Sciences, 2006, 31, 289-292.	0.8	19
1710	The Pathogen-Host Interactions Database (PHI-base) Provides Insights into Generic and Novel Themes of Pathogenicity. Molecular Plant-Microbe Interactions, 2006, 19, 1451-1462.	1.4	68
1711	Variants in the ATM-BRCA2-CHEK2 axis predispose to chronic lymphocytic leukemia. Blood, 2006, 108, 638-644.	0.6	109
1712	Distributional gradient of amino acid repeats in plant proteins. Genome, 2006, 49, 900-905.	0.9	13
1713	Combining biomedical knowledge and transcriptomic data to extract new knowledge on genes. Journal of Integrative Bioinformatics, 2006, 3, 162-176.	1.0	2
1714	Co-expressed gene groups analysis (CGGA): An automatic tool for the interpretation of microarray experiments. Journal of Integrative Bioinformatics, 2006, 3, 188-198.	1.0	2
1715	An assessment of machine and statistical learning approaches to inferring networks of protein-protein interactions. Journal of Integrative Bioinformatics, 2006, 3, 230-246.	1.0	7
1717	Bioinformatics methods for identifying candidate disease genes. Human Genomics, 2006, 2, 429.	1.4	20
1719	Phenotype Data: A Neglected Resource in Biomedical Research?. Current Bioinformatics, 2006, 1, 347-358.	0.7	11
1720	Exploiting Binary Abstractions in Deciphering Gene Interactions. , 2006, 2006, 5858-63.		0
1721	Protein classification using probabilistic chain graphs and the Gene Ontology structure. Bioinformatics, 2006, 22, 1871-1878.	1.8	36

#	ARTICLE	IF	CITATIONS
1723	A classification of tasks for the systematic study of immune response using functional genomics data. <i>Parasitology</i> , 2006, 132, 157.	0.7	10
1724	JOINT LEARNING OF GENE FUNCTIONS " A BAYESIAN NETWORK MODEL APPROACH. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 217-239.	0.3	3
1725	Comparative expression profiling in primary and immortalized endothelial cells: changes in gene expression in response to hydroxy methylglutaryl-coenzyme A reductase inhibition. <i>Blood Coagulation and Fibrinolysis</i> , 2006, 17, 173-180.	0.5	53
1726	Local and Distant Burn Injury Alter Immuno-Inflammatory Gene Expression in Skeletal Muscle. <i>Journal of Trauma</i> , 2006, 61, 280-292.	2.3	18
1727	Microarray expression technology: from start to finish. <i>Pharmacogenomics</i> , 2006, 7, 123-134.	0.6	27
1728	Metabolome, transcriptome, and bioinformatic cis-element analyses point to HNF-4 as a central regulator of gene expression during enterocyte differentiation. <i>Physiological Genomics</i> , 2006, 27, 141-155.	1.0	94
1729	A functional annotation of subproteomes in human plasma. , 2006, , 329-351.		0
1730	Exploring Phenotypic Data at the Rat Genome Database. <i>Current Protocols in Bioinformatics</i> , 2006, 14, 1.14.1-1.14.27.	25.8	15
1731	Diabetes-altered gene expression in rat skeletal muscle corrected by oral administration of vanadyl sulfate. <i>Physiological Genomics</i> , 2006, 26, 192-201.	1.0	42
1732	PANTHER: Protein families and subfamilies modeled on the divergence of function. , 2006, , .		1
1733	A Method to Support Cell Physiological Modelling Using Description Language and Ontology. <i>IPSI Digital Courier</i> , 2006, 2, 726-735.	0.3	5
1734	Screening for Control Genes in Mouse Hippocampus After Transient Forebrain Ischemia Using High-Density Oligonucleotide Array. <i>Journal of Pharmacological Sciences</i> , 2006, 101, 52-57.	1.1	23
1735	Genomic analysis of <i>Xenopus</i> organizer function. <i>BMC Developmental Biology</i> , 2006, 6, 27.	2.1	17
1736	Gene expression profiles in developing nephrons using <i>Lim1</i> metanephric mesenchyme-specific conditional mutant mice. <i>BMC Nephrology</i> , 2006, 7, 1.	0.8	23
1737	Global analysis of X-chromosome dosage compensation. <i>Journal of Biology</i> , 2006, 5, 3.	2.7	294
1738	The interaction map of yeast: terra incognita?. <i>Journal of Biology</i> , 2006, 5, 10.	2.7	2
1739	GARBAN II: An integrative framework for extracting biological information from proteomic and genomic data. <i>Proteomics</i> , 2006, 6, S12-S15.	1.3	6
1740	SPLASH: Systematic proteomics laboratory analysis and storage hub. <i>Proteomics</i> , 2006, 6, 1758-1769.	1.3	5

#	ARTICLE	IF	CITATIONS
1741	Quantitative proteome analysis of breast cancer cell lines using ¹⁸ O-labeling and an accurate mass and time tag strategy. <i>Proteomics</i> , 2006, 6, 2903-2915.	1.3	34
1742	Construction of quantitative proteome reference maps of mouse spleen and lymph node based on two-dimensional gel electrophoresis. <i>Proteomics</i> , 2006, 6, 3833-3844.	1.3	4
1743	Landscape of the hnRNP K protein's protein interactome. <i>Proteomics</i> , 2006, 6, 2395-2406.	1.3	69
1744	Reconstructing protein complexes: From proteomics to systems biology. <i>Proteomics</i> , 2006, 6, 4724-4731.	1.3	18
1745	Optimized proteomic analysis of a mouse model of cerebellar dysfunction using amine-specific isobaric tags. <i>Proteomics</i> , 2006, 6, 4321-4334.	1.3	77
1746	Identification of differentially regulated proteins in response to a compatible interaction between the pathogen <i>Fusarium graminearum</i> and its host, <i>Triticum aestivum</i> . <i>Proteomics</i> , 2006, 6, 4599-4609.	1.3	130
1747	Pilot study of the Human Proteome Organisation Brain Proteome Project: Applying different 2-DE techniques to monitor proteomic changes during murine brain development. <i>Proteomics</i> , 2006, 6, 4899-4913.	1.3	31
1748	Proteome analysis of B-cell maturation. <i>Proteomics</i> , 2006, 6, 5152-5168.	1.3	13
1749	Quantitative proteomic analysis of the budding yeast cell cycle using acid-cleavable isotope-coded affinity tag reagents. <i>Proteomics</i> , 2006, 6, 6146-6157.	1.3	38
1750	Functional annotation of proteins identified in human brain during the HUPO Brain Proteome Project pilot study. <i>Proteomics</i> , 2006, 6, 5059-5075.	1.3	23
1751	Integrating forward and reverse proteomics to unravel protein function. <i>Proteomics</i> , 2006, 6, 5467-5480.	1.3	18
1752	Lipopolysaccharide-stimulated responses in rat aortic endothelial cells by a systems biology approach. <i>Proteomics</i> , 2006, 6, 5915-5928.	1.3	17
1753	Evaluation of different biological data and computational classification methods for use in protein interaction prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 490-500.	1.5	299
1754	How to get the most from fission yeast genome data: a report from the 2006 European Fission Yeast Meeting computing workshop. <i>Yeast</i> , 2006, 23, 905-912.	0.8	3
1755	Gene Ontology annotation status of the fission yeast genome: preliminary coverage approaches 100%. <i>Yeast</i> , 2006, 23, 913-919.	0.8	47
1756	Incorporating gene functional annotations in detecting differential gene expression. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2006, 55, 301-316.	0.5	6
1757	A library of gene expression signatures to illuminate normal and pathological lymphoid biology. <i>Immunological Reviews</i> , 2006, 210, 67-85.	2.8	189
1758	Molecular signature of mice T lymphocytes following tolerance induction by allogeneic BMT and CD40-CD40L costimulation blockade. <i>Transplant International</i> , 2006, 19, 146-157.	0.8	7

#	ARTICLE	IF	CITATIONS
1759	Gene expression analysis identifies novel genes participating in early murine liver development and adult liver regeneration. <i>Differentiation</i> , 2006, 74, 167-173.	1.0	39
1760	Co-ordinate but disproportionate activation of apoptotic, regenerative and inflammatory pathways characterizes the liver response to acute amebic infection. <i>Cellular Microbiology</i> , 2006, 8, 508-522.	1.1	15
1761	Proteomic analysis of rat hippocampal plasma membrane: characterization of potential neuronal-specific plasma membrane proteins. <i>Journal of Neurochemistry</i> , 2006, 98, 1126-1140.	2.1	60
1762	Age-specific hormonal decline is accompanied by transcriptional changes in human sebocytes in vitro. <i>Aging Cell</i> , 2006, 5, 331-344.	3.0	102
1763	The heavy metal hyperaccumulator <i>Thlaspi caerulescens</i> expresses many species-specific genes, as identified by comparative expressed sequence tag analysis. <i>New Phytologist</i> , 2006, 170, 753-766.	3.5	69
1764	Recent trends in knowledge and data integration for the life sciences. <i>Expert Systems</i> , 2006, 23, 330-341.	2.9	9
1765	Comparative RNA expression analyses from small-scale, single-donor platelet samples ¹ . <i>Journal of Thrombosis and Haemostasis</i> , 2006, 4, 349-356.	1.9	26
1766	Comparison of transcription of multiple genes at three developmental stages of the plant pathogen <i>Sclerotinia sclerotiorum</i> . <i>FEMS Microbiology Letters</i> , 2006, 258, 150-160.	0.7	38
1767	Genome-wide screening of dioxin-responsive genes in fetal brain: bioinformatic and experimental approaches. <i>Congenital Anomalies (discontinued)</i> , 2006, 46, 135-143.	0.3	10
1768	Global gene expression profiling of preimplantation embryos. <i>Human Cell</i> , 2006, 19, 98-117.	1.2	133
1769	Comparisons of Graph-structure Clustering Methods for Gene Expression Data. <i>Acta Biochimica Et Biophysica Sinica</i> , 2006, 38, 379-384.	0.9	6
1770	Influence of testosterone on gene expression in the ovariectomized mouse submandibular gland. <i>European Journal of Oral Sciences</i> , 2006, 114, 328-336.	0.7	5
1771	Skin layer-specific transcriptional profiles in normal and recessive yellow (Mc1re/Mc1re) mice. <i>Pigment Cell & Melanoma Research</i> , 2006, 19, 194-205.	4.0	14
1772	Subcellular Localization of Mammalian Type II Membrane Proteins. <i>Traffic</i> , 2006, 7, 613-625.	1.3	19
1773	Microarray profiling of human white adipose tissue after exogenous leptin injection. <i>European Journal of Clinical Investigation</i> , 2006, 36, 153-163.	1.7	21
1774	The molecular ecologist's guide to expressed sequence tags. <i>Molecular Ecology</i> , 2006, 16, 907-924.	2.0	326
1775	From 'omes to biology. <i>Animal Genetics</i> , 2006, 37, 48-56.	0.6	14
1776	Gene expression profiles of O ₃ -treated <i>Arabidopsis</i> plants. <i>Plant, Cell and Environment</i> , 2006, 29, 1686-1702.	2.8	84

#	ARTICLE	IF	CITATIONS
1777	Microarray analysis of the transcriptome as a stepping stone towards understanding biological systems: practical considerations and perspectives. <i>Plant Journal</i> , 2006, 45, 630-650.	2.8	82
1778	The Arabidopsis co-expression tool (act): a WWW-based tool and database for microarray-based gene expression analysis. <i>Plant Journal</i> , 2006, 46, 336-348.	2.8	69
1779	Membrane-associated transcripts in Arabidopsis; their isolation and characterization by DNA microarray analysis and bioinformatics. <i>Plant Journal</i> , 2006, 46, 708-721.	2.8	33
1780	UPSC-BASE -Populustranscriptomics online. <i>Plant Journal</i> , 2006, 48, 806-817.	2.8	53
1781	Analysis of expressed sequence tags from <i>Rhynchosciara americana</i> salivary glands. <i>Insect Molecular Biology</i> , 2006, 15, 109-118.	1.0	10
1782	Caste development and reproduction: a genome-wide analysis of hallmarks of insect eusociality. <i>Insect Molecular Biology</i> , 2006, 15, 703-714.	1.0	73
1783	Protein annotation by EBIMed. <i>Nature Biotechnology</i> , 2006, 24, 902-903.	9.4	19
1784	Are we stuck in the standards?. <i>Nature Biotechnology</i> , 2006, 24, 1374-1376.	9.4	9
1785	Creation and implications of a phenome-genome network. <i>Nature Biotechnology</i> , 2006, 24, 55-62.	9.4	190
1786	The art of gene function prediction. <i>Nature Biotechnology</i> , 2006, 24, 1474-1475.	9.4	69
1787	Hematopoietic stem cell gene transfer in a tumor-prone mouse model uncovers low genotoxicity of lentiviral vector integration. <i>Nature Biotechnology</i> , 2006, 24, 687-696.	9.4	648
1788	ORFeome cloning and global analysis of protein localization in the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Nature Biotechnology</i> , 2006, 24, 841-847.	9.4	508
1789	Modelling data across labs, genomes, space and time. <i>Nature Cell Biology</i> , 2006, 8, 1190-1194.	4.6	30
1790	Genetic regulators of large-scale transcriptional signatures in cancer. <i>Nature Genetics</i> , 2006, 38, 421-430.	9.4	204
1791	A functional genomics guide to the galaxy of neuronal cell types. <i>Nature Neuroscience</i> , 2006, 9, 10-12.	7.1	9
1792	Damaging secretions: chromogranins team up with mutant SOD1. <i>Nature Neuroscience</i> , 2006, 9, 12-14.	7.1	7
1793	Molecular taxonomy of major neuronal classes in the adult mouse forebrain. <i>Nature Neuroscience</i> , 2006, 9, 99-107.	7.1	502
1794	Reverse engineering cellular networks. <i>Nature Protocols</i> , 2006, 1, 662-671.	5.5	345

#	ARTICLE	IF	CITATIONS
1795	The mode-of-action by network identification (MNI) algorithm: a network biology approach for molecular target identification. <i>Nature Protocols</i> , 2006, 1, 2551-2554.	5.5	25
1796	Addressing the problems with life-science databases for traditional uses and systems biology. <i>Nature Reviews Genetics</i> , 2006, 7, 482-488.	7.7	77
1797	Standards for systems biology. <i>Nature Reviews Genetics</i> , 2006, 7, 593-605.	7.7	137
1798	Effect of Exercise on Hepatic Gene Expression in an Obese Mouse Model Using cDNA Microarrays. <i>Obesity</i> , 2006, 14, 1294-1302.	1.5	34
1799	Single-cell proteomic analysis of <i>S. cerevisiae</i> reveals the architecture of biological noise. <i>Nature</i> , 2006, 441, 840-846.	13.7	1,434
1800	A genomic code for nucleosome positioning. <i>Nature</i> , 2006, 442, 772-778.	13.7	1,333
1801	Retroviral vector insertions in T-lymphocytes used for suicide gene therapy occur in gene groups with specific molecular functions. <i>Bone Marrow Transplantation</i> , 2006, 38, 229-235.	1.3	6
1802	Identification of key genes responsible for cytokine-induced erythroid and myeloid differentiation and switching of hematopoietic stem cells by RAGE. <i>Cell Research</i> , 2006, 16, 923-939.	5.7	3
1803	A text-mining analysis of the human phenome. <i>European Journal of Human Genetics</i> , 2006, 14, 535-542.	1.4	588
1804	Organellar proteomics: turning inventories into insights. <i>EMBO Reports</i> , 2006, 7, 874-879.	2.0	185
1805	Identification of novel genes and transcription factors involved in spleen, thymus and immunological development and function. <i>Genes and Immunity</i> , 2006, 7, 101-112.	2.2	11
1806	Deregulated stress system in non-obese diabetic lymphocyte. <i>Genes and Immunity</i> , 2006, 7, 352-358.	2.2	1
1807	Bayesian mapping of genotype \bar{A} - expression interactions in quantitative and qualitative traits. <i>Heredity</i> , 2006, 97, 4-18.	1.2	66
1808	Deregulated expression of fat and muscle genes in B-cell chronic lymphocytic leukemia with high lipoprotein lipase expression. <i>Leukemia</i> , 2006, 20, 1080-1088.	3.3	63
1809	Gene expression profiling identifies molecular subgroups among nodal peripheral T-cell lymphomas. <i>Oncogene</i> , 2006, 25, 1560-1570.	2.6	132
1810	Parallel induction of ATM-dependent pro- and antiapoptotic signals in response to ionizing radiation in murine lymphoid tissue. <i>Oncogene</i> , 2006, 25, 1584-1592.	2.6	69
1811	Identification of target genes in laryngeal squamous cell carcinoma by high-resolution copy number and gene expression microarray analyses. <i>Oncogene</i> , 2006, 25, 6997-7008.	2.6	88
1812	Development of a human mitochondria-focused cDNA microarray (hMitChip) and validation in skeletal muscle cells: implications for pharmaco- and mitogenomics. <i>Pharmacogenomics Journal</i> , 2006, 6, 333-342.	0.9	18

#	ARTICLE	IF	CITATIONS
1813	Gene expression profile differences in left and right liver lobes from mid-gestation fetal baboons: a cautionary tale. <i>Journal of Physiology</i> , 2006, 572, 59-66.	1.3	43
1814	Effect of 30 per cent maternal nutrient restriction from 0.16 to 0.5 gestation on fetal baboon kidney gene expression. <i>Journal of Physiology</i> , 2006, 572, 67-85.	1.3	72
1815	Soft computing agents for e-Health in application to the research and control of unknown diseases. <i>Information Sciences</i> , 2006, 176, 1190-1214.	4.0	39
1816	Analysis of protein interaction networks using mass spectrometry compatible techniques. <i>Analytica Chimica Acta</i> , 2006, 564, 10-18.	2.6	17
1817	Creating hierarchical models of protein families based on Expressed Sequence Tags: The "Sprockets" analysis pipeline. <i>Analytica Chimica Acta</i> , 2006, 564, 123-132.	2.6	0
1818	Identification of critical genes in microarray experiments by a Neuro-Fuzzy approach. <i>Computational Biology and Chemistry</i> , 2006, 30, 372-381.	1.1	11
1819	ONTOFUSION: Ontology-based integration of genomic and clinical databases. <i>Computers in Biology and Medicine</i> , 2006, 36, 712-730.	3.9	90
1820	Using Gene Ontology and genomic controlled vocabularies to analyze high-throughput gene lists: Three tool comparison. <i>Computers in Biology and Medicine</i> , 2006, 36, 731-747.	3.9	13
1821	Computation of semantic similarity within an ontology of breast pathology to assist inter-observer consensus. <i>Computers in Biology and Medicine</i> , 2006, 36, 768-788.	3.9	15
1822	GOHSE: Ontology driven linking of biology resources. <i>Web Semantics</i> , 2006, 4, 155-163.	2.2	14
1823	Semantic web infrastructure for fungal enzyme biotechnologists. <i>Web Semantics</i> , 2006, 4, 168-180.	2.2	31
1824	SAMBO "A system for aligning and merging biomedical ontologies. <i>Web Semantics</i> , 2006, 4, 196-206.	2.2	159
1825	SWAN: A distributed knowledge infrastructure for Alzheimer disease research. <i>Web Semantics</i> , 2006, 4, 222-228.	2.2	38
1826	Identification of early molecular pathways affected by paraquat in rat lung. <i>Toxicology</i> , 2006, 225, 157-172.	2.0	22
1827	Evaluation of the Application of Sodium Deoxycholate to Proteomic Analysis of Rat Hippocampal Plasma Membrane. <i>Journal of Proteome Research</i> , 2006, 5, 2547-2553.	1.8	108
1828	Use of Differentiating Adult Stem Cells (Marrow Stromal Cells) to Identify New Downstream Target Genes for Transcription Factors. <i>Stem Cells</i> , 2006, 24, 642-652.	1.4	20
1829	Selection of Neural Differentiation-Specific Genes by Comparing Profiles of Random Differentiation. <i>Stem Cells</i> , 2006, 24, 1946-1955.	1.4	29
1830	Defining a Developmental Path to Neural Fate by Global Expression Profiling of Mouse Embryonic Stem Cells and Adult Neural Stem/Progenitor Cells. <i>Stem Cells</i> , 2006, 24, 889-895.	1.4	58

#	ARTICLE	IF	CITATIONS
1831	Differential mRNA Processing in Hematopoietic Stem Cells. <i>Stem Cells</i> , 2006, 24, 662-670.	1.4	20
1832	Chemosensation in <i>C. elegans</i> . <i>WormBook</i> , 2006, , 1-29.	5.3	603
1833	Wnt but Not BMP Signaling Is Involved in the Inhibitory Action of Sclerostin on BMP-Stimulated Bone Formation. <i>Journal of Bone and Mineral Research</i> , 2006, 22, 19-28.	3.1	238
1835	A categorization approach to automated ontological function annotation. <i>Protein Science</i> , 2006, 15, 1544-1549.	3.1	59
1836	MachineProse: An Ontological Framework for Scientific Assertions. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2006, 13, 220-232.	2.2	10
1837	Enhancing Text Categorization with Semantic-enriched Representation and Training Data Augmentation. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2006, 13, 526-535.	2.2	38
1838	Math1 Target Genes Are Enriched With Evolutionarily Conserved Clustered E-box Binding Sites. <i>Journal of Molecular Neuroscience</i> , 2006, 28, 211-230.	1.1	26
1839	Identification of estrogen-responsive genes in the testis of sea bream (<i>Sparus auratus</i>) using suppression subtractive hybridization. <i>Molecular Reproduction and Development</i> , 2006, 73, 318-329.	1.0	44
1840	Human spontaneous labor without histologic chorioamnionitis is characterized by an acute inflammation gene expression signature. <i>American Journal of Obstetrics and Gynecology</i> , 2006, 195, 394-405.e12.	0.7	195
1841	Heterogeneity of Breast Cancer among Patients and Implications for Patient Selection for Adjuvant Chemotherapy. <i>Pharmaceutical Research</i> , 2006, 23, 1951-1958.	1.7	11
1842	Conversion of MapMan to Allow the Analysis of Transcript Data from Solanaceous Species: Effects of Genetic and Environmental Alterations in Energy Metabolism in the Leaf. <i>Plant Molecular Biology</i> , 2006, 60, 773-792.	2.0	115
1843	Computational Prediction and Experimental Verification of HVA1-like Abscisic Acid Responsive Promoters in Rice (<i>Oryza sativa</i>). <i>Plant Molecular Biology</i> , 2006, 62, 233-246.	2.0	23
1844	Expressed Sequence Tags from loblolly pine embryos reveal similarities with angiosperm embryogenesis. <i>Plant Molecular Biology</i> , 2006, 62, 485-501.	2.0	69
1845	Transcriptional changes in powdery mildew infected wheat and <i>Arabidopsis</i> leaves undergoing syringolin-triggered hypersensitive cell death at infection sites. <i>Plant Molecular Biology</i> , 2006, 62, 561-578.	2.0	42
1846	GeneGrid: Architecture, Implementation and Application. <i>Journal of Grid Computing</i> , 2006, 4, 209-222.	2.5	6
1847	Genome-wide transcription survey on flavour production in <i>Saccharomyces cerevisiae</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2006, 22, 1347-1356.	1.7	14
1848	Predicting Protein-Protein Interactions by Association Mining. <i>Information Systems Frontiers</i> , 2006, 8, 37-47.	4.1	13
1849	Molecular Analysis of the Magnocellular Neuroendocrine Phenotype: from the Micropunch to Laser Microdissection. <i>Neurochemical Research</i> , 2006, 31, 189-199.	1.6	3

#	ARTICLE	IF	CITATIONS
1850	Clustering Analysis of Gene Expression Data based on Semi-supervised Visual Clustering Algorithm. <i>Soft Computing</i> , 2006, 10, 981-993.	2.1	15
1851	Gene-Dosage Effect on Chromosome 21 Transcriptome in Trisomy 21: Implication in Down Syndrome Cognitive Disorders. <i>Behavior Genetics</i> , 2006, 36, 416-428.	1.4	28
1852	Whole genome expression profiling of the medial and lateral substantia nigra in Parkinson's disease. <i>Neurogenetics</i> , 2006, 7, 1-11.	0.7	212
1853	Evaluating HapMap SNP data transferability in a large-scale genotyping project involving 175 cancer-associated genes. <i>Human Genetics</i> , 2006, 118, 669-679.	1.8	92
1854	Large-scale characterization of public database SNPs causing non-synonymous changes in three ethnic groups. <i>Human Genetics</i> , 2006, 119, 75-83.	1.8	15
1855	Complex patterns of copy number variation at sites of segmental duplications: an important category of structural variation in the human genome. <i>Human Genetics</i> , 2006, 120, 270-284.	1.8	68
1856	Learning accurate and concise naïve Bayes classifiers from attribute value taxonomies and data. <i>Knowledge and Information Systems</i> , 2006, 9, 157-179.	2.1	47
1857	Gene expression profiling of bovine in vitro adipogenesis using a cDNA microarray. <i>Functional and Integrative Genomics</i> , 2006, 6, 235-249.	1.4	53
1859	Gene expression analysis of mouse chromosome substitution strains. <i>Mammalian Genome</i> , 2006, 17, 598-614.	1.0	29
1860	Gene expression analysis in a canine model of X-linked Alport syndrome. <i>Mammalian Genome</i> , 2006, 17, 976-990.	1.0	14
1861	LTR Retrotransposon-Gene Associations in <i>Drosophila melanogaster</i> . <i>Journal of Molecular Evolution</i> , 2006, 62, 111-120.	0.8	21
1862	Testing for Spatial Clustering of Amino Acid Replacements Within Protein Tertiary Structure. <i>Journal of Molecular Evolution</i> , 2006, 62, 682-692.	0.8	11
1863	Gene expression profiles of T lymphocytes are sensitive to the influence of heavy smoking: a pilot study. <i>Immunogenetics</i> , 2006, 59, 37-43.	1.2	25
1864	Rapid identification of target genes for 3-methyl-1-butanol production in <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2006, 70, 237-246.	1.7	35
1865	Puzzling over orphan enzymes. <i>Cellular and Molecular Life Sciences</i> , 2006, 63, 517-523.	2.4	18
1866	Proteomic analysis of low-abundant integral plasma membrane proteins based on gels. <i>Cellular and Molecular Life Sciences</i> , 2006, 63, 1790-1804.	2.4	40
1867	Control of smooth muscle cell proliferation by ferrous iron. <i>Biomaterials</i> , 2006, 27, 2193-2200.	5.7	137
1868	A multiplexed proteomics approach to differentiate neurite outgrowth patterns. <i>Journal of Neuroscience Methods</i> , 2006, 158, 22-29.	1.3	18

#	ARTICLE	IF	CITATIONS
1869	Ontology based text indexing and querying for the semantic web. Knowledge-Based Systems, 2006, 19, 744-754.	4.0	69
1870	Integrating linguistic knowledge into a conditional random field framework to identify biomedical named entities. Expert Systems With Applications, 2006, 30, 117-128.	4.4	39
1871	Bioinformatics and cancer: an essential alliance. Clinical and Translational Oncology, 2006, 8, 409-415.	1.2	13
1872	Comparative analysis of whole-genome sequences of Streptococcus suis. Science Bulletin, 2006, 51, 1199-1209.	1.7	3
1873	Identifying disease feature genes based on cellular localized gene functional modules and regulation networks. Science Bulletin, 2006, 51, 1848-1856.	1.7	3
1874	Comparative analysis of lymphatic metastasis associated genes in mouse hepatocellular carcinoma cell lines with different metastatic potential. Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association, Beijing Institute for Cancer Research, 2006, 18, 26-31.	0.7	2
1875	Comparison of protein expression lists from mass spectrometry of human blood fluids using exact peptide sequences versus BLAST. Clinical Proteomics, 2006, 2, 185-203.	1.1	17
1876	Gene Expression Profiling of Acute Liver Stress During Living Donor Liver Transplantation. American Journal of Transplantation, 2006, 6, 806-824.	2.6	34
1877	Identification and analysis of genes expressed in the adult filarial parasitic nematode Dirofilaria immitis. International Journal for Parasitology, 2006, 36, 829-839.	1.3	15
1878	Knowledge guided analysis of microarray data. Journal of Biomedical Informatics, 2006, 39, 401-411.	2.5	40
1879	Bioinformatics and biological reality. Journal of Biomedical Informatics, 2006, 39, 274-287.	2.5	16
1880	Granularity, scale and collectivity: When size does and does not matter. Journal of Biomedical Informatics, 2006, 39, 333-349.	2.5	49
1881	Beyond the data deluge: Data integration and bio-ontologies. Journal of Biomedical Informatics, 2006, 39, 314-320.	2.5	128
1882	Information integration of protein-protein interactions as essential tools for immunomics. Cellular Immunology, 2006, 244, 84-86.	1.4	4
1883	Immunome: A reference set of genes and proteins for systems biology of the human immune system. Cellular Immunology, 2006, 244, 87-89.	1.4	63
1884	Evolutionary deimmunization: An ancillary mechanism for self-tolerance?. Cellular Immunology, 2006, 244, 148-153.	1.4	27
1885	Anti-oxidant sensitivity of donor age-related gene expression in cultured fibroblasts. European Journal of Pharmacology, 2006, 542, 154-161.	1.7	12
1886	Positive selection on gene expression in the human brain. Current Biology, 2006, 16, R356-R358.	1.8	50

#	ARTICLE	IF	CITATIONS
1887	Chondrocyte genomics: implications for disease modification in osteoarthritis. <i>Drug Discovery Today</i> , 2006, 11, 825-832.	3.2	10
1888	Biological microarray interpretation: The rules of engagement. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2006, 1759, 319-327.	2.4	40
1889	Genome-wide analyses show that nuclear and cytoplasmic RNA levels are differentially affected by dioxin. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2006, 1759, 388-402.	2.4	20
1890	Murine central and peripheral nervous system transcriptomes: Comparative gene expression. <i>Brain Research</i> , 2006, 1107, 24-41.	1.1	19
1891	High-throughput screen for genes predominantly expressed in the ICM of mouse blastocysts by whole mount in situ hybridization. <i>Gene Expression Patterns</i> , 2006, 6, 213-224.	0.3	70
1892	Gender biased differential alternative splicing patterns of the transcriptional cofactor CA150 gene in <i>Schistosoma mansoni</i> . <i>Molecular and Biochemical Parasitology</i> , 2006, 150, 123-131.	0.5	31
1893	Integrative analysis of metabolic networks: from peaks to flux models?. <i>Current Opinion in Plant Biology</i> , 2006, 9, 220-226.	3.5	12
1894	The NEIBank project for ocular genomics: Data-mining gene expression in human and rodent eye tissues. <i>Progress in Retinal and Eye Research</i> , 2006, 25, 43-77.	7.3	32
1895	Comparison of transcripts in <i>Phalaenopsis bellina</i> and <i>Phalaenopsis equestris</i> (Orchidaceae) flowers to deduce monoterpene biosynthesis pathway. <i>BMC Plant Biology</i> , 2006, 6, 14.	1.6	83
1896	An expressed sequence tag (EST) library from developing fruits of an Hawaiian endemic mint (<i>Stenogyne rugosa</i> , Lamiaceae): characterization and microsatellite markers. <i>BMC Plant Biology</i> , 2006, 6, 16.	1.6	30
1897	A transcriptome anatomy of human colorectal cancers. <i>BMC Cancer</i> , 2006, 6, 40.	1.1	21
1898	Lower expression of genes near microRNA in <i>C. elegans</i> germline. <i>BMC Bioinformatics</i> , 2006, 7, 112.	1.2	6
1899	Gene functional similarity search tool (GFSST). <i>BMC Bioinformatics</i> , 2006, 7, 135.	1.2	43
1900	INTEGRATOR: interactive graphical search of large protein interactomes over the Web. <i>BMC Bioinformatics</i> , 2006, 7, 146.	1.2	2
1901	2DDB - a bioinformatics solution for analysis of quantitative proteomics data. <i>BMC Bioinformatics</i> , 2006, 7, 158.	1.2	20
1902	GOPET: a tool for automated predictions of Gene Ontology terms. <i>BMC Bioinformatics</i> , 2006, 7, 161.	1.2	44
1903	An approach for clustering gene expression data with error information. <i>BMC Bioinformatics</i> , 2006, 7, 17.	1.2	30
1904	BioWarehouse: a bioinformatics database warehouse toolkit. <i>BMC Bioinformatics</i> , 2006, 7, 170.	1.2	133

#	ARTICLE	IF	CITATIONS
1905	STEM: a tool for the analysis of short time series gene expression data. BMC Bioinformatics, 2006, 7, 191.	1.2	1,309
1906	A database and tool, IM Browser, for exploring and integrating emerging gene and protein interaction data for Drosophila. BMC Bioinformatics, 2006, 7, 195.	1.2	27
1907	QPath: a method for querying pathways in a protein-protein interaction network. BMC Bioinformatics, 2006, 7, 199.	1.2	140
1908	Cluster analysis of networks generated through homology: automatic identification of important protein communities involved in cancer metastasis. BMC Bioinformatics, 2006, 7, 2.	1.2	148
1909	A phylogenomic gene cluster resource: the Phylogenetically Inferred Groups (PhIGs) database. BMC Bioinformatics, 2006, 7, 201.	1.2	56
1910	GenoLink: a graph-based querying and browsing system for investigating the function of genes and proteins. BMC Bioinformatics, 2006, 7, 21.	1.2	12
1911	Predicting deleterious nsSNPs: an analysis of sequence and structural attributes. BMC Bioinformatics, 2006, 7, 217.	1.2	74
1912	Meta-analysis discovery of tissue-specific DNA sequence motifs from mammalian gene expression data. BMC Bioinformatics, 2006, 7, 229.	1.2	38
1913	Components of the antigen processing and presentation pathway revealed by gene expression microarray analysis following B cell antigen receptor (BCR) stimulation. BMC Bioinformatics, 2006, 7, 237.	1.2	33
1914	Genome wide prediction of protein function via a generic knowledge discovery approach based on evidence integration. BMC Bioinformatics, 2006, 7, 268.	1.2	24
1915	Automated functional classification of experimental and predicted protein structures. BMC Bioinformatics, 2006, 7, 278.	1.2	6
1916	Argument-predicate distance as a filter for enhancing precision in extracting predications on the genetic etiology of disease. BMC Bioinformatics, 2006, 7, 291.	1.2	27
1917	WholePathwayScope: a comprehensive pathway-based analysis tool for high-throughput data. BMC Bioinformatics, 2006, 7, 30.	1.2	188
1918	A new measure for functional similarity of gene products based on Gene Ontology. BMC Bioinformatics, 2006, 7, 302.	1.2	597
1919	The Autoimmune Disease Database: a dynamically compiled literature-derived database. BMC Bioinformatics, 2006, 7, 325.	1.2	29
1920	Cluster analysis of protein array results via similarity of Gene Ontology annotation. BMC Bioinformatics, 2006, 7, 338.	1.2	29
1921	A combined approach to data mining of textual and structured data to identify cancer-related targets. BMC Bioinformatics, 2006, 7, 354.	1.2	68
1922	A direct comparison of protein interaction confidence assignment schemes. BMC Bioinformatics, 2006, 7, 360.	1.2	101

#	ARTICLE	IF	CITATIONS
1923	A literature-based similarity metric for biological processes. BMC Bioinformatics, 2006, 7, 363.	1.2	9
1924	Genome comparison using Gene Ontology (GO) with statistical testing. BMC Bioinformatics, 2006, 7, 374.	1.2	15
1925	Validation and functional annotation of expression-based clusters based on gene ontology. BMC Bioinformatics, 2006, 7, 380.	1.2	14
1926	Methods for evaluating clustering algorithms for gene expression data using a reference set of functional classes. BMC Bioinformatics, 2006, 7, 397.	1.2	133
1927	PhyloPat: phylogenetic pattern analysis of eukaryotic genes. BMC Bioinformatics, 2006, 7, 398.	1.2	13
1928	miTarget: microRNA target gene prediction using a support vector machine. BMC Bioinformatics, 2006, 7, 411.	1.2	195
1929	Correlated fragile site expression allows the identification of candidate fragile genes involved in immunity and associated with carcinogenesis. BMC Bioinformatics, 2006, 7, 413.	1.2	24
1930	Genomes as geography: using GIS technology to build interactive genome feature maps. BMC Bioinformatics, 2006, 7, 416.	1.2	16
1931	Analysis with respect to instrumental variables for the exploration of microarray data structures. BMC Bioinformatics, 2006, 7, 422.	1.2	55
1932	Grouping Gene Ontology terms to improve the assessment of gene set enrichment in microarray data. BMC Bioinformatics, 2006, 7, 426.	1.2	40
1933	A graph-search framework for associating gene identifiers with documents. BMC Bioinformatics, 2006, 7, 440.	1.2	19
1934	GOLEM: an interactive graph-based gene-ontology navigation and analysis tool. BMC Bioinformatics, 2006, 7, 443.	1.2	52
1935	Comparison of protein interaction networks reveals species conservation and divergence. BMC Bioinformatics, 2006, 7, 457.	1.2	44
1936	Rapid and asymmetric divergence of duplicate genes in the human gene coexpression network. BMC Bioinformatics, 2006, 7, 46.	1.2	45
1937	ProFAT: a web-based tool for the functional annotation of protein sequences. BMC Bioinformatics, 2006, 7, 466.	1.2	9
1938	GeneTools – application for functional annotation and statistical hypothesis testing. BMC Bioinformatics, 2006, 7, 470.	1.2	78
1939	Using local gene expression similarities to discover regulatory binding site modules. BMC Bioinformatics, 2006, 7, 505.	1.2	12
1940	IntNetDB v1.0: an integrated protein-protein interaction network database generated by a probabilistic model. BMC Bioinformatics, 2006, 7, 508.	1.2	73

#	ARTICLE	IF	CITATIONS
1941	PageMan: An interactive ontology tool to generate, display, and annotate overview graphs for profiling experiments. BMC Bioinformatics, 2006, 7, 535.	1.2	309
1942	Integrated analysis of gene expression by Association Rules Discovery. BMC Bioinformatics, 2006, 7, 54.	1.2	100
1943	Identifying biological concepts from a protein-related corpus with a probabilistic topic model. BMC Bioinformatics, 2006, 7, 58.	1.2	46
1944	Bayesian detection of periodic mRNA time profiles without use of training examples. BMC Bioinformatics, 2006, 7, 63.	1.2	14
1945	BIOZON: a system for unification, management and analysis of heterogeneous biological data. BMC Bioinformatics, 2006, 7, 70.	1.2	79
1946	GO-Diff: mining functional differentiation between EST-based transcriptomes. BMC Bioinformatics, 2006, 7, 72.	1.2	16
1947	BayGO: Bayesian analysis of ontology term enrichment in microarray data. BMC Bioinformatics, 2006, 7, 86.	1.2	56
1948	GONOME: measuring correlations between GO terms and genomic positions. BMC Bioinformatics, 2006, 7, 94.	1.2	14
1949	The Ontology Lookup Service, a lightweight cross-platform tool for controlled vocabulary queries. BMC Bioinformatics, 2006, 7, 97.	1.2	170
1950	Determination of strongly overlapping signaling activity from microarray data. BMC Bioinformatics, 2006, 7, 99.	1.2	25
1951	Choosing negative examples for the prediction of protein-protein interactions. BMC Bioinformatics, 2006, 7, S2.	1.2	189
1952	GOFFA: Gene Ontology For Functional Analysis – A FDA Gene Ontology Tool for Analysis of Genomic and Proteomic Data. BMC Bioinformatics, 2006, 7, S23.	1.2	51
1953	The relationship between protein sequences and their gene ontology functions. BMC Bioinformatics, 2006, 7, S11.	1.2	11
1954	SPIDer: Saccharomyces protein-protein interaction database. BMC Bioinformatics, 2006, 7, S16.	1.2	22
1955	Comparative genomics in cyprinids: common carp ESTs help the annotation of the zebrafish genome. BMC Bioinformatics, 2006, 7, S2.	1.2	40
1956	Evaluation and comparison of mammalian subcellular localization prediction methods. BMC Bioinformatics, 2006, 7, S3.	1.2	52
1957	Eleven ancestral gene families lost in mammals and vertebrates while otherwise universally conserved in animals. BMC Evolutionary Biology, 2006, 6, 5.	3.2	33
1958	Global similarity and local divergence in human and mouse gene co-expression networks. BMC Evolutionary Biology, 2006, 6, 70.	3.2	75

#	ARTICLE	IF	CITATIONS
1959	Cell-type specific gene expression profiles of leukocytes in human peripheral blood. BMC Genomics, 2006, 7, 115.	1.2	275
1960	Differential gene expression in abdomens of the malaria vector mosquito, <i>Anopheles gambiae</i> , after sugar feeding, blood feeding and <i>Plasmodium berghei</i> infection. BMC Genomics, 2006, 7, 119.	1.2	27
1961	Causal inference of regulator-target pairs by gene mapping of expression phenotypes. BMC Genomics, 2006, 7, 125.	1.2	69
1962	Transcriptome analysis of <i>Deinagkistrodon acutus</i> venomous gland focusing on cellular structure and functional aspects using expressed sequence tags. BMC Genomics, 2006, 7, 152.	1.2	61
1963	Gene identification and analysis of transcripts differentially regulated in fracture healing by EST sequencing in the domestic sheep. BMC Genomics, 2006, 7, 172.	1.2	23
1964	Finding function: evaluation methods for functional genomic data. BMC Genomics, 2006, 7, 187.	1.2	189
1965	Generation, annotation and analysis of ESTs from <i>Trichoderma harzianum</i> CECT 2413. BMC Genomics, 2006, 7, 193.	1.2	60
1966	High degree of conservancy among secreted salivary gland proteins from two geographically distant <i>Phlebotomus duboscqi</i> sandflies populations (Mali and Kenya). BMC Genomics, 2006, 7, 226.	1.2	93
1967	Analysis and functional annotation of expressed sequence tags from the fall armyworm <i>Spodoptera frugiperda</i> . BMC Genomics, 2006, 7, 264.	1.2	16
1968	Simultaneous host and parasite expression profiling identifies tissue-specific transcriptional programs associated with susceptibility or resistance to experimental cerebral malaria. BMC Genomics, 2006, 7, 295.	1.2	62
1969	Systematic interpretation of microarray data using experiment annotations. BMC Genomics, 2006, 7, 319.	1.2	16
1970	Conservation of noncoding microsatellites in plants: implication for gene regulation. BMC Genomics, 2006, 7, 323.	1.2	72
1971	EST2Prot: Mapping EST sequences to proteins. BMC Genomics, 2006, 7, 41.	1.2	3
1972	Development of a chicken 5 K microarray targeted towards immune function. BMC Genomics, 2006, 7, 49.	1.2	32
1973	Comparative salivary gland transcriptomics of sandfly vectors of visceral leishmaniasis. BMC Genomics, 2006, 7, 52.	1.2	148
1974	Whitefly (<i>Bemisia tabaci</i>) genome project: analysis of sequenced clones from egg, instar, and adult (viruliferous and non-viruliferous) cDNA libraries. BMC Genomics, 2006, 7, 79.	1.2	79
1975	In vivo vs in vitro toxicogenomic comparison of TCDD-elicited gene expression in Hepa1c1c7 mouse hepatoma cells and C57BL/6 hepatic tissue. BMC Genomics, 2006, 7, 80.	1.2	50
1976	Microarray based comparison of two <i>Escherichia coli</i> O157:H7 lineages. BMC Microbiology, 2006, 6, 30.	1.3	44

#	ARTICLE	IF	CITATIONS
1977	Generation, annotation, and analysis of an extensive <i>Aspergillus niger</i> EST collection. <i>BMC Microbiology</i> , 2006, 6, 7.	1.3	34
1978	Model storage, exchange and integration. <i>BMC Neuroscience</i> , 2006, 7, S11.	0.8	66
1979	Ontologies for data and knowledge sharing in biology: plant ROS signaling as a case study. <i>BioEssays</i> , 2006, 28, 199-210.	1.2	7
1980	Genome-wide prediction of genetic interactions in a metazoan. <i>BioEssays</i> , 2006, 28, 1087-1090.	1.2	4
1982	Analysis of pigmented villonodular synovitis with genome-wide complementary DNA microarray and tissue array technology reveals insight into potential novel therapeutic approaches. <i>Arthritis and Rheumatism</i> , 2006, 54, 1009-1019.	6.7	37
1983	Identification of genes modulated in rheumatoid arthritis using complementary DNA microarray analysis of lymphoblastoid B cell lines from disease-discordant monozygotic twins. <i>Arthritis and Rheumatism</i> , 2006, 54, 2047-2060.	6.7	100
1984	EST-based profiling and comparison of gene expression in the silkworm fat body during metamorphosis. <i>Archives of Insect Biochemistry and Physiology</i> , 2006, 61, 10-23.	0.6	30
1985	System-wide analysis of hepatotoxicological responses: Tissocks is key. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2006, 69A, 612-619.	1.1	7
1986	Transforming omics data into context: Bioinformatics on genomics and proteomics raw data. <i>Electrophoresis</i> , 2006, 27, 2659-2675.	1.3	33
1987	Comparative gene expression profiling reveals partially overlapping but distinct genomic actions of different antiestrogens in human breast cancer cells. <i>Journal of Cellular Biochemistry</i> , 2006, 98, 1163-1184.	1.2	43
1988	Correlating Expression Data with Gene Function Using Gene Ontology. <i>Chinese Journal of Chemistry</i> , 2006, 24, 1247-1254.	2.6	1
1989	Modeling tumor predisposing FH mutations in yeast: Effects on fumarase activity, growth phenotype and gene expression profile. <i>International Journal of Cancer</i> , 2006, 118, 1340-1345.	2.3	7
1990	Regulation of lipocalin-2 gene by the cancer chemopreventive retinoid 4-HPR. <i>International Journal of Cancer</i> , 2006, 119, 1599-1606.	2.3	15
1991	Patterns and mechanisms of genome organization in the mouse. <i>Journal of Experimental Zoology Part A, Comparative Experimental Biology</i> , 2006, 305A, 683-688.	1.3	15
1992	Lentiviral vector integration sites in human NOD/SCID repopulating cells. <i>Journal of Gene Medicine</i> , 2006, 8, 1197-1207.	1.4	46
1993	Comparison of schwann cell and sciatic nerve transcriptomes indicates that mouse is a valid model for the human peripheral nervous system. <i>Journal of Neuroscience Research</i> , 2006, 84, 542-552.	1.3	2
1994	Batten disease (JNCL) is linked to disturbances in mitochondrial, cytoskeletal, and synaptic compartments. <i>Journal of Neuroscience Research</i> , 2006, 84, 1124-1138.	1.3	65
1995	Tetrahymena Genome Database (TGD): a new genomic resource for Tetrahymena thermophila research. <i>Nucleic Acids Research</i> , 2006, 34, D500-D503.	6.5	107

#	ARTICLE	IF	CITATIONS
1996	VIRGO: computational prediction of gene functions. Nucleic Acids Research, 2006, 34, W340-W344.	6.5	25
1997	The Relationship between Protein Sequences and their Gene Ontology Functions. , 2006, , .		2
1998	Accomplishments and Challenges of Protein Ontology. , 2006, , .		0
1999	All I Really Need To Know I Learned in Genetics Class. American Entomologist, 2006, 52, 132-133.	0.1	0
2000	Using Information From Public <i>Arabidopsis</i> Databases to Aid Research. , 2006, 323, 187-212.		1
2001	Improving missing value estimation in microarray data with gene ontology. Bioinformatics, 2006, 22, 566-572.	1.8	101
2002	XQTav: an XQuery processor for Taverna environment. Bioinformatics, 2006, 22, 1280-1281.	1.8	1
2003	FlyTF: a systematic review of site-specific transcription factors in the fruit fly <i>Drosophila melanogaster</i> . Bioinformatics, 2006, 22, 1532-1533.	1.8	90
2004	Integrative Array Analyzer: a software package for analysis of cross-platform and cross-species microarray data. Bioinformatics, 2006, 22, 1665-1667.	1.8	13
2005	A top-level ontology of functions and its application in the Open Biomedical Ontologies. Bioinformatics, 2006, 22, e66-e73.	1.8	40
2006	Additional Gene Ontology structure for improved biological reasoning. Bioinformatics, 2006, 22, 2020-2027.	1.8	177
2007	ADGO: analysis of differentially expressed gene sets using composite GO annotation. Bioinformatics, 2006, 22, 2249-2253.	1.8	36
2008	Global topological features of cancer proteins in the human interactome. Bioinformatics, 2006, 22, 2291-2297.	1.8	458
2009	Extending MapMan: application to legume genome arrays. Bioinformatics, 2006, 22, 2958-2959.	1.8	33
2010	CisView: A Browser and Database of cis-regulatory Modules Predicted in the Mouse Genome. DNA Research, 2006, 13, 123-134.	1.5	28
2011	Identification of gene expression signatures in autoimmune disease without the influence of familial resemblance. Human Molecular Genetics, 2006, 15, 501-509.	1.4	19
2012	NOPdb: Nucleolar Proteome Database. Nucleic Acids Research, 2006, 34, D218-D220.	6.5	93
2013	The Gene Ontology (GO) project in 2006. Nucleic Acids Research, 2006, 34, D322-D326.	6.5	923

#	ARTICLE	IF	CITATIONS
2014	PhytoME: a platform for plant comparative genomics. <i>Nucleic Acids Research</i> , 2006, 34, D724-D730.	6.5	35
2015	RNAi Codex: a portal/database for short-hairpin RNA (shRNA) gene-silencing constructs. <i>Nucleic Acids Research</i> , 2006, 34, D153-D157.	6.5	41
2016	LOCATE: a mouse protein subcellular localization database. <i>Nucleic Acids Research</i> , 2006, 34, D213-D217.	6.5	72
2017	dictyBase, the model organism database for <i>Dictyostelium discoideum</i> . <i>Nucleic Acids Research</i> , 2006, 34, D423-D427.	6.5	101
2018	TiProD: the Tissue-specific Promoter Database. <i>Nucleic Acids Research</i> , 2006, 34, D104-D107.	6.5	29
2019	The UCSC Archaeal Genome Browser. <i>Nucleic Acids Research</i> , 2006, 34, D407-D410.	6.5	107
2020	The UCSC Genome Browser Database: update 2006. <i>Nucleic Acids Research</i> , 2006, 34, D590-D598.	6.5	1,156
2021	A new method to remove hybridization bias for interspecies comparison of global gene expression profiles uncovers an association between mRNA sequence divergence and differential gene expression in <i>Xenopus</i> . <i>Nucleic Acids Research</i> , 2006, 34, 185-200.	6.5	37
2022	PubMed: a web-based biomedical literature search interface. <i>Nucleic Acids Research</i> , 2006, 34, W745-W747.	6.5	52
2023	JAFa: a protein function annotation meta-server. <i>Nucleic Acids Research</i> , 2006, 34, W379-W381.	6.5	31
2024	metaSHARK: a WWW platform for interactive exploration of metabolic networks. <i>Nucleic Acids Research</i> , 2006, 34, W725-W728.	6.5	23
2025	New Onto-Tools: Promoter-Express, nsSNPCounter and Onto-Translate. <i>Nucleic Acids Research</i> , 2006, 34, W626-W631.	6.5	17
2026	Prediction of yeast protein-protein interaction network: insights from the Gene Ontology and annotations. <i>Nucleic Acids Research</i> , 2006, 34, 2137-2150.	6.5	193
2027	CRSD: a comprehensive web server for composite regulatory signature discovery. <i>Nucleic Acids Research</i> , 2006, 34, W571-W577.	6.5	35
2028	Detecting uber-operons in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2006, 34, 2418-2427.	6.5	33
2029	AGMIAL: implementing an annotation strategy for prokaryote genomes as a distributed system. <i>Nucleic Acids Research</i> , 2006, 34, 3533-3545.	6.5	84
2030	An open-access long oligonucleotide microarray resource for analysis of the human and mouse transcriptomes. <i>Nucleic Acids Research</i> , 2006, 34, e87-e87.	6.5	89
2031	Apoptosis resistance downstream of eIF4E: posttranscriptional activation of an anti-apoptotic transcript carrying a consensus hairpin structure. <i>Nucleic Acids Research</i> , 2006, 34, 4375-4386.	6.5	61

#	ARTICLE	IF	CITATIONS
2032	Identifying functional gene sets from hierarchically clustered expression data: map of abiotic stress regulated genes in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2006, 34, e124-e124.	6.5	13
2033	A systematic approach to infer biological relevance and biases of gene network structures. <i>Nucleic Acids Research</i> , 2006, 34, e6-e6.	6.5	15
2034	Gene Expression Profile of Human Airway Epithelium Induced by Hyperoxia In Vivo. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2006, 35, 424-435.	1.4	22
2035	dictyBase and the Dicty Stock Center. , 2006, 346, 51-74.		17
2036	Creating Fungal Pathway/Genome Databases Using Pathway Tools. <i>Applied Mycology and Biotechnology</i> , 2006, 6, 209-225.	0.3	0
2037	Systematic identification and functional screens of uncharacterized proteins associated with eukaryotic ribosomal complexes. <i>Genes and Development</i> , 2006, 20, 1294-1307.	2.7	248
2038	IDENTIFYING BIOLOGICAL PATHWAYS VIA PHASE DECOMPOSITION AND PROFILE EXTRACTION. , 2006, , .		1
2039	The RCSB PDB information portal for structural genomics. <i>Nucleic Acids Research</i> , 2006, 34, D302-D305.	6.5	334
2040	Panzea: a database and resource for molecular and functional diversity in the maize genome. <i>Nucleic Acids Research</i> , 2006, 34, D752-D757.	6.5	89
2041	Towards applying text mining and natural language processing for biomedical ontology acquisition. , 2006, , .		10
2042	Engineering Approaches Toward Biological Information Integration at the Systems Level. <i>Current Bioinformatics</i> , 2006, 1, 85-93.	0.7	3
2043	Microarray RNA transcriptional profiling: Part II. Analytical considerations and annotation. <i>Expert Review of Molecular Diagnostics</i> , 2006, 6, 703-715.	1.5	12
2044	MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , 2006, 34, D169-D172.	6.5	348
2045	Computational Analyses of Ancient Polyploidy. <i>Current Bioinformatics</i> , 2006, 1, 131-146.	0.7	5
2046	Methods for Identifying and Mapping Recent Segmental and Gene Duplications in Eukaryotic Genomes. , 2006, 338, 9-20.		13
2047	The YEASTRACT database: a tool for the analysis of transcription regulatory associations in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2006, 34, D446-D451.	6.5	421
2048	The Stanford Microarray Database: A User's Guide. , 2006, 338, 191-208.		16
2049	Estradiol Regulates Different Genes in Human Breast Tumor Xenografts Compared with the Identical Cells in Culture. <i>Endocrinology</i> , 2006, 147, 700-713.	1.4	46

#	ARTICLE	IF	CITATIONS
2050	Knowledge modeling and its application in life sciences. , 2006, , .		24
2051	Clustering microarray gene expression data using weighted Chinese restaurant process. Bioinformatics, 2006, 22, 1988-1997.	1.8	110
2052	Computational analysis of tissue-specific combinatorial gene regulation: predicting interaction between transcription factors in human tissues. Nucleic Acids Research, 2006, 34, 4925-4936.	6.5	134
2053	Discovering significant OPSM subspace clusters in massive gene expression data. , 2006, , .		23
2054	POXO: a web-enabled tool series to discover transcription factor binding sites. Nucleic Acids Research, 2006, 34, W534-W540.	6.5	10
2055	Towards a Phenotypic Semantic Web. Current Bioinformatics, 2006, 1, 235-246.	0.7	6
2056	[17] Using Ontologies to Annotate Microarray Experiments. Methods in Enzymology, 2006, 411, 325-339.	0.4	9
2057	GeneChips in Stem Cell Research. Methods in Enzymology, 2006, 420, 162-224.	0.4	4
2058	Clustering pair-wise dissimilarity data into partially ordered sets. , 2006, , .		5
2059	Relative contributions of structural designability and functional diversity in molecular evolution of duplicates. Bioinformatics, 2006, 22, e440-e445.	1.8	8
2060	GO for gene documents. , 2006, , .		1
2061	Polyglutamine expansion causes neurodegeneration by altering the neuronal differentiation program. Human Molecular Genetics, 2006, 15, 691-703.	1.4	67
2062	Phytophthora functional genomics database (PFGD): functional genomics of phytophthora-plant interactions. Nucleic Acids Research, 2006, 34, D465-D470.	6.5	20
2063	Issues in Comparative Fungal Genomics. Applied Mycology and Biotechnology, 2006, , 99-122.	0.3	0
2064	SubLoc: a server/client suite for protein subcellular location based on SOAP. Bioinformatics, 2006, 22, 376-377.	1.8	47
2065	A graphical model for predicting protein molecular function. , 2006, , .		7
2066	Identification and function of hypoxia-response genes in Drosophila melanogaster. Physiological Genomics, 2006, 25, 134-141.	1.0	69
2067	Identification of a novel putative mitogen-activated kinase cascade on human chromosome 21 by computational approaches. Bioinformatics, 2006, 22, 775-778.	1.8	13

#	ARTICLE	IF	CITATIONS
2068	A Mixture model with random-effects components for clustering correlated gene-expression profiles. <i>Bioinformatics</i> , 2006, 22, 1745-1752.	1.8	143
2069	Combination of text-mining algorithms increases the performance. <i>Bioinformatics</i> , 2006, 22, 2151-2157.	1.8	20
2070	Analysis of multiple tissue-specific cDNA libraries from the Pacific whiteleg shrimp, <i>Litopenaeus vannamei</i> . <i>Integrative and Comparative Biology</i> , 2006, 46, 931-939.	0.9	28
2071	Metagenome Analyses. , 2006, , 261-286.		1
2072	Striking Similarities in the Genomic Distribution of Tandemly Arrayed Genes in Arabidopsis and Rice. <i>PLoS Computational Biology</i> , 2006, 2, e115.	1.5	265
2073	Resources and Tools for Investigating Biomolecular Networks in Mammals. <i>Current Pharmaceutical Design</i> , 2006, 12, 3723-34.	0.9	3
2074	Mice and Men: Their Promoter Properties. <i>PLoS Genetics</i> , 2006, 2, e54.	1.5	95
2075	Expression Microarray Proteomics and the Search for Cancer Biomarkers. <i>Current Genomics</i> , 2006, 7, 399-426.	0.7	13
2076	Analysis of Gene Expression Using Gene Sets Discriminates Cancer Patients with and without Late Radiation Toxicity. <i>PLoS Medicine</i> , 2006, 3, e422.	3.9	117
2077	Positive Selection, Relaxation, and Acceleration in the Evolution of the Human and Chimp Genome. <i>PLoS Computational Biology</i> , 2006, 2, e38.	1.5	128
2078	The Effect of Multifunctionality on the Rate of Evolution in Yeast. <i>Molecular Biology and Evolution</i> , 2006, 23, 721-722.	3.5	52
2079	Mining literature for systems biology. <i>Briefings in Bioinformatics</i> , 2006, 7, 399-406.	3.2	41
2080	Identification of the Proliferation/Differentiation Switch in the Cellular Network of Multicellular Organisms. <i>PLoS Computational Biology</i> , 2006, 2, e145.	1.5	91
2081	Genome-Scale Identification of Membrane-Associated Human mRNAs. <i>PLoS Genetics</i> , 2006, 2, e11.	1.5	84
2082	Understanding Mammalian Genetic Systems: The Challenge of Phenotyping in the Mouse. <i>PLoS Genetics</i> , 2006, 2, e118.	1.5	82
2083	Bias of Selection on Human Copy-Number Variants. <i>PLoS Genetics</i> , 2006, 2, e20.	1.5	237
2084	The LCB Data Warehouse. <i>Bioinformatics</i> , 2006, 22, 1024-1026.	1.8	34
2085	Transgenic and Gene Replacement Models of Epilepsy: Targeting Ion Channel and Neurotransmission Pathways in Mice. , 2006, , 199-222.		4

#	ARTICLE	IF	CITATIONS
2086	An extensible automated protein annotation tool: standardizing input and output using validated XML. <i>Bioinformatics</i> , 2006, 22, 291-296.	1.8	1
2087	A scalable method for integration and functional analysis of multiple microarray datasets. <i>Bioinformatics</i> , 2006, 22, 2890-2897.	1.8	127
2088	A data-driven clustering method for time course gene expression data. <i>Nucleic Acids Research</i> , 2006, 34, 1261-1269.	6.5	156
2089	Incorporating biological knowledge into distance-based clustering analysis of microarray gene expression data. <i>Bioinformatics</i> , 2006, 22, 1259-1268.	1.8	103
2090	Reversible Kinetic Analysis of Myc Targets In vivo Provides Novel Insights into Myc-Mediated Tumorigenesis. <i>Cancer Research</i> , 2006, 66, 4591-4601.	0.4	71
2091	A novel sensitive method for the detection of user-defined compositional bias in biological sequences. <i>Bioinformatics</i> , 2006, 22, 1055-1063.	1.8	16
2092	DBD: a transcription factor prediction database. <i>Nucleic Acids Research</i> , 2006, 34, D74-D81.	6.5	186
2093	Transcription Factor Map Alignment of Promoter Regions. <i>PLoS Computational Biology</i> , 2006, 2, e49.	1.5	50
2094	Functional Classification Using Phylogenomic Inference. <i>PLoS Computational Biology</i> , 2006, 2, e77.	1.5	61
2095	Intrinsic Disorder Is a Common Feature of Hub Proteins from Four Eukaryotic Interactomes. <i>PLoS Computational Biology</i> , 2006, 2, e100.	1.5	512
2096	Phylogenetic Reconstruction of Orthology, Paralogy, and Conserved Synteny for Dog and Human. <i>PLoS Computational Biology</i> , 2006, 2, e133.	1.5	130
2097	Forces Shaping the Fastest Evolving Regions in the Human Genome. <i>PLoS Genetics</i> , 2006, 2, e168.	1.5	399
2098	Antigen-induced differential gene expression in lymphocytes and gene expression profile in synovium prior to the onset of arthritis. <i>Autoimmunity</i> , 2006, 39, 663-673.	1.2	10
2099	Hierarchical multi-label prediction of gene function. <i>Bioinformatics</i> , 2006, 22, 830-836.	1.8	422
2100	Dynamic Changes in Subgraph Preference Profiles of Crucial Transcription Factors. <i>PLoS Computational Biology</i> , 2006, 2, e47.	1.5	14
2101	Transcriptional Profiling of Aging in Human Muscle Reveals a Common Aging Signature. <i>PLoS Genetics</i> , 2006, 2, e115.	1.5	331
2102	Incorporating gene functions as priors in model-based clustering of microarray gene expression data. <i>Bioinformatics</i> , 2006, 22, 795-801.	1.8	91
2103	Bacterial Postgenomics: the Promise and Peril of Systems Biology \hat{a} - \hat{z} . <i>Journal of Bacteriology</i> , 2006, 188, 7999-8004.	1.0	3

#	ARTICLE	IF	CITATIONS
2104	Assessing semantic similarity measures for the characterization of human regulatory pathways. <i>Bioinformatics</i> , 2006, 22, 967-973.	1.8	212
2105	Expression of Late Cell Cycle Genes and an Increased Proliferative Capacity Characterize Very Early Relapse of Childhood Acute Lymphoblastic Leukemia. <i>Clinical Cancer Research</i> , 2006, 12, 4553-4561.	3.2	51
2106	PIANA: protein interactions and network analysis. <i>Bioinformatics</i> , 2006, 22, 1015-1017.	1.8	55
2107	Genome-Wide Analysis of mRNAs Regulated by Droscha and Argonaute Proteins in <i>Drosophila melanogaster</i> . <i>Molecular and Cellular Biology</i> , 2006, 26, 2965-2975.	1.1	125
2108	A systematic comparison and evaluation of biclustering methods for gene expression data. <i>Bioinformatics</i> , 2006, 22, 1122-1129.	1.8	782
2109	Development and Characterization of a Normalized Canine Retinal cDNA Library for Genomic and Expression Studies. , 2006, 47, 2632.		9
2110	From genomes to systems: the path with yeast. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 477-482.	1.8	37
2111	The Life Sciences Semantic Web is Full of Creeps!. <i>Briefings in Bioinformatics</i> , 2006, 7, 275-286.	3.2	73
2112	Identification of function-associated loop motifs and application to protein function prediction. <i>Bioinformatics</i> , 2006, 22, 2237-2243.	1.8	41
2113	Effects of replacing the unreliable cDNA microarray measurements on the disease classification based on gene expression profiles and functional modules. <i>Bioinformatics</i> , 2006, 22, 2883-2889.	1.8	36
2114	Thrombin and NAD(P)H Oxidase-Mediated Regulation of CD44 and BMP4-Id Pathway in VSMC, Restenosis, and Atherosclerosis. <i>Circulation Research</i> , 2006, 98, 1254-1263.	2.0	84
2115	Likelihood-Based Inference on Haplotype Effects in Genetic Association Studies. <i>Journal of the American Statistical Association</i> , 2006, 101, 89-104.	1.8	127
2116	MiGenes: a searchable interspecies database of mitochondrial proteins curated using gene ontology annotation. <i>Bioinformatics</i> , 2006, 22, 485-492.	1.8	19
2117	Thematic review series: Systems Biology Approaches to Metabolic and Cardiovascular Disorders Approaches to lipid metabolism gene identification and characterization in the postgenomic era. <i>Journal of Lipid Research</i> , 2006, 47, 1891-1907.	2.0	1
2118	Biological characterization of gene response in Rpe65 mouse model of Leber's congenital amaurosis during progression of the disease. <i>FASEB Journal</i> , 2006, 20, 2036-2049.	0.2	46
2119	Variants in the GH-IGF axis confer susceptibility to lung cancer. <i>Genome Research</i> , 2006, 16, 693-701.	2.4	102
2120	A global assembly of cotton ESTs. <i>Genome Research</i> , 2006, 16, 441-450.	2.4	138
2121	DNA Microarray and Proteomic Analyses of the RpoS Regulon in <i>Geobacter sulfurreducens</i> . <i>Journal of Bacteriology</i> , 2006, 188, 2792-2800.	1.0	62

#	ARTICLE	IF	CITATIONS
2122	Expression Profileâ€œDefined Classification of Lung Adenocarcinoma Shows Close Relationship With Underlying Major Genetic Changes and Clinicopathologic Behaviors. <i>Journal of Clinical Oncology</i> , 2006, 24, 1679-1688.	0.8	296
2123	System-wide Genomic and Biochemical Comparisons of Sialic Acid Biology Among Primates and Rodents. <i>Journal of Biological Chemistry</i> , 2006, 281, 25689-25702.	1.6	52
2124	Transcriptional profiling of reporter genes used for molecular imaging of embryonic stem cell transplantation. <i>Physiological Genomics</i> , 2006, 25, 29-38.	1.0	76
2125	Babel's tower revisited: a universal resource for cross-referencing across annotation databases. <i>Bioinformatics</i> , 2006, 22, 2934-2939.	1.8	39
2126	A transcriptome analysis of the <i>Aedes aegypti</i> vitellogenic fat body. <i>Journal of Insect Science</i> , 2006, 6, 1-26.	0.6	18
2127	Heterozygous carriers of Nijmegen Breakage Syndrome have a distinct gene expression phenotype. <i>Genome Research</i> , 2006, 16, 973-979.	2.4	17
2129	Behavioural Genetics of the Honey Bee <i>Apis mellifera</i> . <i>Advances in Insect Physiology</i> , 2006, , 1-49.	1.1	40
2130	An Improved Statistic for Detecting Over-Represented Gene Ontology Annotations in Gene Sets. <i>Lecture Notes in Computer Science</i> , 2006, , 85-98.	1.0	15
2131	Celecoxib Treatment Alters the Gene Expression Profile of Normal Colonic Mucosa. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 1382-1391.	1.1	31
2132	Toward a Molecular Understanding of Pleiotropy. <i>Genetics</i> , 2006, 173, 1885-1891.	1.2	182
2133	Geneâ€œExpression Profiling Discriminates between Cerebral Malaria (CM)â€œSusceptible Mice and CMâ€œResistant Mice. <i>Journal of Infectious Diseases</i> , 2006, 193, 312-321.	1.9	50
2134	Quantitative Comparison of Caste Differences in Honeybee Hemolymph. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2252-2262.	2.5	133
2135	Analysis of protein sequence and interaction data for candidate disease gene prediction. <i>Nucleic Acids Research</i> , 2006, 34, e130-e130.	6.5	138
2136	Genetics of Asthma and Chronic Obstructive Pulmonary Disease. , 0, , .		3
2137	Genome-Wide Expression Profiling Reveals EBV-Associated Inhibition of MHC Class I Expression in Nasopharyngeal Carcinoma. <i>Cancer Research</i> , 2006, 66, 7999-8006.	0.4	207
2138	Anatomic Demarcation by Positional Variation in Fibroblast Gene Expression Programs. <i>PLoS Genetics</i> , 2006, 2, e119.	1.5	413
2139	Genome-Wide Search of Gene Conversions in Duplicated Genes of Mouse and Rat. <i>Molecular Biology and Evolution</i> , 2006, 23, 927-940.	3.5	76
2140	BAFF controls B cell metabolic fitness through a PKC β - and Akt-dependent mechanism. <i>Journal of Experimental Medicine</i> , 2006, 203, 2551-2562.	4.2	178

#	ARTICLE	IF	CITATIONS
2141	Computer Support for Physiological Cell Modelling using an Ontology on Cell Physiology. , 2006, 2006, 4171-4.		0
2143	Genome-Wide Discovery of Modulators of Transcriptional Interactions in Human B Lymphocytes. Lecture Notes in Computer Science, 2006, , 348-362.	1.0	23
2144	Microarrays in breast cancer research and clinical practice – the future lies ahead. Endocrine-Related Cancer, 2006, 13, 1017-1031.	1.6	22
2145	Autoregulation of Ribosome Biosynthesis by a Translational Response in Fission Yeast. Molecular and Cellular Biology, 2006, 26, 1731-1742.	1.1	41
2146	Lipopolysaccharide-induced gene expression in murine macrophages is enhanced by prior exposure to oxLDL. Journal of Lipid Research, 2006, 47, 2259-2267.	2.0	45
2147	Genes Associated With Breast Cancer Metastatic to Bone. Journal of Clinical Oncology, 2006, 24, 2261-2267.	0.8	278
2148	Post-genomic approaches to understanding the mechanisms of environmentally induced phenotypic plasticity. Journal of Experimental Biology, 2006, 209, 2328-2336.	0.8	87
2149	RNA editing in Drosophila melanogaster: New targets and functional consequences. Rna, 2006, 12, 1922-1932.	1.6	51
2150	Piroxicam and Cisplatin in a Mouse Model of Peritoneal Mesothelioma. Clinical Cancer Research, 2006, 12, 6133-6143.	3.2	39
2151	Acute Myeloid Leukemia-Associated Mkl1 (Mrtf-a) Is a Key Regulator of Mammary Gland Function. Molecular and Cellular Biology, 2006, 26, 5809-5826.	1.1	154
2152	GENE ONTOLOGY SIMILARITY MEASURES BASED ON LINEAR ORDER STATISTICS. International Journal of Uncertainty, Fuzziness and Knowledge-Based Systems, 2006, 14, 639-661.	0.9	10
2153	Robust multi-scale clustering of large DNA microarray datasets with the consensus algorithm. Bioinformatics, 2006, 22, 58-67.	1.8	72
2154	Functional bioinformatics for Arabidopsis thaliana. Bioinformatics, 2006, 22, 1130-1136.	1.8	28
2155	Search for low penetrance alleles for colorectal cancer through a scan of 1467 non-synonymous SNPs in 2575 cases and 2707 controls with validation by kin-cohort analysis of 14...704 first-degree relatives. Human Molecular Genetics, 2006, 15, 3263-3271.	1.4	61
2156	Short blocks from the noncoding parts of the human genome have instances within nearly all known genes and relate to biological processes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6605-6610.	3.3	111
2157	A global topology map of the Saccharomyces cerevisiae membrane proteome. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11142-11147.	3.3	124
2158	Global analysis of gene function in yeast by quantitative phenotypic profiling. Molecular Systems Biology, 2006, 2, 2006.0001.	3.2	142
2159	The Forkhead transcription factor Hcm1 regulates chromosome segregation genes and fills the S-phase gap in the transcriptional circuitry of the cell cycle. Genes and Development, 2006, 20, 2266-2278.	2.7	250

#	ARTICLE	IF	CITATIONS
2160	A measure of semantic similarity between gene ontology terms based on semantic pathway covering*. Progress in Natural Science: Materials International, 2006, 16, 721-726.	1.8	11
2161	Bioinformatics Approaches to Integrate Metabolomics and Other Systems Biology Data. , 2006, , 105-115.		14
2162	Genome-wide in silico identification and analysis of cis natural antisense transcripts (cis-NATs) in ten species. Nucleic Acids Research, 2006, 34, 3465-3475.	6.5	155
2163	Focused Microarray Analysis: Characterization of Phenomes by Gene Expression Profiling. Current Pharmacogenomics and Personalized Medicine: the International Journal for Expert Reviews in Pharmacogenomics, 2006, 4, 245-260.	0.3	9
2164	KOBAS server: a web-based platform for automated annotation and pathway identification. Nucleic Acids Research, 2006, 34, W720-W724.	6.5	682
2165	Sequencing and analysis of 10,967 full-length cDNA clones from <i>Xenopus laevis</i> and <i>Xenopus tropicalis</i> reveals post-tetraploidization transcriptome remodeling. Genome Research, 2006, 16, 796-803.	2.4	73
2166	Hypoxia Modifies the Transcriptome of Primary Human Monocytes: Modulation of Novel Immune-Related Genes and Identification Of CC-Chemokine Ligand 20 as a New Hypoxia-Inducible Gene. Journal of Immunology, 2006, 177, 1941-1955.	0.4	189
2167	Reliable gene signatures for microarray classification: assessment of stability and performance. Bioinformatics, 2006, 22, 2356-2363.	1.8	79
2168	Sex-Related Effect on Gene Expression in the Mouse Meibomian Gland. Current Eye Research, 2006, 31, 119-128.	0.7	24
2169	Development of FuGO: An Ontology for Functional Genomics Investigations. OMICS A Journal of Integrative Biology, 2006, 10, 199-204.	1.0	56
2170	<i>Brucella melitensis</i> Triggers Time-Dependent Modulation of Apoptosis and Down-Regulation of Mitochondrion-Associated Gene Expression in Mouse Macrophages. Infection and Immunity, 2006, 74, 5035-5046.	1.0	85
2171	Functional Interpretation of Microarray Experiments. OMICS A Journal of Integrative Biology, 2006, 10, 398-410.	1.0	74
2172	A Corpus-Driven Approach for Design, Evolution and Alignment of Ontologies. , 2006, , .		3
2173	Application of Bioinformatics in the Design of Gene Expression Microarrays. , 2006, , .		4
2174	Bio-Ontology and text: bridging the modeling gap. Bioinformatics, 2006, 22, 2421-2429.	1.8	28
2175	On Methods for Gene Function Scoring as a Means of Facilitating the Interpretation of Microarray Results. Journal of Computational Biology, 2006, 13, 798-809.	0.8	21
2176	Combining Gene Annotations and Gene Expression Data in Model-Based Clustering: Weighted Method. OMICS A Journal of Integrative Biology, 2006, 10, 28.	1.0	15
2178	National Center for Biomedical Ontology: Advancing Biomedicine through Structured Organization of Scientific Knowledge. OMICS A Journal of Integrative Biology, 2006, 10, 185-198.	1.0	149

#	ARTICLE	IF	CITATIONS
2179	CLUSTERING BIOLOGICAL ANNOTATIONS AND GENE EXPRESSION DATA TO IDENTIFY PUTATIVELY CO-REGULATED BIOLOGICAL PROCESSES. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 833-852.	0.3	21
2181	GeneGrid: From "Virtual" Bioinformatics Laboratory to "Smart" Bioinformatics Laboratory. , 2006, , .		1
2182	BABELOMICS: a systems biology perspective in the functional annotation of genome-scale experiments. <i>Nucleic Acids Research</i> , 2006, 34, W472-W476.	6.5	240
2183	Challenges for Modeling and Simulation Methods in Systems Biology. , 2006, , .		13
2184	Extracting Metadata from Biological Experimental Data. , 0, , .		1
2185	Cross-species analysis of biological networks by Bayesian alignment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10967-10972.	3.3	136
2186	Microarray Analysis of Mouse Ear Tissue Exposed to Bis-(2-chloroethyl) Sulfide: Gene Expression Profiles Correlate with Treatment Efficacy and An Established Clinical Endpoint. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2006, 317, 76-87.	1.3	29
2187	Molecular Evolution and Population Genetic Analysis of Candidate Female Reproductive Genes in <i>Drosophila</i> . <i>Genetics</i> , 2006, 173, 2039-2047.	1.2	50
2188	Genomic dissection of behavioral maturation in the honey bee. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16068-16075.	3.3	216
2189	WEGO: a web tool for plotting GO annotations. <i>Nucleic Acids Research</i> , 2006, 34, W293-W297.	6.5	2,529
2190	Radiation-Induced Changes in Gene Expression Involve Recruitment of Existing Messenger RNAs to and away from Polysomes. <i>Cancer Research</i> , 2006, 66, 1052-1061.	0.4	120
2191	In-depth analysis of the membrane and cytosolic proteome of red blood cells. <i>Blood</i> , 2006, 108, 791-801.	0.6	388
2192	Prediction of Genomic Functional Elements. <i>Annual Review of Genomics and Human Genetics</i> , 2006, 7, 315-338.	2.5	40
2193	Improving reliability and performance of DNA microarrays. <i>Expert Review of Molecular Diagnostics</i> , 2006, 6, 481-492.	1.5	13
2195	A System-Based Approach to Interpret Dose- and Time-Dependent Microarray Data: Quantitative Integration of Gene Ontology Analysis for Risk Assessment. <i>Toxicological Sciences</i> , 2006, 92, 560-577.	1.4	50
2196	Importance of dosage standardization for interpreting transcriptomal signature profiles: Evidence from studies of xenoestrogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12033-12038.	3.3	60
2197	Improving Identification of Differentially Expressed Genes by Integrative Analysis of Affymetrix and Illumina Arrays. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 369-380.	1.0	7
2198	Genome Snapshot: a new resource at the <i>Saccharomyces</i> Genome Database (SGD) presenting an overview of the <i>Saccharomyces cerevisiae</i> genome. <i>Nucleic Acids Research</i> , 2006, 34, D442-D445.	6.5	91

#	ARTICLE	IF	CITATIONS
2199	Integrative Genomics Identifies Distinct Molecular Classes of Neuroblastoma and Shows That Multiple Genes Are Targeted by Regional Alterations in DNA Copy Number. <i>Cancer Research</i> , 2006, 66, 6050-6062.	0.4	178
2200	Profiles of Growth Hormone (GH)-regulated Genes Reveal Time-dependent Responses and Identify a Mechanism for Regulation of Activating Transcription Factor 3 By GH. <i>Journal of Biological Chemistry</i> , 2006, 281, 4132-4141.	1.6	40
2201	Genome-Wide Prediction of <i>C. elegans</i> Genetic Interactions. <i>Science</i> , 2006, 311, 1481-1484.	6.0	258
2202	Cockayne syndrome group B protein (CSB) plays a general role in chromatin maintenance and remodeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9613-9618.	3.3	141
2203	Retroviral vector integration deregulates gene expression but has no consequence on the biology and function of transplanted T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1457-1462.	3.3	172
2204	GOBASE—a database of organelle and bacterial genome information. <i>Nucleic Acids Research</i> , 2006, 34, D697-D699.	6.5	19
2205	[18] Interpreting Experimental Results Using Gene Ontologies. <i>Methods in Enzymology</i> , 2006, 411, 340-352.	0.4	52
2206	Improved scoring of functional groups from gene expression data by decorrelating GO graph structure. <i>Bioinformatics</i> , 2006, 22, 1600-1607.	1.8	1,927
2207	Downregulation of Electron Transport Chain Genes in Visceral Adipose Tissue in Type 2 Diabetes Independent of Obesity and Possibly Involving Tumor Necrosis Factor- α . <i>Diabetes</i> , 2006, 55, 1792-1799.	0.3	162
2208	SNP500Cancer: a public resource for sequence validation, assay development, and frequency analysis for genetic variation in candidate genes. <i>Nucleic Acids Research</i> , 2006, 34, D617-D621.	6.5	242
2209	Evaluation of the Transcriptome and Genome to Inform the Study of Metabolic Control in Plants. , 0, , 1-23.		3
2210	Interferon type I and type II responses in an Atlantic salmon (<i>Salmo salar</i>) SHK-1 cell line by the salmon TRAITS/SGP microarray. <i>Physiological Genomics</i> , 2007, 32, 33-44.	1.0	80
2211	Hippocampal Expression Analyses Reveal Selective Association of Immediate-Early, Neuroenergetic, and Myelinogenic Pathways with Cognitive Impairment in Aged Rats. <i>Journal of Neuroscience</i> , 2007, 27, 3098-3110.	1.7	201
2212	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
2213	Gallus GBrowse: a unified genomic database for the chicken. <i>Nucleic Acids Research</i> , 2007, 36, D719-D723.	6.5	9
2215	Informatics in neuroscience. <i>Briefings in Bioinformatics</i> , 2007, 8, 446-456.	3.2	13
2216	Increased glycolytic flux as an outcome of whole-genome duplication in yeast. <i>Molecular Systems Biology</i> , 2007, 3, 129.	3.2	197
2217	Attenuation of Allergic Contact Dermatitis Through the Endocannabinoid System. <i>Science</i> , 2007, 316, 1494-1497.	6.0	302

#	ARTICLE	IF	CITATIONS
2218	Species-specific endogenous retroviruses shape the transcriptional network of the human tumor suppressor protein p53. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18613-18618.	3.3	364
2219	Single-Cell Transcript Profiling of Barley Attacked by the Powdery Mildew Fungus. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 235-246.	1.4	42
2220	Evidence of spatially bound gene regulation in <i>Mus musculus</i> : Decreased gene expression proximal to microRNA genomic location. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5020-5025.	3.3	2
2221	Transcriptome Analysis of Cold Syndrome Using Microarray. <i>The American Journal of Chinese Medicine</i> , 2007, 35, 609-620.	1.5	19
2222	Domain Architecture Comparison for Multidomain Homology Identification. <i>Journal of Computational Biology</i> , 2007, 14, 496-516.	0.8	34
2223	A statistical approach using network structure in the prediction of protein characteristics. <i>Bioinformatics</i> , 2007, 23, 2314-2321.	1.8	6
2224	Gene symbol disambiguation using knowledge-based profiles. <i>Bioinformatics</i> , 2007, 23, 1015-1022.	1.8	50
2225	Genomic and Phenotypic Diversity of Coastal <i>Vibrio cholerae</i> Strains Is Linked to Environmental Factors. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3705-3714.	1.4	70
2226	Transcriptional signature with differential expression of BCL6 target genes accurately identifies BCL6-dependent diffuse large B cell lymphomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3207-3212.	3.3	130
2227	Restoration of Liver Mass after Injury Requires Proliferative and Not Embryonic Transcriptional Patterns. <i>Journal of Biological Chemistry</i> , 2007, 282, 11197-11204.	1.6	77
2228	Analysis of Temporal Gene Expression during <i>Bacillus subtilis</i> Spore Germination and Outgrowth. <i>Journal of Bacteriology</i> , 2007, 189, 3624-3634.	1.0	112
2229	Adaptive genic evolution in the <i>Drosophila</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2271-2276.	3.3	210
2230	A SYSTEMS BIOLOGY APPROACH TO THE STUDY OF CISPLATIN DRUG RESISTANCE IN OVARIAN CANCERS. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 383-405.	0.3	19
2231	Transcriptional Profiling of Antigen-Dependent Murine B Cell Differentiation and Memory Formation. <i>Journal of Immunology</i> , 2007, 179, 6808-6819.	0.4	145
2232	Functional Genomic Analysis Reveals Cross-talk between Peroxisome Proliferator-activated Receptor β and Calcium Signaling in Human Colorectal Cancer Cells. <i>Journal of Biological Chemistry</i> , 2007, 282, 23387-23401.	1.6	29
2233	DISEASE-RELATED CONCEPT MINING BY KNOWLEDGE-BASED TWO-DIMENSIONAL GENE MAPPING. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 1047-1067.	0.3	4
2234	Systems Biology and Computational Proteomics. <i>Lecture Notes in Computer Science</i> , 2007, , .	1.0	1
2235	Targeted discovery of novel human exons by comparative genomics. <i>Genome Research</i> , 2007, 17, 1763-1773.	2.4	42

#	ARTICLE	IF	CITATIONS
2236	Insights into rubber biosynthesis from transcriptome analysis of <i>Hevea brasiliensis</i> latex. <i>Journal of Experimental Botany</i> , 2007, 58, 2429-2440.	2.4	163
2237	Transcriptome Profile of Human Colorectal Adenomas. <i>Molecular Cancer Research</i> , 2007, 5, 1263-1275.	1.5	428
2238	Thousands of human mobile element fragments undergo strong purifying selection near developmental genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8005-8010.	3.3	219
2239	Defining functional distance using manifold embeddings of gene ontology annotations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11334-11339.	3.3	34
2240	Evola: Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees. <i>Nucleic Acids Research</i> , 2007, 36, D787-D792.	6.5	33
2241	Modeling complex genetic interactions in a simple eukaryotic genome: actin displays a rich spectrum of complex haploinsufficiencies. <i>Genes and Development</i> , 2007, 21, 148-159.	2.7	80
2242	A genome-wide approach to identify genetic variants that contribute to etoposide-induced cytotoxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9758-9763.	3.3	195
2243	Gyrase inhibitors induce an oxidative damage cellular death pathway in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2007, 3, 91.	3.2	397
2244	Ontologies for Molecular Biology. , 0, , 1061-1086.		1
2245	Mining Protein Pathway from Proteomic Data. , 2007, , .		1
2246	Integrating Biological Databases. , 0, , 1525-1571.		3
2247	Gpos-PLoc: an ensemble classifier for predicting subcellular localization of Gram-positive bacterial proteins. <i>Protein Engineering, Design and Selection</i> , 2007, 20, 39-46.	1.0	146
2248	Unsupervised Clustering of Gene Expression Time Series with Conditional Random Fields. , 2007, , .		4
2249	BioNetBuilder: automatic integration of biological networks. <i>Bioinformatics</i> , 2007, 23, 392-393.	1.8	82
2250	Detection of eQTL modules mediated by activity levels of transcription factors. <i>Bioinformatics</i> , 2007, 23, 2290-2297.	1.8	35
2251	An efficient strategy for extensive integration of diverse biological data for protein function prediction. <i>Bioinformatics</i> , 2007, 23, 3364-3373.	1.8	56
2252	Gene3D: comprehensive structural and functional annotation of genomes. <i>Nucleic Acids Research</i> , 2007, 36, D414-D418.	6.5	68
2253	Annotation-based distance measures for patient subgroup discovery in clinical microarray studies. <i>Bioinformatics</i> , 2007, 23, 2256-2264.	1.8	12

#	ARTICLE	IF	CITATIONS
2254	Gene Duplication and Adaptive Evolution of Digestive Proteases in <i>Drosophila arizonae</i> Female Reproductive Tracts. <i>PLoS Genetics</i> , 2007, 3, e148.	1.5	70
2255	Incorporating prior knowledge of predictors into penalized classifiers with multiple penalty terms. <i>Bioinformatics</i> , 2007, 23, 1775-1782.	1.8	62
2256	Web Services at the European Bioinformatics Institute. <i>Nucleic Acids Research</i> , 2007, 35, W6-W11.	6.5	166
2257	Where Have All the Interactions Gone? Estimating the Coverage of Two-Hybrid Protein Interaction Maps. <i>PLoS Computational Biology</i> , 2007, 3, e214.	1.5	151
2258	Conservation of Regional Gene Expression in Mouse and Human Brain. <i>PLoS Genetics</i> , 2007, 3, e59.	1.5	91
2259	The (In)dependence of Alternative Splicing and Gene Duplication. <i>PLoS Computational Biology</i> , 2007, 3, e33.	1.5	66
2260	Inferring Function Using Patterns of Native Disorder in Proteins. <i>PLoS Computational Biology</i> , 2007, 3, e162.	1.5	124
2261	Predicting Protein Function with Hierarchical Phylogenetic Profiles: The Gene3D Phylo-Tuner Method Applied to Eukaryotic Genomes. <i>PLoS Computational Biology</i> , 2007, 3, e237.	1.5	41
2262	Superfamily Assignments for the Yeast Proteome through Integration of Structure Prediction with the Gene Ontology. <i>PLoS Biology</i> , 2007, 5, e76.	2.6	48
2263	Improved detection of overrepresentation of Gene-Ontology annotations with parent-child analysis. <i>Bioinformatics</i> , 2007, 23, 3024-3031.	1.8	370
2264	Ontology development for biological systems: immunology. <i>Bioinformatics</i> , 2007, 23, 913-915.	1.8	49
2265	Predicting Experimental Properties of Proteins from Sequence by Machine Learning Techniques. <i>Current Protein and Peptide Science</i> , 2007, 8, 121-133.	0.7	13
2266	Exploiting inter-gene information for microarray data integration. , 2007, , .		5
2267	Adrenal transcription regulatory genes modulated by angiotensin II and their role in steroidogenesis. <i>Physiological Genomics</i> , 2007, 30, 26-34.	1.0	50
2268	PPAR α Regulates a Molecular Signature of Marrow Mesenchymal Stem Cells. <i>PPAR Research</i> , 2007, 2007, 1-13.	1.1	26
2269	OBO to OWL: a protege OWL tab to read/save OBO ontologies. <i>Bioinformatics</i> , 2007, 23, 1868-1870.	1.8	50
2270	EBIMed-text crunching to gather facts for proteins from Medline. <i>Bioinformatics</i> , 2007, 23, e237-e244.	1.8	174
2271	Computing the maximum similarity bi-clusters of gene expression data. <i>Bioinformatics</i> , 2007, 23, 50-56.	1.8	142

#	ARTICLE	IF	CITATIONS
2272	EuSplice: a unified resource for the analysis of splice signals and alternative splicing in eukaryotic genes. <i>Bioinformatics</i> , 2007, 23, 1815-1823.	1.8	25
2273	Computational identification of candidate loci for recessively inherited mutation using high-throughput SNP arrays. <i>Bioinformatics</i> , 2007, 23, 1952-1961.	1.8	2
2274	Systematic construction of gene coexpression networks with applications to human T helper cell differentiation process. <i>Bioinformatics</i> , 2007, 23, 2096-2103.	1.8	94
2275	Prediction of Gene Expression in Embryonic Structures of <i>Drosophila melanogaster</i> . <i>PLoS Computational Biology</i> , 2007, 3, e144.	1.5	13
2277	Elucidating the Altered Transcriptional Programs in Breast Cancer using Independent Component Analysis. <i>PLoS Computational Biology</i> , 2007, 3, e161.	1.5	108
2278	Getting Started in Probabilistic Graphical Models. <i>PLoS Computational Biology</i> , 2007, 3, e252.	1.5	42
2279	Genome-Wide Profiling of DNA Methylation Reveals a Class of Normally Methylated CpG Island Promoters. <i>PLoS Genetics</i> , 2007, 3, e181.	1.5	319
2280	Characterization of phloem-sap transcription profile in melon plants. <i>Journal of Experimental Botany</i> , 2007, 58, 3645-3656.	2.4	132
2281	ApiDB: integrated resources for the apicomplexan bioinformatics resource center. <i>Nucleic Acids Research</i> , 2007, 35, D427-D430.	6.5	94
2282	Query-driven module discovery in microarray data. <i>Bioinformatics</i> , 2007, 23, 2573-2580.	1.8	25
2283	Mouse Embryology Research Techniques and a Comparison of Embryonic Development between Bouse and Man. , 2007, , 165-209.		2
2284	Challenges and Solutions in Proteomics. <i>Current Genomics</i> , 2007, 8, 21-28.	0.7	12
2285	Specificity and Evolvability in Eukaryotic Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2007, 3, e25.	1.5	111
2286	AGEMAP: A Gene Expression Database for Aging in Mice. <i>PLoS Genetics</i> , 2007, 3, e201.	1.5	355
2287	SPINE: a framework for signaling-regulatory pathway inference from cause-effect experiments. <i>Bioinformatics</i> , 2007, 23, i359-i366.	1.8	93
2288	An insight into the sialome of the oriental rat flea, <i>Xenopsylla cheopis</i> (Rots). <i>BMC Genomics</i> , 2007, 8, 102.	1.2	70
2289	A structural alignment kernel for protein structures. <i>Bioinformatics</i> , 2007, 23, 1090-1098.	1.8	38
2290	Comparative analysis of microarray normalization procedures: effects on reverse engineering gene networks. <i>Bioinformatics</i> , 2007, 23, i282-i288.	1.8	163

#	ARTICLE	IF	CITATIONS
2291	GeneTrail-advanced gene set enrichment analysis. <i>Nucleic Acids Research</i> , 2007, 35, W186-W192.	6.5	321
2292	Extensions to gene set enrichment. <i>Bioinformatics</i> , 2007, 23, 306-313.	1.8	195
2293	Neutrality, Compensation, and Negative Selection during Evolution of B-Cell Development Transcriptomes. <i>Molecular Biology and Evolution</i> , 2007, 24, 2610-2618.	3.5	7
2294	FatiGO +: a functional profiling tool for genomic data. Integration of functional annotation, regulatory motifs and interaction data with microarray experiments. <i>Nucleic Acids Research</i> , 2007, 35, W91-W96.	6.5	248
2295	Towards clustering of incomplete microarray data without the use of imputation. <i>Bioinformatics</i> , 2007, 23, 107-113.	1.8	15
2296	Proteomic Analysis of a Membrane Preparation from Rat Olfactory Sensory Cilia. <i>Chemical Senses</i> , 2007, 33, 145-162.	1.1	73
2297	PRIDE: new developments and new datasets. <i>Nucleic Acids Research</i> , 2007, 36, D878-D883.	6.5	124
2298	Mining co-regulated gene profiles for the detection of functional associations in gene expression data. <i>Bioinformatics</i> , 2007, 23, 1927-1935.	1.8	31
2299	A semantic web approach applied to integrative bioinformatics experimentation: a biological use case with genomics data. <i>Bioinformatics</i> , 2007, 23, 3080-3087.	1.8	41
2300	Enhancing the functional annotation of PDB structures in PDBsum using key figures extracted from the literature. <i>Bioinformatics</i> , 2007, 23, 1824-1827.	1.8	64
2301	In Vivo Validation of a Computationally Predicted Conserved Ath5 Target Gene Set. <i>PLoS Genetics</i> , 2007, 3, e159.	1.5	45
2302	Regeneration of the adult thymus is preceded by the expansion of K5+K8+ epithelial cell progenitors and by increased expression of Trp63, cMyc and Tcf3 transcription factors in the thymic stroma. <i>International Immunology</i> , 2007, 19, 1249-1260.	1.8	38
2303	A Transcriptional Program Mediating Entry into Cellular Quiescence. <i>PLoS Genetics</i> , 2007, 3, e91.	1.5	67
2304	Ageing Hematopoietic Stem Cells Decline in Function and Exhibit Epigenetic Dysregulation. <i>PLoS Biology</i> , 2007, 5, e201.	2.6	677
2305	RegulonDB (version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription, active (experimental) annotated promoters and Textpresso navigation. <i>Nucleic Acids Research</i> , 2007, 36, D120-D124.	6.5	395
2306	Identification of Putative Androgen Receptor Interaction Protein Modules. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 252-271.	2.5	51
2307	Analyzing microarray data using CLANS. <i>Bioinformatics</i> , 2007, 23, 1170-1171.	1.8	10
2308	Organelle DB: an updated resource of eukaryotic protein localization and function. <i>Nucleic Acids Research</i> , 2007, 35, D810-D814.	6.5	31

#	ARTICLE	IF	CITATIONS
2309	Hedgehog Signaling Pathway Database: a repository of current annotation efforts and resources for the Hh research community. <i>Nucleic Acids Research</i> , 2007, 35, D595-D598.	6.5	4
2310	The SUPERFAMILY database in 2007: families and functions. <i>Nucleic Acids Research</i> , 2007, 35, D308-D313.	6.5	216
2311	MISt: a microbial signal transduction database. <i>Nucleic Acids Research</i> , 2007, 35, D386-D390.	6.5	103
2312	Operon prediction in <i>Pyrococcus furiosus</i> . <i>Nucleic Acids Research</i> , 2007, 35, 11-20.	6.5	33
2313	MBGD: a platform for microbial comparative genomics based on the automated construction of orthologous groups. <i>Nucleic Acids Research</i> , 2007, 35, D343-D346.	6.5	69
2314	The Rat Genome Database, update 2007--Easing the path from disease to data and back again. <i>Nucleic Acids Research</i> , 2007, 35, D658-D662.	6.5	119
2315	Enteropathogen Resource Integration Center (ERIC): bioinformatics support for research on biodefense-relevant enterobacteria. <i>Nucleic Acids Research</i> , 2007, 36, D519-D523.	6.5	14
2316	Prominent use of distal 5' transcription start sites and discovery of a large number of additional exons in ENCODE regions. <i>Genome Research</i> , 2007, 17, 746-759.	2.4	173
2317	Patterns of Selection and Tissue-Specific Expression among Maize Domestication and Crop Improvement Loci. <i>Plant Physiology</i> , 2007, 144, 1642-1653.	2.3	17
2318	Genes misregulated in <i>C. elegans</i> deficient in Dicer, RDE-4, or RDE-1 are enriched for innate immunity genes. <i>Rna</i> , 2007, 13, 1090-1102.	1.6	47
2319	Variable Strength of Translational Selection Among 12 <i>Drosophila</i> Species. <i>Genetics</i> , 2007, 177, 1337-1348.	1.2	37
2320	Investigating the Genetic Circuitry of Mastermind in <i>Drosophila</i> , a Notch Signal Effector. <i>Genetics</i> , 2007, 177, 2493-2505.	1.2	57
2321	<i>Drosophila</i> Polymorphism Database (DPDB) A Portal for Nucleotide Polymorphism in <i>Drosophila</i> . <i>Fly</i> , 2007, 1, 205-211.	0.9	3
2322	Associative Artificial Neural Network for Discovery of Highly Correlated Gene Groups Based on Gene Ontology and Gene Expression. , 2007, , .		0
2323	Using <i>Drosophila melanogaster</i> Data to Discover Disease-Related Protein Interactions in Humans. , 2007, , .		0
2324	MULTIOBJECTIVE EVOLUTIONARY APPROACH TO FUZZY CLUSTERING OF MICROARRAY DATA. <i>Science, Engineering, and Biology Informatics</i> , 2007, , 303-328.	0.1	15
2325	Systematic variation in mRNA 3' processing signals during mouse spermatogenesis. <i>Nucleic Acids Research</i> , 2007, 35, 234-246.	6.5	114
2326	Using GOstats to test gene lists for GO term association. <i>Bioinformatics</i> , 2007, 23, 257-258.	1.8	1,870

#	ARTICLE	IF	CITATIONS
2327	Functional Differentiation of SWI/SNF Remodelers in Transcription and Cell Cycle Control. <i>Molecular and Cellular Biology</i> , 2007, 27, 651-661.	1.1	123
2328	Evolutionary analysis of enzymes using Chisel. <i>Bioinformatics</i> , 2007, 23, 2961-2968.	1.8	1
2329	Incorporating prior knowledge of gene functional groups into regularized discriminant analysis of microarray data. <i>Bioinformatics</i> , 2007, 23, 3170-3177.	1.8	57
2330	Identifying clusters of functionally related genes in genomes. <i>Bioinformatics</i> , 2007, 23, 1053-1060.	1.8	117
2331	Computational Approaches to Phenotyping: High-Throughput Phenomics. <i>Proceedings of the American Thoracic Society</i> , 2007, 4, 18-25.	3.5	56
2332	Novel Insights into Lung Transplant Rejection by Microarray Analysis. <i>Proceedings of the American Thoracic Society</i> , 2007, 4, 44-51.	3.5	42
2333	Gene expression profiles of human proximal tubular epithelial cells in proteinuric nephropathies. <i>Kidney International</i> , 2007, 71, 325-335.	2.6	63
2334	The Postimplantation Embryo Differentially Regulates Endometrial Gene Expression and Decidualization. <i>Endocrinology</i> , 2007, 148, 4173-4184.	1.4	64
2335	Estrogen Regulation of Genes Important for K ⁺ Channel Signaling in the Arcuate Nucleus. <i>Endocrinology</i> , 2007, 148, 4937-4951.	1.4	81
2336	Activation of Peroxisome Proliferator-Activated Receptor $\hat{1}^3$ (PPAR $\hat{1}^3$) by Rosiglitazone Suppresses Components of the Insulin-Like Growth Factor Regulatory System in Vitro and in Vivo. <i>Endocrinology</i> , 2007, 148, 903-911.	1.4	130
2337	TIGRFAMs and Genome Properties: tools for the assignment of molecular function and biological process in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2007, 35, D260-D264.	6.5	266
2338	Directed network modules. <i>New Journal of Physics</i> , 2007, 9, 186-186.	1.2	108
2339	Domain-enhanced analysis of microarray data using GO annotations. <i>Bioinformatics</i> , 2007, 23, 1225-1234.	1.8	23
2340	Building a comprehensive ontology to refine video concept detection. , 2007, , .		41
2341	Information theory applied to the sparse gene ontology annotation network to predict novel gene function. <i>Bioinformatics</i> , 2007, 23, i529-i538.	1.8	148
2342	Immunity genes and their orthologs: a multi-species database. <i>International Immunology</i> , 2007, 19, 1361-1370.	1.8	13
2343	The high-level similarity of some disparate gene expression measures. <i>Bioinformatics</i> , 2007, 23, 3032-3038.	1.8	15
2344	An ensemble framework for clustering protein-protein interaction networks. <i>Bioinformatics</i> , 2007, 23, i29-i40.	1.8	189

#	ARTICLE	IF	CITATIONS
2345	eggNOG: automated construction and annotation of orthologous groups of genes. <i>Nucleic Acids Research</i> , 2007, 36, D250-D254.	6.5	428
2346	A novel pattern based clustering methodology for time-series microarray data. <i>International Journal of Computer Mathematics</i> , 2007, 84, 585-597.	1.0	15
2347	Predicting Protein N-glycosylation by Combining Functional Domain and Secretion Information. <i>Journal of Biomolecular Structure and Dynamics</i> , 2007, 25, 49-54.	2.0	11
2348	Positive Adaptive State: Microarray Evaluation of Gene Expression in <i>Salmonella enterica</i> Typhimurium Exposed to Nalidixic Acid. <i>Foodborne Pathogens and Disease</i> , 2007, 4, 187-200.	0.8	20
2349	A New Metric to Measure Gene Product Similarity. , 2007, , .		3
2350	Methodology development for predicting subcellular localization and other attributes of proteins. <i>Expert Review of Proteomics</i> , 2007, 4, 453-463.	1.3	36
2351	Graph Kernel-Based Learning for Gene Function Prediction from Gene Interaction Network. , 2007, , .		6
2352	Extracting Biological Knowledge by Fuzzy Association Rule Mining. <i>IEEE International Conference on Fuzzy Systems</i> , 2007, , .	0.0	7
2353	Auto-Extraction, Representation and Integration of a Diabetes Ontology Using Bayesian Networks. <i>Proceedings of the IEEE Symposium on Computer-Based Medical Systems</i> , 2007, , .	0.0	7
2354	Predicting and Annotating Catalytic Residues: An Information Theoretic Approach. <i>Journal of Computational Biology</i> , 2007, 14, 1058-1073.	0.8	24
2355	Arabidopsis Transcriptome Changes in Response to Phloem-Feeding Silverleaf Whitefly Nymphs. Similarities and Distinctions in Responses to Aphids. <i>Plant Physiology</i> , 2007, 143, 849-865.	2.3	344
2356	Transcription factor modularity in a gene-centered <i>C. elegans</i> core neuronal protein-DNA interaction network. <i>Genome Research</i> , 2007, 17, 1061-1071.	2.4	87
2357	On the Effectiveness of Constraints Sets in Clustering Genes. , 2007, , .		6
2358	A Systematic Approach to Quantifying Evolutionary Functional Trends Across the Universal Tree of Life. , 2007, , .		1
2359	Large-scale mapping of human protein-protein interactions by mass spectrometry. <i>Molecular Systems Biology</i> , 2007, 3, 89.	3.2	850
2360	Genomic drift and copy number variation of sensory receptor genes in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20421-20426.	3.3	139
2361	Incorporating Uncertainty Metrics into a General-Purpose Data Integration System. <i>International Conference on Scientific and Statistical Database Management: [proceedings] International Conference on Scientific and Statistical Database Management</i> , 2007, , .	0.0	11
2362	Scalable, Dynamic Analysis and Visualization for Genomic Datasets. , 2007, , .		1

#	ARTICLE	IF	CITATIONS
2363	Learning Imbalanced Data Sets with a Min-Max Modular Support Vector Machine. <i>Neural Networks (IJCNN), International Joint Conference on</i> , 2007, , .	0.0	3
2364	An Efficient Algorithm for Mining Coherent Patterns from Heterogeneous Microarrays. <i>International Conference on Scientific and Statistical Database Management: [proceedings] International Conference on Scientific and Statistical Database Management</i> , 2007, , .	0.0	2
2365	A Web-enabled Database of Human Gene Expression Controlled Annotations for Gene List Functional Evaluation. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2007, 2007, 394-7.	0.5	4
2367	Microarray-based Analysis of Ventilator-induced Lung Injury. <i>Proceedings of the American Thoracic Society</i> , 2007, 4, 77-84.	3.5	68
2368	Probing the mRNA processing body using protein macroarrays and "autoantigenomics". <i>Rna</i> , 2007, 13, 704-712.	1.6	78
2369	Decidual Stromal Cell Response to Paracrine Signals from the Trophoblast: Amplification of Immune and Angiogenic Modulators ¹ . <i>Biology of Reproduction</i> , 2007, 76, 102-117.	1.2	258
2370	Selective Regulation of Bone Cell Apoptosis by Translational Isoforms of the Glucocorticoid Receptor. <i>Molecular and Cellular Biology</i> , 2007, 27, 7143-7160.	1.1	132
2371	Current trends in the bioinformatic sequence analysis of metabolic pathways in prokaryotes. <i>Briefings in Bioinformatics</i> , 2007, 9, 34-45.	3.2	4
2372	Rapid Evolution of Female-Biased, but Not Male-Biased, Genes Expressed in the Avian Brain. <i>Molecular Biology and Evolution</i> , 2007, 24, 2698-2706.	3.5	72
2373	Functional Analysis of Gene Duplications in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2007, 175, 933-943.	1.2	148
2374	Enrichment analysis in high-throughput genomicsâ€”accounting for dependency in the NULL. <i>Briefings in Bioinformatics</i> , 2007, 8, 71-77.	3.2	16
2375	Cellular Processes and Pathways That Protect <i>Saccharomyces cerevisiae</i> Cells against the Plasma Membrane-Perturbing Compound Chitosan. <i>Eukaryotic Cell</i> , 2007, 6, 600-608.	3.4	62
2376	PEDE (Pig EST Data Explorer) has been expanded into Pig Expression Data Explorer, including 10 147 porcine full-length cDNA sequences. <i>Nucleic Acids Research</i> , 2007, 35, D650-D653.	6.5	60
2377	Gene-expression profiling in Parkinsonâ€™s disease: discovery of valid biomarkers, molecular targets and biochemical pathways. <i>Future Neurology</i> , 2007, 2, 29-38.	0.9	8
2378	Discovery of Candidate Tumor Markers for Prostate Cancer via Proteomic Analysis of Cell Cultureâ€”Conditioned Medium. <i>Clinical Chemistry</i> , 2007, 53, 429-437.	1.5	75
2379	Selective Sweeps Reveal Candidate Genes for Adaptation to Drought and Salt Tolerance in Common Sunflower, <i>Helianthus annuus</i> . <i>Genetics</i> , 2007, 175, 1823-1834.	1.2	112
2380	Activation of protective responses in oral epithelial cells by <i>Fusobacterium nucleatum</i> and human Î²-defensin-2. <i>Journal of Medical Microbiology</i> , 2007, 56, 976-987.	0.7	45
2381	Why Are There Still Over 1000 Uncharacterized Yeast Genes?. <i>Genetics</i> , 2007, 176, 7-14.	1.2	130

#	ARTICLE	IF	CITATIONS
2382	Effect of in vitro fertilization on gene expression and development of mouse preimplantation embryos. <i>Reproduction</i> , 2007, 134, 63-72.	1.1	142
2383	Serpin Peptidase Inhibitor Clade A Member 1 as a Potential Marker for Malignancy in Insulinomas. <i>Clinical Cancer Research</i> , 2007, 13, 5322-5330.	3.2	30
2384	KI 2007: Advances in Artificial Intelligence. <i>Lecture Notes in Computer Science</i> , 2007, , .	1.0	5
2385	Genomic resources for songbird research and their use in characterizing gene expression during brain development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6834-6839.	3.3	53
2386	Cancer genetics of epigenetic genes. <i>Human Molecular Genetics</i> , 2007, 16, R28-R49.	1.4	223
2387	Current progress in network research; toward reference networks for key model organisms. <i>Briefings in Bioinformatics</i> , 2007, 8, 318-332.	3.2	46
2388	DBAli tools: mining the protein structure space. <i>Nucleic Acids Research</i> , 2007, 35, W393-W397.	6.5	25
2389	GoSh: a web-based database for goat and sheep EST sequences. <i>Bioinformatics</i> , 2007, 23, 1043-1045.	1.8	8
2390	Resources, standards and tools for systems biology. <i>Briefings in Functional Genomics & Proteomics</i> , 2007, 6, 240-251.	3.8	63
2391	ESTExplorer: an expressed sequence tag (EST) assembly and annotation platform. <i>Nucleic Acids Research</i> , 2007, 35, W143-W147.	6.5	60
2392	Extracting biology from high-dimensional biological data. <i>Journal of Experimental Biology</i> , 2007, 210, 1507-1517.	0.8	44
2393	Statistical assessment of functional categories of genes deregulated in pathological conditions by using microarray data. <i>Bioinformatics</i> , 2007, 23, 2063-2072.	1.8	22
2394	PhosPhAt: a database of phosphorylation sites in <i>Arabidopsis thaliana</i> and a plant-specific phosphorylation site predictor. <i>Nucleic Acids Research</i> , 2007, 36, D1015-D1021.	6.5	302
2395	The Edinburgh human metabolic network reconstruction and its functional analysis. <i>Molecular Systems Biology</i> , 2007, 3, 135.	3.2	364
2396	Qualitative and Quantitative Analyses of Protein Phosphorylation in Naive and Stimulated Mouse Synaptosomal Preparations. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 283-293.	2.5	211
2397	Significant gene content variation characterizes the genomes of inbred mouse strains. <i>Genome Research</i> , 2007, 17, 1743-1754.	2.4	89
2398	Analyzing gene expression data in terms of gene sets: methodological issues. <i>Bioinformatics</i> , 2007, 23, 980-987.	1.8	690
2399	An improved algorithm for clustering gene expression data. <i>Bioinformatics</i> , 2007, 23, 2859-2865.	1.8	239

#	ARTICLE	IF	CITATIONS
2400	Patterns of Host Genomeâ€“Wide Gene Transcript Abundance in the Peripheral Blood of Patients with Acute Dengue Hemorrhagic Fever. <i>Journal of Infectious Diseases</i> , 2007, 195, 1097-1107.	1.9	159
2401	Identification of distinct changes in gene expression after modulation of melanoma tumor antigen p97 (melanotransferrin) in multiple models in vitro and in vivo. <i>Carcinogenesis</i> , 2007, 28, 2172-2183.	1.3	34
2402	Systematic condition-dependent annotation of metabolic genes. <i>Genome Research</i> , 2007, 17, 1626-1633.	2.4	22
2403	ATDB: a uni-database platform for animal toxins. <i>Nucleic Acids Research</i> , 2007, 36, D293-D297.	6.5	70
2404	Gene Ontology annotations at SGD: new data sources and annotation methods. <i>Nucleic Acids Research</i> , 2007, 36, D577-D581.	6.5	218
2405	IFN- γ Alters the Response of <i>Borrelia burgdorferi</i> -Activated Endothelium to Favor Chronic Inflammation. <i>Journal of Immunology</i> , 2007, 178, 1172-1179.	0.4	35
2406	Mapping biomedical concepts onto the human genome by mining literature on chromosomal aberrations. <i>Nucleic Acids Research</i> , 2007, 35, 2533-2543.	6.5	27
2408	Identifying the biologically relevant gene categories based on gene expression and biological data: an example on prostate cancer. <i>Bioinformatics</i> , 2007, 23, 1503-1510.	1.8	14
2409	Functional annotation of regulatory pathways. <i>Bioinformatics</i> , 2007, 23, i377-i386.	1.8	17
2410	Exploring the functional landscape of gene expression: directed search of large microarray compendia. <i>Bioinformatics</i> , 2007, 23, 2692-2699.	1.8	243
2411	A High-Throughput Approach To Protein Structure Analysis. , 2007, 28, 105-128.		9
2412	Upgrades to StellaBase facilitate medical and genetic studies on the starlet sea anemone, <i>Nematostella vectensis</i> . <i>Nucleic Acids Research</i> , 2007, 36, D607-D611.	6.5	21
2413	Annotating gene function by combining expression data with a modular gene network. <i>Bioinformatics</i> , 2007, 23, i468-i478.	1.8	27
2414	Berkeley Phylogenomics Group web servers: resources for structural phylogenomic analysis. <i>Nucleic Acids Research</i> , 2007, 35, W27-W32.	6.5	24
2415	Quantifying the Impact of Protein Tertiary Structure on Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2007, 24, 1769-1782.	3.5	54
2416	The anatomy of microbial cell state transitions in response to oxygen. <i>Genome Research</i> , 2007, 17, 1399-1413.	2.4	59
2417	A Chado case study: an ontology-based modular schema for representing genome-associated biological information. <i>Bioinformatics</i> , 2007, 23, i337-i346.	1.8	216
2418	Interpretation of ANOVA models for microarray data using PCA. <i>Bioinformatics</i> , 2007, 23, 184-190.	1.8	70

#	ARTICLE	IF	CITATIONS
2419	Comparison of human protein-protein interaction maps. <i>Bioinformatics</i> , 2007, 23, 605-611.	1.8	85
2420	The Zebrafish Information Network: the zebrafish model organism database provides expanded support for genotypes and phenotypes. <i>Nucleic Acids Research</i> , 2007, 36, D768-D772.	6.5	137
2421	Genome Sequence of Avery's Virulent Serotype 2 Strain D39 of <i>Streptococcus pneumoniae</i> and Comparison with That of Unencapsulated Laboratory Strain R6. <i>Journal of Bacteriology</i> , 2007, 189, 38-51.	1.0	429
2422	Extracting binary signals from microarray time-course data. <i>Nucleic Acids Research</i> , 2007, 35, 3705-3712.	6.5	145
2423	firestar-prediction of functionally important residues using structural templates and alignment reliability. <i>Nucleic Acids Research</i> , 2007, 35, W573-W577.	6.5	91
2424	Statistical Absolute Evaluation of Gene Ontology Terms with Gene Expression Data. , 2007, , 146-157.		6
2425	Semantic Web Approach to Database Integration in the Life Sciences. , 2007, , 11-30.		12
2426	Nonparametric pathway-based regression models for analysis of genomic data. <i>Biostatistics</i> , 2007, 8, 265-284.	0.9	74
2427	Ultraconserved elements are associated with homeostatic control of splicing regulators by alternative splicing and nonsense-mediated decay. <i>Genes and Development</i> , 2007, 21, 708-718.	2.7	470
2428	Reliable prediction of regulator targets using 12 <i>Drosophila</i> genomes. <i>Genome Research</i> , 2007, 17, 1919-1931.	2.4	141
2429	g:Profiler-a web-based toolset for functional profiling of gene lists from large-scale experiments. <i>Nucleic Acids Research</i> , 2007, 35, W193-W200.	6.5	1,203
2430	Macrophage Scavenger Receptor-Deficient Mice Are Resistant Against Diabetic Nephropathy Through Amelioration of Microinflammation. <i>Diabetes</i> , 2007, 56, 363-372.	0.3	86
2431	Analysis of the In Vitro Transcriptional Response of Human Pharyngeal Epithelial Cells to Adherent <i>Streptococcus pneumoniae</i> : Evidence for a Distinct Response to Encapsulated Strains. <i>Infection and Immunity</i> , 2007, 75, 5489-5499.	1.0	50
2432	Averaged gene expressions for regression. <i>Biostatistics</i> , 2007, 8, 212-227.	0.9	123
2433	Context-sensitive data integration and prediction of biological networks. <i>Bioinformatics</i> , 2007, 23, 2322-2330.	1.8	101
2434	PlantTribes: a gene and gene family resource for comparative genomics in plants. <i>Nucleic Acids Research</i> , 2007, 36, D970-D976.	6.5	93
2435	Differential Expression of Drug Resistance-Related Genes between Sensitive and Resistant Blasts in Acute Myeloid Leukemia. <i>Acta Haematologica</i> , 2007, 117, 8-15.	0.7	38
2436	WormBase 2007. <i>Nucleic Acids Research</i> , 2007, 36, D612-D617.	6.5	95

#	ARTICLE	IF	CITATIONS
2437	COXPRESdb: a database of coexpressed gene networks in mammals. <i>Nucleic Acids Research</i> , 2007, 36, D77-D82.	6.5	120
2438	YEASTRACT-DISCOVERER: new tools to improve the analysis of transcriptional regulatory associations in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2007, 36, D132-D136.	6.5	140
2439	Genetic Regulatory Networks. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2007, 2007, 1-2.	1.4	3
2440	Gene Systems Network Inferred from Expression Profiles in Hepatocellular Carcinogenesis by Graphical Gaussian Model. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2007, 2007, 1-11.	1.4	3
2441	Effect of 21 Different Nitrogen Sources on Global Gene Expression in the Yeast <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2007, 27, 3065-3086.	1.1	237
2442	Expression Profiling of Huntington's Disease Models Suggests That Brain-Derived Neurotrophic Factor Depletion Plays a Major Role in Striatal Degeneration. <i>Journal of Neuroscience</i> , 2007, 27, 11758-11768.	1.7	197
2443	GOing from functional genomics to biological significance. <i>Cytogenetic and Genome Research</i> , 2007, 117, 278-287.	0.6	15
2444	cDNA Microarray Analysis of Adaptive Changes after Renal Ablation in a Sclerosis-Resistant Mouse Strain. <i>Kidney and Blood Pressure Research</i> , 2007, 30, 377-387.	0.9	8
2445	Analysis of phosphorylation sites on proteins from <i>Saccharomyces cerevisiae</i> by electron transfer dissociation (ETD) mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2193-2198.	3.3	541
2446	Immediate-Early and Delayed Primary Response Genes Are Distinct in Function and Genomic Architecture*. <i>Journal of Biological Chemistry</i> , 2007, 282, 23981-23995.	1.6	159
2447	MethyCancer: the database of human DNA methylation and cancer. <i>Nucleic Acids Research</i> , 2007, 36, D836-D841.	6.5	127
2448	Assessing Significance of Connectivity and Conservation in Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2007, 14, 747-764.	0.8	52
2449	Identification of conserved protein complexes based on a model of protein network evolution. <i>Bioinformatics</i> , 2007, 23, e170-e176.	1.8	93
2450	Structural templates predict novel protein interactions and targets from pancreas tumour gene expression data. <i>Bioinformatics</i> , 2007, 23, i115-i124.	1.8	19
2451	Clustering microarray-derived gene lists through implicit literature relationships. <i>Bioinformatics</i> , 2007, 23, 1995-2003.	1.8	16
2452	Mining experimental evidence of molecular function claims from the literature. <i>Bioinformatics</i> , 2007, 23, 3232-3240.	1.8	11
2453	Reconstructing dynamic regulatory maps. <i>Molecular Systems Biology</i> , 2007, 3, 74.	3.2	183
2454	Prediction of phenotype and gene expression for combinations of mutations. <i>Molecular Systems Biology</i> , 2007, 3, 96.	3.2	43

#	ARTICLE	IF	CITATIONS
2455	Revealing static and dynamic modular architecture of the eukaryotic protein interaction network. <i>Molecular Systems Biology</i> , 2007, 3, 110.	3.2	127
2456	Temporal and spatial transcriptional profiles of aging in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2007, 17, 1236-1243.	2.4	91
2457	A multidimensional analysis of genes mutated in breast and colorectal cancers. <i>Genome Research</i> , 2007, 17, 1304-1318.	2.4	121
2458	Expressed Sequence Tags from <i>Phytophthora sojae</i> Reveal Genes Specific to Development and Infection. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 781-793.	1.4	59
2459	INTEGRATING HIERARCHICAL CONTROLLED VOCABULARIES WITH OWL ONTOLOGY: A CASE STUDY FROM THE DOMAIN OF MOLECULAR INTERACTIONS. , 2007, , .		2
2460	Mining Information on Protein Function from Text. , 0, , 1253-1295.		1
2461	Random-set methods identify distinct aspects of the enrichment signal in gene-set analysis. <i>Annals of Applied Statistics</i> , 2007, 1, 85.	0.5	199
2462	Genomics and Proteomics of Foodborne Microorganisms. , 2007, , 935-951.		2
2463	DNA Microarray Technology and Applications” An Overview. , 0, , 899-928.		0
2464	Classification of Patients. , 0, , 957-991.		2
2466	Between the cross and the sword: the crisis of the gene concept. <i>Genetics and Molecular Biology</i> , 2007, 30, 297-307.	0.6	26
2467	Course 12 Statistical modelling and analysis of biological networks. <i>Les Houches Summer School Proceedings</i> , 2007, , 447-471.	0.2	0
2468	Modeling the regulatory network of histone acetylation in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2007, 3, 153.	3.2	32
2469	Transcriptomic analysis of the cardiac left ventricle in a rodent model of diabetic cardiomyopathy: molecular snapshot of a severe myocardial disease. <i>Physiological Genomics</i> , 2007, 28, 284-293.	1.0	26
2470	Inferring Protein Function from Protein Structure. , 0, , 1211-1252.		1
2471	A case study of integrating protein interaction data using semantic web technology. <i>International Journal of Bioinformatics Research and Applications</i> , 2007, 3, 286.	0.1	16
2472	A database ontology for signal transduction pathways. <i>International Journal of Bioinformatics Research and Applications</i> , 2007, 3, 326.	0.1	7
2473	Visualization of Biological Data. , 0, , 1573-1626.		1

#	ARTICLE	IF	CITATIONS
2474	Histone Modification Enzymes Induced during Chemical Hepatocarcinogenesis. <i>Yakugaku Zasshi</i> , 2007, 127, 469-479.	0.0	2
2475	The thymic theme of acetylcholinesterase splice variants in myasthenia gravis. <i>Blood</i> , 2007, 109, 4383-4391.	0.6	35
2476	Lesional gene expression profiling in cutaneous T-cell lymphoma reveals natural clusters associated with disease outcome. <i>Blood</i> , 2007, 110, 3015-3027.	0.6	115
2477	Hot spots of retroviral integration in human CD34+ hematopoietic cells. <i>Blood</i> , 2007, 110, 1770-1778.	0.6	248
2478	Building the bridges to bioinformatics in nutrition research. <i>American Journal of Clinical Nutrition</i> , 2007, 86, 1261-1269.	2.2	28
2479	Developing a Systems Biology Approach to Study Disease Progression Caused by <i>Heterodera glycines</i> in <i>Glycine max</i> . <i>Gene Regulation and Systems Biology</i> , 2007, 1, 117762500700100.	2.3	0
2480	Variability of DNA Microarray Gene Expression Profiles in Cultured Rat Primary Hepatocytes. <i>Gene Regulation and Systems Biology</i> , 2007, 1, 117762500700100.	2.3	0
2481	A Two-Step Clustering for 3-D Gene Expression Data Reveals the Main Features of the Arabidopsis Stress Response. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 81-93.	1.0	4
2482	Data Linkage Graph: computation, querying and knowledge discovery of life science database networks. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 101-111.	1.0	3
2483	Functional and Transcriptional Coherency of Modules in the Human Protein Interaction Network. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 198-207.	1.0	3
2484	Prediction of protein-protein interactions using one-class classification methods and integrating diverse biological data. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 208-223.	1.0	9
2485	CIDA: An integrated software for the design, characterisation and global comparison of microarrays. <i>Journal of Integrative Bioinformatics</i> , 2007, 4, 224-242.	1.0	0
2486	Oncogene Coexpression in Mesenchymal Neoplasia Correlates with EGF Transcription. <i>Clinical Orthopaedics and Related Research</i> , 2007, 459, 14-21.	0.7	3
2487	Gender-specific differences in expression in human lymphoblastoid cell lines. <i>Pharmacogenetics and Genomics</i> , 2007, 17, 447-450.	0.7	29
2488	Gene-Expression Profiles and Age of Donor Kidney Biopsies Obtained Before Transplantation Distinguish Medium Term Graft Function. <i>Transplantation</i> , 2007, 83, 1048-1054.	0.5	34
2489	Genome Wide Expression Profiling of Human Peripheral Blood Mononuclear Cells Stimulated With BAY 50-4798, a Novel T Cell Selective Interleukin-2 Analog. <i>Journal of Immunotherapy</i> , 2007, 30, 150-168.	1.2	2
2490	Frequency-dependent response of the vascular endothelium to pulsatile shear stress. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2007, 293, H645-H653.	1.5	112
2491	Molecular and genetic association of interleukin-6 in tacrine-induced hepatotoxicity. <i>Pharmacogenetics and Genomics</i> , 2007, 17, 961-972.	0.7	30

#	ARTICLE	IF	CITATIONS
2492	Semantic Analysis of Genome Annotations using Weighting Schemes. , 2007, , .		10
2493	Prediction of Co-Regulated Gene Groups through Gene Ontology. , 2007, , .		0
2494	Motifs and Modules in Fractured Functional Yeast Networks. , 2007, , .		4
2495	Distinct profiles of expressed sequence tags during intestinal regeneration in the sea cucumber <i>Holothuria glaberrima</i> . <i>Physiological Genomics</i> , 2007, 31, 203-215.	1.0	60
2496	Evolutionary rate analyses of orthologs and paralogs from 12 <i>Drosophila</i> genomes. <i>Genome Research</i> , 2007, 17, 1837-1849.	2.4	131
2497	Distinct gene expression profiles in peripheral blood mononuclear cells from patients infected with vaccinia virus, yellow fever 17D virus, or upper respiratory infections. <i>Vaccine</i> , 2007, 25, 6458-6473.	1.7	31
2498	Activity-dependent neuroprotective protein (ADNP) differentially interacts with chromatin to regulate genes essential for embryogenesis. <i>Developmental Biology</i> , 2007, 303, 814-824.	0.9	158
2499	hORFeome v3.1: A resource of human open reading frames representing over 10,000 human genes. <i>Genomics</i> , 2007, 89, 307-315.	1.3	248
2500	Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. <i>Genomics</i> , 2007, 89, 580-587.	1.3	56
2501	Global transcriptional response of porcine mesenteric lymph nodes to <i>Salmonella enterica</i> serovar Typhimurium. <i>Genomics</i> , 2007, 90, 72-84.	1.3	36
2502	Parent genes of retrotransposition-generated gene duplicates in <i>Drosophila melanogaster</i> have distinct expression profiles. <i>Genomics</i> , 2007, 90, 334-343.	1.3	11
2503	Knot/Collier and Cut Control Different Aspects of Dendrite Cytoskeleton and Synergize to Define Final Arbor Shape. <i>Neuron</i> , 2007, 56, 963-978.	3.8	170
2504	Sensitization to the conditioned rewarding effects of morphine modulates gene expression in rat hippocampus. <i>Neuropharmacology</i> , 2007, 52, 430-435.	2.0	16
2505	PathExpress: a web-based tool to identify relevant pathways in gene expression data. <i>Nucleic Acids Research</i> , 2007, 35, W176-W181.	6.5	66
2506	An extensive resource of single nucleotide polymorphism markers associated with Atlantic salmon (<i>Salmo salar</i>) expressed sequences. <i>Aquaculture</i> , 2007, 265, 82-90.	1.7	110
2507	Discovery of genes involved in defense/immunity functions in a haemocytes cDNA library from <i>Fenneropenaeus chinensis</i> by ESTs annotation. <i>Aquaculture</i> , 2007, 272, 208-215.	1.7	28
2508	Microarray analysis in the zebrafish (<i>Danio rerio</i>) liver and telencephalon after exposure to low concentration of 17alpha-ethinylestradiol. <i>Aquatic Toxicology</i> , 2007, 84, 38-49.	1.9	117
2509	Exploration of PPAR functions by microarray technologyâ€”A paradigm for nutrigenomics. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2007, 1771, 1046-1064.	1.2	43

#	ARTICLE	IF	CITATIONS
2510	Microarray analysis of gene expression in Men1 knockout embryoid body reveals genetic events involved in early mouse embryonic development. <i>Biochemical and Biophysical Research Communications</i> , 2007, 352, 456-462.	1.0	5
2511	Hum-mPloc: An ensemble classifier for large-scale human protein subcellular location prediction by incorporating samples with multiple sites. <i>Biochemical and Biophysical Research Communications</i> , 2007, 355, 1006-1011.	1.0	214
2512	Identification and characterization of expressed sequence tags from the liver of rare minnow (<i>Gobiocypris rarus</i>). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2007, 2, 356-362.	0.4	8
2513	Identification of over-expressed proteins in oral squamous cell carcinoma (OSCC) patients by clinical proteomic analysis. <i>Clinica Chimica Acta</i> , 2007, 376, 101-107.	0.5	125
2514	A Common Mechanism of Cellular Death Induced by Bactericidal Antibiotics. <i>Cell</i> , 2007, 130, 797-810.	13.5	2,334
2515	Global Analysis of mRNA Localization Reveals a Prominent Role in Organizing Cellular Architecture and Function. <i>Cell</i> , 2007, 131, 174-187.	13.5	878
2516	SMAUG Is a Major Regulator of Maternal mRNA Destabilization in <i>Drosophila</i> and Its Translation Is Activated by the PAN GU Kinase. <i>Developmental Cell</i> , 2007, 12, 143-155.	3.1	280
2517	Comparative analysis of cis-encoded antisense RNAs in eukaryotes. <i>Gene</i> , 2007, 392, 134-141.	1.0	29
2518	Globally predicting protein functions based on co-expressed protein-protein interaction networks and ontology taxonomy similarities. <i>Gene</i> , 2007, 391, 113-119.	1.0	26
2519	A domain of the thyroid adenoma associated gene (THADA) conserved in vertebrates becomes destroyed by chromosomal rearrangements observed in thyroid adenomas. <i>Gene</i> , 2007, 403, 110-117.	1.0	29
2520	Identification of a gene-pathway associated with non-alcoholic steatohepatitis. <i>Journal of Hepatology</i> , 2007, 46, 708-718.	1.8	52
2521	Towards Fully Automated Structure-based Function Prediction in Structural Genomics: A Case Study. <i>Journal of Molecular Biology</i> , 2007, 367, 1511-1522.	2.0	79
2522	Comparative genomics of elastin: Sequence analysis of a highly repetitive protein. <i>Matrix Biology</i> , 2007, 26, 524-540.	1.5	67
2523	Application of Bayesian networks for inferring cause-effect relations from gene expression profiles of cancer versus normal cells. <i>Mathematical Biosciences</i> , 2007, 209, 528-546.	0.9	10
2524	A Universal Framework for Regulatory Element Discovery across All Genomes and Data Types. <i>Molecular Cell</i> , 2007, 28, 337-350.	4.5	277
2525	Cutaneous immune responses in the common carp detected using transcript analysis. <i>Molecular Immunology</i> , 2007, 44, 1664-1679.	1.0	64
2526	Immunological systems biology: Gene expression analysis of B-cell development in Ramos B-cells. <i>Molecular Immunology</i> , 2007, 44, 3537-3551.	1.0	4
2527	The aryl hydrocarbon receptor agonist 3,3',4,4',5-pentachlorobiphenyl induces distinct patterns of gene expression between hepatoma and glioma cells: Chromatin remodeling as a mechanism for selective effects. <i>NeuroToxicology</i> , 2007, 28, 594-612.	1.4	17

#	ARTICLE	IF	CITATIONS
2528	An insight into the sialome of the adult female mosquito <i>Aedes albopictus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 107-127.	1.2	119
2529	SAGE analysis of early oogenesis in the silkworm, <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 147-154.	1.2	15
2530	An insight into the sialome of <i>Anopheles funestus</i> reveals an emerging pattern in anopheline salivary protein families. <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 164-175.	1.2	101
2531	The sialotranscriptome of the blood-sucking bug <i>Triatoma brasiliensis</i> (Hemiptera, Triatominae). <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 702-712.	1.2	78
2532	An insight into the sialotranscriptome of the seed-feeding bug, <i>Oncopeltus fasciatus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 903-910.	1.2	29
2533	High-Throughput Analysis of Promoter Occupancy Reveals Direct Neural Targets of FOXP2, a Gene Mutated in Speech and Language Disorders. <i>American Journal of Human Genetics</i> , 2007, 81, 1232-1250.	2.6	232
2534	Pathway-Based Approaches for Analysis of Genomewide Association Studies. <i>American Journal of Human Genetics</i> , 2007, 81, 1278-1283.	2.6	782
2535	Restauro-G: A Rapid Genome Re-Annotation System for Comparative Genomics. <i>Genomics, Proteomics and Bioinformatics</i> , 2007, 5, 53-58.	3.0	17
2536	Integration of Known Transcription Factor Binding Site Information and Gene Expression Data to Advance from Co-Expression to Co-Regulation. <i>Genomics, Proteomics and Bioinformatics</i> , 2007, 5, 86-101.	3.0	17
2537	Multilineage hematopoietic reconstitution without clonal selection in ADA-SCID patients treated with stem cell gene therapy. <i>Journal of Clinical Investigation</i> , 2007, 117, 2233-2240.	3.9	231
2538	Using the Tools and Resources of the RCSB Protein Data Bank. <i>Current Protocols in Bioinformatics</i> , 2007, 20, Unit1.9.	25.8	12
2539	Rice Genome Annotation: Beginnings of Functional Genomics. , 2007, , 21-30.		3
2540	The morphologies of breast cancer cell lines in three-dimensional assays correlate with their profiles of gene expression. <i>Molecular Oncology</i> , 2007, 1, 84-96.	2.1	872
2541	Effect of Menopause on Gene Expression Profiles of Circulating Monocytes: A Pilot in vivo Microarray Study. <i>Journal of Genetics and Genomics</i> , 2007, 34, 974-983.	1.7	12
2542	Origin and Evolution of Human microRNAs From Transposable Elements. <i>Genetics</i> , 2007, 176, 1323-1337.	1.2	311
2543	Experimental and Computational Procedures for the Assessment of Protein Complexes on a Genome-wide Scale. <i>Chemical Reviews</i> , 2007, 107, 3585-3600.	23.0	18
2544	Web Intelligence Meets Brain Informatics. <i>Lecture Notes in Computer Science</i> , 2007, , .	1.0	9
2545	Protein Targeting Protocols. , 2007, , .		1

#	ARTICLE	IF	CITATIONS
2547	Expression of truncated Int6/eIF3e in mammary alveolar epithelium leads to persistent hyperplasia and tumorigenesis. <i>Breast Cancer Research</i> , 2007, 9, R42.	2.2	25
2548	Prediction of synergistic transcription factors by function conservation. <i>Genome Biology</i> , 2007, 8, R257.	13.9	24
2549	Transcriptional profiling of MnSOD-mediated lifespan extension in <i>Drosophila</i> reveals a species-general network of aging and metabolic genes. <i>Genome Biology</i> , 2007, 8, R262.	13.9	123
2550	GeneChip analysis of human embryonic stem cell differentiation into hemangioblasts: an in silico dissection of mixed phenotypes. <i>Genome Biology</i> , 2007, 8, R240.	13.9	23
2551	Genome-wide expression profiling and bioinformatics analysis of diurnally regulated genes in the mouse prefrontal cortex. <i>Genome Biology</i> , 2007, 8, R247.	13.9	37
2552	All duplicates are not equal: the difference between small-scale and genome duplication. <i>Genome Biology</i> , 2007, 8, R209.	13.9	163
2553	Harnessing naturally randomized transcription to infer regulatory relationships among genes. <i>Genome Biology</i> , 2007, 8, R219.	13.9	109
2554	Simplified ontologies allowing comparison of developmental mammalian gene expression. <i>Genome Biology</i> , 2007, 8, R229.	13.9	12
2555	The LeFE algorithm: embracing the complexity of gene expression in the interpretation of microarray data. <i>Genome Biology</i> , 2007, 8, R187.	13.9	16
2556	Identification of novel stem cell markers using gap analysis of gene expression data. <i>Genome Biology</i> , 2007, 8, R193.	13.9	9
2557	Exploration of the omics evidence landscape: adding qualitative labels to predicted protein-protein interactions. <i>Genome Biology</i> , 2007, 8, R197.	13.9	3
2558	Transcriptomic and phenotypic analysis of murine embryonic stem cell derived BMP2+ lineage cells: an insight into mesodermal patterning. <i>Genome Biology</i> , 2007, 8, R184.	13.9	22
2559	InSite: a computational method for identifying protein-protein interaction binding sites on a proteome-wide scale. <i>Genome Biology</i> , 2007, 8, R192.	13.9	53
2560	The roles of binding site arrangement and combinatorial targeting in microRNA repression of gene expression. <i>Genome Biology</i> , 2007, 8, R166.	13.9	131
2561	FlyMine: an integrated database for <i>Drosophila</i> and <i>Anopheles</i> genomics. <i>Genome Biology</i> , 2007, 8, R129.	13.9	345
2562	Global analysis of patterns of gene expression during <i>Drosophila</i> embryogenesis. <i>Genome Biology</i> , 2007, 8, R145.	13.9	387
2563	Novel metrics for evaluating the functional coherence of protein groups via protein semantic network. <i>Genome Biology</i> , 2007, 8, R153.	13.9	13
2564	A proteome-wide protein interaction map for <i>Campylobacter jejuni</i> . <i>Genome Biology</i> , 2007, 8, R130.	3.8	214

#	ARTICLE	IF	CITATIONS
2565	Evolutionary conservation of regulated longevity assurance mechanisms. <i>Genome Biology</i> , 2007, 8, R132.	13.9	173
2566	Housekeeping genes tend to show reduced upstream sequence conservation. <i>Genome Biology</i> , 2007, 8, R140.	13.9	64
2567	Combined analysis reveals a core set of cycling genes. <i>Genome Biology</i> , 2007, 8, R146.	13.9	36
2568	Celsius: a community resource for Affymetrix microarray data. <i>Genome Biology</i> , 2007, 8, R112.	13.9	57
2569	Computational and transcriptional evidence for microRNAs in the honey bee genome. <i>Genome Biology</i> , 2007, 8, R97.	13.9	82
2570	LongSAGE profiling of nine human embryonic stem cell lines. <i>Genome Biology</i> , 2007, 8, R113.	13.9	21
2571	Global transcriptional responses of fission and budding yeast to changes in copper and iron levels: a comparative study. <i>Genome Biology</i> , 2007, 8, R73.	13.9	54
2572	Threshold-free high-power methods for the ontological analysis of genome-wide gene-expression studies. <i>Genome Biology</i> , 2007, 8, R74.	13.9	20
2573	Global analyses of mRNA translational control during early <i>Drosophila</i> embryogenesis. <i>Genome Biology</i> , 2007, 8, R63.	13.9	74
2574	Functional dissection of the <i>ash2</i> and <i>ash1</i> transcriptomes provides insights into the transcriptional basis of wing phenotypes and reveals conserved protein interactions. <i>Genome Biology</i> , 2007, 8, R67.	13.9	31
2575	Global transcriptome analysis of murine embryonic stem cell-derived cardiomyocytes. <i>Genome Biology</i> , 2007, 8, R56.	13.9	54
2576	Porcine transcriptome analysis based on 97 non-normalized cDNA libraries and assembly of 1,021,891 expressed sequence tags. <i>Genome Biology</i> , 2007, 8, R45.	13.9	67
2577	GOTax: investigating biological processes and biochemical activities along the taxonomic tree. <i>Genome Biology</i> , 2007, 8, R33.	13.9	20
2578	Reactome: a knowledge base of biologic pathways and processes. <i>Genome Biology</i> , 2007, 8, R39.	13.9	539
2579	Parallel evolution of conserved non-coding elements that target a common set of developmental regulatory genes from worms to humans. <i>Genome Biology</i> , 2007, 8, R15.	13.9	117
2580	Signaling netwErks get the global treatment. <i>Genome Biology</i> , 2007, 8, 202.	3.8	12
2581	An annotated cDNA library and microarray for large-scale gene-expression studies in the ant <i>Solenopsis invicta</i> . <i>Genome Biology</i> , 2007, 8, R9.	13.9	47
2582	GENECODIS: a web-based tool for finding significant concurrent annotations in gene lists. <i>Genome Biology</i> , 2007, 8, R3.	13.9	554

#	ARTICLE	IF	CITATIONS
2583	Topics in Biostatistics. <i>Methods in Molecular Biology</i> , 2007, , .	0.4	33
2584	Fine Mapping of Mouse QTLs for Fatness Using SNP Data. <i>OMICS A Journal of Integrative Biology</i> , 2007, 11, 341-350.	1.0	3
2587	Mitochondria. <i>Methods in Molecular Biology</i> , 2007, , .	0.4	5
2588	Analysis of Expression Data: An Overview. <i>Current Protocols in Human Genetics</i> , 2007, 54, Unit11.4.	3.5	5
2590	Gene Function Analysis. <i>Methods in Molecular Biology</i> , 2007, 408, vii-ix.	0.4	2
2591	Microarray Data Analysis. <i>Methods in Molecular Biology</i> , 2007, , .	0.4	5
2592	Characterization of the drugged human genome. <i>Pharmacogenomics</i> , 2007, 8, 1063-1073.	0.6	65
2593	Tissue-specific transcription factor HNF4 β inhibits cell proliferation and induces apoptosis in the pancreatic INS-1 β -cell line. <i>Biological Chemistry</i> , 2007, 388, 91-106.	1.2	25
2595	Clustering " Class Discovery in the Post-Genomic Era. , 2007, , 123-148.		1
2596	Text Mining in Genomics and Proteomics. , 2007, , 251-274.		3
2597	A modular network model of aging. <i>Molecular Systems Biology</i> , 2007, 3, 147.	3.2	151
2598	Gene response of human monocytic cells for the detection of antimigraine activity of feverfew extractsThis article is one of a selection of papers published in this special issue (part 2 of 2) on the Safety and Efficacy of Natural Health Products.. <i>Canadian Journal of Physiology and Pharmacology</i> , 2007, 85, 1108-1115.	0.7	5
2600	Functional Genomics of the Chicken" A Model Organism. <i>Poultry Science</i> , 2007, 86, 2059-2094.	1.5	95
2601	Artificial Intelligence in Medicine. <i>Lecture Notes in Computer Science</i> , 2007, , .	1.0	6
2602	Glucocorticoids induce differentiation of a specifically activated, anti-inflammatory subtype of human monocytes. <i>Blood</i> , 2007, 109, 1265-1274.	0.6	336
2604	Counting potentially functional variants in BRCA1, BRCA2 and ATM predicts breast cancer susceptibility. <i>Human Molecular Genetics</i> , 2007, 16, 1051-1057.	1.4	109
2605	Identification of higher-order functional domains in the human ENCODE regions. <i>Genome Research</i> , 2007, 17, 917-927.	2.4	120
2606	Computational prediction of host-pathogen protein"protein interactions. <i>Bioinformatics</i> , 2007, 23, i159-i166.	1.8	164

#	ARTICLE	IF	CITATIONS
2607	Lifetime Proteomic Profiling of an A30P Î±-Synuclein in <i>Drosophila</i> Model of Parkinson's Disease. <i>Journal of Proteome Research</i> , 2007, 6, 3729-3738.	1.8	32
2608	Sembowser - Semantic Biological Web Services Registry. , 2007, , 317-340.		2
2609	Protein Annotation at Genomic Scale: The Current Status. <i>Chemical Reviews</i> , 2007, 107, 3448-3466.	23.0	66
2610	Global reconstruction of the human metabolic network based on genomic and bibliomic data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1777-1782.	3.3	1,259
2611	The Reacquisition of Biotin Prototrophy in <i>Saccharomyces cerevisiae</i> Involved Horizontal Gene Transfer, Gene Duplication and Gene Clustering. <i>Genetics</i> , 2007, 177, 2293-2307.	1.2	147
2612	An HV-SVM Classifier to Infer TF-TF Interactions Using Protein Domains and GO Annotations. , 2007, , .		0
2613	A Preliminary Study of Correlation between Depth and Path Length of GO Nodes with Gene Sequence Similarity. , 2007, , .		0
2614	Comparing Protein Interaction Networks via a Graph Match-and-Split Algorithm. <i>Journal of Computational Biology</i> , 2007, 14, 892-907.	0.8	61
2615	XOA: Web-Enabled Cross-Ontological Analytics. , 2007, , .		11
2616	An Information Theoretic Approach to Quantifying Evolutionary Functional Trends. , 2007, , .		0
2617	BRAIN GENE ONTOLOGY AND SIMULATION SYSTEM (BGOS) FOR A BETTER UNDERSTANDING OF THE BRAIN. <i>Cybernetics and Systems</i> , 2007, 38, 495-508.	1.6	4
2618	Entrez Gene. <i>Journal of Electronic Resources in Medical Libraries</i> , 2007, 4, 53-78.	0.2	3
2620	Using SVG to Model and Query Image Annotations and Their History. , 2007, , .		1
2621	Evolving Brain-Genome Ontology System (EBGOS): Towards Integrating Bioinformatics and Neuroinformatics Data to Facilitate Discoveries. <i>Neural Networks (IJCNN), International Joint Conference on</i> , 2007, , .	0.0	5
2622	Identification of Conserved Domain Combinations in <i>S.cerevisiae</i> Proteins. , 2007, , .		2
2623	Gene Name Service: No-Nonsense Alias Resolution Service for Homo Sapiens Genes. , 2007, , .		3
2624	Interactive Semisupervised Learning for Microarray Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 190-203.	1.9	8
2625	The Requirements for Ontologies in Medical Data Integration: A Case Study. , 2007, , .		10

#	ARTICLE	IF	CITATIONS
2626	Identifying Genomic Regulators of Set-Wise Co-Expression. , 2007, 2007, 433-439.		1
2627	A weighted k-nearest neighbor method for gene ontology based protein function prediction. , 2007, , .		20
2628	Resolving Scientific Service Interoperability With Schema Mapping. , 2007, , .		2
2629	Multi-stage Framework to Infer Protein Functional Modules from Mass Spectrometry Pull-Down Data with Assessment of Biological Relevance. , 2007, , .		4
2630	Gene Expression Analysis of Endometrium Reveals Progesterone Resistance and Candidate Susceptibility Genes in Women with Endometriosis. Endocrinology, 2007, 148, 3814-3826.	1.4	642
2631	KAAS: an automatic genome annotation and pathway reconstruction server. Nucleic Acids Research, 2007, 35, W182-W185.	6.5	3,517
2632	Visualizing Quantitative Proteomics Datasets using Treemaps. Proceedings / International Conference on Information Visualisation, 2007, , .	0.0	4
2633	WoLF PSORT: protein localization predictor. Nucleic Acids Research, 2007, 35, W585-W587.	6.5	3,028
2634	Characterizing Proteins with Finer Functions: A Case Study for Translational Functions of Yeast Proteins. , 2007, , .		1
2635	Biometric Identity Information Integration with Semantics. , 2007, , .		0
2636	Connecting Seed Lists of Mammalian Proteins Using Steiner Trees. Conference Record of the Asilomar Conference on Signals, Systems and Computers, 2007, , .	0.0	4
2637	Computational identification of cellular networks and pathways. Molecular BioSystems, 2007, 3, 478.	2.9	20
2638	Linking Protein Mass with Function via Organismal Massome Networks. , 2007, , .		0
2639	ailSemantic Web-based data representation and reasoning applied to disease mechanism and pharmacology. , 2007, , .		1
2640	New method for ranking arabic web sites using ontology concepts. , 2007, , .		4
2641	Biomedical ontologies: a functional perspective. Briefings in Bioinformatics, 2007, 9, 75-90.	3.2	218
2642	SynDB: a Synapse protein DataBase based on synapse ontology. Nucleic Acids Research, 2007, 35, D737-D741.	6.5	43
2643	Biodiversity informatics: organizing and linking information across the spectrum of life. Briefings in Bioinformatics, 2007, 8, 347-357.	3.2	55

#	ARTICLE	IF	CITATIONS
2644	Analysis of Time Series Data with Predictive Clustering Trees. , 2006, , 63-80.		20
2645	Identification of Candidate Biomarker Proteins Released by Human Endometrial and Cervical Cancer Cells Using Two-Dimensional Liquid Chromatography/Tandem Mass Spectrometry. Journal of Proteome Research, 2007, 6, 2615-2622.	1.8	25
2646	Proteomic Identification of Endothelial Proteins Isolated in Situ from Atherosclerotic Aorta via Systemic Perfusion. Journal of Proteome Research, 2007, 6, 4728-4736.	1.8	25
2647	Immunoaffinity Purification of Plasma Membrane with Secondary Antibody Superparamagnetic Beads for Proteomic Analysis. Journal of Proteome Research, 2007, 6, 34-43.	1.8	38
2648	2-D DIGE Analysis of Liver and Red Blood Cells Provides Further Evidence for Oxidative Stress in Schizophrenia. Journal of Proteome Research, 2007, 6, 141-149.	1.8	104
2649	Gene Promoter Scan Methodology for Identifying and Classifying Coregulated Promoters. Methods in Enzymology, 2007, 422, 361-385.	0.4	4
2650	Euk-mPLOC: A Fusion Classifier for Large-Scale Eukaryotic Protein Subcellular Location Prediction by Incorporating Multiple Sites. Journal of Proteome Research, 2007, 6, 1728-1734.	1.8	341
2651	Examining the Proteome of Drosophila Across Organism Lifespan. Journal of Proteome Research, 2007, 6, 3637-3647.	1.8	30
2652	Practical Applications of Bacterial Functional Genomics. Biotechnology and Genetic Engineering Reviews, 2007, 24, 213-242.	2.4	5
2653	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	6.0	1,283
2654	The Chronic Fatigue Syndrome: A Comparative Pathway Analysis. Journal of Computational Biology, 2007, 14, 961-972.	0.8	77
2655	Tools for visually exploring biological networks. Bioinformatics, 2007, 23, 2651-2659.	1.8	220
2656	Proteomics of Neuroendocrine Secretory Vesicles Reveal Distinct Functional Systems for Biosynthesis and Exocytosis of Peptide Hormones and Neurotransmitters. Journal of Proteome Research, 2007, 6, 1652-1665.	1.8	44
2657	Identification of Marker Genes for Intestinal Immunomodulating Effect of a Fructooligosaccharide by DNA Microarray Analysis. Journal of Agricultural and Food Chemistry, 2007, 55, 3174-3179.	2.4	29
2658	Increased expression of extracellular matrix proteins in rapid atrial pacing-induced atrial fibrillation. Heart Rhythm, 2007, 4, 938-949.	0.3	56
2659	Pattern Recognition in Bioinformatics. Lecture Notes in Computer Science, 2007, , .	1.0	1
2660	Comparing the Contribution of Syntactic and Semantic Features in Closed versus Open Domain Question Answering. , 2007, , .		2
2662	Searchable High-Resolution 2D Gel Proteome of the Human Colon Crypt. Journal of Proteome Research, 2007, 6, 2232-2238.	1.8	15

#	ARTICLE	IF	CITATIONS
2663	Applications of medical informatics in allergy/immunology. <i>Annals of Allergy, Asthma and Immunology</i> , 2007, 99, 2-10.	0.5	3
2664	Molecular portrait of cisplatin induced response in human testis cancer cell lines based on gene expression profiles. <i>Molecular Cancer</i> , 2007, 6, 53.	7.9	56
2665	Comparative proteome analysis of human epithelial ovarian cancer. <i>Proteome Science</i> , 2007, 5, 16.	0.7	47
2666	Intrinsic Disorder and Functional Proteomics. <i>Biophysical Journal</i> , 2007, 92, 1439-1456.	0.2	643
2667	Transcriptional Profiling of Bipotential Embryonic Liver Cells to Identify Liver Progenitor Cell Surface Markers. <i>Stem Cells</i> , 2007, 25, 2476-2487.	1.4	32
2668	APC Inactivation Associates With Abnormal Mitosis Completion and Concomitant BUB1B/MAD2L1 Up-Regulation. <i>Gastroenterology</i> , 2007, 132, 2448-2458.	0.6	36
2669	An ontology for describing and synthesizing ecological observation data. <i>Ecological Informatics</i> , 2007, 2, 279-296.	2.3	209
2670	Atherosclerosis. <i>Journal of the American College of Cardiology</i> , 2007, 49, 1589-1599.	1.2	63
2671	Interpreting physiological responses to environmental change through gene expression profiling. <i>Journal of Experimental Biology</i> , 2007, 210, 1584-1592.	0.8	103
2672	Sparse Nonnegative Matrix Factorization with Genetic Algorithms for Microarray Analysis. <i>Neural Networks (IJCNN), International Joint Conference on</i> , 2007, , .	0.0	12
2673	Gene3D and Understanding Proteome Evolution. <i>Biological and Medical Physics Series</i> , 2007, , 37-55.	0.3	0
2674	Amino-Acid Properties and Consequences of Substitutions. , 0, , 311-342.		88
2675	Needle in a Haystack? Dealing with 500 000 SNP Genome Scans. , 0, , 447-493.		1
2676	Network-based prediction of protein function. <i>Molecular Systems Biology</i> , 2007, 3, 88.	3.2	918
2679	Analysis of Expression Data: An Overview. <i>Current Protocols in Bioinformatics</i> , 2007, 17, Unit 7.1.	25.8	9
2680	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. <i>PLoS Biology</i> , 2007, 5, e16.	2.6	736
2681	Evolution of Symbiotic Bacteria in the Distal Human Intestine. <i>PLoS Biology</i> , 2007, 5, e156.	2.6	490
2682	A Family of Human MicroRNA Genes from Miniature Inverted-Repeat Transposable Elements. <i>PLoS ONE</i> , 2007, 2, e203.	1.1	264

#	ARTICLE	IF	CITATIONS
2683	Probabilistic Protein Function Prediction from Heterogeneous Genome-Wide Data. PLoS ONE, 2007, 2, e337.	1.1	84
2684	Phenotypic Diversity and Altered Environmental Plasticity in Arabidopsis thaliana with Reduced Hsp90 Levels. PLoS ONE, 2007, 2, e648.	1.1	159
2685	Wide-Scale Analysis of Human Functional Transcription Factor Binding Reveals a Strong Bias towards the Transcription Start Site. PLoS ONE, 2007, 2, e807.	1.1	55
2686	Proteomic Shifts in Embryonic Stem Cells with Gene Dose Modifications Suggest the Presence of Balancer Proteins in Protein Regulatory Networks. PLoS ONE, 2007, 2, e1218.	1.1	24
2687	Gene-Centric Characteristics of Genome-Wide Association Studies. PLoS ONE, 2007, 2, e1262.	1.1	7
2688	Familial aggregation analysis of gene expressions. BMC Proceedings, 2007, 1, S49.	1.8	1
2689	Searching for master regulators of transcription in a human gene expression data set. BMC Proceedings, 2007, 1, S81.	1.8	3
2690	Inferring Protein Function from Sequence. , 0, , 1087-1119.		2
2691	Conjugated Linoleic Acid Alters Global Gene Expression in Human Intestinal-Like Caco-2 Cells in an Isomer-Specific Manner ³ . Journal of Nutrition, 2007, 137, 2359-2365.	1.3	26
2692	Gene projects: a genome web tool for ongoing mining and annotation applied to CitEST. Genetics and Molecular Biology, 2007, 30, 1030-1036.	0.6	8
2693	Frequency and distribution of microsatellites from ESTs of citrus. Genetics and Molecular Biology, 2007, 30, 1009-1018.	0.6	37
2694	Public Databases and Software for the Pathway Analysis of Cancer Genomes. Cancer Informatics, 2007, 3, 117693510700300.	0.9	9
2695	Integration of Transcriptome and Proteome Data from Human-Pathogenic Fungi by Using a Data Warehouse. Journal of Integrative Bioinformatics, 2007, 4, 51-63.	1.0	14
2696	Using Data Warehouse Technology in Crop Plant Bioinformatics. Journal of Integrative Bioinformatics, 2007, 4, 145-159.	1.0	4
2697	Finding cis-regulatory elements using comparative genomics: Some lessons from ENCODE data. Genome Research, 2007, 17, 775-786.	2.4	69
2698	Microarray analysis of gene expression profile of multidrug resistance in pancreatic cancer. Chinese Medical Journal, 2007, 120, 1743-1752.	0.9	24
2699	Including Functional Annotations and Extending the Collection of Structural Classifications of Protein Loops (ArchDB). Bioinformatics and Biology Insights, 2007, 1, 117793220700100.	1.0	2
2700	The Research Collaboratory for Structural Bioinformatics Protein Data Bank. , 2007, , 373-388.		2

#	ARTICLE	IF	CITATIONS
2701	On the use of organisation modelling techniques to address biological organisation. Multiagent and Grid Systems, 2007, 3, 199-223.	0.5	3
2702	A Measurement Ontology Generalizable for Emerging Domain Applications on the Semantic Web. Journal of Database Management, 2007, 18, 20-42.	1.0	16
2703	Análisis de micromatrices de ADN revela genes asociados a metástasis en líneas celulares de cáncer de próstata de rata. Biomedica, 2007, 27, 192.	0.3	7
2704	Functional genomics analysis of low concentration of ethanol in human hepatocellular carcinoma (HepG2) cells. Role of genes involved in transcriptional and translational processes. International Journal of Medical Sciences, 2007, 4, 28-35.	1.1	15
2705	ChIP-on-chip significance analysis reveals large-scale binding and regulation by human transcription factor oncogenes. Nature Precedings, 2007, , .	0.1	0
2706	Bridging the gap between social tagging and semantic annotation: E.D. the Entity Describer. Nature Precedings, 2007, , .	0.1	4
2707	Bridging the gap between social tagging and semantic annotation: E.D. the Entity Describer. Nature Precedings, 2007, , .	0.1	0
2708	Section 7: Bioinformatics: Bioinformatics Linkage of Heterogeneous Clinical and Genomic Information in Support of Personalized Medicine. Yearbook of Medical Informatics, 2007, 16, 98-105.	0.8	3
2710	Computational prediction of microRNA targets in vertebrates, fruitflies and nematodes. , 0, , 172-186.		0
2711	Computational approaches to elucidate miRNA biology. , 2007, , 187-198.		2
2712	Data Syndication Techniques for Bioinformatics Applications. , 0, , 157-177.		0
2713	GeneBrowser: an approach for integration and functional classification of genomic data. Journal of Integrative Bioinformatics, 2007, 4, 264-273.	1.0	7
2714	Functional genomics of plant infection by the rice blast fungus Magnaporthe grisea. , 0, , 227-254.		0
2717	Integrating Functional Knowledge during Sample Clustering for Microarray Data using Unsupervised Decision Trees. Biometrical Journal, 2007, 49, 214-229.	0.6	5
2718	Virus-Ploc: A fusion classifier for predicting the subcellular localization of viral proteins within host and virus-infected cells. Biopolymers, 2007, 85, 233-240.	1.2	154
2719	Automated System for Gene Annotation and Metabolic Pathway Reconstruction Using General Sequence Databases. Chemistry and Biodiversity, 2007, 4, 2593-2602.	1.0	27
2720	Ontologies on the Semantic Web. Annual Review of Information Science & Technology, 2007, 41, 407-451.	2.6	16
2721	Long-term course and mutational spectrum of <i>spatacsin</i> -linked spastic paraplegia. Annals of Neurology, 2007, 62, 656-665.	2.8	113

#	ARTICLE	IF	CITATIONS
2722	Down-regulation of insulin-like growth factor binding protein-5 (IGFBP-5): Novel marker for cervical carcinogenesis. <i>International Journal of Cancer</i> , 2007, 120, 2068-2077.	2.3	18
2723	A gene expression signature associated with metastatic cells in effusions of breast carcinoma patients. <i>International Journal of Cancer</i> , 2007, 121, 1036-1046.	2.3	29
2724	Gene expression abnormalities in histologically normal breast epithelium of breast cancer patients. <i>International Journal of Cancer</i> , 2008, 122, 1557-1566.	2.3	105
2725	Gene expression analysis of estrogenic compounds in the liver of common carp (<i>Cyprinus</i> Tj ETQq1 1 0.784314 rgBT /Overlock 1001121, 299-311.	1.4	51
2726	Large-scale plant protein subcellular location prediction. <i>Journal of Cellular Biochemistry</i> , 2007, 100, 665-678.	1.2	209
2727	Bioinformatics. <i>Journal of Cellular Physiology</i> , 2007, 213, 365-369.	2.0	20
2728	Neural precursor cells from a fatal human motoneuron disease differentiate despite aberrant gene expression. <i>Developmental Neurobiology</i> , 2007, 67, 270-284.	1.5	9
2729	Genome-wide association analyses of expression phenotypes. <i>Genetic Epidemiology</i> , 2007, 31, S7-S11.	0.6	0
2730	Data mining of RNA expression and DNA genotype data: Presentation Group 5 contributions to Genetic Analysis Workshop 15. <i>Genetic Epidemiology</i> , 2007, 31, S43-S50.	0.6	1
2731	Cardiotrophin-1 is an essential factor in the natural defense of the liver against apoptosis. <i>Hepatology</i> , 2007, 45, 639-648.	3.6	36
2732	Genome-level analysis of genetic regulation of liver gene expression networks. <i>Hepatology</i> , 2007, 46, 548-557.	3.6	49
2733	Transcriptional oncogenomic hot spots in Barrett's adenocarcinomas: Serial analysis of gene expression. <i>Genes Chromosomes and Cancer</i> , 2007, 46, 914-928.	1.5	18
2734	The use of evolutionary biology concepts for genome annotation. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2007, 308B, 26-36.	0.6	4
2735	Wide gene expression profiling of ischemia-reperfusion injury in human liver transplantation. <i>Liver Transplantation</i> , 2007, 13, 99-113.	1.3	47
2736	Parasitic nematodes—From genomes to control. <i>Veterinary Parasitology</i> , 2007, 148, 31-42.	0.7	43
2737	Prion infection-impaired functional blocks identified by proteomics enlighten the targets and the curing pathways of an anti-prion drug. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 154-167.	1.1	13
2738	Annotating the human proteome: Beyond establishing a parts list. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 175-191.	1.1	32
2739	Addressing the challenges of multiscale model management in systems biology. <i>Computers and Chemical Engineering</i> , 2007, 31, 962-979.	2.0	24

#	ARTICLE	IF	CITATIONS
2740	Computational methodologies for genome evolution and functional association. <i>Computers and Chemical Engineering</i> , 2007, 31, 943-949.	2.0	1
2741	Ontology annotation: mapping genomic regions to biological function. <i>Current Opinion in Chemical Biology</i> , 2007, 11, 4-11.	2.8	76
2742	Recent progress in protein subcellular location prediction. <i>Analytical Biochemistry</i> , 2007, 370, 1-16.	1.1	864
2743	Functional gene expression differences between inbred alcohol-preferring and "non-preferring rats in five brain regions. <i>Alcohol</i> , 2007, 41, 95-132.	0.8	107
2744	Systems Biology and grid technologies: Challenges for understanding complex cell signaling networks. <i>Future Generation Computer Systems</i> , 2007, 23, 428-434.	4.9	5
2745	Using OWL to model biological knowledge. <i>International Journal of Human Computer Studies</i> , 2007, 65, 583-594.	3.7	59
2746	Haplotype-Based Analysis of Genes Associated With Risk of Adverse Skin Reactions After Radiotherapy in Breast Cancer Patients. <i>International Journal of Radiation Oncology Biology Physics</i> , 2007, 69, 685-693.	0.4	63
2747	Development of bioinformatic tools to support EST-sequencing, in silico- and microarray-based transcriptome profiling in mycorrhizal symbioses. <i>Phytochemistry</i> , 2007, 68, 19-32.	1.4	49
2748	A method of gene-function annotation based on variable precision rough sets. <i>Journal of Bionic Engineering</i> , 2007, 4, 177-184.	2.7	17
2749	Concept of Intelligent Mechanical Design for autonomous mobile robots. <i>Journal of Bionic Engineering</i> , 2007, 4, 217-226.	2.7	22
2750	The first trimester human trophoblast cell line ACH-3P: A novel tool to study autocrine/paracrine regulatory loops of human trophoblast subpopulations " TNF- α stimulates MMP15 expression. <i>BMC Developmental Biology</i> , 2007, 7, 137.	2.1	79
2751	Molecular determinants of caste differentiation in the highly eusocial honeybee <i>Apis mellifera</i> . <i>BMC Developmental Biology</i> , 2007, 7, 70.	2.1	226
2752	Genetic mapping of a new heart rate QTL on chromosome 8 of spontaneously hypertensive rats. <i>BMC Medical Genetics</i> , 2007, 8, 17.	2.1	30
2753	Common molecular pathways involved in human CD133+/CD34+ progenitor cell expansion and cancer. <i>Cancer Cell International</i> , 2007, 7, 11.	1.8	15
2754	Gene expression and the evolution of phenotypic diversity in social wasps. <i>BMC Biology</i> , 2007, 5, 23.	1.7	55
2755	Identification of novel conserved peptide uORF homology groups in Arabidopsis and rice reveals ancient eukaryotic origin of select groups and preferential association with transcription factor-encoding genes. <i>BMC Biology</i> , 2007, 5, 32.	1.7	147
2756	Growth control of the eukaryote cell: a systems biology study in yeast. <i>Journal of Biology</i> , 2007, 6, 4.	2.7	234
2757	A global analysis of genetic interactions in <i>Caenorhabditis elegans</i> . <i>Journal of Biology</i> , 2007, 6, 8.	2.7	144

#	ARTICLE	IF	CITATIONS
2758	Analysis of effects of the herbal preparation circulat on gene expression levels in cultured human fibroblasts. <i>Phytotherapy Research</i> , 2007, 21, 777-789.	2.8	3
2759	Non-heme iron through the three domains of life. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 317-324.	1.5	70
2760	Assessment of predictions submitted for the CASP7 function prediction category. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 165-174.	1.5	54
2761	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
2762	Proteomic analysis of protein expression changes in a model of gliomagenesis. <i>Proteomics - Clinical Applications</i> , 2007, 1, 1485-1498.	0.8	3
2763	A review of standards for data exchange within systems biology. <i>Proteomics</i> , 2007, 7, 857-867.	1.3	54
2764	Identifying functional modules in the physical interactome of <i>Saccharomyces cerevisiae</i> . <i>Proteomics</i> , 2007, 7, 944-960.	1.3	135
2765	Evaluation of an in vitro model of androgen ablation and identification of the androgen responsive proteome in LNCaP cells. <i>Proteomics</i> , 2007, 7, 47-63.	1.3	31
2766	A multivariate analysis approach to the integration of proteomic and gene expression data. <i>Proteomics</i> , 2007, 7, 2162-2171.	1.3	70
2767	Modeling the proteome of a Marek's disease transformed cell line: a natural animal model for CD30 overexpressing lymphomas. <i>Proteomics</i> , 2007, 7, 1316-1326.	1.3	41
2768	Subcellular proteomics of cell differentiation: Quantitative analysis of the plasma membrane proteome of Caco-2 cells. <i>Proteomics</i> , 2007, 7, 2201-2215.	1.3	53
2769	Proteome and phosphoproteome analysis of chromatin associated proteins in rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overloc 1.3 65	1.3	65
2770	Differentially androgen-modulated genes in ovarian epithelial cells from BRCA mutation carriers and control patients predict ovarian cancer survival and disease progression. <i>Oncogene</i> , 2007, 26, 198-214.	2.6	36
2771	Serrated carcinomas form a subclass of colorectal cancer with distinct molecular basis. <i>Oncogene</i> , 2007, 26, 312-320.	2.6	136
2772	Identification of a metastasis signature and the DLX4 homeobox protein as a regulator of metastasis by combined transcriptome approach. <i>Oncogene</i> , 2007, 26, 4600-4608.	2.6	43
2773	Molecular signatures of metaplastic carcinoma of the breast by large-scale transcriptional profiling: identification of genes potentially related to epithelial-mesenchymal transition. <i>Oncogene</i> , 2007, 26, 7859-7871.	2.6	183
2774	Mechanisms of skeletal muscle injury and repair revealed by gene expression studies in mouse models. <i>Journal of Physiology</i> , 2007, 582, 825-841.	1.3	117
2775	Identification of glucocorticoid-regulated genes that control cell proliferation during murine respiratory development. <i>Journal of Physiology</i> , 2007, 585, 187-201.	1.3	45

#	ARTICLE	IF	CITATIONS
2776	Genome sequence of the lignocellulose-bioconverting and xylose-fermenting yeast <i>Pichia stipitis</i> . <i>Nature Biotechnology</i> , 2007, 25, 319-326.	9.4	449
2777	Towards zoomable multidimensional maps of the cell. <i>Nature Biotechnology</i> , 2007, 25, 547-554.	9.4	84
2778	Decoding global gene expression programs in liver cancer by noninvasive imaging. <i>Nature Biotechnology</i> , 2007, 25, 675-680.	9.4	510
2779	RNA polymerase stalling at developmental control genes in the <i>Drosophila melanogaster</i> embryo. <i>Nature Genetics</i> , 2007, 39, 1512-1516.	9.4	671
2780	A genome-wide map of diversity in <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 113-119.	9.4	320
2781	Genome variation and evolution of the malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 120-125.	9.4	184
2782	Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. <i>Nature Genetics</i> , 2007, 39, 199-206.	9.4	294
2783	A genome-wide association study of global gene expression. <i>Nature Genetics</i> , 2007, 39, 1202-1207.	9.4	882
2784	A high-resolution atlas of nucleosome occupancy in yeast. <i>Nature Genetics</i> , 2007, 39, 1235-1244.	9.4	765
2785	Population genomics of human gene expression. <i>Nature Genetics</i> , 2007, 39, 1217-1224.	9.4	1,072
2786	A critical developmental switch defines the kinetics of kidney cyst formation after loss of <i>Pkd1</i> . <i>Nature Medicine</i> , 2007, 13, 1490-1495.	15.2	370
2787	Genome-wide resources of endoribonuclease-prepared short interfering RNAs for specific loss-of-function studies. <i>Nature Methods</i> , 2007, 4, 337-344.	9.0	167
2788	Integration of biological networks and gene expression data using Cytoscape. <i>Nature Protocols</i> , 2007, 2, 2366-2382.	5.5	2,275
2789	High-throughput electronic biology: mining information for drug discovery. <i>Nature Reviews Drug Discovery</i> , 2007, 6, 220-230.	21.5	82
2790	The versatile worm: genetic and genomic resources for <i>Caenorhabditis elegans</i> research. <i>Nature Reviews Genetics</i> , 2007, 8, 518-532.	7.7	116
2791	A unified classification system for eukaryotic transposable elements. <i>Nature Reviews Genetics</i> , 2007, 8, 973-982.	7.7	2,396
2792	Predicting protein function from sequence and structure. <i>Nature Reviews Molecular Cell Biology</i> , 2007, 8, 995-1005.	16.1	485
2793	Enrichment of HapMap recombination hotspot predictions around human nervous system genes: evidence for positive selection ?. <i>European Journal of Human Genetics</i> , 2007, 15, 1071-1078.	1.4	14

#	ARTICLE	IF	CITATIONS
2794	Expression Profiling Identifies the CRH/CRH-R1 System as a Modulator of Neurovascular Gene Activity. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2007, 27, 1476-1495.	2.4	24
2795	A Web-Based Data Warehouse on Gene Expression in Human Malignant Melanoma. <i>Journal of Investigative Dermatology</i> , 2007, 127, 394-399.	0.3	40
2796	Gene Expression Time Course in the Human Skin during Elicitation of Allergic Contact Dermatitis. <i>Journal of Investigative Dermatology</i> , 2007, 127, 2585-2595.	0.3	41
2797	Disrupted in Schizophrenia 1 Interactome: evidence for the close connectivity of risk genes and a potential synaptic basis for schizophrenia. <i>Molecular Psychiatry</i> , 2007, 12, 74-86.	4.1	386
2798	Lack of serotonin1B receptor expression leads to age-related motor dysfunction, early onset of brain molecular aging and reduced longevity. <i>Molecular Psychiatry</i> , 2007, 12, 1042-1056.	4.1	51
2799	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	13.7	661
2800	Natural history and evolutionary principles of gene duplication in fungi. <i>Nature</i> , 2007, 449, 54-61.	13.7	611
2801	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007, 450, 219-232.	13.7	573
2802	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
2803	Identification of candidate transcriptional modulators involved in successful regeneration after nerve injury. <i>European Journal of Neuroscience</i> , 2007, 25, 3629-3637.	1.2	117
2804	A β treatment and P301L tau expression in an Alzheimer's disease tissue culture model act synergistically to promote aberrant cell cycle re-entry. <i>European Journal of Neuroscience</i> , 2007, 26, 60-72.	1.2	31
2805	Novel genes differentially expressed in cortical regions during late neurogenesis. <i>European Journal of Neuroscience</i> , 2007, 26, 33-50.	1.2	22
2806	Using gene chips to identify organ-specific, smooth muscle responses to experimental diabetes: potential applications to urological diseases. <i>BJU International</i> , 2007, 99, 418-430.	1.3	28
2807	Hepatopancreatic multi-transcript expression patterns in the crayfish <i>Cherax quadricarinatus</i> during the moult cycle. <i>Insect Molecular Biology</i> , 2007, 16, 661-674.	1.0	35
2808	Heterologous microarray experiments used to identify the early gene response to heat stress in a coral reef fish. <i>Molecular Ecology</i> , 2007, 16, 1749-1763.	2.0	97
2809	Patterns of genetic diversity and candidate genes for ecological divergence in a homoploid hybrid sunflower, <i>Helianthus anomalus</i> . <i>Molecular Ecology</i> , 2007, 16, 5017-5029.	2.0	16
2810	In vitro transcriptional response of polymorphonuclear leukocytes following contact with different antigens. <i>European Journal of Clinical Investigation</i> , 2007, 37, 860-869.	1.7	5
2811	Signatures of Positive Selection in Genes Associated with Human Skin Pigmentation as Revealed from Analyses of Single Nucleotide Polymorphisms. <i>Annals of Human Genetics</i> , 2007, 71, 354-369.	0.3	212

#	ARTICLE	IF	CITATIONS
2812	Identification and Analysis of Genomic Regions with Large Between-Population Differentiation in Humans. <i>Annals of Human Genetics</i> , 2008, 72, 99-110.	0.3	62
2813	Specific transcriptional responses induced by 8-methoxypsoralen and UVA in yeast. <i>FEMS Yeast Research</i> , 2007, 7, 866-878.	1.1	16
2814	Generation and annotation of lodgepole pine and oleoresin-induced expressed sequences from the blue-stain fungus <i>Ophiostoma clavigerum</i> , a Mountain Pine Beetle-associated pathogen. <i>FEMS Microbiology Letters</i> , 2007, 267, 151-158.	0.7	42
2815	Automatic mining of the literature to generate new hypotheses for the possible link between periodontitis and atherosclerosis: lipopolysaccharide as a case study. <i>Journal of Clinical Periodontology</i> , 2007, 34, 1016-1024.	2.3	40
2816	Systematic analysis of alternative first exons in plant genomes. <i>BMC Plant Biology</i> , 2007, 7, 55.	1.6	24
2817	Pathway aberrations of murine melanoma cells observed in Paired-End diTag transcriptomes. <i>BMC Cancer</i> , 2007, 7, 109.	1.1	10
2818	Cross-study analysis of gene expression data for intermediate neuroblastoma identifies two biological subtypes. <i>BMC Cancer</i> , 2007, 7, 89.	1.1	29
2819	Simultaneous clustering of gene expression data with clinical chemistry and pathological evaluations reveals phenotypic prototypes. <i>BMC Systems Biology</i> , 2007, 1, 15.	3.0	48
2820	A search engine to identify pathway genes from expression data on multiple organisms. <i>BMC Systems Biology</i> , 2007, 1, 20.	3.0	6
2821	Revealing cell cycle control by combining model-based detection of periodic expression with novel cis-regulatory descriptors. <i>BMC Systems Biology</i> , 2007, 1, 45.	3.0	8
2822	CoryneCenter – An online resource for the integrated analysis of corynebacterial genome and transcriptome data. <i>BMC Systems Biology</i> , 2007, 1, 55.	3.0	11
2823	Identification of functional modules using network topology and high-throughput data. <i>BMC Systems Biology</i> , 2007, 1, 8.	3.0	267
2825	HMM-ModE – Improved classification using profile hidden Markov models by optimising the discrimination threshold and modifying emission probabilities with negative training sequences. <i>BMC Bioinformatics</i> , 2007, 8, 104.	1.2	31
2826	Locational distribution of gene functional classes in <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2007, 8, 112.	1.2	10
2827	From genes to functional classes in the study of biological systems. <i>BMC Bioinformatics</i> , 2007, 8, 114.	1.2	108
2828	Multiple non-collinear TF-map alignments of promoter regions. <i>BMC Bioinformatics</i> , 2007, 8, 138.	1.2	10
2829	Detecting multivariate differentially expressed genes. <i>BMC Bioinformatics</i> , 2007, 8, 150.	1.2	28
2830	MPHASYS: a mouse phenotype analysis system. <i>BMC Bioinformatics</i> , 2007, 8, 183.	1.2	5

#	ARTICLE	IF	CITATIONS
2831	GenMAPP 2: new features and resources for pathway analysis. BMC Bioinformatics, 2007, 8, 217.	1.2	224
2832	Automatic extraction of gene ontology annotation and its correlation with clusters in protein networks. BMC Bioinformatics, 2007, 8, 243.	1.2	46
2833	Nearest Neighbor Networks: clustering expression data based on gene neighborhoods. BMC Bioinformatics, 2007, 8, 250.	1.2	59
2834	Difference-based clustering of short time-course microarray data with replicates. BMC Bioinformatics, 2007, 8, 253.	1.2	13
2835	HoughFeature, a novel method for assessing drug effects in three-color cDNA microarray experiments. BMC Bioinformatics, 2007, 8, 256.	1.2	14
2836	False positive reduction in protein-protein interaction predictions using gene ontology annotations. BMC Bioinformatics, 2007, 8, 262.	1.2	58
2837	Using contextual and lexical features to restructure and validate the classification of biomedical concepts. BMC Bioinformatics, 2007, 8, 264.	1.2	14
2838	Bayesian hierarchical model for transcriptional module discovery by jointly modeling gene expression and ChIP-chip data. BMC Bioinformatics, 2007, 8, 283.	1.2	25
2839	Exploring inconsistencies in genome-wide protein function annotations: a machine learning approach. BMC Bioinformatics, 2007, 8, 284.	1.2	33
2840	Computation of significance scores of unweighted Gene Set Enrichment Analyses. BMC Bioinformatics, 2007, 8, 290.	1.2	46
2841	Quantitative sequence-function relationships in proteins based on gene ontology. BMC Bioinformatics, 2007, 8, 294.	1.2	68
2842	PARE: A tool for comparing protein abundance and mRNA expression data. BMC Bioinformatics, 2007, 8, 309.	1.2	18
2843	Gene analogue finder: a GRID solution for finding functionally analogous gene products. BMC Bioinformatics, 2007, 8, 329.	1.2	6
2844	How to decide which are the most pertinent overly-represented features during gene set enrichment analysis. BMC Bioinformatics, 2007, 8, 332.	1.2	11
2845	EDISA: extracting biclusters from multiple time-series of gene expression profiles. BMC Bioinformatics, 2007, 8, 334.	1.2	52
2846	PathFinder: mining signal transduction pathway segments from protein-protein interaction networks. BMC Bioinformatics, 2007, 8, 335.	1.2	101
2847	OntologyWidget – a reusable, embeddable widget for easily locating ontology terms. BMC Bioinformatics, 2007, 8, 338.	1.2	2
2848	Classification of microarray data using gene networks. BMC Bioinformatics, 2007, 8, 35.	1.2	191

#	ARTICLE	IF	CITATIONS
2849	Combining classifiers to predict gene function in <i>Arabidopsis thaliana</i> using large-scale gene expression measurements. <i>BMC Bioinformatics</i> , 2007, 8, 358.	1.2	33
2850	Linking microarray reporters with protein functions. <i>BMC Bioinformatics</i> , 2007, 8, 360.	1.2	12
2851	Representing default knowledge in biomedical ontologies: application to the integration of anatomy and phenotype ontologies. <i>BMC Bioinformatics</i> , 2007, 8, 377.	1.2	38
2852	FUNC: a package for detecting significant associations between gene sets and ontological annotations. <i>BMC Bioinformatics</i> , 2007, 8, 41.	1.2	180
2853	DAVID Knowledgebase: a gene-centered database integrating heterogeneous gene annotation resources to facilitate high-throughput gene functional analysis. <i>BMC Bioinformatics</i> , 2007, 8, 426.	1.2	510
2854	CoryneRegNet 4.0 – A reference database for corynebacterial gene regulatory networks. <i>BMC Bioinformatics</i> , 2007, 8, 429.	1.2	61
2855	Identifications of conserved 7-mers in 3'-UTRs and microRNAs in <i>Drosophila</i> . <i>BMC Bioinformatics</i> , 2007, 8, 432.	1.2	12
2856	Identification of tissue-specific cis-regulatory modules based on interactions between transcription factors. <i>BMC Bioinformatics</i> , 2007, 8, 437.	1.2	27
2857	Transcription factor target prediction using multiple short expression time series from <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2007, 8, 454.	1.2	28
2858	Predicting gene ontology functions from protein's regional surface structures. <i>BMC Bioinformatics</i> , 2007, 8, 475.	1.2	19
2859	PARPs database: A LIMS systems for protein-protein interaction data mining or laboratory information management system. <i>BMC Bioinformatics</i> , 2007, 8, 483.	1.2	17
2860	Userscripts for the Life Sciences. <i>BMC Bioinformatics</i> , 2007, 8, 487.	1.2	14
2861	BiolInfer: a corpus for information extraction in the biomedical domain. <i>BMC Bioinformatics</i> , 2007, 8, 50.	1.2	288
2862	PLAN: a web platform for automating high-throughput BLAST searches and for managing and mining results. <i>BMC Bioinformatics</i> , 2007, 8, 53.	1.2	36
2863	Understanding and using the meaning of statements in a bio-ontology: recasting the Gene Ontology in OWL. <i>BMC Bioinformatics</i> , 2007, 8, 57.	1.2	37
2864	GeneBins: a database for classifying gene expression data, with application to plant genome arrays. <i>BMC Bioinformatics</i> , 2007, 8, 87.	1.2	41
2865	ESTuber db: an online database for <i>Tuber borchii</i> EST sequences. <i>BMC Bioinformatics</i> , 2007, 8, S13.	1.2	9
2866	Statistical analysis of genomic protein family and domain controlled annotations for functional investigation of classified gene lists. <i>BMC Bioinformatics</i> , 2007, 8, S14.	1.2	3

#	ARTICLE	IF	CITATIONS
2867	The Genopolis Microarray Database. BMC Bioinformatics, 2007, 8, S21.	1.2	8
2868	Semi-supervised learning for the identification of syn-expressed genes from fused microarray and in situ image data. BMC Bioinformatics, 2007, 8, S3.	1.2	15
2869	Analyzing in situ gene expression in the mouse brain with image registration, feature extraction and block clustering. BMC Bioinformatics, 2007, 8, S5.	1.2	27
2870	A mixture of feature experts approach for protein-protein interaction prediction. BMC Bioinformatics, 2007, 8, S6.	1.2	53
2871	Validating module network learning algorithms using simulated data. BMC Bioinformatics, 2007, 8, S5.	1.2	34
2872	e-Science and biological pathway semantics. BMC Bioinformatics, 2007, 8, S3.	1.2	36
2873	AlzPharm: integration of neurodegeneration data using RDF. BMC Bioinformatics, 2007, 8, S4.	1.2	38
2874	LinkHub: a Semantic Web system that facilitates cross-database queries and information retrieval in proteomics. BMC Bioinformatics, 2007, 8, S5.	1.2	27
2875	Towards Semantic e-Science for Traditional Chinese Medicine. BMC Bioinformatics, 2007, 8, S6.	1.2	24
2877	The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. BMC Bioinformatics, 2007, 8, S4.	1.2	36
2878	Using structural motif descriptors for sequence-based binding site prediction. BMC Bioinformatics, 2007, 8, S5.	1.2	22
2879	An improved method for identifying functionally linked proteins using phylogenetic profiles. BMC Bioinformatics, 2007, 8, S7.	1.2	44
2880	Using indirect protein interactions for the prediction of Gene Ontology functions. BMC Bioinformatics, 2007, 8, S8.	1.2	54
2881	Inferring cellular networks – a review. BMC Bioinformatics, 2007, 8, S5.	1.2	311
2882	Dissecting complex transcriptional responses using pathway-level scores based on prior information. BMC Bioinformatics, 2007, 8, S6.	1.2	19
2883	Graphs in molecular biology. BMC Bioinformatics, 2007, 8, S8.	1.2	106
2884	Current approaches to gene regulatory network modelling. BMC Bioinformatics, 2007, 8, S9.	1.2	218
2885	Cloning, analysis and functional annotation of expressed sequence tags from the Earthworm Eisenia fetida. BMC Bioinformatics, 2007, 8, S7.	1.2	52

#	ARTICLE	IF	CITATIONS
2886	T2DM-GeneMiner a web resource for meta-analysis and marker identification for type 2 diabetes mellitus. BMC Bioinformatics, 2007, 8, .	1.2	1
2887	GO for gene documents. BMC Bioinformatics, 2007, 8, S3.	1.2	10
2888	DNA indels in coding regions reveal selective constraints on protein evolution in the human lineage. BMC Evolutionary Biology, 2007, 7, 191.	3.2	42
2889	Thermal evolution of gene expression profiles in <i>Drosophila subobscura</i> . BMC Evolutionary Biology, 2007, 7, 42.	3.2	58
2890	The use of global transcriptional analysis to reveal the biological and cellular events involved in distinct development phases of <i>Trichophyton rubrum</i> conidial germination. BMC Genomics, 2007, 8, 100.	1.2	67
2891	A cricket Gene Index: a genomic resource for studying neurobiology, speciation, and molecular evolution. BMC Genomics, 2007, 8, 109.	1.2	32
2892	Transcriptome analysis of the venom gland of the Mexican scorpion <i>Hadrurus gertschi</i> (Arachnida: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.2	128
2893	CAG-encoded polyglutamine length polymorphism in the human genome. BMC Genomics, 2007, 8, 126.	1.2	78
2894	ConiferEST: an integrated bioinformatics system for data reprocessing and mining of conifer expressed sequence tags (ESTs). BMC Genomics, 2007, 8, 134.	1.2	14
2895	Generation and analysis of ESTs from the eastern oyster, <i>Crassostrea virginica</i> Gmelin and identification of microsatellite and SNP markers. BMC Genomics, 2007, 8, 157.	1.2	65
2896	Re-annotation and re-analysis of the <i>Campylobacter jejuni</i> NCTC11168 genome sequence. BMC Genomics, 2007, 8, 162.	1.2	189
2897	Generation and analysis of expressed sequence tags from the ciliate protozoan parasite <i>Ichthyophthirius multifiliis</i> . BMC Genomics, 2007, 8, 176.	1.2	29
2898	Combining mouse mammary gland gene expression and comparative mapping for the identification of candidate genes for QTL of milk production traits in cattle. BMC Genomics, 2007, 8, 183.	1.2	52
2899	Evidence for systems-level molecular mechanisms of tumorigenesis. BMC Genomics, 2007, 8, 185.	1.2	31
2900	Gene discovery for the carcinogenic human liver fluke, <i>Opisthorchis viverrini</i> . BMC Genomics, 2007, 8, 189.	1.2	90
2901	Effects of DNA-targeted ionizing radiation produced by 5-[125I]iodo-2'-deoxyuridine on global gene expression in primary human cells. BMC Genomics, 2007, 8, 192.	1.2	10
2902	Species differences in brain gene expression profiles associated with adult behavioral maturation in honey bees. BMC Genomics, 2007, 8, 202.	1.2	43
2903	Toward accurate high-throughput SNP genotyping in the presence of inherited copy number variation. BMC Genomics, 2007, 8, 211.	1.2	9

#	ARTICLE	IF	CITATIONS
2904	Quantitative assessment of relationship between sequence similarity and function similarity. BMC Genomics, 2007, 8, 222.	1.2	77
2905	An analysis of expression patterns of genes encoding proteins with catalytic activities. BMC Genomics, 2007, 8, 232.	1.2	35
2906	Whole genome expression profiling reveals a significant role for immune function in human abdominal aortic aneurysms. BMC Genomics, 2007, 8, 237.	1.2	149
2907	Mouse SNP Miner: an annotated database of mouse functional single nucleotide polymorphisms. BMC Genomics, 2007, 8, 24.	1.2	15
2908	Exploiting combinatorial cultivation conditions to infer transcriptional regulation. BMC Genomics, 2007, 8, 25.	1.2	42
2909	Pathways and genes differentially expressed in the motor cortex of patients with sporadic amyotrophic lateral sclerosis. BMC Genomics, 2007, 8, 26.	1.2	130
2910	ESTs and EST-linked polymorphisms for genetic mapping and phylogenetic reconstruction in the guppy, <i>Poecilia reticulata</i> . BMC Genomics, 2007, 8, 269.	1.2	21
2911	Design and evaluation of Actichip, a thematic microarray for the study of the actin cytoskeleton. BMC Genomics, 2007, 8, 294.	1.2	5
2912	MELOGEN: an EST database for melon functional genomics. BMC Genomics, 2007, 8, 306.	1.2	87
2913	A transcriptomic analysis of the adult stage of the bovine lungworm, <i>Dictyocaulus viviparus</i> . BMC Genomics, 2007, 8, 311.	1.2	17
2914	Unravelling the hidden heterogeneities of diffuse large B-cell lymphoma based on coupled two-way clustering. BMC Genomics, 2007, 8, 332.	1.2	7
2915	Collembase: a repository for springtail genomics and soil quality assessment. BMC Genomics, 2007, 8, 341.	1.2	44
2916	Androgen-induced masculinization in rainbow trout results in a marked dysregulation of early gonadal gene expression profiles. BMC Genomics, 2007, 8, 357.	1.2	59
2917	From transcriptome to biological function: environmental stress in an ectothermic vertebrate, the coral reef fish <i>Pomacentrus moluccensis</i> . BMC Genomics, 2007, 8, 358.	1.2	64
2918	Global comparative analysis of ESTs from the southern cattle tick, <i>Rhipicephalus (Boophilus) microplus</i> . BMC Genomics, 2007, 8, 368.	1.2	53
2919	Genes involved in TGF β 21-driven epithelial-mesenchymal transition of renal epithelial cells are topologically related in the human interactome map. BMC Genomics, 2007, 8, 383.	1.2	20
2920	A systems-biology analysis of isogenic megakaryocytic and granulocytic cultures identifies new molecular components of megakaryocytic apoptosis. BMC Genomics, 2007, 8, 384.	1.2	18
2921	Functional genomic delineation of TLR-induced transcriptional networks. BMC Genomics, 2007, 8, 394.	1.2	28

#	ARTICLE	IF	CITATIONS
2922	Ganoderma lucidum polysaccharides in human monocytic leukemia cells: from gene expression to network construction. <i>BMC Genomics</i> , 2007, 8, 411.	1.2	57
2923	Profiling sex-biased gene expression during parthenogenetic reproduction in <i>Daphnia pulex</i> . <i>BMC Genomics</i> , 2007, 8, 464.	1.2	51
2924	Surviving extreme polar winters by desiccation: clues from Arctic springtail (<i>Onychiurus arcticus</i>) EST libraries. <i>BMC Genomics</i> , 2007, 8, 475.	1.2	61
2925	Analysis of a set of Australian northern brown bandicoot expressed sequence tags with comparison to the genome sequence of the South American grey short tailed opossum. <i>BMC Genomics</i> , 2007, 8, 50.	1.2	14
2926	Differential regulation of gene products in newly synthesized <i>Brassica napus</i> allotetraploids is not related to protein function nor subcellular localization. <i>BMC Genomics</i> , 2007, 8, 56.	1.2	36
2927	An annotated catalogue of salivary gland transcripts in the adult female mosquito, <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2007, 8, 6.	1.2	219
2928	Gene expression profiling of aging reveals activation of a p53-mediated transcriptional program. <i>BMC Genomics</i> , 2007, 8, 80.	1.2	161
2929	Spotted cotton oligonucleotide microarrays for gene expression analysis. <i>BMC Genomics</i> , 2007, 8, 81.	1.2	43
2930	Gene function in early mouse embryonic stem cell differentiation. <i>BMC Genomics</i> , 2007, 8, 85.	1.2	123
2931	Identification and characterization of insect-specific proteins by genome data analysis. <i>BMC Genomics</i> , 2007, 8, 93.	1.2	38
2932	Gene expression trees in lymphoid development. <i>BMC Immunology</i> , 2007, 8, 25.	0.9	6
2933	Transcriptional control in embryonic <i>Drosophila</i> midline guidance assessed through a whole genome approach. <i>BMC Neuroscience</i> , 2007, 8, 59.	0.8	9
2934	Pathway and gene ontology based analysis of gene expression in a rat model of cerebral ischemic tolerance. <i>Brain Research</i> , 2007, 1177, 103-123.	1.1	33
2935	The <i>Schistosoma mansoni</i> transcriptome: An update. <i>Experimental Parasitology</i> , 2007, 117, 229-235.	0.5	23
2936	Gene functional annotation by statistical analysis of biomedical articles. <i>International Journal of Medical Informatics</i> , 2007, 76, 601-613.	1.6	18
2937	A method exploiting syntactic patterns and the UMLS semantics for aligning biomedical ontologies: The case of OBO disease ontologies. <i>International Journal of Medical Informatics</i> , 2007, 76, S353-S361.	1.6	18
2938	Inferring gene regulatory networks by integrating static and dynamic data. <i>International Journal of Medical Informatics</i> , 2007, 76, S462-S475.	1.6	7
2939	Data integration and genomic medicine. <i>Journal of Biomedical Informatics</i> , 2007, 40, 5-16.	2.5	147

#	ARTICLE	IF	CITATIONS
2940	An agent- and ontology-based system for integrating public gene, protein, and disease databases. <i>Journal of Biomedical Informatics</i> , 2007, 40, 17-29.	2.5	75
2941	Co-clustering and visualization of gene expression data and gene ontology terms for <i>Saccharomyces cerevisiae</i> using self-organizing maps. <i>Journal of Biomedical Informatics</i> , 2007, 40, 160-173.	2.5	55
2942	Measures of semantic similarity and relatedness in the biomedical domain. <i>Journal of Biomedical Informatics</i> , 2007, 40, 288-299.	2.5	434
2943	Enrichment of OBO ontologies. <i>Journal of Biomedical Informatics</i> , 2007, 40, 300-315.	2.5	30
2944	Natural language processing and visualization in the molecular imaging domain. <i>Journal of Biomedical Informatics</i> , 2007, 40, 270-281.	2.5	7
2945	Interface analysis between GSVML and HL7 version 3. <i>Journal of Biomedical Informatics</i> , 2007, 40, 527-538.	2.5	1
2946	Conceptual knowledge acquisition in biomedicine: A methodological review. <i>Journal of Biomedical Informatics</i> , 2007, 40, 582-602.	2.5	53
2947	Towards knowledge-based gene expression data mining. <i>Journal of Biomedical Informatics</i> , 2007, 40, 787-802.	2.5	70
2948	From broken to old: DNA damage, IGF1 endocrine suppression and aging. <i>DNA Repair</i> , 2007, 6, 1386-1390.	1.3	12
2949	Genes that may modulate longevity in <i>C. elegans</i> in both dauer larvae and long-lived daf-2 adults. <i>Experimental Gerontology</i> , 2007, 42, 825-839.	1.2	26
2950	Gene Ontology analysis in multiple gene clusters under multiple hypothesis testing framework. <i>Artificial Intelligence in Medicine</i> , 2007, 41, 105-115.	3.8	11
2951	Large scale analysis of genes contributing to the herbal preparation dependent hippocampal plasticity in postischemic rehabilitation. <i>Vascular Pharmacology</i> , 2007, 47, 319-327.	1.0	4
2952	Endocan is a VEGF-A and PI3K regulated gene with increased expression in human renal cancer. <i>Experimental Cell Research</i> , 2007, 313, 1285-1294.	1.2	112
2953	Analyses of human-chimpanzee orthologous gene pairs to explore evolutionary hypotheses of aging. <i>Mechanisms of Ageing and Development</i> , 2007, 128, 355-364.	2.2	34
2954	Effect of bisphenol A on human chorionic gonadotrophin-stimulated gene expression of cultured mouse Leydig tumour cells. <i>Reproductive Toxicology</i> , 2007, 24, 265-275.	1.3	21
2955	Protein function space: viewing the limits or limited by our view?. <i>Current Opinion in Structural Biology</i> , 2007, 17, 362-369.	2.6	37
2956	Functional Differentiation of Proteins: Implications for Structural Genomics. <i>Structure</i> , 2007, 15, 405-415.	1.6	9
2957	Detection of novel skeletogenesis target genes by comprehensive analysis of a Runx2 ^{+/+} /Δ mouse model. <i>Gene Expression Patterns</i> , 2007, 7, 102-112.	0.3	82

#	ARTICLE	IF	CITATIONS
2958	A portrait of cisplatin-induced transcriptional changes in mouse embryonic stem cells reveals a dominant p53-like response. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2007, 617, 58-70.	0.4	16
2959	Effects of gender on nigral gene expression and parkinson disease. <i>Neurobiology of Disease</i> , 2007, 26, 606-614.	2.1	206
2960	Palmitoyl protein thioesterase 1 (Ppt1)-deficient mouse neurons show alterations in cholesterol metabolism and calcium homeostasis prior to synaptic dysfunction. <i>Neurobiology of Disease</i> , 2007, 28, 52-64.	2.1	42
2961	Predicting Gene Ontology functions based on support vector machines and statistical significance estimation. <i>Neurocomputing</i> , 2007, 70, 718-725.	3.5	21
2962	Cytogenetic characterization and gene expression profiling in the rat reflux-induced esophageal tumor model. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2007, 133, 763-769.e10.	0.4	31
2963	Management and Analysis of Genomic Functional and Phenotypic Controlled Annotations to Support Biomedical Investigation and Practice. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2007, 11, 376-385.	3.6	14
2964	Psychiatric Consultation Record Retrieval Using Scenario-Based Representation and Multilevel Mixture Model. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2007, 11, 415-427.	3.6	12
2965	The Application of Proteomic Techniques to Fungal Protein Identification and Quantification. <i>Annals of the New York Academy of Sciences</i> , 2007, 1111, 133-146.	1.8	8
2966	Histamine Receptor H1 and Dermatopontin: New Downstream Targets of the Vitamin D Receptor. <i>Journal of Bone and Mineral Research</i> , 2007, 22, 1338-1349.	3.1	24
2967	Microarray analysis of bast fibre producing tissues of <i>Cannabis sativa</i> identifies transcripts associated with conserved and specialised processes of secondary wall development. <i>Functional Plant Biology</i> , 2007, 34, 737.	1.1	22
2968	Muscular Transcriptome in Postmenopausal Women With or Without Hormone Replacement. <i>Rejuvenation Research</i> , 2007, 10, 485-500E.	0.9	34
2969	A Bioinformatics Reference Model: Towards a Framework for Developing and Organising Bioinformatic Resources. <i>AIP Conference Proceedings</i> , 2007, , .	0.3	3
2970	Classification analysis of microarray data based on ontological engineering. <i>Journal of Zhejiang University: Science A</i> , 2007, 8, 638-643.	1.3	3
2971	Fibroblast Growth Factor 2 Modulates Transforming Growth Factor β^2 Signaling in Mouse Embryonic Fibroblasts and Human ESCs (hESCs) to Support hESC Self-Renewal. <i>Stem Cells</i> , 2007, 25, 455-464.	1.4	212
2972	Molecular Signature of Quiescent Satellite Cells in Adult Skeletal Muscle. <i>Stem Cells</i> , 2007, 25, 2448-2459.	1.4	402
2973	HEPATIC RESPONSES OF GENE EXPRESSION IN JUVENILE BROWN TROUT (<i>SALMO TRUTTA LACUSTRIS</i>) EXPOSED TO THREE MODEL CONTAMINANTS APPLIED SINGLY AND IN COMBINATION. <i>Environmental Toxicology and Chemistry</i> , 2007, 26, 100.	2.2	28
2974	Distinct subsets of microRNAs are expressed differentially in the human placentas of patients with preeclampsia. <i>American Journal of Obstetrics and Gynecology</i> , 2007, 196, 261.e1-261.e6.	0.7	373
2975	Differential expression of microRNAs with progression of gestation and inflammation in the human chorioamniotic membranes. <i>American Journal of Obstetrics and Gynecology</i> , 2007, 197, 289.e1-289.e6.	0.7	45

#	ARTICLE	IF	CITATIONS
2976	Leveraging Model Legume Information to Find Candidate Genes for Soybean Sudden Death Syndrome Using the Legume Information System. , 2007, 406, 245-259.		6
2977	BGI-RIS V2. , 2007, 406, 275-299.		4
2978	Discovering Sequence Motifs. <i>Methods in Molecular Biology</i> , 2007, 395, 271-292.	0.4	13
2979	Analysis and prediction of functionally important sites in proteins. <i>Protein Science</i> , 2007, 16, 4-13.	3.1	44
2980	Semantic Classification of Biomedical Concepts Using Distributional Similarity. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2007, 14, 467-477.	2.2	35
2981	A genome-wide transcriptional analysis of producer and non-producer NSO myeloma cell lines. <i>Biotechnology and Applied Biochemistry</i> , 2007, 47, 85.	1.4	24
2982	Comparing classical pathways and modern networks: towards the development of an edge ontology. <i>Trends in Biochemical Sciences</i> , 2007, 32, 320-331.	3.7	59
2983	Co-immunoprecipitations revisited: an update on experimental concepts and their implementation for sensitive interactome investigations of endogenous proteins. <i>Analytical and Bioanalytical Chemistry</i> , 2007, 389, 461-473.	1.9	74
2984	Protein Polymorphism Is Negatively Correlated with Conservation of Intronic Sequences and Complexity of Expression Patterns in <i>Drosophila melanogaster</i> . <i>Journal of Molecular Evolution</i> , 2007, 64, 511-518.	0.8	5
2985	Molecular characterization of the immune system: emergence of proteins, processes, and domains. <i>Immunogenetics</i> , 2007, 59, 333-348.	1.2	43
2986	Expressed sequence tags-based identification of genes in the biocontrol agent <i>Chaetomium cupreum</i> . <i>Applied Microbiology and Biotechnology</i> , 2007, 74, 650-658.	1.7	28
2987	Generation, annotation, and analysis of ESTs from four different <i>Trichoderma</i> strains grown under conditions related to biocontrol. <i>Applied Microbiology and Biotechnology</i> , 2007, 75, 853-862.	1.7	39
2988	Genes expression analyses of sea-island cotton (<i>Gossypium barbadense</i> L.) during fiber development. <i>Plant Cell Reports</i> , 2007, 26, 1309-1320.	2.8	81
2989	The HSP70 heat shock response in the Antarctic fish <i>Harpagifer antarcticus</i> . <i>Polar Biology</i> , 2007, 31, 171-180.	0.5	87
2990	Systems developmental biology: the use of ontologies in annotating models and in identifying gene function within and across species. <i>Mammalian Genome</i> , 2007, 18, 402-411.	1.0	15
2991	Transcript profiles of dendritic cells of PLOSL patients link demyelinating CNS disorders with abnormalities in pathways of actin bundling and immune response. <i>Journal of Molecular Medicine</i> , 2007, 85, 971-983.	1.7	24
2993	Characterization of genes encoding novel peptidases in the biocontrol fungus <i>Trichoderma harzianum</i> CECT 2413 using the TrichoEST functional genomics approach. <i>Current Genetics</i> , 2007, 51, 331-342.	0.8	71
2994	Computational protein function prediction: Are we making progress?. <i>Cellular and Molecular Life Sciences</i> , 2007, 64, 2505-2511.	2.4	46

#	ARTICLE	IF	CITATIONS
2995	Distinct reorganization of the genome transcription associates with organogenesis of somatic embryo, shoots, and roots in rice. <i>Plant Molecular Biology</i> , 2007, 63, 337-349.	2.0	26
2996	Detecting inconsistency in biological molecular databases using ontologies. <i>Data Mining and Knowledge Discovery</i> , 2007, 15, 275-296.	2.4	15
2997	Microarray analysis reveals potential mechanisms of BRMS1-mediated metastasis suppression. <i>Clinical and Experimental Metastasis</i> , 2007, 24, 551-565.	1.7	46
2998	Influence of Temperature on the Ontogenetic Expression of Neural Development-Related Genes from Developing Tilapia Brain Expressed Sequence Tags. <i>Marine Biotechnology</i> , 2007, 9, 243-261.	1.1	7
2999	A cDNA Microarray for <i>Crassostrea virginica</i> and <i>C. gigas</i> . <i>Marine Biotechnology</i> , 2007, 9, 577-591.	1.1	62
3000	Differentiation of the two rice subspecies <i>indica</i> and <i>japonica</i> : a Gene Ontology perspective. <i>Functional and Integrative Genomics</i> , 2007, 7, 135-151.	1.4	8
3001	Prot@G@: A Tool for Managing and Using Terminology in Radiology Applications. <i>Journal of Digital Imaging</i> , 2007, 20, 34-46.	1.6	71
3002	Tissue-driven Hypothesis with Gene Ontology (GO) Analysis. <i>Annals of Biomedical Engineering</i> , 2007, 35, 1088-1094.	1.3	8
3003	Genetics and diagnostic refinement. <i>Behavior Genetics</i> , 2007, 37, 535-545.	1.4	5
3004	Euk-PLoc: an ensemble classifier for large-scale eukaryotic protein subcellular location prediction. <i>Amino Acids</i> , 2007, 33, 57-67.	1.2	156
3005	Gene transcript and metabolite profiling of elicitor-induced opium poppy cell cultures reveals the coordinate regulation of primary and secondary metabolism. <i>Planta</i> , 2007, 225, 1085-1106.	1.6	98
3006	Cytoview: Development of a cell modelling framework. <i>Journal of Biosciences</i> , 2007, 32, 965-977.	0.5	4
3007	Systems biology via redescription and ontologies (I): finding phase changes with applications to malaria temporal data. <i>Systems and Synthetic Biology</i> , 2007, 1, 197-205.	1.0	4
3008	Widely predicting specific protein functions based on protein-protein interaction data and gene expression profile. <i>Science in China Series C: Life Sciences</i> , 2007, 50, 125-134.	1.3	10
3009	Evaluation of strategy for analyzing mouse liver plasma membrane proteome. <i>Science in China Series C: Life Sciences</i> , 2007, 50, 731-738.	1.3	6
3010	Comparing the biological coherence of network clusters identified by different detection algorithms. <i>Science Bulletin</i> , 2007, 52, 2938-2944.	1.7	5
3011	Finding finer functions for partially characterized proteins by protein-protein interaction networks. <i>Science Bulletin</i> , 2007, 52, 3363-3370.	1.7	1
3012	Biological relation extraction and query answering from MEDLINE abstracts using ontology-based text mining. <i>Data and Knowledge Engineering</i> , 2007, 61, 228-262.	2.1	31

#	ARTICLE	IF	CITATIONS
3013	Long-term phytosterol treatment alters gene expression in the liver of apo E-deficient mice. <i>Journal of Nutritional Biochemistry</i> , 2008, 19, 545-554.	1.9	24
3014	AondÃª: An ontology Web service for interoperability across biodiversity applications. <i>Information Systems</i> , 2008, 33, 724-753.	2.4	26
3015	A compression algorithm for pre-simulated Monte Carlo p-value functions: Application to the ontological analysis of microarray studies. <i>Pattern Recognition Letters</i> , 2008, 29, 768-772.	2.6	2
3016	Bayesian Weibull tree models for survival analysis of clinico-genomic data. <i>Statistical Methodology</i> , 2008, 5, 238-262.	0.5	10
3017	Actin cytoskeletal mediators of motility and invasion amplified and overexpressed in head and neck cancer. <i>Clinical and Experimental Metastasis</i> , 2008, 25, 289-304.	1.7	37
3018	Decision trees for hierarchical multi-label classification. <i>Machine Learning</i> , 2008, 73, 185-214.	3.4	497
3019	Individual-based Modelling: An Essential Tool for Microbiology. <i>Journal of Biological Physics</i> , 2008, 34, 19-37.	0.7	77
3020	Amino Acid Biases in the N- and C-termini of Proteins are Evolutionarily Conserved and are Conserved Between Functionally Related Proteins. <i>Protein Journal</i> , 2008, 27, 283-291.	0.7	10
3021	Exposure to radiation from global system for mobile communications at 1,800MHz significantly changes gene expression in rat hippocampus and cortex. <i>The Environmentalist</i> , 2008, 28, 458-465.	0.7	19
3022	MAIDS resistance-associated gene expression patterns in secondary lymphoid organs. <i>Immunogenetics</i> , 2008, 60, 485-494.	1.2	0
3023	The effect of temperature on Natural Antisense Transcript (NAT) expression in <i>Aspergillus flavus</i> . <i>Current Genetics</i> , 2008, 54, 241-269.	0.8	41
3024	Structure and expression of MdfBCP1, encoding an F-box-containing protein 1, during Fuji apple (<i>Malus</i>) Tj ETQq1 1 0.784314 rgBT /Ov 2.8 10	0.7	10
3025	Critical immunological pathways are downregulated in APECED patient dendritic cells. <i>Journal of Molecular Medicine</i> , 2008, 86, 1139-1152.	1.7	40
3026	Identifying cancer genes from cancer mutation profiles by cancer functions. <i>Science in China Series C: Life Sciences</i> , 2008, 51, 569-574.	1.3	1
3027	Prediction of anther-expressed gene regulation in <i>Arabidopsis</i> . <i>Science Bulletin</i> , 2008, 53, 3198-3203.	4.3	2
3028	Renewal and preliminary study of expressed sequence tags database on human fetal liver aged 22 wk of gestation. <i>Science Bulletin</i> , 2008, 53, 3204-3210.	4.3	0
3029	In silico analysis of candidate genes involved in light sensing and signal transduction pathways in soybean. <i>Plant Biotechnology Reports</i> , 2008, 2, 59-73.	0.9	1
3030	Fas Death Pathway in Sarcomas Correlates with Epidermal Growth Factor Transcription. <i>Clinical Orthopaedics and Related Research</i> , 2008, 466, 2092-2098.	0.7	3

#	ARTICLE	IF	CITATIONS
3031	Domain-Specific Data Sharing in Neuroscience: What Do We Have to Learn from Each Other?. <i>Neuroinformatics</i> , 2008, 6, 117-121.	1.5	24
3032	Terminology for Neuroscience Data Discovery: Multi-tree Syntax and Investigator-Derived Semantics. <i>Neuroinformatics</i> , 2008, 6, 161-174.	1.5	14
3033	Textpresso for Neuroscience: Searching the Full Text of Thousands of Neuroscience Research Papers. <i>Neuroinformatics</i> , 2008, 6, 195-204.	1.5	46
3034	The NIFSTD and BIRNLex Vocabularies: Building Comprehensive Ontologies for Neuroscience. <i>Neuroinformatics</i> , 2008, 6, 175-194.	1.5	130
3035	The Genome Browser at UCSC for Locating Genes, and Much More!. <i>Molecular Biotechnology</i> , 2008, 38, 269-275.	1.3	15
3036	MitoP2: An Integrative Tool for the Analysis of the Mitochondrial Proteome. <i>Molecular Biotechnology</i> , 2008, 40, 306-315.	1.3	69
3037	The Value of Nonmodel Genomes and an Example Using SynMap Within CoGe to Dissect the Hexaploidy that Predates the Rosids. <i>Tropical Plant Biology</i> , 2008, 1, 181-190.	1.0	193
3038	Bioinformatics and cancer research: building bridges for translational research. <i>Clinical and Translational Oncology</i> , 2008, 10, 85-95.	1.2	15
3039	Issues in an inference platform for generating deductive knowledge: a case study in cultural heritage digital libraries using the CIDOC CRM. <i>International Journal on Digital Libraries</i> , 2008, 8, 115-132.	1.1	17
3040	Global correlation analysis for micro-RNA and mRNA expression profiles in human cell lines. <i>Journal of Human Genetics</i> , 2008, 53, 515-523.	1.1	77
3041	Protein function prediction with high-throughput data. <i>Amino Acids</i> , 2008, 35, 517-530.	1.2	33
3042	Bridging protein local structures and protein functions. <i>Amino Acids</i> , 2008, 35, 627-650.	1.2	37
3043	Pollution-Affected Fish Hepatic Transcriptome and Its Expression Patterns on Exposure to Cadmium. <i>Marine Biotechnology</i> , 2008, 10, 250-261.	1.1	26
3044	Genome-wide analysis for identification of salt-responsive genes in common wheat. <i>Functional and Integrative Genomics</i> , 2008, 8, 277-286.	1.4	84
3045	Expression patterns in soybean resistant to <i>Phakopsora pachyrhizi</i> reveal the importance of peroxidases and lipoxygenases. <i>Functional and Integrative Genomics</i> , 2008, 8, 341-359.	1.4	54
3046	Monitoring of multiple sclerosis immunotherapy. <i>Journal of Neurology</i> , 2008, 255, 48-57.	1.8	84
3047	Gene expression changes induced by space flight in single-cells of the fern <i>Ceratopteris richardii</i> . <i>Planta</i> , 2008, 229, 151-159.	1.6	65
3048	Differential expression of cancer-related genes by single and permanent exposure to bone morphogenetic protein 2. <i>Journal of Cancer Research and Clinical Oncology</i> , 2008, 134, 1237-1245.	1.2	18

#	ARTICLE	IF	CITATIONS
3049	Small RNAs and the regulation of cis-natural antisense transcripts in Arabidopsis. BMC Molecular Biology, 2008, 9, 6.	3.0	120
3050	Web GIS in practice VI: a demo playlist of geo-mashups for public health neogeographers. International Journal of Health Geographics, 2008, 7, 38.	1.2	43
3051	Duplicate gene expression in allopolyploid Gossypium reveals two temporally distinct phases of expression evolution. BMC Biology, 2008, 6, 16.	1.7	235
3052	Effects of aging and calorie restriction on the global gene expression profiles of mouse testis and ovary. BMC Biology, 2008, 6, 24.	1.7	59
3053	Outlining eicosanoid biosynthesis in the crustacean Daphnia. Frontiers in Zoology, 2008, 5, 11.	0.9	80
3054	Expressed sequence tags (ESTs) from immune tissues of turbot (Scophthalmus maximus) challenged with pathogens. BMC Veterinary Research, 2008, 4, 37.	0.7	61
3055	Tobacco use induces anti-apoptotic, proliferative patterns of gene expression in circulating leukocytes of Caucasian males. BMC Medical Genomics, 2008, 1, 38.	0.7	12
3056	The Comparative Toxicogenomics Database facilitates identification and understanding of chemical-gene-disease associations: arsenic as a case study. BMC Medical Genomics, 2008, 1, 48.	0.7	60
3057	Pathways affected by asbestos exposure in normal and tumour tissue of lung cancer patients. BMC Medical Genomics, 2008, 1, 55.	0.7	13
3058	Biological processes, properties and molecular wiring diagrams of candidate low-penetrance breast cancer susceptibility genes. BMC Medical Genomics, 2008, 1, 62.	0.7	13
3059	Identification of molecular pathways affected by pterostilbene, a natural dimethylether analog of resveratrol. BMC Medical Genomics, 2008, 1, 7.	0.7	37
3060	Fast Gene Ontology based clustering for microarray experiments. BioData Mining, 2008, 1, 11.	2.2	89
3061	A survey of visualization tools for biological network analysis. BioData Mining, 2008, 1, 12.	2.2	173
3062	Modeling gene-by-environment interaction in comorbid depression with alcohol use disorders via an integrated bioinformatics approach. BioData Mining, 2008, 1, 2.	2.2	39
3063	Fast approximate hierarchical clustering using similarity heuristics. BioData Mining, 2008, 1, 9.	2.2	14
3064	'Validation' in genome-scale research. Journal of Biology, 2008, 8, 3.	2.7	21
3065	A Caenorhabditis elegans genetic-interaction map wiggles into view. Journal of Biology, 2008, 7, 8.	2.7	6
3066	Identifying candidate genes affecting developmental time in Drosophila melanogaster: pervasive pleiotropy and gene-by-environment interaction. BMC Developmental Biology, 2008, 8, 78.	2.1	47

#	ARTICLE	IF	CITATIONS
3067	BrainProfileDB â€“ a platform for integration of functional genomics data. <i>Proteomics</i> , 2008, 8, 1162-1164.	1.3	7
3068	Physical and computational analysis of the yeast <i>Kluyveromyces lactis</i> secreted proteome. <i>Proteomics</i> , 2008, 8, 2714-2723.	1.3	30
3069	Protein Information Crawler (PIC): Extensive spidering of multiple protein information resources for large protein sets. <i>Proteomics</i> , 2008, 8, 42-44.	1.3	4
3070	Establishment of a PF2Dâ€MS/MS platform for rapid profiling and semiquantitative analysis of membrane protein biomarkers. <i>Proteomics</i> , 2008, 8, 2168-2177.	1.3	21
3071	Chemical proteomic study of isoprenoid chain interactome with a synthetic photoaffinity probe. <i>Proteomics</i> , 2008, 8, 3094-3104.	1.3	15
3072	Cardiovascular GO Annotation Initiative Year 1 Report: Why Cardiovascular GO?. <i>Proteomics</i> , 2008, 8, 1950-1953.	1.3	15
3073	A novel stepwise analysis procedure of genomeâ€wide expression profiles identifies transcript signatures of thiamine genes as classifiers of mitochondrial mutants. <i>Yeast</i> , 2008, 25, 129-140.	0.8	2
3074	Global gene expression profile of <i>Saccharomyces cerevisiae</i> induced by dictamnine. <i>Yeast</i> , 2008, 25, 631-641.	0.8	19
3075	Exploration of the normal human bronchoalveolar lavage fluid proteome. <i>Proteomics - Clinical Applications</i> , 2008, 2, 585-595.	0.8	51
3076	Characterization of the renal cyst fluid proteome in autosomal dominant polycystic kidney disease (ADPKD) patients. <i>Proteomics - Clinical Applications</i> , 2008, 2, 1140-1152.	0.8	49
3077	The urine proteome as a biomarker of radiation injury. <i>Proteomics - Clinical Applications</i> , 2008, 2, 1065-1086.	0.8	25
3078	Protein domain annotation with integration of heterogeneous information sources. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 461-473.	1.5	20
3079	An integrated approach to inferring geneâ€disease associations in humans. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 1030-1037.	1.5	153
3080	Proteomics in gramâ€negative bacterial outer membrane vesicles. <i>Mass Spectrometry Reviews</i> , 2008, 27, 535-555.	2.8	288
3081	Modulation of several waves of gene expression during FGFâ€1 induced epithelialâ€mesenchymal transition of carcinoma cells. <i>Journal of Cellular Biochemistry</i> , 2008, 104, 826-839.	1.2	56
3082	<i>CYR61</i> is a novel gene associated with temperatureâ€dependent changes in fish metabolism as revealed by cDNA microarray analysis on a medaka <i>Oryzias latipes</i> cell line. <i>Journal of Cellular Biochemistry</i> , 2008, 104, 1297-1310.	1.2	7
3083	Genomeâ€wide expression analysis of cells expressing gain of function mutant D374Yâ€PCSK9. <i>Journal of Cellular Physiology</i> , 2008, 217, 459-467.	2.0	34
3084	Removal of highâ€abundance proteins for nuclear subproteome studies in rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.3	42

#	ARTICLE	IF	CITATIONS
3085	On the utility of gene set methods in genomewide association studies of quantitative traits. <i>Genetic Epidemiology</i> , 2008, 32, 658-668.	0.6	52
3086	CANDID: a flexible method for prioritizing candidate genes for complex human traits. <i>Genetic Epidemiology</i> , 2008, 32, 779-790.	0.6	75
3087	Gene profile analysis implicates Klotho as an important contributor to aging changes in brain white matter of the rhesus monkey. <i>Glia</i> , 2008, 56, 106-117.	2.5	118
3088	Comparative gene expression profiling of olfactory ensheathing glia and Schwann cells indicates distinct tissue repair characteristics of olfactory ensheathing glia. <i>Glia</i> , 2008, 56, 1285-1298.	2.5	56
3089	CAVEman: Standardized anatomical context for biomedical data mapping. <i>Anatomical Sciences Education</i> , 2008, 1, 10-18.	2.5	14
3090	Statistical Inference for Microarray Studies. , 2008, , 231-266.		1
3092	Genetic diversity and composition of a plasmid metagenome from a wastewater treatment plant. <i>Journal of Biotechnology</i> , 2008, 136, 65-76.	1.9	87
3093	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. <i>Journal of Biotechnology</i> , 2008, 136, 91-101.	1.9	202
3094	Interactive data analysis and clustering of genomic data. <i>Neural Networks</i> , 2008, 21, 368-378.	3.3	31
3095	Accuracy and robustness of clustering algorithms for small-size applications in bioinformatics. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2008, 387, 6310-6318.	1.2	4
3096	An insight into the salivary transcriptome and proteome of the soft tick and vector of epizootic bovine abortion, <i>Ornithodoros coriaceus</i> . <i>Journal of Proteomics</i> , 2008, 71, 493-512.	1.2	84
3097	A new geometric biclustering algorithm based on the Hough transform for analysis of large-scale microarray data. <i>Journal of Theoretical Biology</i> , 2008, 251, 264-274.	0.8	51
3098	Large-scale estimates of cellular origins of mRNAs: Enhancing the yield of transcriptome analyses. <i>Journal of Neuroscience Methods</i> , 2008, 167, 198-206.	1.3	13
3099	Differential gene expression involved in oxidative stress response caused by triethylene glycol dimethacrylate. <i>Biomaterials</i> , 2008, 29, 1377-1387.	5.7	89
3100	Vertex coloring acyclic digraphs and their corresponding hypergraphs. <i>Discrete Applied Mathematics</i> , 2008, 156, 1918-1928.	0.5	1
3101	In situ migration of handcrafted ontologies to reason-able forms. <i>Data and Knowledge Engineering</i> , 2008, 66, 147-162.	2.1	10
3102	Subsequence-based feature map for protein function classification. <i>Computational Biology and Chemistry</i> , 2008, 32, 122-130.	1.1	19
3103	On application of directons to functional classification of genes in prokaryotes. <i>Computational Biology and Chemistry</i> , 2008, 32, 176-184.	1.1	3

#	ARTICLE	IF	CITATIONS
3104	Complex phylogenetic profiling reveals fundamental genotype-phenotype associations. <i>Computational Biology and Chemistry</i> , 2008, 32, 412-416.	1.1	8
3105	Identification of regulatory mechanisms of the hepatic response to thermal injury. <i>Computers and Chemical Engineering</i> , 2008, 32, 356-369.	2.0	3
3106	Standardizing experimental protocols. <i>Current Opinion in Biotechnology</i> , 2008, 19, 354-359.	3.3	20
3107	Sodium-deoxycholate-assisted tryptic digestion and identification of proteolytically resistant proteins. <i>Analytical Biochemistry</i> , 2008, 377, 259-266.	1.1	104
3108	Abstract interpretation and types for systems biology. <i>Theoretical Computer Science</i> , 2008, 403, 52-70.	0.5	61
3109	The contact allergen dinitrochlorobenzene (DNCB) and respiratory allergy in the Th2-prone Brown Norway rat. <i>Toxicology</i> , 2008, 246, 213-221.	2.0	26
3110	The proteome of the human neuroblastoma cell line SH-SY5Y: An enlarged proteome. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 983-985.	1.1	30
3111	Integrating evolving brain gene ontology and connectionist-based system for modeling and knowledge discovery. <i>Neural Networks</i> , 2008, 21, 266-275.	3.3	7
3112	Cerebellar development transcriptome database (CDT-DB): Profiling of spatio-temporal gene expression during the postnatal development of mouse cerebellum. <i>Neural Networks</i> , 2008, 21, 1056-1069.	3.3	64
3113	Global gene expression profiles for life stages of the deadly amphibian pathogen <i>Batrachochytrium dendrobatidis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17034-17039.	3.3	101
3114	Identifying targets for drug discovery using bioinformatics. <i>Expert Opinion on Therapeutic Targets</i> , 2008, 12, 383-389.	1.5	70
3115	Predicting enzyme family class in a hybridization space. <i>Protein Science</i> , 2008, 13, 2857-2863.	3.1	75
3116	Searching Biomedical Literature with Anatomy Ontologies. , 2008, , 177-194.		1
3117	Selected reaction monitoring for quantitative proteomics: a tutorial. <i>Molecular Systems Biology</i> , 2008, 4, 222.	3.2	1,215
3118	New paradigm in protein function prediction for large scale omics analysis. <i>Molecular BioSystems</i> , 2008, 4, 223.	2.9	31
3119	Human Multipotent Stromal Cells Undergo Sharp Transition from Division to Development in Culture. <i>Stem Cells</i> , 2008, 26, 193-201.	1.4	90
3120	Genes Involved in Post-Transcriptional Regulation Are Overrepresented in Stem/Progenitor Spermatogonia of Cryptorchid Mouse Testes. <i>Stem Cells</i> , 2008, 26, 927-938.	1.4	36
3121	Molecular Signature of Cardiomyocyte Clusters Derived from Human Embryonic Stem Cells. <i>Stem Cells</i> , 2008, 26, 1831-1840.	1.4	78

#	ARTICLE	IF	CITATIONS
3122	MicroRNA Discovery and Profiling in Human Embryonic Stem Cells by Deep Sequencing of Small RNA Libraries. <i>Stem Cells</i> , 2008, 26, 2496-2505.	1.4	273
3123	Plasma Proteome Profiling of a Mouse Model of Breast Cancer Identifies a Set of Up-Regulated Proteins in Common with Human Breast Cancer Cells. <i>Journal of Proteome Research</i> , 2008, 7, 1481-1489.	1.8	54
3124	Molecular Genetics of Addiction and Related Heritable Phenotypes. <i>Annals of the New York Academy of Sciences</i> , 2008, 1141, 318-381.	1.8	134
3125	Cell image analysis ontology. <i>Pattern Recognition and Image Analysis</i> , 2008, 18, 332-341.	0.6	8
3126	Evaluation of Genetic Variation Contributing to Differences in Gene Expression between Populations. <i>American Journal of Human Genetics</i> , 2008, 82, 631-640.	2.6	192
3127	Epigenomic Profiling Reveals DNA-Methylation Changes Associated with Major Psychosis. <i>American Journal of Human Genetics</i> , 2008, 82, 696-711.	2.6	725
3128	The Human Phenotype Ontology: A Tool for Annotating and Analyzing Human Hereditary Disease. <i>American Journal of Human Genetics</i> , 2008, 83, 610-615.	2.6	797
3129	Comparison Analysis of Transcripts from the Halophyte <i>Thellungiella halophila</i> . <i>Journal of Integrative Plant Biology</i> , 2008, 50, 1327-1335.	4.1	50
3130	Dynamics of the yeast transcriptome during wine fermentation reveals a novel fermentation stress response. <i>FEMS Yeast Research</i> , 2008, 8, 35-52.	1.1	173
3131	Genomic resources and microarrays for the common carp <i>Cyprinus carpio</i> L.. <i>Journal of Fish Biology</i> , 2008, 72, 2095-2117.	0.7	60
3132	Use of a 15 k gene microarray to determine gene expression changes in response to acute and chronic methylmercury exposure in the fathead minnow <i>Pimephales promelas</i> Rafinesque. <i>Journal of Fish Biology</i> , 2008, 72, 2207-2280.	0.7	43
3133	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	13.7	1,003
3134	Synergistic response to oncogenic mutations defines gene class critical to cancer phenotype. <i>Nature</i> , 2008, 453, 1112-1116.	13.7	142
3135	The impact of microRNAs on protein output. <i>Nature</i> , 2008, 455, 64-71.	13.7	3,270
3136	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	9.4	155
3137	Identification of Information Flow-Modulating Drug Targets: A Novel Bridging Paradigm for Drug Discovery. <i>Clinical Pharmacology and Therapeutics</i> , 2008, 84, 563-572.	2.3	97
3138	High expression of DNA repair pathways is associated with metastasis in melanoma patients. <i>Oncogene</i> , 2008, 27, 565-573.	2.6	228
3139	Genes involved in cell adhesion, cell motility and mitogenic signaling are altered due to HPV 16 E5 protein expression. <i>Oncogene</i> , 2008, 27, 2532-2541.	2.6	60

#	ARTICLE	IF	CITATIONS
3140	<i>ITN1</i> , a novel gene encoding an ankyrin repeat protein that affects the ABA-mediated production of reactive oxygen species and is involved in salt stress tolerance in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2008, 56, 411-422.	2.8	95
3141	Assessment of Diet-induced Obese Rats as an Obesity Model by Comparative Functional Genomics. <i>Obesity</i> , 2008, 16, 811-818.	1.5	61
3142	DAX1, a direct target of EWS/FLI1 oncoprotein, is a principal regulator of cell-cycle progression in Ewing's tumor cells. <i>Oncogene</i> , 2008, 27, 6034-6043.	2.6	100
3143	Prediction of future metastasis and molecular characterization of head and neck squamous-cell carcinoma based on transcriptome and genome analysis by microarrays. <i>Oncogene</i> , 2008, 27, 6607-6622.	2.6	134
3144	MicroRNA-21 promotes cell transformation by targeting the programmed cell death 4 gene. <i>Oncogene</i> , 2008, 27, 4373-4379.	2.6	648
3145	A modular approach for integrative analysis of large-scale gene-expression and drug-response data. <i>Nature Biotechnology</i> , 2008, 26, 531-539.	9.4	111
3146	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	9.4	1,116
3147	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008, 26, 1155-1160.	9.4	530
3148	Gene expression signatures and small-molecule compounds link a protein kinase to <i>Plasmodium falciparum</i> motility. <i>Nature Chemical Biology</i> , 2008, 4, 347-356.	3.9	203
3149	Many sequence variants affecting diversity of adult human height. <i>Nature Genetics</i> , 2008, 40, 609-615.	9.4	615
3150	Identification and characterization of high-flux-control genes of yeast through competition analyses in continuous cultures. <i>Nature Genetics</i> , 2008, 40, 113-117.	9.4	93
3151	What everybody should know about the rat genome and its online resources. <i>Nature Genetics</i> , 2008, 40, 523-527.	9.4	43
3152	Stromal gene expression predicts clinical outcome in breast cancer. <i>Nature Medicine</i> , 2008, 14, 518-527.	15.2	1,497
3153	Functional organization of the transcriptome in human brain. <i>Nature Neuroscience</i> , 2008, 11, 1271-1282.	7.1	743
3154	Cell-PLoc: a package of Web servers for predicting subcellular localization of proteins in various organisms. <i>Nature Protocols</i> , 2008, 3, 153-162.	5.5	969
3155	The Mouse Tumor Biology database. <i>Nature Reviews Cancer</i> , 2008, 8, 459-465.	12.8	60
3156	Use and misuse of the gene ontology annotations. <i>Nature Reviews Genetics</i> , 2008, 9, 509-515.	7.7	518
3157	Towards a cyberinfrastructure for the biological sciences: progress, visions and challenges. <i>Nature Reviews Genetics</i> , 2008, 9, 678-688.	7.7	145

#	ARTICLE	IF	CITATIONS
3158	Haplotype patterns in cancer-related genes with long-range linkage disequilibrium: no evidence of association with breast cancer or positive selection. <i>European Journal of Human Genetics</i> , 2008, 16, 252-260.	1.4	7
3159	Targeting lipid metabolism by the lipoprotein lipase inhibitor orlistat results in apoptosis of B-cell chronic lymphocytic leukemia cells. <i>Leukemia</i> , 2008, 22, 585-592.	3.3	88
3160	Preliminary analysis of genomic abnormalities in canine meningiomas. <i>Veterinary and Comparative Oncology</i> , 2008, 6, 182-192.	0.8	14
3161	Possible role of the innate immunity in temporal lobe epilepsy. <i>Epilepsia</i> , 2008, 49, 1055-1065.	2.6	90
3162	Comprehensive gene expression atlas for the <i>Arabidopsis</i> MAP kinase signalling pathways. <i>New Phytologist</i> , 2008, 179, 643-662.	3.5	105
3163	Gene expression in the rat brain during prostaglandin D ₂ and adenosinergically induced sleep. <i>Journal of Neurochemistry</i> , 2008, 105, 1480-1498.	2.1	8
3164	Gene expression of AGS cells stimulated with released proteins by <i>Helicobacter pylori</i> . <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2008, 23, 643-651.	1.4	8
3165	Mu opioid receptor activation induces transcriptional plasticity in the central extended amygdala. <i>European Journal of Neuroscience</i> , 2008, 27, 2973-2984.	1.2	74
3166	Gene expression profiling in the developing prostate. <i>Differentiation</i> , 2008, 76, 624-640.	1.0	36
3167	Gene expression profiling of diffuse large B-cell lymphoma supervised by CD21 expression. <i>British Journal of Haematology</i> , 2008, 142, 562-570.	1.2	12
3168	Biocompatibility of haemodialysis membranes determined by gene expression of human leucocytes: a crossover study. <i>European Journal of Clinical Investigation</i> , 2008, 38, 918-924.	1.7	9
3169	Access to immunology through the Gene Ontology. <i>Immunology</i> , 2008, 125, 154-160.	2.0	33
3170	A microarray-based analysis of transcriptional compartmentalization in the alimentary canal of <i>Anopheles gambiae</i> (Diptera: Culicidae) larvae. <i>Insect Molecular Biology</i> , 2008, 17, 61-72.	1.0	63
3171	Anatomical ontologies of mosquitoes and ticks, and their web browsers in VectorBase. <i>Insect Molecular Biology</i> , 2008, 17, 87-89.	1.0	18
3172	Serine proteases identified from a <i>Costelytra zealandica</i> (White) (Coleoptera: Scarabaeidae) midgut EST library and their expression through insect development. <i>Insect Molecular Biology</i> , 2008, 17, 247-259.	1.0	17
3173	<i>In silico</i> prediction and characterization of microRNAs from red flour beetle (<i>Tribolium</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 155	1.0	55
3174	Rapid transcriptome characterization for a nonmodel organism using 454 pyrosequencing. <i>Molecular Ecology</i> , 2008, 17, 1636-1647.	2.0	624
3175	Population transcriptomics of life-history variation in the genus <i>Salmo</i> . <i>Molecular Ecology</i> , 2008, 17, 3095-3108.	2.0	41

#	ARTICLE	IF	CITATIONS
3176	Gene expression analysis in citrus reveals the role of gibberellins on photosynthesis and stress. <i>Plant, Cell and Environment</i> , 2008, 31, 1620-1633.	2.8	41
3177	Transcriptional regulation by an NAC (NAM-ATAF1,2-CUC2) transcription factor attenuates ABA signalling for efficient basal defence towards <i>Blumeria graminis</i> f. sp. <i>hordei</i> in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2008, 56, 867-880.	2.8	210
3178	A high-resolution survey of the effects of 5-aza-dC treatment on the chromatin state of MCF7 breast cancer cells [Engineering in Genomics]. <i>IEEE Engineering in Medicine and Biology Magazine</i> , 2008, 27, 86-100.	1.1	1
3179	The EDGE hypothesis: Epigenetically directed genetic errors in repeat-containing proteins (RCPs) involved in evolution, neuroendocrine signaling, and cancer. <i>Frontiers in Neuroendocrinology</i> , 2008, 29, 428-444.	2.5	20
3180	Corpus annotation for mining biomedical events from literature. <i>BMC Bioinformatics</i> , 2008, 9, 10.	1.2	244
3181	PDTD: a web-accessible protein database for drug target identification. <i>BMC Bioinformatics</i> , 2008, 9, 104.	1.2	249
3182	High-precision high-coverage functional inference from integrated data sources. <i>BMC Bioinformatics</i> , 2008, 9, 119.	1.2	33
3183	DBMLoc: a Database of proteins with multiple subcellular localizations. <i>BMC Bioinformatics</i> , 2008, 9, 127.	1.2	48
3184	Term-tissue specific models for prediction of gene ontology biological processes using transcriptional profiles of aging in <i>drosophila melanogaster</i> . <i>BMC Bioinformatics</i> , 2008, 9, 129.	1.2	7
3185	Mining phenotypes for gene function prediction. <i>BMC Bioinformatics</i> , 2008, 9, 136.	1.2	41
3186	Goldsurfer2 (Gs2): A comprehensive tool for the analysis and visualization of genome wide association studies. <i>BMC Bioinformatics</i> , 2008, 9, 138.	1.2	11
3187	Synonym set extraction from the biomedical literature by lexical pattern discovery. <i>BMC Bioinformatics</i> , 2008, 9, 159.	1.2	31
3188	Prediction of enzyme function based on 3D templates of evolutionarily important amino acids. <i>BMC Bioinformatics</i> , 2008, 9, 17.	1.2	70
3189	annot8r: GO, EC and KEGG annotation of EST datasets. <i>BMC Bioinformatics</i> , 2008, 9, 180.	1.2	87
3190	Improving protein function prediction methods with integrated literature data. <i>BMC Bioinformatics</i> , 2008, 9, 198.	1.2	24
3191	Network motif-based identification of transcription factor-target gene relationships by integrating multi-source biological data. <i>BMC Bioinformatics</i> , 2008, 9, 203.	1.2	35
3192	Identification of coherent patterns in gene expression data using an efficient biclustering algorithm and parallel coordinate visualization. <i>BMC Bioinformatics</i> , 2008, 9, 210.	1.2	75
3193	M-BISON: Microarray-based integration of data sources using networks. <i>BMC Bioinformatics</i> , 2008, 9, 214.	1.2	8

#	ARTICLE	IF	CITATIONS
3194	MelInfoText: associated gene methylation and cancer information from text mining. BMC Bioinformatics, 2008, 9, 22.	1.2	34
3195	A visual analytics approach for understanding biclustering results from microarray data. BMC Bioinformatics, 2008, 9, 247.	1.2	46
3196	StAR: a simple tool for the statistical comparison of ROC curves. BMC Bioinformatics, 2008, 9, 265.	1.2	163
3197	Microarray data mining: A novel optimization-based approach to uncover biologically coherent structures. BMC Bioinformatics, 2008, 9, 268.	1.2	27
3198	Discovering functional interaction patterns in protein-protein interaction networks. BMC Bioinformatics, 2008, 9, 276.	1.2	13
3199	Partial mixture model for tight clustering of gene expression time-course. BMC Bioinformatics, 2008, 9, 287.	1.2	17
3200	Genome-scale cluster analysis of replicated microarrays using shrinkage correlation coefficient. BMC Bioinformatics, 2008, 9, 288.	1.2	24
3201	Literature-aided meta-analysis of microarray data: a compendium study on muscle development and disease. BMC Bioinformatics, 2008, 9, 291.	1.2	21
3202	Relating gene expression data on two-component systems to functional annotations in Escherichia coli. BMC Bioinformatics, 2008, 9, 294.	1.2	7
3203	Gene Ontology term overlap as a measure of gene functional similarity. BMC Bioinformatics, 2008, 9, 327.	1.2	168
3204	Performing statistical analyses on quantitative data in Taverna workflows: An example using R and maxdBrowse to identify differentially-expressed genes from microarray data. BMC Bioinformatics, 2008, 9, 334.	1.2	38
3205	Gene Vector Analysis (Geneva): A unified method to detect differentially-regulated gene sets and similar microarray experiments. BMC Bioinformatics, 2008, 9, 348.	1.2	13
3206	Testing gene set enrichment for subset of genes: Sub-GSE. BMC Bioinformatics, 2008, 9, 362.	1.2	18
3207	OntoDas – a tool for facilitating the construction of complex queries to the Gene Ontology. BMC Bioinformatics, 2008, 9, 437.	1.2	4
3208	Evading the annotation bottleneck: using sequence similarity to search non-sequence gene data. BMC Bioinformatics, 2008, 9, 442.	1.2	14
3209	Assessment of protein set coherence using functional annotations. BMC Bioinformatics, 2008, 9, 444.	1.2	11
3210	Information-based methods for predicting gene function from systematic gene knock-downs. BMC Bioinformatics, 2008, 9, 463.	1.2	5
3211	Gene set analyses for interpreting microarray experiments on prokaryotic organisms. BMC Bioinformatics, 2008, 9, 469.	1.2	13

#	ARTICLE	IF	CITATIONS
3212	Evaluation of GO-based functional similarity measures using <i>S. cerevisiae</i> protein interaction and expression profile data. BMC Bioinformatics, 2008, 9, 472.	1.2	91
3213	Expression profiles of switch-like genes accurately classify tissue and infectious disease phenotypes in model-based classification. BMC Bioinformatics, 2008, 9, 486.	1.2	8
3214	EST2uni: an open, parallel tool for automated EST analysis and database creation, with a data mining web interface and microarray expression data integration. BMC Bioinformatics, 2008, 9, 5.	1.2	54
3215	Microarray-based gene set analysis: a comparison of current methods. BMC Bioinformatics, 2008, 9, 502.	1.2	62
3216	Unsupervised reduction of random noise in complex data by a row-specific, sorted principal component-guided method. BMC Bioinformatics, 2008, 9, 508.	1.2	3
3217	The contrasting properties of conservation and correlated phylogeny in protein functional residue prediction. BMC Bioinformatics, 2008, 9, 51.	1.2	38
3218	GeneTrailExpress: a web-based pipeline for the statistical evaluation of microarray experiments. BMC Bioinformatics, 2008, 9, 552.	1.2	69
3219	Gene function prediction using labeled and unlabeled data. BMC Bioinformatics, 2008, 9, 57.	1.2	74
3220	CASCADE: a novel quasi all paths-based network analysis algorithm for clustering biological interactions. BMC Bioinformatics, 2008, 9, 64.	1.2	22
3221	OpenDMP: An open source, ontology-driven concept analysis engine, with applications to capturing knowledge regarding protein transport, protein interactions and cell-type-specific gene expression. BMC Bioinformatics, 2008, 9, 78.	1.2	112
3222	ProLoc-GO: Utilizing informative Gene Ontology terms for sequence-based prediction of protein subcellular localization. BMC Bioinformatics, 2008, 9, 80.	1.2	101
3223	The Annotation, Mapping, Expression and Network (AMEN) suite of tools for molecular systems biology. BMC Bioinformatics, 2008, 9, 86.	1.2	73
3224	Microarray data mining using landmark gene-guided clustering. BMC Bioinformatics, 2008, 9, 92.	1.2	20
3225	In silico analysis of expressed sequence tags from <i>Trichostrongylus vitrinus</i> (Nematoda): comparison of the automated ESTExplorer workflow platform with conventional database searches. BMC Bioinformatics, 2008, 9, S10.	1.2	17
3226	Cascaded classifiers for confidence-based chemical named entity recognition. BMC Bioinformatics, 2008, 9, S4.	1.2	48
3227	A protein interaction based model for schizophrenia study. BMC Bioinformatics, 2008, 9, S23.	1.2	13
3228	Finding microRNA regulatory modules in human genome using rule induction. BMC Bioinformatics, 2008, 9, S5.	1.2	82
3229	Version VI of the ESTree db: an improved tool for peach transcriptome analysis. BMC Bioinformatics, 2008, 9, S9.	1.2	22

#	ARTICLE	IF	CITATIONS
3230	Monitoring the evolutionary aspect of the Gene Ontology to enhance predictability and usability. BMC Bioinformatics, 2008, 9, S7.	1.2	13
3231	Terminologies for text-mining; an experiment in the lipoprotein metabolism domain. BMC Bioinformatics, 2008, 9, S2.	1.2	16
3232	Ontology-based, Tissue MicroArray oriented, image centered tissue bank. BMC Bioinformatics, 2008, 9, S4.	1.2	13
3233	RDFScape: Semantic Web meets Systems Biology. BMC Bioinformatics, 2008, 9, S6.	1.2	24
3234	Reconstructing networks of pathways via significance analysis of their intersections. BMC Bioinformatics, 2008, 9, S9.	1.2	25
3235	Ontology Design Patterns for bio-ontologies: a case study on the Cell Cycle Ontology. BMC Bioinformatics, 2008, 9, S1.	1.2	49
3236	Integrating protein-protein interactions and text mining for protein function prediction. BMC Bioinformatics, 2008, 9, S2.	1.2	36
3237	Measuring the prevalence of regional mutation rates: an analysis of silent substitutions in mammals, fungi, and insects. BMC Evolutionary Biology, 2008, 8, 186.	3.2	27
3238	Coordinated evolution of co-expressed gene clusters in the Drosophila transcriptome. BMC Evolutionary Biology, 2008, 8, 2.	3.2	30
3239	Protein evolution in deep sea bacteria: an analysis of amino acids substitution rates. BMC Evolutionary Biology, 2008, 8, 313.	3.2	37
3240	MADIBA: A web server toolkit for biological interpretation of Plasmodium and plant gene clusters. BMC Genomics, 2008, 9, 105.	1.2	21
3241	Can subtle changes in gene expression be consistently detected with different microarray platforms?. BMC Genomics, 2008, 9, 124.	1.2	45
3242	An anatomy ontology to represent biological knowledge in Dictyostelium discoideum. BMC Genomics, 2008, 9, 130.	1.2	39
3243	Comparative analysis of the acute response of the trout, <i>O. mykiss</i> , head kidney to in vivo challenge with virulent and attenuated infectious hematopoietic necrosis virus and LPS-induced inflammation. BMC Genomics, 2008, 9, 141.	1.2	67
3244	cDNA-AFLP analysis of plant and pathogen genes expressed in grapevine infected with <i>Plasmopara viticola</i> . BMC Genomics, 2008, 9, 142.	1.2	109
3245	Brain gene expression profiles of <i>Cln1</i> and <i>Cln5</i> deficient mice unravels common molecular pathways underlying neuronal degeneration in NCL diseases. BMC Genomics, 2008, 9, 146.	1.2	46
3246	The unique genomic properties of sex-biased genes: Insights from avian microarray data. BMC Genomics, 2008, 9, 148.	1.2	79
3247	The midgut transcriptome of <i>Lutzomyia longipalpis</i> : comparative analysis of cDNA libraries from sugar-fed, blood-fed, post-digested and <i>Leishmania infantum</i> chagasi-infected sand flies. BMC Genomics, 2008, 9, 15.	1.2	94

#	ARTICLE	IF	CITATIONS
3248	Mining small RNA structure elements in untranslated regions of human and mouse mRNAs using structure-based alignment. BMC Genomics, 2008, 9, 189.	1.2	15
3249	Simultaneous gene expression profiling in human macrophages infected with Leishmania major parasites using SAGE. BMC Genomics, 2008, 9, 238.	1.2	68
3250	Transcriptome profiling of developmental and xenobiotic responses in a keystone soil animal, the oligochaete annelid Lumbricus rubellus. BMC Genomics, 2008, 9, 266.	1.2	93
3251	Transcriptome analysis of Loxosceles laeta (Araneae, Sicariidae) spider venomous gland using expressed sequence tags. BMC Genomics, 2008, 9, 279.	1.2	110
3252	Proteomic profile of dormant Trichophyton Rubrum conidia. BMC Genomics, 2008, 9, 303.	1.2	36
3253	A genome-wide 20 K citrus microarray for gene expression analysis. BMC Genomics, 2008, 9, 318.	1.2	49
3254	T2D-Db: An integrated platform to study the molecular basis of Type 2 diabetes. BMC Genomics, 2008, 9, 320.	1.2	36
3255	Evolutionary conservation of zinc finger transcription factor binding sites in promoters of genes co-expressed with WT1 in prostate cancer. BMC Genomics, 2008, 9, 337.	1.2	21
3256	WildSilkbase: An EST database of wild silkmoths. BMC Genomics, 2008, 9, 338.	1.2	38
3257	Structural conservation versus functional divergence of maternally expressed microRNAs in the Dlk1/Gtl2 imprinting region. BMC Genomics, 2008, 9, 346.	1.2	49
3258	Trait correlated expression combined with expression QTL analysis reveals biological pathways and candidate genes affecting water holding capacity of muscle. BMC Genomics, 2008, 9, 367.	1.2	80
3259	SoyXpress: A database for exploring the soybean transcriptome. BMC Genomics, 2008, 9, 368.	1.2	24
3260	Splice-mediated Variants of Proteins (SpliVaP) – data and characterization of changes in signatures among protein isoforms due to alternative splicing. BMC Genomics, 2008, 9, 453.	1.2	8
3261	DroID: the Drosophila Interactions Database, a comprehensive resource for annotated gene and protein interactions. BMC Genomics, 2008, 9, 461.	1.2	107
3262	Prioritizing genes of potential relevance to diseases affected by sex hormones: an example of Myasthenia Gravis. BMC Genomics, 2008, 9, 481.	1.2	8
3263	BioVenn – a web application for the comparison and visualization of biological lists using area-proportional Venn diagrams. BMC Genomics, 2008, 9, 488.	1.2	1,371
3264	Matching curated genome databases: a non trivial task. BMC Genomics, 2008, 9, 501.	1.2	2
3265	Meta-analysis of genome-wide expression patterns associated with behavioral maturation in honey bees. BMC Genomics, 2008, 9, 503.	1.2	20

#	ARTICLE	IF	CITATIONS
3266	Towards the understanding of the cocoa transcriptome: Production and analysis of an exhaustive dataset of ESTs of <i>Theobroma cacao</i> L. generated from various tissues and under various conditions. BMC Genomics, 2008, 9, 512.	1.2	112
3267	Analyses of expressed sequence tags from the maize foliar pathogen <i>Cercospora zeae-maydis</i> identify novel genes expressed during vegetative, infectious, and reproductive growth. BMC Genomics, 2008, 9, 523.	1.2	12
3268	Gene expression profiling in chicken heterophils with <i>Salmonella enteritidis</i> stimulation using a chicken 44 K Agilent microarray. BMC Genomics, 2008, 9, 526.	1.2	73
3269	Temporal and functional profile of the transcriptional regulatory network in the early regenerative response to partial hepatectomy in the rat. BMC Genomics, 2008, 9, 527.	1.2	25
3270	Analysis of the <i>Pythium ultimum</i> transcriptome using Sanger and Pyrosequencing approaches. BMC Genomics, 2008, 9, 542.	1.2	78
3271	Prediction of alternatively skipped exons and splicing enhancers from exon junction arrays. BMC Genomics, 2008, 9, 551.	1.2	9
3272	Exploring the mialome of ticks: An annotated catalogue of midgut transcripts from the hard tick, <i>Dermacentor variabilis</i> (Acari: Ixodidae). BMC Genomics, 2008, 9, 552.	1.2	109
3273	A cross-species transcriptomics approach to identify genes involved in leaf development. BMC Genomics, 2008, 9, 589.	1.2	37
3274	EST analysis of male accessory glands from <i>Heliconius</i> butterflies with divergent mating systems. BMC Genomics, 2008, 9, 592.	1.2	33
3275	Characterization of a newly developed chicken 44K Agilent microarray. BMC Genomics, 2008, 9, 60.	1.2	68
3276	Combinatorial control of gene expression by the three yeast repressors Mig1, Mig2 and Mig3. BMC Genomics, 2008, 9, 601.	1.2	86
3277	Transcriptome profiling of the feeding-to-fasting transition in chicken liver. BMC Genomics, 2008, 9, 611.	1.2	83
3278	Comparison of the transcriptomic "stress response" evoked by antimycin A and oxygen deprivation in <i>saccharomyces cerevisiae</i> . BMC Genomics, 2008, 9, 627.	1.2	18
3279	Human and mouse switch-like genes share common transcriptional regulatory mechanisms for bimodality. BMC Genomics, 2008, 9, 628.	1.2	12
3280	Transcriptomic dissection of tongue squamous cell carcinoma. BMC Genomics, 2008, 9, 69.	1.2	276
3281	In silico discovery of transcription regulatory elements in <i>Plasmodium falciparum</i> . BMC Genomics, 2008, 9, 70.	1.2	104
3282	Activation of counter-regulatory mechanisms in a rat renal acute rejection model. BMC Genomics, 2008, 9, 71.	1.2	24
3283	Large-scale analysis of <i>Macaca fascicularis</i> transcripts and inference of genetic divergence between <i>M. fascicularis</i> and <i>M. mulatta</i> . BMC Genomics, 2008, 9, 90.	1.2	40

#	ARTICLE	IF	CITATIONS
3284	Annotation of expressed sequence tags for the East African cichlid fish <i>Astatotilapia burtoni</i> and evolutionary analyses of cichlid ORFs. <i>BMC Genomics</i> , 2008, 9, 96.	1.2	48
3285	Semantically linking and browsing PubMed abstracts with gene ontology. <i>BMC Genomics</i> , 2008, 9, S10.	1.2	34
3286	Batch Blast Extractor: an automated blastx parser application. <i>BMC Genomics</i> , 2008, 9, S10.	1.2	32
3287	The FEATURE framework for protein function annotation: modeling new functions, improving performance, and extending to novel applications. <i>BMC Genomics</i> , 2008, 9, S2.	1.2	47
3288	The Innate Immune Database (IIDB). <i>BMC Immunology</i> , 2008, 9, 7.	0.9	45
3289	Identification of a set of genes showing regionally enriched expression in the mouse brain. <i>BMC Neuroscience</i> , 2008, 9, 66.	0.8	25
3290	Transcriptomic identification of candidate genes involved in sunflower responses to chilling and salt stresses based on cDNA microarray analysis. <i>BMC Plant Biology</i> , 2008, 8, 11.	1.6	69
3291	Large-scale collection and annotation of full-length enriched cDNAs from a model halophyte, <i>Thellungiella halophila</i> . <i>BMC Plant Biology</i> , 2008, 8, 115.	1.6	57
3292	Characterization of paralogous protein families in rice. <i>BMC Plant Biology</i> , 2008, 8, 18.	1.6	58
3293	Development of a novel data mining tool to find cis-elements in rice gene promoter regions. <i>BMC Plant Biology</i> , 2008, 8, 20.	1.6	26
3294	VitisExpDB: A database resource for grape functional genomics. <i>BMC Plant Biology</i> , 2008, 8, 23.	1.6	16
3295	Analysis of tall fescue ESTs representing different abiotic stresses, tissue types and developmental stages. <i>BMC Plant Biology</i> , 2008, 8, 27.	1.6	23
3296	Global expression profiling in leaves of free-growing aspen. <i>BMC Plant Biology</i> , 2008, 8, 61.	1.6	29
3297	Heterogeneous in vitro effects of doxorubicin on gene expression in primary human liposarcoma cultures. <i>BMC Cancer</i> , 2008, 8, 313.	1.1	21
3298	Arena3D: visualization of biological networks in 3D. <i>BMC Systems Biology</i> , 2008, 2, 104.	3.0	95
3299	One hub-one process: a tool based view on regulatory network topology. <i>BMC Systems Biology</i> , 2008, 2, 25.	3.0	2
3300	Extracting expression modules from perturbational gene expression compendia. <i>BMC Systems Biology</i> , 2008, 2, 33.	3.0	16
3301	Defining a Modular Signalling Network from the Fly Interactome. <i>BMC Systems Biology</i> , 2008, 2, 45.	3.0	10

#	ARTICLE	IF	CITATIONS
3302	The use of Gene Ontology terms for predicting highly-connected 'hub' nodes in protein-protein interaction networks. <i>BMC Systems Biology</i> , 2008, 2, 80.	3.0	55
3303	Employing conservation of co-expression to improve functional inference. <i>BMC Systems Biology</i> , 2008, 2, 81.	3.0	5
3304	Age and gender related differences in human parotid gland gene expression. <i>Archives of Oral Biology</i> , 2008, 53, 1058-1070.	0.8	49
3305	Reversible commitment to differentiation by human multipotent stromal cells in single-cell derived colonies. <i>Experimental Hematology</i> , 2008, 36, 1390-1402.	0.2	46
3306	<i>Eimeria tenella</i> : Analysis of differentially expressed genes in the monensin- and maduramicin-resistant lines using cDNA array. <i>Experimental Parasitology</i> , 2008, 119, 264-271.	0.5	14
3307	<i>Opisthorchis viverrini</i> : Gene expression profiling of carcinogenic adult liver fluke worms using 5â€² SAGE. <i>Experimental Parasitology</i> , 2008, 120, 306-313.	0.5	6
3308	An in situ hybridization-based screen for heterogeneously expressed genes in mouse ES cells. <i>Gene Expression Patterns</i> , 2008, 8, 181-198.	0.3	74
3309	A cDNA-AFLP approach to study ochratoxin A production in <i>Aspergillus carbonarius</i> . <i>International Journal of Food Microbiology</i> , 2008, 127, 105-115.	2.1	18
3310	Global profiling of influence of intra-ischemic brain temperature on gene expression in rat brain. <i>Brain Research Reviews</i> , 2008, 58, 171-191.	9.1	23
3311	Systemic evaluation of gene expression changes in major target organs induced by atorvastatin. <i>European Journal of Pharmacology</i> , 2008, 584, 376-389.	1.7	12
3312	Gene expression of jojoba (<i>Simmondsia chinensis</i>) leaves exposed to drying. <i>Environmental and Experimental Botany</i> , 2008, 63, 137-146.	2.0	10
3313	Literature-based concept profiles for gene annotation: The issue of weighting. <i>International Journal of Medical Informatics</i> , 2008, 77, 354-362.	1.6	35
3314	Gene ontology annotation as text categorization: An empirical study. <i>Information Processing and Management</i> , 2008, 44, 1754-1770.	5.4	7
3315	caCORE version 3: Implementation of a model driven, service-oriented architecture for semantic interoperability. <i>Journal of Biomedical Informatics</i> , 2008, 41, 106-123.	2.5	90
3316	Non-linear correlation of content and metadata information extracted from biomedical article datasets. <i>Journal of Biomedical Informatics</i> , 2008, 41, 202-216.	2.5	8
3317	Taxonomy-based partitioning of the Gene Ontology. <i>Journal of Biomedical Informatics</i> , 2008, 41, 282-292.	2.5	22
3318	Extracting interactions between proteins from the literature. <i>Journal of Biomedical Informatics</i> , 2008, 41, 393-407.	2.5	66
3319	SEGS: Search for enriched gene sets in microarray data. <i>Journal of Biomedical Informatics</i> , 2008, 41, 588-601.	2.5	41

#	ARTICLE	IF	CITATIONS
3320	State of the nation in data integration for bioinformatics. <i>Journal of Biomedical Informatics</i> , 2008, 41, 687-693.	2.5	244
3321	Combining Semantic Web technologies with Multi-Agent Systems for integrated access to biological resources. <i>Journal of Biomedical Informatics</i> , 2008, 41, 848-859.	2.5	45
3322	Dynamic sub-ontology evolution for traditional Chinese medicine web ontology. <i>Journal of Biomedical Informatics</i> , 2008, 41, 790-805.	2.5	19
3323	Human metabolic network reconstruction and its impact on drug discovery and development. <i>Drug Discovery Today</i> , 2008, 13, 402-408.	3.2	52
3324	Biomarker candidates for cardiovascular disease and bone metabolism disorders in chronic kidney disease: a systems biology perspective. <i>Journal of Cellular and Molecular Medicine</i> , 2008, 12, 1177-1187.	1.6	19
3325	Gene Expression Profiling of Human Liver Transplants Identifies an Early Transcriptional Signature Associated with Initial Poor Graft Function. <i>American Journal of Transplantation</i> , 2008, 8, 1221-1236.	2.6	32
3326	Complement C5 regulates the expression of insulin-like growth factor binding proteins in chronic experimental allergic encephalomyelitis. <i>Journal of Neuroimmunology</i> , 2008, 203, 94-103.	1.1	18
3327	How can ontologies help vector biology?. <i>Trends in Parasitology</i> , 2008, 24, 249-252.	1.5	9
3328	The current excitement about copy-number variation: how it relates to gene duplications and protein families. <i>Current Opinion in Structural Biology</i> , 2008, 18, 366-374.	2.6	92
3329	Differential gene expression in the nucleus accumbens with ethanol self-administration in inbred alcohol-preferring rats. <i>Pharmacology Biochemistry and Behavior</i> , 2008, 89, 481-498.	1.3	80
3330	Scale relativity theory and integrative systems biology: 1. <i>Progress in Biophysics and Molecular Biology</i> , 2008, 97, 79-114.	1.4	75
3331	Diabetic neuropathy: Mechanisms to management. , 2008, 120, 1-34.		588
3332	Cell cycle-dependent gene networks relevant to cancer. <i>Progress in Natural Science: Materials International</i> , 2008, 18, 945-952.	1.8	3
3333	A feature ensemble technology to identify molecular mechanisms for distinction between multiple subtypes of lymphoma. <i>Progress in Natural Science: Materials International</i> , 2008, 18, 1491-1500.	1.8	1
3334	Cold hardening processes in the Antarctic springtail, <i>Cryptopygus antarcticus</i> : Clues from a microarray. <i>Journal of Insect Physiology</i> , 2008, 54, 1356-1362.	0.9	39
3335	Harnessing Knowledge from Structural Genomics. <i>Structure</i> , 2008, 16, 16-18.	1.6	7
3336	Detection of Functionally Important Regions in "Hypothetical Proteins" of Known Structure. <i>Structure</i> , 2008, 16, 1755-1763.	1.6	63
3337	Response of human renal tubular cells to cyclosporine and sirolimus: A toxicogenomic study. <i>Toxicology and Applied Pharmacology</i> , 2008, 229, 184-196.	1.3	51

#	ARTICLE	IF	CITATIONS
3338	Gene expression profiles in the cerebellum and hippocampus following exposure to a neurotoxicant, Aroclor 1254: Developmental effects†. <i>Toxicology and Applied Pharmacology</i> , 2008, 231, 165-178.	1.3	25
3339	Gene expression profiling analysis reveals arsenic-induced cell cycle arrest and apoptosis in p53-proficient and p53-deficient cells through differential gene pathways. <i>Toxicology and Applied Pharmacology</i> , 2008, 233, 389-403.	1.3	28
3340	Chemogenomics and biotechnology. <i>Trends in Biotechnology</i> , 2008, 26, 252-258.	4.9	32
3341	Insights into the connection between cancer and alternative splicing. <i>Trends in Genetics</i> , 2008, 24, 7-10.	2.9	146
3342	Chance and necessity in chromosomal gene distributions. <i>Trends in Genetics</i> , 2008, 24, 216-219.	2.9	22
3343	The quest for orthologs: finding the corresponding gene across genomes. <i>Trends in Genetics</i> , 2008, 24, 539-551.	2.9	258
3344	Inferring molecular function: contributions from functional linkages. <i>Trends in Genetics</i> , 2008, 24, 587-590.	2.9	5
3345	The canine hookworm genome: Analysis and classification of <i>Ancylostoma caninum</i> survey sequences. <i>Molecular and Biochemical Parasitology</i> , 2008, 157, 187-192.	0.5	36
3346	Genes and pathways differentially expressed in the brains of Fxr2 knockout mice. <i>Neurobiology of Disease</i> , 2008, 32, 510-520.	2.1	13
3347	Hybridizing sparse component analysis with genetic algorithms for microarray analysis. <i>Neurocomputing</i> , 2008, 71, 2356-2376.	3.5	14
3348	Plant Structure Ontology (PSO)â€” A Morphological and Anatomical Ontology of Flowering Plants. , 2008, , 27-42.		2
3349	The Gene Ontology (GO) Project: Structured Vocabularies for Molecular Biology and Their Application to Genome and Expression Analysis. <i>Current Protocols in Bioinformatics</i> , 2008, 23, Unit 7.2.	25.8	94
3350	Plasmodium in the Postgenomic Era: New Insights into the Molecular Cell Biology of Malaria Parasites. <i>International Review of Cell and Molecular Biology</i> , 2008, 266, 85-156.	1.6	62
3351	Target Selection for Structural Genomics: An Overview. <i>Methods in Molecular Biology</i> , 2008, 426, 3-25.	0.4	28
3354	Protein Function Prediction via Analysis of Interactomes. , 2008, , 231-258.		1
3358	Clinical Uses of Microarrays in Cancer Research. <i>Methods in Molecular Medicine</i> , 2008, 141, 87-113.	0.8	18
3360	MYCNâ€”nonâ€”amplified metastatic neuroblastoma with good prognosis and spontaneous regression: A molecular portrait of stage 4S. <i>Molecular Oncology</i> , 2008, 2, 261-271.	2.1	63
3361	Evidence for lifespan extension and delayed ageâ€”related biomarkers in insulin receptor substrate 1 null mice. <i>FASEB Journal</i> , 2008, 22, 807-818.	0.2	487

#	ARTICLE	IF	CITATIONS
3362	Coclustering of Human Cancer Microarrays Using Minimum Sum-Squared Residue Coclustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 385-400.	1.9	54
3363	WGCNA: an R package for weighted correlation network analysis. BMC Bioinformatics, 2008, 9, 559.	1.2	17,294
3364	Genetic interactions: the missing links for a better understanding of cancer susceptibility, progression and treatment. Molecular Cancer, 2008, 7, 4.	7.9	10
3365	Identification of differentially expressed proteins in spontaneous thymic lymphomas from knockout mice with deletion of p53. Proteome Science, 2008, 6, 18.	0.7	13
3366	Dramatic down-regulation of oxidoreductases in human hepatocellular carcinoma hepG2 cells: proteomics and gene ontology unveiling new frontiers in cancer enzymology. Proteome Science, 2008, 6, 29.	0.7	19
3367	Sample prep for proteomics of breast cancer: proteomics and gene ontology reveal dramatic differences in protein solubilization preferences of radioimmunoprecipitation assay and urea lysis buffers. Proteome Science, 2008, 6, 30.	0.7	75
3368	Identification of differentially expressed ovarian genes during primary and early secondary oocyte growth in coho salmon, <i>Oncorhynchus kisutch</i> . Reproductive Biology and Endocrinology, 2008, 6, 2.	1.4	133
3369	MicroRNA miR-146a and further oncogenesis-related cellular microRNAs are dysregulated in HTLV-1-transformed T lymphocytes. Retrovirology, 2008, 5, 100.	0.9	98
3370	The evolution of domain-content in bacterial genomes. Biology Direct, 2008, 3, 51.	1.9	26
3371	From Biomedical Literature to Knowledge: Mining Protein-Protein Interactions. Studies in Computational Intelligence, 2008, , 397-421.	0.7	2
3373	Informatics and computational strategies for the study of lipids. Molecular BioSystems, 2008, 4, 121-127.	2.9	189
3374	Ontology Alignment and Merging. Computational Biology, 2008, , 133-149.	0.1	15
3375	Linking genes to literature: text mining, information extraction, and retrieval applications for biology. Genome Biology, 2008, 9, S8.	3.8	181
3376	Practical and theoretical advances in predicting the function of a protein by its phylogenetic distribution. Journal of the Royal Society Interface, 2008, 5, 151-170.	1.5	97
3377	The <i>cis</i> -regulatory map of <i>Shewanella</i> genomes. Nucleic Acids Research, 2008, 36, 5376-5390.	6.5	17
3378	Fish toxicogenomics. Advances in Experimental Biology, 2008, 2, 75-325.	0.1	9
3379	Advanced Protocols in Oxidative Stress I. Methods in Molecular Biology, 2008, , .	0.4	5
3380	Semantic Grid: Model, Methodology, and Applications. Advanced Topics in Science and Technology in China, 2008, , .	0.0	4

#	ARTICLE	IF	CITATIONS
3381	Occurrence of Copper Proteins through the Three Domains of Life: A Bioinformatic Approach. <i>Journal of Proteome Research</i> , 2008, 7, 209-216.	1.8	184
3382	<i>Pseudomonas syringae</i> Pathovars and Related Pathogens Identification, <i>Epidemiology and Genomics.</i> , 2008, , .		9
3383	A weighted average difference method for detecting differentially expressed genes from microarray data. <i>Algorithms for Molecular Biology</i> , 2008, 3, 8.	0.3	104
3384	Prioritizing functional modules mediating genetic perturbations and their phenotypic effects: a global strategy. <i>Genome Biology</i> , 2008, 9, R174.	13.9	4
3385	Selective maintenance of <i>Drosophila</i> tandemly arranged duplicated genes during evolution. <i>Genome Biology</i> , 2008, 9, R176.	13.9	20
3386	Rapid identification of PAX2/5/8 direct downstream targets in the otic vesicle by combinatorial use of bioinformatics tools. <i>Genome Biology</i> , 2008, 9, R145.	13.9	18
3387	Changes in protein expression during honey bee larval development. <i>Genome Biology</i> , 2008, 9, R156.	13.9	60
3388	Systematic bioinformatic analysis of expression levels of 17,330 human genes across 9,783 samples from 175 types of healthy and pathological tissues. <i>Genome Biology</i> , 2008, 9, R139.	13.9	234
3389	NetGrep: fast network schema searches in interactomes. <i>Genome Biology</i> , 2008, 9, R138.	13.9	34
3390	Modeling synthetic lethality. <i>Genome Biology</i> , 2008, 9, R135.	13.9	47
3391	Metabolic changes in schizophrenia and human brain evolution. <i>Genome Biology</i> , 2008, 9, R124.	13.9	89
3392	Global transcriptome analysis reveals circadian regulation of key pathways in plant growth and development. <i>Genome Biology</i> , 2008, 9, R130.	13.9	677
3393	Anni 2.0: a multipurpose text-mining tool for the life sciences. <i>Genome Biology</i> , 2008, 9, R96.	13.9	104
3394	GMODWeb: a web framework for the generic model organism database. <i>Genome Biology</i> , 2008, 9, R102.	13.9	39
3395	Gene expression profiling of human prostate cancer stem cells reveals a pro-inflammatory phenotype and the importance of extracellular matrix interactions. <i>Genome Biology</i> , 2008, 9, R83.	13.9	191
3396	Transcriptome analysis reveals new insight into appressorium formation and function in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Genome Biology</i> , 2008, 9, R85.	13.9	169
3397	Perceiving molecular evolution processes in <i>Escherichia coli</i> by comprehensive metabolite and gene expression profiling. <i>Genome Biology</i> , 2008, 9, R72.	13.9	17
3398	Natural selection of protein structural and functional properties: a SNP perspective. <i>Genome Biology</i> , 2008, 9, R69.	13.9	54

#	ARTICLE	IF	CITATIONS
3399	Proteomic analysis of the secretome of <i>Leishmania donovani</i> . <i>Genome Biology</i> , 2008, 9, R35.	13.9	262
3400	Systems biology meets stress ecology: linking molecular and organismal stress responses in <i>Daphnia magna</i> . <i>Genome Biology</i> , 2008, 9, R40.	13.9	130
3401	Concept recognition for extracting protein interaction relations from biomedical text. <i>Genome Biology</i> , 2008, 9, S9.	3.8	34
3402	Adipose tissue transcriptomic signature highlights the pathological relevance of extracellular matrix in human obesity. <i>Genome Biology</i> , 2008, 9, R14.	13.9	372
3403	High-resolution analysis of condition-specific regulatory modules in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2008, 9, R2.	13.9	6
3404	The SeqFEATURE library of 3D functional site models: comparison to existing methods and applications to protein function annotation. <i>Genome Biology</i> , 2008, 9, R8.	13.9	20
3405	Inferring mouse gene functions from genomic-scale data using a combined functional network/classification strategy. <i>Genome Biology</i> , 2008, 9, S5.	13.9	66
3406	A critical assessment of <i>Mus musculus</i> gene function prediction using integrated genomic evidence. <i>Genome Biology</i> , 2008, 9, S2.	13.9	214
3407	GeneMANIA: a real-time multiple association network integration algorithm for predicting gene function. <i>Genome Biology</i> , 2008, 9, S4.	13.9	795
3408	An en masse phenotype and function prediction system for <i>Mus musculus</i> . <i>Genome Biology</i> , 2008, 9, S8.	13.9	20
3409	Functional Proteomics. <i>Methods in Molecular Biology</i> , 2008, 484, v-vii.	0.4	7
3412	Comparative Genome Sequence Analysis of Multidrug-Resistant <i>Acinetobacter baumannii</i> . <i>Journal of Bacteriology</i> , 2008, 190, 8053-8064.	1.0	429
3413	An Introduction to Metabolic Networks and Their Structural Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 594-617.	1.9	103
3414	Study on Ontology Partition Based on Ant Colony Algorithm. , 2008, , .		1
3415	Expression and Microarrays. <i>Methods in Molecular Biology</i> , 2008, 453, 245-255.	0.4	1
3416	A Unified Scoring Scheme for Detecting Essential Proteins in Protein Interaction Networks. , 2008, , .		13
3417	Lr34-Mediated Leaf Rust Resistance in Wheat: Transcript Profiling Reveals a High Energetic Demand Supported by Transient Recruitment of Multiple Metabolic Pathways. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 1515-1527.	1.4	99
3418	Cell Identity Mediates the Response of <i>Arabidopsis</i> Roots to Abiotic Stress. <i>Science</i> , 2008, 320, 942-945.	6.0	700

#	ARTICLE	IF	CITATIONS
3419	OntoDM: An Ontology of Data Mining. , 2008, , .		72
3421	High-throughput functional annotation and data mining with the Blast2GO suite. <i>Nucleic Acids Research</i> , 2008, 36, 3420-3435.	6.5	3,905
3422	An insight into the sialome of the soft tick, <i>Ornithodoros parkeri</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 1-21.	1.2	105
3423	An insight into the sialome of the blood-sucking bug <i>Triatoma infestans</i> , a vector of Chagas's™ disease. <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 213-232.	1.2	114
3424	An insight into the sialotranscriptome of the non-blood feeding <i>Toxorhynchites amboinensis</i> mosquito. <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 499-507.	1.2	21
3425	Protease proteomics: Revealing protease in vivo functions using systems biology approaches. <i>Molecular Aspects of Medicine</i> , 2008, 29, 339-358.	2.7	84
3426	Engrailed-2 regulates genes related to vesicle formation and transport in cerebellar Purkinje cells. <i>Molecular and Cellular Neurosciences</i> , 2008, 38, 495-504.	1.0	17
3427	The Cell Centered Database project: An update on building community resources for managing and sharing 3D imaging data. <i>Journal of Structural Biology</i> , 2008, 161, 220-231.	1.3	84
3428	Molecular Phenotypic Descriptors of Dupuytren's™ Disease Defined Using Informatics Analysis of the Transcriptome. <i>Journal of Hand Surgery</i> , 2008, 33, 359-372.	0.7	54
3429	Virogenomics: the virus's™ host interaction revisited. <i>Current Opinion in Microbiology</i> , 2008, 11, 461-466.	2.3	7
3430	Granulocyte chemotactic properties of <i>M. tuberculosis</i> versus <i>M. bovis</i> -infected bovine alveolar macrophages. <i>Molecular Immunology</i> , 2008, 45, 740-749.	1.0	36
3431	Overexpression of DNA repair genes is associated with metastasis: A new hypothesis. <i>Mutation Research - Reviews in Mutation Research</i> , 2008, 659, 49-55.	2.4	79
3432	Exploring functional genomics for drug target and therapeutics discovery in <i>Plasmodia</i> . <i>Acta Tropica</i> , 2008, 105, 113-123.	0.9	17
3433	The Brazilian contribution to the study of the <i>Schistosoma mansoni</i> transcriptome. <i>Acta Tropica</i> , 2008, 108, 179-182.	0.9	11
3434	Genomic Anatomy of the Hippocampus. <i>Neuron</i> , 2008, 60, 1010-1021.	3.8	337
3435	Transcriptome analysis revealed novel possible venom components and cellular processes of the tarantula <i>Chilobrachys jingzhao</i> venom gland. <i>Toxicon</i> , 2008, 52, 794-806.	0.8	42
3436	Advancing ecological research with ontologies. <i>Trends in Ecology and Evolution</i> , 2008, 23, 159-168.	4.2	174
3437	CYP26A1 knockout embryonic stem cells exhibit reduced differentiation and growth arrest in response to retinoic acid. <i>Developmental Biology</i> , 2008, 315, 331-354.	0.9	40

#	ARTICLE	IF	CITATIONS
3438	Combinatorial effects of four histone modifications in transcription and differentiation. <i>Genomics</i> , 2008, 91, 41-51.	1.3	45
3439	Altered myocardial gene expression reveals possible maladaptive processes in heterozygous and homozygous cardiac myosin-binding protein C knockout mice. <i>Genomics</i> , 2008, 91, 52-60.	1.3	12
3440	Differential gene expression analysis of iodide-treated rat thyroid follicular cell line PCCl3. <i>Genomics</i> , 2008, 91, 356-366.	1.3	29
3441	Genomic expression patterns distinguish long-term from short-term glioblastoma survivors: A preliminary feasibility study. <i>Genomics</i> , 2008, 91, 395-406.	1.3	45
3442	Functional classification analysis of somatically mutated genes in human breast and colorectal cancers. <i>Genomics</i> , 2008, 91, 508-511.	1.3	48
3443	Characterizing the mouse ES cell transcriptome with Illumina sequencing. <i>Genomics</i> , 2008, 92, 187-194.	1.3	79
3444	Genome-wide identification of osmotic stress response gene in <i>Arabidopsis thaliana</i> . <i>Genomics</i> , 2008, 92, 488-493.	1.3	21
3445	An overview of cardiac systems biology. <i>Journal of Molecular and Cellular Cardiology</i> , 2008, 44, 460-469.	0.9	16
3446	MicroRNA Regulation of Cell Lineages in Mouse and Human Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2008, 2, 219-229.	5.2	577
3447	Efficient Homing of Multipotent Adult Mesenchymal Stem Cells Depends on FROUNT-Mediated Clustering of CCR2. <i>Cell Stem Cell</i> , 2008, 2, 566-575.	5.2	249
3448	Changes in gene expression induced by polycyclic aromatic hydrocarbons in the human cell lines HepG2 and A549. <i>Toxicology in Vitro</i> , 2008, 22, 411-421.	1.1	52
3449	Discovering Sequence Motifs. <i>Methods in Molecular Biology</i> , 2008, 452, 231-251.	0.4	30
3450	Protein glycosylation pathways in filamentous fungi. <i>Glycobiology</i> , 2008, 18, 626-637.	1.3	157
3451	Evolutionary Conservation of Human Drug Targets in Organisms used for Environmental Risk Assessments. <i>Environmental Science & Technology</i> , 2008, 42, 5807-5813.	4.6	475
3452	A Combinatorial Code for CPE-Mediated Translational Control. <i>Cell</i> , 2008, 132, 434-448.	13.5	360
3453	Global Chromatin Domain Organization of the <i>Drosophila</i> Genome. <i>PLoS Genetics</i> , 2008, 4, e1000045.	1.5	72
3454	Biological data integration using Semantic Web technologies. <i>Biochimie</i> , 2008, 90, 584-594.	1.3	40
3455	Identification of differentially expressed genes after PPM1D silencing in breast cancer. <i>Cancer Letters</i> , 2008, 259, 61-70.	3.2	28

#	ARTICLE	IF	CITATIONS
3456	Gene expression profiles in liver of zebrafish treated with microcystin-LR. <i>Environmental Toxicology and Pharmacology</i> , 2008, 26, 6-12.	2.0	40
3457	Dual role of Nr2e3 in photoreceptor development and maintenance. <i>Experimental Eye Research</i> , 2008, 87, 35-48.	1.2	38
3458	Genomic response programs of <i>Saccharomyces cerevisiae</i> following protoplasting and regeneration. <i>Fungal Genetics and Biology</i> , 2008, 45, 253-265.	0.9	6
3459	Increasing genomic information in bivalves through new EST collections in four species: Development of new genetic markers for environmental studies and genome evolution. <i>Gene</i> , 2008, 408, 27-36.	1.0	132
3460	Analysis of <i>Sus scrofa</i> liver proteome and identification of proteins differentially expressed between genders, and conventional and genetically enhanced lines. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2008, 3, 234-242.	0.4	19
3461	Mistranslation of Membrane Proteins and Two-Component System Activation Trigger Antibiotic-Mediated Cell Death. <i>Cell</i> , 2008, 135, 679-690.	13.5	459
3462	A Translational Profiling Approach for the Molecular Characterization of CNS Cell Types. <i>Cell</i> , 2008, 135, 738-748.	13.5	1,007
3463	Identification of the up-regulated expression genes in hemocytes of variously colored abalone (<i>Haliotis diversicolor</i> Reeve, 1846) challenged with bacteria. <i>Developmental and Comparative Immunology</i> , 2008, 32, 1326-1347.	1.0	96
3464	The ontology of biological taxa. <i>Bioinformatics</i> , 2008, 24, i313-i321.	1.8	20
3465	Functional Annotation from Meta-analysis of Microarray Datasets. , 2008, , .		1
3466	PhyloSort: a user-friendly phylogenetic sorting tool and its application to estimating the cyanobacterial contribution to the nuclear genome of <i>Chlamydomonas</i> . <i>BMC Evolutionary Biology</i> , 2008, 8, 6.	3.2	53
3467	Meta-Analysis Approach identifies Candidate Genes and associated Molecular Networks for Type-2 Diabetes Mellitus. <i>BMC Genomics</i> , 2008, 9, 310.	1.2	51
3468	Network Analysis Tools: from biological networks to clusters and pathways. <i>Nature Protocols</i> , 2008, 3, 1616-1629.	5.5	101
3469	A Multiobjective Evolutionary Conceptual Clustering Methodology for Gene Annotation Within Structural Databases: A Case of Study on the <i>Gene Ontology</i> Database. <i>IEEE Transactions on Evolutionary Computation</i> , 2008, 12, 679-701.	7.5	33
3470	Mapping the Integrin-Linked Kinase Interactome Using SILAC. <i>Journal of Proteome Research</i> , 2008, 7, 1740-1749.	1.8	90
3471	Heterogeneity of Human Macrophages in Culture and in Atherosclerotic Plaques. <i>American Journal of Pathology</i> , 2008, 172, 1112-1126.	1.9	213
3472	Class A macrophage scavenger receptor gene expression levels in peripheral blood mononuclear cells specifically increase in patients with acute coronary syndrome. <i>Atherosclerosis</i> , 2008, 198, 426-433.	0.4	25
3473	The surface properties of nanocrystalline diamond and nanoparticulate diamond powder and their suitability as cell growth support surfaces. <i>Biomaterials</i> , 2008, 29, 4275-4284.	5.7	96

#	ARTICLE	IF	CITATIONS
3474	Identification of differentially expressed genes in spontaneously regressing melanoma using the MeLiM Swine Model. <i>Pigment Cell and Melanoma Research</i> , 2008, 21, 147-161.	1.5	24
3475	Ionomics and the Study of the Plant Ionome. <i>Annual Review of Plant Biology</i> , 2008, 59, 709-733.	8.6	480
3476	Bioinformatics and Database of the Rice Genome. <i>Biotechnology in Agriculture and Forestry</i> , 2008, , 13-21.	0.2	0
3477	Identification of Semaphorin 5A Interacting Protein by Applying Apriori Knowledge and Peptide Complementarity Related to Protein Evolution and Structure. <i>Genomics, Proteomics and Bioinformatics</i> , 2008, 6, 163-174.	3.0	14
3478	Network integration and graph analysis in mammalian molecular systems biology. <i>IET Systems Biology</i> , 2008, 2, 206-221.	0.8	42
3479	Activation of MAP Kinase Signaling Through ERK5 But Not ERK1 Expression Is Associated with Lymph Node Metastases in Oral Squamous Cell Carcinoma (OSCC). <i>Neoplasia</i> , 2008, 10, 462-IN4.	2.3	68
3480	Interactive Three-Dimensional Visualization and Contextual Analysis of Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2008, 7, 104-112.	1.8	37
3481	Data Storage and Analysis in ArrayExpress and Expression Profiler. <i>Current Protocols in Bioinformatics</i> , 2008, 23, Unit 7.13.	25.8	12
3482	Expression of genes in normal human monocytes in response to <i>Aspergillus fumigatus</i> . <i>Medical Mycology</i> , 2008, 46, 327-336.	0.3	21
3483	Copy number variation and evolution in humans and chimpanzees. <i>Genome Research</i> , 2008, 18, 1698-1710.	2.4	215
3484	The SWI/SNF Chromatin-Remodeling Complex and Glucocorticoid Resistance in Acute Lymphoblastic Leukemia. <i>Journal of the National Cancer Institute</i> , 2008, 100, 1792-1803.	3.0	61
3485	caBIG™: Opportunities and challenges to creating a federated global network of interoperable information systems. , 2008, , .		2
3487	Exploring Heterogeneous Biological Data Sources. , 2008, , .		1
3488	Ontological Analysis and Pathway Modelling in Drug Discovery. <i>Pharmaceutical Medicine</i> , 2008, 22, 99-105.	1.0	2
3489	Development of a <i>Brassica</i> seed cDNA microarray. <i>Genome</i> , 2008, 51, 236-242.	0.9	25
3490	Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. <i>Genome Research</i> , 2008, 18, 610-621.	2.4	964
3491	The Mouse Resource Browser (MRB) - A near-complete registry of mouse resources. , 2008, , .		1
3492	The Gene Ontology project in 2008. <i>Nucleic Acids Research</i> , 2008, 36, D440-D444.	6.5	699

#	ARTICLE	IF	CITATIONS
3493	Protein robustness promotes evolutionary innovations on large evolutionary time-scales. Proceedings of the Royal Society B: Biological Sciences, 2008, 275, 1595-1602.	1.2	63
3494	Prospective Study of Metal Fume-Induced Responses of Global Gene Expression Profiling in Whole Blood. Inhalation Toxicology, 2008, 20, 1233-1244.	0.8	10
3495	GOMA: Web utility for direct finding of enriched Gene Ontology terms from gene expression profile. , 2008, , .		0
3496	Identification of active biological networks and common expression conditions. , 2008, , .		8
3497	Incorporating Gene Functions into Regression Analysis of DNA-Protein Binding Data and Gene Expression Data to Construct Transcriptional Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 401-415.	1.9	5
3498	CARE: Finding Local Linear Correlations in High Dimensional Data. , 2008, 24, 130-139.		16
3499	CASIMIR: Coordination and Sustainability of International Mouse Informatics Resources. , 2008, , .		7
3500	<i>Short Communication:</i> Cataloguing the HIV Type 1 Human Protein Interaction Network. AIDS Research and Human Retroviruses, 2008, 24, 1497-1502.	0.5	126
3501	Conserved Domain Combination Identification in Human Proteins. , 2008, , .		0
3502	Evolving models of biological sequence similarity. , 2008, , .		0
3503	Analysis of the Zebrafish Proteome during Embryonic Development. Molecular and Cellular Proteomics, 2008, 7, 981-994.	2.5	112
3504	Multiple views for ontology-based formal concept lattices. , 2008, , .		1
3505	Bipolarity of the Saccharomyces Cerevisiae Genome. , 2008, , .		0
3506	ESTplus: An Integrative System for Comprehensive and Customized EST Analysis and Proteomic Data Matching. , 2008, , .		2
3507	Toward an Online Repository of Standard Operating Procedures (SOPs) for (Meta)genomic Annotation. OMICS A Journal of Integrative Biology, 2008, 12, 137-141.	1.0	598
3508	A new cluster validity measure for bioinformatics relational datasets. , 2008, , .		10
3509	Protein-Protein Interaction Prediction and Assessment from Model Organisms. , 2008, , .		4
3510	An outlook into ultra-scale visualization of large-scale biological data. , 2008, , .		4

#	ARTICLE	IF	CITATIONS
3511	Use of Protein Ontology to Enable Data Exchange for Complex Proteomic Experiments. , 2008, , .		0
3512	ProLoc-rGO: Using rule-based knowledge with Gene Ontology terms for prediction of protein subnuclear localization. , 2008, , .		2
3513	Finding common aberrations in array CGH data. , 2008, , .		2
3514	Characteristics of Genomic Signatures Derived Using Univariate Methods and Mechanistically Anchored Functional Descriptors for Predicting Drug- and Xenobiotic-Induced Nephrotoxicity. Toxicology Mechanisms and Methods, 2008, 18, 267-276.	1.3	13
3515	Multi-platform investigation of the metabolome in a leptin receptor defective murine model of type 2 diabetes. Molecular BioSystems, 2008, 4, 1015.	2.9	22
3516	Hybrid Integration Approach for Heterogenous Information Sources: Applied to Medical Resources and Patients Medical Documents. , 2008, , .		1
3517	Toxicogenomics: A Regulatory Perspective. , 0, , 353-364.		0
3518	Evolving Models of Biological Sequence Similarity. , 2008, , .		0
3519	Ontology-Based Protein-Protein Interactions Extraction from Literature Using the Hidden Vector State Model. , 2008, , .		1
3520	Combining multiple types of biological data in constraint-based learning of gene regulatory networks. , 2008, , .		11
3521	Development and Application of a Two-Phase, On-Membrane Digestion Method in the Analysis of Membrane Proteome. Journal of Proteome Research, 2008, 7, 1778-1783.	1.8	17
3522	DOMINE: a database of protein domain interactions. Nucleic Acids Research, 2008, 36, D656-D661.	6.5	122
3523	A New Path Length Measure Based on GO for Gene Similarity with Evaluation using SGD Pathways. , 2008, , .		37
3524	Expression Profiling of Muscle Reveals Transcripts Differentially Expressed in Muscle That Affect Water-Holding Capacity of Pork. Journal of Agricultural and Food Chemistry, 2008, 56, 10311-10317.	2.4	40
3525	Subtypes of Breast Cancer Show Preferential Site of Relapse. Cancer Research, 2008, 68, 3108-3114.	0.4	674
3526	Genome-Wide Computational and Expression Analyses Reveal G-Quadruplex DNA Motifs as Conserved cis-Regulatory Elements in Human and Related Species. Journal of Medicinal Chemistry, 2008, 51, 5641-5649.	2.9	188
3527	Effect of Transgenes on Global Gene Expression in Soybean Is within the Natural Range of Variation of Conventional Cultivars. Journal of Agricultural and Food Chemistry, 2008, 56, 3057-3067.	2.4	67
3528	Hepatocystin Is Not Secreted in Cyst Fluid of Hepatocystin Mutant Polycystic Liver Patients. Journal of Proteome Research, 2008, 7, 2490-2495.	1.8	7

#	ARTICLE	IF	CITATIONS
3529	Generating GO Slim Using Relational Database Management Systems to Support Proteomics Analysis. , 2008, , .		5
3530	Curated databases. , 2008, , .		85
3531	High-Throughput Analysis of Rat Liver Plasma Membrane Proteome by a Nonelectrophoretic In-Gel Tryptic Digestion Coupled with Mass Spectrometry Identification. Journal of Proteome Research, 2008, 7, 535-545.	1.8	42
3532	Data-driven Networking Reveals 5-Genes Signature for Early Detection of Lung Cancer. , 2008, , .		1
3533	ConFuncâ€”functional annotation in the twilight zone. Bioinformatics, 2008, 24, 798-806.	1.8	95
3534	Evaluation of Gene Expression in a Single Antibiotic Exposureâ€”Derived Isolate of <i>Salmonella enterica</i> Typhimurium 14028 Possessing Resistance to Multiple Antibiotics. Foodborne Pathogens and Disease, 2008, 5, 205-221.	0.8	16
3535	A quality assessment of genetic association studies supporting susceptibility and outcome in acute lung injury. Critical Care, 2008, 12, R130.	2.5	38
3536	Proteome Response to the Panneural Expression of Human Wild-Type α -Synuclein: A <i>Drosophila</i> Model of Parkinsonâ€™s Disease. Journal of Proteome Research, 2008, 7, 3911-3921.	1.8	19
3537	ACOPIN: An ACO Algorithm with TSP Approach for Clustering Proteins from Protein Interaction Network. , 2008, , .		17
3538	Comparisons of Mass Spectrometry Compatible Surfactants for Global Analysis of the Mammalian Brain Proteome. Analytical Chemistry, 2008, 80, 8694-8701.	3.2	89
3539	2D Difference Gel Electrophoresis of Prepubertal and Pubertal Rat Mammary Gland Proteomes. Journal of Proteome Research, 2008, 7, 4638-4650.	1.8	4
3540	Deep Coverage Mouse Red Blood Cell Proteome. Molecular and Cellular Proteomics, 2008, 7, 1317-1330.	2.5	59
3541	Analysis of a Gibbs sampler method for model-based clustering of gene expression data. Bioinformatics, 2008, 24, 176-183.	1.8	59
3542	MANTIS: a phylogenetic framework for multi-species genome comparisons. Bioinformatics, 2008, 24, 151-157.	1.8	33
3543	From pull-down data to protein interaction networks and complexes with biological relevance. Bioinformatics, 2008, 24, 979-986.	1.8	141
3544	Inferring differentiation pathways from gene expression. Bioinformatics, 2008, 24, i156-i164.	1.8	16
3545	Annotation-Modules: a tool for finding significant combinations of multisource annotations for gene lists. Bioinformatics, 2008, 24, 1386-1393.	1.8	32
3546	An assessment of the uses of homologous interactions. Bioinformatics, 2008, 24, 689-695.	1.8	22

#	ARTICLE	IF	CITATIONS
3547	OREST: the online resource for EST analysis. <i>Nucleic Acids Research</i> , 2008, 36, W140-W144.	6.5	6
3548	Bio-ontologies as Tools for Integration in Biology. <i>Biological Theory</i> , 2008, 3, 7-11.	0.8	27
3549	Alternative Splicing at NAGNAG Acceptor Sites Shares Common Properties in Land Plants and Mammals. <i>Molecular Biology and Evolution</i> , 2008, 25, 709-718.	3.5	25
3550	GOSLING: a rule-based protein annotator using BLAST and GO. <i>Bioinformatics</i> , 2008, 24, 2628-2629.	1.8	12
3551	Chronic CD4 ⁺ T-Cell Activation and Depletion in Human Immunodeficiency Virus Type 1 Infection: Type I Interferon-Mediated Disruption of T-Cell Dynamics. <i>Journal of Virology</i> , 2008, 82, 1870-1883.	1.5	155
3552	COMPARE, a multi-organism system for cross-species data comparison and transfer of information. <i>Bioinformatics</i> , 2008, 24, 447-449.	1.8	11
3553	Microarray Analysis of a <i>Chlamydia pneumoniae</i> Infected Human Epithelial Cell Line by Use of Gene Ontology Hierarchy. <i>Journal of Infectious Diseases</i> , 2008, 197, 156-162.	1.9	43
3554	Network-guided genetic screening: building, testing and using gene networks to predict gene function. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 7, 217-227.	3.8	24
3555	Variations in the progranulin gene affect global gene expression in frontotemporal lobar degeneration. <i>Human Molecular Genetics</i> , 2008, 17, 1349-1362.	1.4	121
3556	BioTop: An upper domain ontology for the life sciences. <i>Applied Ontology</i> , 2008, 3, 205-212.	1.0	74
3558	Inhibition of Foxo1 Protects Pancreatic Islet β -Cells Against Fatty Acid and Endoplasmic Reticulum Stress-Induced Apoptosis. <i>Diabetes</i> , 2008, 57, 846-859.	0.3	204
3559	Potential Bias in GO::TermFinder. <i>Briefings in Bioinformatics</i> , 2008, 10, 289-294.	3.2	9
3560	A Chemical Genomic Screen in <i>Saccharomyces cerevisiae</i> Reveals a Role for Diphthamidation of Translation Elongation Factor 2 in Inhibition of Protein Synthesis by Sordarin. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 1623-1629.	1.4	28
3561	Phenobabelomics—mouse phenotype data resources. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 6, 292-301.	3.8	13
3562	Ordered Organelle Degradation during Starvation-induced Autophagy. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2419-2428.	2.5	166
3563	Predicting Clinical Outcome through Molecular Profiling in Stage III Melanoma. <i>Clinical Cancer Research</i> , 2008, 14, 5173-5180.	3.2	62
3564	Incorporating gene networks into statistical tests for genomic data via a spatially correlated mixture model. <i>Bioinformatics</i> , 2008, 24, 404-411.	1.8	75
3565	Genomic Analysis of <i>Drosophila</i> Neuronal Remodeling: A Role for the RNA-Binding Protein Boule as a Negative Regulator of Axon Pruning. <i>Journal of Neuroscience</i> , 2008, 28, 6092-6103.	1.7	46

#	ARTICLE	IF	CITATIONS
3566	Probabilistic Cross-Species Inference of Orthologous Genomic Regions Created by Whole-Genome Duplication in Yeast. <i>Genetics</i> , 2008, 179, 1681-1692.	1.2	50
3567	GENE ONTOLOGY-BASED SEMANTIC ALIGNMENT OF BIOLOGICAL PATHWAYS BY EVOLUTIONARY SEARCH. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 825-842.	0.3	5
3568	Proteomic Analysis of Laser-Captured Paraffin-Embedded Tissues: A Molecular Portrait of Head and Neck Cancer Progression. <i>Clinical Cancer Research</i> , 2008, 14, 1002-1014.	3.2	179
3569	Comparative analysis of copy number variation in primate genomes. <i>Cytogenetic and Genome Research</i> , 2008, 123, 288-296.	0.6	5
3570	Identifying gene-disease associations using centrality on a literature mined gene-interaction network. <i>Bioinformatics</i> , 2008, 24, i277-i285.	1.8	314
3571	Human Proteinpedia as a Resource for Clinical Proteomics. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2038-2047.	2.5	17
3572	GlobalANCOVA: exploration and assessment of gene group effects. <i>Bioinformatics</i> , 2008, 24, 78-85.	1.8	127
3573	Microarray data analysis and mining approaches. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 6, 265-281.	3.8	59
3574	MassNet: a functional annotation service for protein mass spectrometry data. <i>Nucleic Acids Research</i> , 2008, 36, W491-W495.	6.5	9
3575	Systematic functional characterization of cis-regulatory motifs in human core promoters. <i>Genome Research</i> , 2008, 18, 477-488.	2.4	57
3576	BioScout. , 2008, , .		3
3577	Assessing the functional structure of genomic data. <i>Bioinformatics</i> , 2008, 24, i330-i338.	1.8	15
3578	Protein Function Predictions Based on the Phylogenetic Profile Method. <i>Critical Reviews in Biotechnology</i> , 2008, 28, 233-238.	5.1	11
3579	Copy number variation in the mouse genome: implications for the mouse as a model organism for human disease. <i>Cytogenetic and Genome Research</i> , 2008, 123, 297-306.	0.6	20
3580	A Functional Proteomic Approach to the Identification and Characterization of Protein Composition in Wheat Leaf. <i>Current Proteomics</i> , 2008, 5, 253-266.	0.1	3
3581	Human and mouse introns are linked to the same processes and functions through each genome's most frequent non-conserved motifs. <i>Nucleic Acids Research</i> , 2008, 36, 3484-3493.	6.5	30
3582	Genomic analysis of estrogen cascade reveals histone variant H2A.Z associated with breast cancer progression. <i>Molecular Systems Biology</i> , 2008, 4, 188.	3.2	158
3583	The Emerging World of Wikis. <i>Science</i> , 2008, 320, 1289-1290.	6.0	23

#	ARTICLE	IF	CITATIONS
3584	NutriGeneOntology: A Biomedical Ontology for Nutrigenomics Research. , 2008, , .		2
3585	Commonality of functional annotation: a method for prioritization of candidate genes from genome-wide linkage studies. Nucleic Acids Research, 2008, 36, e26-e26.	6.5	24
3586	The biological function of some human transcription factor binding motifs varies with position relative to the transcription start site. Nucleic Acids Research, 2008, 36, 2777-2786.	6.5	19
3587	Molecular predictors for anaemia after kidney transplantation. Nephrology Dialysis Transplantation, 2008, 24, 1015-1023.	0.4	5
3588	Using whole genome presence/absence data to untangle function in 12 Drosophila genomes. Fly, 2008, 2, 291-299.	0.9	10
3589	Effect of profound hypothermia on genomics of hippocampus following complete cerebral ischemia in rats. Neurological Research, 2008, 30, 536-541.	0.6	8
3590	Protein function prediction using decision trees. , 2008, , .		1
3591	Maps: An integrated system for protein sequence annotation using support vector machine. Journal of the Chinese Institute of Engineers, Transactions of the Chinese Institute of Engineers, Series A/Chung-kuo Kung Ch'eng Hsueh K'an, 2008, 31, 781-790.	0.6	0
3592	Gaining confidence in biological interpretation of the microarray data: the functional consistence of the significant GO categories. Bioinformatics, 2008, 24, 265-271.	1.8	49
3593	Gene clustering using an evolutionary algorithm. , 2008, , .		0
3594	Formal concept analysis for ontologies and their annotation files. , 2008, , .		7
3595	Classification of Gene Expression Profiles: Comparison of K-means and Expectation Maximization Algorithms. , 2008, , .		7
3596	Consistently predicting protein function based on MKL. , 2008, , .		0
3597	Divisive Correlation Clustering Algorithm (DCCA) for grouping of genes: detecting varying patterns in expression profiles. Bioinformatics, 2008, 24, 1359-1366.	1.8	56
3598	ClusFCM: AN ALGORITHM FOR PREDICTING PROTEIN FUNCTIONS USING HOMOLOGIES AND PROTEIN INTERACTIONS. Journal of Bioinformatics and Computational Biology, 2008, 06, 203-222.	0.3	8
3599	A threading-based method (FINDSITE) for ligand-binding site prediction and functional annotation. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 129-134.	3.3	287
3600	JUDGMENT ALGORITHM FOR PERIODICITY OF TIME SERIES DATA BASED ON BAYESIAN INFORMATION CRITERION. Journal of Bioinformatics and Computational Biology, 2008, 06, 747-757.	0.3	2
3603	Tools for Interpreting Large-scale Protein Profiling in Microbiology. Journal of Dental Research, 2008, 87, 1004-1015.	2.5	21

#	ARTICLE	IF	CITATIONS
3604	QNet: A Tool for Querying Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2008, 15, 913-925.	0.8	86
3605	Transcriptional profiling in human HaCaT keratinocytes in response to kaempferol and identification of potential transcription factors for regulating differential gene expression. <i>Experimental and Molecular Medicine</i> , 2008, 40, 208.	3.2	24
3606	A Genome-Wide Expression Analysis in Blood Identifies Pre-Elafin as a Biomarker in ARDS. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2008, 38, 724-732.	1.4	62
3607	Structure system correlation identifies a gene regulatory Mediator submodule. <i>Genes and Development</i> , 2008, 22, 872-877.	2.7	31
3608	MicroRNAs in the miR-106b Family Regulate p21/CDKN1A and Promote Cell Cycle Progression. <i>Molecular and Cellular Biology</i> , 2008, 28, 2167-2174.	1.1	513
3609	Analysis of the Genome Sequence of <i>Lactobacillus gasseri</i> ATCC 33323 Reveals the Molecular Basis of an Autochthonous Intestinal Organism. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4610-4625.	1.4	152
3610	Functional evolution of the p53 regulatory network through its target response elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 944-949.	3.3	67
3611	Profiling MicroRNA Expression in Hepatocellular Carcinoma Reveals MicroRNA-224 Up-regulation and Apoptosis Inhibitor-5 as a MicroRNA-224-specific Target. <i>Journal of Biological Chemistry</i> , 2008, 283, 13205-13215.	1.6	341
3612	Characterization of genome-wide p53-binding sites upon stress response. <i>Nucleic Acids Research</i> , 2008, 36, 3639-3654.	6.5	199
3613	Uncharacterized/hypothetical proteins in biomedical 'omics' experiments: is novelty being swept under the carpet?. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 7, 283-290.	3.8	25
3614	Identification of a nonkinase target mediating cytotoxicity of novel kinase inhibitors. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 3490-3498.	1.9	107
3615	Prediction of phosphotyrosine signaling networks using a scoring matrix-assisted ligand identification approach. <i>Nucleic Acids Research</i> , 2008, 36, 3263-3273.	6.5	52
3616	Hierarchical testing of variable importance. <i>Biometrika</i> , 2008, 95, 265-278.	1.3	109
3617	Quantitative Analysis of Synaptic Phosphorylation and Protein Expression. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 684-696.	2.5	188
3618	Identification of Transformation-Related Pathways in a Breast Epithelial Cell Model Using a Ribonomics Approach. <i>Cancer Research</i> , 2008, 68, 7730-7735.	0.4	43
3619	A LINEAR-TIME ALGORITHM FOR PREDICTING FUNCTIONAL ANNOTATIONS FROM PPI NETWORKS. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 1049-1065.	0.3	6
3620	Modularity of stress response evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7500-7505.	3.3	53
3621	Uncovering signal transduction networks from high-throughput data by integer linear programming. <i>Nucleic Acids Research</i> , 2008, 36, e48-e48.	6.5	118

#	ARTICLE	IF	CITATIONS
3622	Trans-natural antisense transcripts including noncoding RNAs in 10 species: implications for expression regulation. <i>Nucleic Acids Research</i> , 2008, 36, 4833-4844.	6.5	51
3623	The Protein Feature Ontology: a tool for the unification of protein feature annotations. <i>Bioinformatics</i> , 2008, 24, 2767-2772.	1.8	19
3624	Transcriptional adaptation to Clcn5 knockout in proximal tubules of mouse kidney. <i>Physiological Genomics</i> , 2008, 33, 341-354.	1.0	25
3625	CadA Negatively Regulates <i>Escherichia coli</i> O157:H7 Adherence and Intestinal Colonization. <i>Infection and Immunity</i> , 2008, 76, 5072-5081.	1.0	29
3626	Generation and analysis of an <i>Eucalyptus globulus</i> cDNA library constructed from seedlings subjected to low temperature conditions. <i>Electronic Journal of Biotechnology</i> , 2008, 11, 0-0.	1.2	18
3627	Genetic and Computational Identification of a Conserved Bacterial Metabolic Module. <i>PLoS Genetics</i> , 2008, 4, e1000310.	1.5	26
3628	Coordination of Growth Rate, Cell Cycle, Stress Response, and Metabolic Activity in Yeast. <i>Molecular Biology of the Cell</i> , 2008, 19, 352-367.	0.9	524
3629	Physical protein-protein interactions predicted from microarrays. <i>Bioinformatics</i> , 2008, 24, 2608-2614.	1.8	40
3630	BOLOS. , 2008, , .		0
3631	Identification of Melatonin-Regulated Genes in the Ovine Pituitary Pars Tuberalis, a Target Site for Seasonal Hormone Control. <i>Endocrinology</i> , 2008, 149, 5527-5539.	1.4	65
3632	Adaptive discriminant analysis for microarray-based classification. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2008, 2, 1-20.	2.5	1
3633	Deletion of the WNT Target and Cancer Stem Cell Marker CD44 in <i>Apc</i> (Min/+) Mice Attenuates Intestinal Tumorigenesis. <i>Cancer Research</i> , 2008, 68, 3655-3661.	0.4	163
3634	Evolutionarily Conserved Substrate Substructures for Automated Annotation of Enzyme Superfamilies. <i>PLoS Computational Biology</i> , 2008, 4, e1000142.	1.5	21
3635	Network Inference Algorithms Elucidate Nrf2 Regulation of Mouse Lung Oxidative Stress. <i>PLoS Computational Biology</i> , 2008, 4, e1000166.	1.5	78
3636	Heterozygous Screen in <i>Saccharomyces cerevisiae</i> Identifies Dosage-Sensitive Genes That Affect Chromosome Stability. <i>Genetics</i> , 2008, 178, 1193-1207.	1.2	24
3637	Performance and Scalability of Discriminative Metrics for Comparative Gene Identification in 12 <i>Drosophila</i> Genomes. <i>PLoS Computational Biology</i> , 2008, 4, e1000067.	1.5	45
3638	A Genomewide Functional Network for the Laboratory Mouse. <i>PLoS Computational Biology</i> , 2008, 4, e1000165.	1.5	103
3639	Developmental Constraints on Vertebrate Genome Evolution. <i>PLoS Genetics</i> , 2008, 4, e1000311.	1.5	99

#	ARTICLE	IF	CITATIONS
3640	PaLS: filtering common literature, biological terms and pathway information. <i>Nucleic Acids Research</i> , 2008, 36, W364-W367.	6.5	8
3641	Analyzing ChIP-chip Data Using Bioconductor. <i>PLoS Computational Biology</i> , 2008, 4, e1000227.	1.5	17
3642	Hypermutable Genes in Homo sapiens Due to the Hosting of Long Mono-SSR. <i>Molecular Biology and Evolution</i> , 2008, 26, 111-121.	3.5	17
3643	Efficient algorithms for accurate hierarchical clustering of huge datasets: tackling the entire protein space. <i>Bioinformatics</i> , 2008, 24, i41-i49.	1.8	100
3644	Neurotoxic Consequences of Chronic Alcohol Withdrawal: Expression Profiling Reveals Importance of Gender Over Withdrawal Severity. <i>Neuropsychopharmacology</i> , 2008, 33, 1084-1096.	2.8	74
3645	Assessing the Performance of Single-Copy Genes for Recovering Robust Phylogenies. <i>Systematic Biology</i> , 2008, 57, 613-627.	2.7	162
3646	Supervised principal component analysis for gene set enrichment of microarray data with continuous or survival outcomes. <i>Bioinformatics</i> , 2008, 24, 2474-2481.	1.8	73
3647	An Integrated Approach for the Analysis of Biological Pathways using Mixed Models. <i>PLoS Genetics</i> , 2008, 4, e1000115.	1.5	59
3648	A General Definition and Nomenclature for Alternative Splicing Events. <i>PLoS Computational Biology</i> , 2008, 4, e1000147.	1.5	232
3649	Monte Carlo feature selection for supervised classification. <i>Bioinformatics</i> , 2008, 24, 110-117.	1.8	262
3650	Genomic Islands in the Pathogenic Filamentous Fungus <i>Aspergillus fumigatus</i> . <i>PLoS Genetics</i> , 2008, 4, e1000046.	1.5	473
3651	Discovering Sequence Motifs with Arbitrary Insertions and Deletions. <i>PLoS Computational Biology</i> , 2008, 4, e1000071.	1.5	292
3652	BioLit: integrating biological literature with databases. <i>Nucleic Acids Research</i> , 2008, 36, W385-W389.	6.5	30
3653	Optimal stepwise experimental design for pairwise functional interaction studies. <i>Bioinformatics</i> , 2008, 24, 2733-2739.	1.8	12
3654	Integrating Global Gene Expression Analysis and Genetics. <i>Advances in Genetics</i> , 2008, 60, 571-601.	0.8	48
3655	Genetic Identification of a Network of Factors that Functionally Interact with the Nucleosome Remodeling ATPase ISWI. <i>PLoS Genetics</i> , 2008, 4, e1000089.	1.5	28
3656	Evaluation of Paired-End Sequencing Strategies for Detection of Genome Rearrangements in Cancer. <i>PLoS Computational Biology</i> , 2008, 4, e1000051.	1.5	72
3657	A Feature-Based Approach to Modeling Protein-DNA Interactions. <i>PLoS Computational Biology</i> , 2008, 4, e1000154.	1.5	89

#	ARTICLE	IF	CITATIONS
3658	Gene Set Enrichment in eQTL Data Identifies Novel Annotations and Pathway Regulators. PLoS Genetics, 2008, 4, e1000070.	1.5	90
3659	Estimating node degree in bait-prey graphs. Bioinformatics, 2008, 24, 218-224.	1.8	17
3660	Identification of differentially expressed gene categories in microarray studies using nonparametric multivariate analysis. Bioinformatics, 2008, 24, 192-201.	1.8	60
3661	GraphWeb: mining heterogeneous biological networks for gene modules with functional significance. Nucleic Acids Research, 2008, 36, W452-W459.	6.5	81
3662	SerbGO: searching for the best GO tool. Nucleic Acids Research, 2008, 36, W368-W371.	6.5	12
3663	Onto-CC: a web server for identifying Gene Ontology conceptual clusters. Nucleic Acids Research, 2008, 36, W352-W357.	6.5	8
3664	Combinatorial influence of environmental parameters on transcription factor activity. Bioinformatics, 2008, 24, i172-i181.	1.8	6
3665	An unsupervised conditional random fields approach for clustering gene expression time series. Bioinformatics, 2008, 24, 2467-2473.	1.8	23
3666	The relative value of operon predictions. Briefings in Bioinformatics, 2008, 9, 367-375.	3.2	94
3667	Pediatric Malignant Germ Cell Tumors Show Characteristic Transcriptome Profiles. Cancer Research, 2008, 68, 4239-4247.	0.4	83
3668	Distinct Modes of Regulation by Chromatin Encoded through Nucleosome Positioning Signals. PLoS Computational Biology, 2008, 4, e1000216.	1.5	393
3669	Transcription Factors Bind Thousands of Active and Inactive Regions in the Drosophila Blastoderm. PLoS Biology, 2008, 6, e27.	2.6	428
3670	Identification of OBO nonalignments and its implications for OBO enrichment. Bioinformatics, 2008, 24, 1448-1455.	1.8	23
3671	Functional coherence in domain interaction networks. Bioinformatics, 2008, 24, i28-i34.	1.8	28
3672	Revealing Targeted Therapy for Human Cancer by Gene Module Maps. Cancer Research, 2008, 68, 369-378.	0.4	58
3673	Protein function prediction and annotation in an integrated environment powered by web services (AFAWE). Bioinformatics, 2008, 24, 2393-2394.	1.8	11
3674	Ontologizer 2.0—a multifunctional tool for GO term enrichment analysis and data exploration. Bioinformatics, 2008, 24, 1650-1651.	1.8	466
3675	Functional meta-analysis of double connectivity in gene coexpression networks in mammals. Physiological Genomics, 2008, 34, 34-41.	1.0	21

#	ARTICLE	IF	CITATIONS
3676	Predicting and Validating Protein Interactions Using Network Structure. <i>PLoS Computational Biology</i> , 2008, 4, e1000118.	1.5	30
3677	Differential Gene Expression Profiling in HELLP Syndrome Placentas. <i>Reproductive Sciences</i> , 2008, 15, 285-294.	1.1	8
3678	Diverse RNA-Binding Proteins Interact with Functionally Related Sets of RNAs, Suggesting an Extensive Regulatory System. <i>PLoS Biology</i> , 2008, 6, e255.	2.6	540
3679	Genes and (Common) Pathways Underlying Drug Addiction. <i>PLoS Computational Biology</i> , 2008, 4, e2.	1.5	210
3680	Nonnegative Matrix Factorization: An Analytical and Interpretive Tool in Computational Biology. <i>PLoS Computational Biology</i> , 2008, 4, e1000029.	1.5	332
3681	Local Function Conservation in Sequence and Structure Space. <i>PLoS Computational Biology</i> , 2008, 4, e1000105.	1.5	20
3682	Protein Meta-Functional Signatures from Combining Sequence, Structure, Evolution, and Amino Acid Property Information. <i>PLoS Computational Biology</i> , 2008, 4, e1000181.	1.5	37
3683	Comparative analysis of oocyte transcript profiles reveals a high degree of conservation among species. <i>Reproduction</i> , 2008, 135, 439-448.	1.1	36
3684	Transcriptome response of enterocytes to dietary lipids: impact on cell architecture, signaling, and metabolism genes. <i>American Journal of Physiology - Renal Physiology</i> , 2008, 295, G942-G952.	1.6	13
3685	Linking Fold, Function and Phylogeny: A Comparative Genomics View on Protein (Domain) Evolution. <i>Current Genomics</i> , 2008, 9, 88-96.	0.7	6
3686	Domain Tree-Based Analysis of Protein Architecture Evolution. <i>Molecular Biology and Evolution</i> , 2008, 25, 254-264.	3.5	98
3687	Genome Size Reduction in the Chicken Has Involved Massive Loss of Ancestral Protein-Coding Genes. <i>Molecular Biology and Evolution</i> , 2008, 25, 2681-2688.	3.5	50
3688	Effect of destrin mutations on the gene expression profile in vivo. <i>Physiological Genomics</i> , 2008, 34, 9-21.	1.0	32
3689	TreeGenes: A Forest Tree Genome Database. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-7.	2.2	89
3690	Combined Inhibition of PLC β -1 and c-Src Abrogates Epidermal Growth Factor Receptor-Mediated Head and Neck Squamous Cell Carcinoma Invasion. <i>Clinical Cancer Research</i> , 2008, 14, 4336-4344.	3.2	38
3691	Multiple testing on the directed acyclic graph of gene ontology. <i>Bioinformatics</i> , 2008, 24, 537-544.	1.8	79
3692	Predicting protein function from domain content. <i>Bioinformatics</i> , 2008, 24, 1681-1687.	1.8	83
3693	Improving subcellular localization prediction using text classification and the gene ontology. <i>Bioinformatics</i> , 2008, 24, 2512-2517.	1.8	42

#	ARTICLE	IF	CITATIONS
3694	A Microtubule Interactome: Complexes with Roles in Cell Cycle and Mitosis. <i>PLoS Biology</i> , 2008, 6, e98.	2.6	105
3695	In Silico Detection of Sequence Variations Modifying Transcriptional Regulation. <i>PLoS Computational Biology</i> , 2008, 4, e5.	1.5	94
3696	Entropy Measures Quantify Global Splicing Disorders in Cancer. <i>PLoS Computational Biology</i> , 2008, 4, e1000011.	1.5	53
3697	Predicting Co-Complexed Protein Pairs from Heterogeneous Data. <i>PLoS Computational Biology</i> , 2008, 4, e1000054.	1.5	65
3698	Sequence Similarity Network Reveals Common Ancestry of Multidomain Proteins. <i>PLoS Computational Biology</i> , 2008, 4, e1000063.	1.5	60
3699	Advanced Genomic Data Mining. <i>PLoS Computational Biology</i> , 2008, 4, e1000121.	1.5	13
3700	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
3701	The Landscape of Human Proteins Interacting with Viruses and Other Pathogens. <i>PLoS Pathogens</i> , 2008, 4, e32.	2.1	297
3702	MPSQ: a web tool for protein-state searching. <i>Bioinformatics</i> , 2008, 24, 2412-2413.	1.8	4
3703	A Chemical Genomics Study Identifies Snf1 as a Repressor of GCN4 Translation. <i>Journal of Biological Chemistry</i> , 2008, 283, 35889-35898.	1.6	47
3704	Arabidopsis thaliana regulatory element analyzer. <i>Bioinformatics</i> , 2008, 24, 2263-2264.	1.8	2
3705	Molecular Characterization of Trimellitic Anhydride-induced Respiratory Allergy in Brown Norway Rats. <i>Toxicologic Pathology</i> , 2008, 36, 985-998.	0.9	8
3706	VisANT: an integrative framework for networks in systems biology. <i>Briefings in Bioinformatics</i> , 2008, 9, 317-325.	3.2	121
3707	Gene Characterization Index: Assessing the Depth of Gene Annotation. <i>PLoS ONE</i> , 2008, 3, e1440.	1.1	9
3708	What can we learn from gene expression profiling of mouse oocytes?. <i>Reproduction</i> , 2008, 135, 581-592.	1.1	33
3709	Gene Ontology annotation quality analysis in model eukaryotes. <i>Nucleic Acids Research</i> , 2008, 36, e12-e12.	6.5	45
3710	Babelomics: advanced functional profiling of transcriptomics, proteomics and genomics experiments. <i>Nucleic Acids Research</i> , 2008, 36, W341-W346.	6.5	73
3711	The Death Ligand TRAIL in Diabetic Nephropathy. <i>Journal of the American Society of Nephrology: JASN</i> , 2008, 19, 904-914.	3.0	100

#	ARTICLE	IF	CITATIONS
3712	A probabilistic generative model for GO enrichment analysis. <i>Nucleic Acids Research</i> , 2008, 36, e109-e109.	6.5	74
3713	Dynamics of gene expression and the regulatory inference problem. <i>Europhysics Letters</i> , 2008, 82, 28010.	0.7	12
3714	The <i>Cladosporium fulvum</i> Virulence Protein Avr2 Inhibits Host Proteases Required for Basal Defense. <i>Plant Cell</i> , 2008, 20, 1948-1963.	3.1	230
3715	Mammalian Nonsynonymous Sites Are Not Overdispersed: Comparative Genomic Analysis of Index of Dispersion of Mammalian Proteins. <i>Molecular Biology and Evolution</i> , 2008, 25, 634-642.	3.5	6
3716	Categorization of services for seeking information in biomedical literature: a typology for improvement of practice. <i>Briefings in Bioinformatics</i> , 2008, 9, 452-465.	3.2	25
3717	GOfetcher: a database with complex searching facility for gene ontology. <i>Bioinformatics</i> , 2008, 24, 2561-2563.	1.8	9
3718	Repetitive Ischemia by Coronary Stenosis Induces a Novel Window of Ischemic Preconditioning. <i>Circulation</i> , 2008, 118, 1961-1969.	1.6	44
3719	Defining genetic interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3461-3466.	3.3	399
3720	Facts from text: can text mining help to scale-up high-quality manual curation of gene products with ontologies?. <i>Briefings in Bioinformatics</i> , 2008, 9, 466-478.	3.2	80
3721	Population genetic analysis of shotgun assemblies of genomic sequences from multiple individuals. <i>Genome Research</i> , 2008, 18, 1020-1029.	2.4	85
3722	Afferent Deprivation Elicits a Transcriptional Response Associated with Neuronal Survival after a Critical Period in the Mouse Cochlear Nucleus. <i>Journal of Neuroscience</i> , 2008, 28, 10990-11002.	1.7	25
3723	Global Liver Proteomics of Rats Exposed for 5 Days to Phenobarbital Identifies Changes Associated with Cancer and with CYP Metabolism. <i>Toxicological Sciences</i> , 2008, 106, 556-569.	1.4	21
3724	Statistical search on the Semantic Web. <i>Bioinformatics</i> , 2008, 24, 1002-1010.	1.8	26
3725	Arabidopsis Reactome: A Foundation Knowledgebase for Plant Systems Biology. <i>Plant Cell</i> , 2008, 20, 1426-1436.	3.1	52
3726	Quantitative Whole-Cell Proteome Analysis of Pseudorabies Virus-Infected Cells. <i>Journal of Virology</i> , 2008, 82, 9689-9699.	1.5	28
3727	Comprehensive detection of human terminal oligo-pyrimidine (TOP) genes and analysis of their characteristics. <i>Nucleic Acids Research</i> , 2008, 36, 3707-3715.	6.5	103
3728	Transcription factor and microRNA motif discovery: The Amadeus platform and a compendium of metazoan target sets. <i>Genome Research</i> , 2008, 18, 1180-1189.	2.4	166
3729	Acute Rejection Modulates Gene Expression in the Collecting Duct. <i>Journal of the American Society of Nephrology: JASN</i> , 2008, 19, 538-546.	3.0	23

#	ARTICLE	IF	CITATIONS
3730	Quantitative Proteomics of a Presymptomatic A53T α -Synuclein Drosophila Model of Parkinson Disease. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1191-1203.	2.5	52
3731	Associating transcription factor-binding site motifs with target GO terms and target genes. <i>Nucleic Acids Research</i> , 2008, 36, 4108-4117.	6.5	25
3732	GeneChips in Regenerative Medicine. , 2008, , 562-578.		2
3733	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
3734	A nearest neighbor approach for automated transporter prediction and categorization from protein sequences. <i>Bioinformatics</i> , 2008, 24, 1129-1136.	1.8	35
3735	Bioconductor Case Studies. , 2008, , .		65
3736	ProfCom: a web tool for profiling the complex functionality of gene groups identified from high-throughput data. <i>Nucleic Acids Research</i> , 2008, 36, W347-W351.	6.5	66
3737	A quantitative atlas of mitotic phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10762-10767.	3.3	1,435
3738	PRINCESS, a Protein Interaction Confidence Evaluation System with Multiple Data Sources. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1043-1052.	2.5	52
3739	InteroPORC: automated inference of highly conserved protein interaction networks. <i>Bioinformatics</i> , 2008, 24, 1625-1631.	1.8	39
3740	Annotating proteins with generalized functional linkages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17700-17705.	3.3	14
3741	Quantitative gene expression profiling of mouse brain regions reveals differential transcripts conserved in human and affected in disease models. <i>Physiological Genomics</i> , 2008, 33, 170-179.	1.0	40
3742	Identification of Arx transcriptional targets in the developing basal forebrain. <i>Human Molecular Genetics</i> , 2008, 17, 3740-3760.	1.4	121
3743	Genome Structure of the Legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 2008, 15, 227-239.	1.5	691
3744	Time-synchronized clustering of gene expression trajectories. <i>Biostatistics</i> , 2008, 10, 32-45.	0.9	30
3745	Text processing through Web services: calling Whatizit. <i>Bioinformatics</i> , 2008, 24, 296-298.	1.8	196
3746	Gene Expression Signatures Predictive of Early Response and Outcome in High-Risk Childhood Acute Lymphoblastic Leukemia: A Children's Oncology Group Study. <i>Journal of Clinical Oncology</i> , 2008, 26, 4376-4384.	0.8	102
3747	Transcriptional Changes Induced by Bovine Papillomavirus Type 1 in Equine Fibroblasts. <i>Journal of Virology</i> , 2008, 82, 6481-6491.	1.5	28

#	ARTICLE	IF	CITATIONS
3748	Interoperability with Moby 1.0--It's better than sharing your toothbrush!. Briefings in Bioinformatics, 2008, 9, 220-231.	3.2	91
3749	Positional distribution of human transcription factor binding sites. Nucleic Acids Research, 2008, 36, 6795-6805.	6.5	64
3750	ONTO-PERL: An API for supporting the development and analysis of bio-ontologies. Bioinformatics, 2008, 24, 885-887.	1.8	17
3751	Profiling Gene Expression in Human Placentae of Different Gestational Ages: An OPRU Network and UIW SCOR Study. Reproductive Sciences, 2008, 15, 866-877.	1.1	121
3752	Recombination rates of genes expressed in human tissues. Human Molecular Genetics, 2008, 17, 577-586.	1.4	9
3753	Gene expression analysis of human endometrial endothelial cells exposed to α -DDT. Molecular Human Reproduction, 2008, 14, 97-106.	1.3	12
3754	Predicting functional transcription factor binding through alignment-free and affinity-based analysis of orthologous promoter sequences. Bioinformatics, 2008, 24, i165-i171.	1.8	54
3755	GOEAST: a web-based software toolkit for Gene Ontology enrichment analysis. Nucleic Acids Research, 2008, 36, W358-W363.	6.5	569
3756	FFPred: an integrated feature-based function prediction server for vertebrate proteomes. Nucleic Acids Research, 2008, 36, W297-W302.	6.5	47
3757	Mitochondrial processes are impaired in hereditary inclusion body myopathy. Human Molecular Genetics, 2008, 17, 3663-3674.	1.4	49
3758	The Preferential Retention of Starch Synthesis Genes Reveals the Impact of Whole-Genome Duplication on Grass Evolution. Molecular Biology and Evolution, 2008, 25, 1003-1006.	3.5	37
3759	Clues about the Genetic Basis of Adaptation Emerge from Comparing the Proteomes of Two <i>Ostreococcus</i> Ecotypes (Chlorophyta, Prasinophyceae). Molecular Biology and Evolution, 2008, 25, 2293-2300.	3.5	39
3760	Liver-Specific Hepatocyte Nuclear Factor-4 β Deficiency: Greater Impact on Gene Expression in Male than in Female Mouse Liver. Molecular Endocrinology, 2008, 22, 1274-1286.	3.7	87
3762	Sex-Specific Early Growth Hormone Response Genes in Rat Liver. Molecular Endocrinology, 2008, 22, 1962-1974.	3.7	69
3763	Role of Secretoglobin 3A2 in Lung Development. American Journal of Respiratory and Critical Care Medicine, 2008, 178, 389-398.	2.5	50
3764	Candesartan-Induced Gene Expression in Five Organs of Stroke-Prone Spontaneously Hypertensive Rats. Hypertension Research, 2008, 31, 1963-1975.	1.5	3
3765	Enabling ontology-based document classification and management in ebXML registries. , 2008, , .		3
3766	The CONCUR framework for community maintenance of curated resources. , 2008, , .		1

#	ARTICLE	IF	CITATIONS
3767	Identification of temporal association rules from time-series microarray data set. , 2008, , .		0
3768	Coordination of Growth and Endoplasmic Reticulum Stress Signaling by Regulator of Calcineurin 1 (RCAN1), a Novel ATF6-inducible Gene. <i>Journal of Biological Chemistry</i> , 2008, 283, 14012-14021.	1.6	90
3769	Beyond the "best" match: machine learning annotation of protein sequences by integration of different sources of information. <i>Bioinformatics</i> , 2008, 24, 621-628.	1.8	12
3770	<i>Bioinformatics of Protein Function.</i> , 2008, , 79-119.		0
3771	Myocardial Gene Expression Associated with Genetic Cardiac Hypertrophy in the Absence of Hypertension. <i>Hypertension Research</i> , 2008, 31, 941-955.	1.5	9
3772	Translating the COPD Transcriptome: Insights into Pathogenesis and Tools for Clinical Management. <i>Proceedings of the American Thoracic Society</i> , 2008, 5, 834-841.	3.5	36
3774	Fundamental statistical features and self-similar properties of tagged networks. <i>New Journal of Physics</i> , 2008, 10, 123026.	1.2	43
3775	Combining Clustering and Bayesian Network for Gene Network Inference. , 2008, , .		4
3776	Adaptive Evolution of Proteins Secreted during Sperm Maturation: An Analysis of the Mouse Epididymal Transcriptome. <i>Molecular Biology and Evolution</i> , 2008, 25, 383-392.	3.5	49
3777	The scale-free nature of semantic web ontology. , 2008, , .		11
3778	Group additive regression models for genomic data analysis. <i>Biostatistics</i> , 2008, 9, 100-113.	0.9	40
3779	Local coherence in genetic interaction patterns reveals prevalent functional versatility. <i>Bioinformatics</i> , 2008, 24, 2376-2383.	1.8	26
3780	ENDEAVOUR update: a web resource for gene prioritization in multiple species. <i>Nucleic Acids Research</i> , 2008, 36, W377-W384.	6.5	202
3781	Compositional mining of multirelational biological datasets. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2008, 2, 1-35.	2.5	132
3782	ANALYSIS OF NONLINEAR RELATIONS BETWEEN EXPRESSION PROFILES BY THE PRINCIPAL CURVES OF ORIENTED-POINTS APPROACH. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 367-386.	0.3	7
3783	Widespread Ultraconservation Divergence in Primates. <i>Molecular Biology and Evolution</i> , 2008, 25, 1668-1676.	3.5	18
3784	Proteomic profiling and identification in peritoneal fluid of children treated by peritoneal dialysis. <i>Nephrology Dialysis Transplantation</i> , 2008, 23, 2402-2405.	0.4	32
3785	Genetic-linkage mapping of complex hereditary disorders to a whole-genome molecular-interaction network. <i>Genome Research</i> , 2008, 18, 1150-1162.	2.4	63

#	ARTICLE	IF	CITATIONS
3786	Dispensability of mammalian DNA. <i>Genome Research</i> , 2008, 18, 1743-1751.	2.4	42
3787	A Genomic Scan for Selection Reveals Candidates for Genes Involved in the Evolution of Cultivated Sunflower (<i>Helianthus annuus</i>). <i>Plant Cell</i> , 2008, 20, 2931-2945.	3.1	269
3788	A data integration method for exploring gene regulatory mechanisms. , 2008, , .		0
3789	Key pathways associated with heart failure development revealed by gene networks correlated with cardiac remodeling. <i>Physiological Genomics</i> , 2008, 35, 222-230.	1.0	44
3790	Gene Ontology-driven transcriptional analysis of CD34 ⁺ cell-initiated megakaryocytic cultures identifies new transcriptional regulators of megakaryopoiesis. <i>Physiological Genomics</i> , 2008, 33, 159-169.	1.0	23
3791	Gene-environment interactions reveal a homeostatic role for cholesterol metabolism during dietary folate perturbation in mice. <i>Physiological Genomics</i> , 2008, 35, 182-190.	1.0	13
3792	Meta-analysis and profiling of cardiac expression modules. <i>Physiological Genomics</i> , 2008, 35, 305-315.	1.0	12
3793	Thyroid Hormone Action in the Adult Brain: Gene Expression Profiling of the Effects of Single and Multiple Doses of Triiodo-L-Thyronine in the Rat Striatum. <i>Endocrinology</i> , 2008, 149, 3989-4000.	1.4	68
3794	Protein supporting structure discovery by rigid structure identification via one-dimensional structural signature. , 2008, , .		0
3795	Chapter 17 A System Biology Approach to Understand Functional Activity of Cell Communication Systems. <i>Methods in Cell Biology</i> , 2008, 90, 399-415.	0.5	30
3796	An Extensible, Scalable Architecture for Managing Bioinformatics Data and Analyses. , 2008, , .		7
3797	Ontology-based information retrieval: Overview and new proposition. , 2008, , .		11
3798	Bioinformatics and Its Relevance to Weed Science. <i>Weed Science</i> , 2008, 56, 297-305.	0.8	3
3799	BioDEAL: Biological data-evidence-annotation linkage system. , 2008, , .		1
3800	Genome-wide profiling of PPAR γ :RXR and RNA polymerase II occupancy reveals temporal activation of distinct metabolic pathways and changes in RXR dimer composition during adipogenesis. <i>Genes and Development</i> , 2008, 22, 2953-2967.	2.7	475
3801	An Ontological Model for Knowledge Representation of the Genetic Regulation Networks. , 2008, , .		0
3802	Validating Clustering for Gene Expression Data Based on Semantic Distance of Gene Ontology Terms. , 2008, , .		0
3803	TcruziKB: Enabling Complex Queries for Genomic Data Exploration. , 2008, , .		14

#	ARTICLE	IF	CITATIONS
3804	Mining functional biclusters of DNA microarray gene expression data. Conference Proceedings IEEE International Conference on Systems, Man, and Cybernetics, 2008, , .	0.0	0
3805	Probabilistic framework for gene expression clustering validation based on gene ontology and graph theory. Proceedings of the IEEE International Conference on Acoustics, Speech, and Signal Processing, 2008, , .	1.8	0
3806	Network Legos: Building Blocks of Cellular Wiring Diagrams. Journal of Computational Biology, 2008, 15, 829-844.	0.8	5
3807	Reassessing the limit of data integration for the prediction of protein-protein interactions in <i>Saccharomyces cerevisiae</i> . , 2008, , .		1
3808	Global gene expression analyses reveal changes in biological processes after hyperthermia in a rat glioma model. International Journal of Hyperthermia, 2008, 24, 425-441.	1.1	17
3809	Chapter 16 Gene Discovery: Macroarrays and Microarrays. Methods in Cell Biology, 2008, 87, 297-312.	0.5	2
3811	Validating Annotations for Uncharacterized Proteins in <i>Shewanella oneidensis</i> . OMICS A Journal of Integrative Biology, 2008, 12, 211-215.	1.0	5
3812	Improving feature representation of natural language gene functional annotations using automatic term expansion. , 2008, , .		0
3813	A novel 6C assay uncovers Polycomb-mediated higher order chromatin conformations. Genome Research, 2008, 18, 1171-1179.	2.4	111
3814	The PRIDE Proteomics Identifications Database: Data Submission, Query, and Dataset Comparison. Methods in Molecular Biology, 2008, 484, 287-303.	0.4	21
3815	An Instant Cell Recognition System Using a Microfabricated Coordinate Standard Chip Useful for Combinable Cell Observation with Multiple Microscopic Apparatuses. Microscopy and Microanalysis, 2008, 14, 236-242.	0.2	8
3816	Classification of Protein Structures. , 2008, , 153-188.		1
3817	An unsupervised learning framework for discovering the site-specific ontology from multiple Web pages. , 2008, , .		2
3818	Data Pushing: A Fly-Centric Guide to Bioinformatics Tools. Fly, 2008, 2, 1-18.	0.9	20
3819	Expression of <i>Medicago truncatula</i> Genes Responsive to Nitric Oxide in Pathogenic and Symbiotic Conditions. Molecular Plant-Microbe Interactions, 2008, 21, 781-790.	1.4	89
3820	Infection with <i>Rhizoctonia solani</i> Induces Defense Genes and Systemic Resistance in Potato Sprouts Grown Without Light. Phytopathology, 2008, 98, 1190-1198.	1.1	50
3821	GOSAP: Gene Ontology-Based Semantic Alignment of Biological Pathways. International Journal of Bioinformatics Research and Applications, 2008, 4, 274.	0.1	5
3822	Creating gene set activity profiles with time-series expression data. International Journal of Bioinformatics Research and Applications, 2008, 4, 306.	0.1	2

#	ARTICLE	IF	CITATIONS
3823	Towards predicting Protein-Protein Interactions in novel organisms. International Journal of Computational Biology and Drug Design, 2008, 1, 235.	0.3	0
3824	An integrated probabilistic approach for gene function prediction using multiple sources of high-throughput data. International Journal of Computational Biology and Drug Design, 2008, 1, 254.	0.3	4
3825	Scoring and summarising gene product clusters using the Gene Ontology. International Journal of Data Mining and Bioinformatics, 2008, 2, 216.	0.1	4
3826	DACE: Differential Allelic Co-Expression test for estimating regulatory associations of SNP and biological pathway. International Journal of Functional Informatics and Personalised Medicine, 2008, 1, 407.	0.4	1
3827	Indirectly driven knowledge modelling in ecology. International Journal of Metadata, Semantics and Ontologies, 2008, 3, 210.	0.2	7
3829	Chapter 3 Description Logics. Foundations of Artificial Intelligence, 2008, , 135-179.	0.9	115
3830	InnateDB: facilitating systems-level analyses of the mammalian innate immune response. Molecular Systems Biology, 2008, 4, 218.	3.2	330
3831	Niche-Specificity and the Variable Fraction of the <i>Pectobacterium</i> Pan-Genome. Molecular Plant-Microbe Interactions, 2008, 21, 1549-1560.	1.4	93
3832	Kapitel 14. Ontologie. , 0, , .		0
3833	PAIRWISE ALIGNMENT OF INTERACTION NETWORKS BY FAST IDENTIFICATION OF MAXIMAL CONSERVED PATTERNS. , 2008, , .		13
3834	DISSECTING THE INTERFACE BETWEEN SIGNALING AND TRANSCRIPTIONAL REGULATION IN HUMAN B CELLS. , 2008, , .		7
3835	PREDICTION OF INTERACTIONS BETWEEN HIV-1 AND HUMAN PROTEINS BY INFORMATION INTEGRATION. , 2008, , .		58
3836	A map of human protein interactions derived from co-expression of human mRNAs and their orthologs. Molecular Systems Biology, 2008, 4, 180.	3.2	77
3837	Transcriptional upregulation of p21/WAF/Cip1 in myeloid leukemic blasts expressing AML1-ETO. Haematologica, 2008, 93, 1728-1733.	1.7	27
3838	Models and computational strategies linking physiological response to molecular networks from large-scale data. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2008, 366, 3067-3089.	1.6	11
3839	Life Sciences and the web: a new era for collaboration. Molecular Systems Biology, 2008, 4, 201.	3.2	29
3840	Genome-wide identification of genetic determinants for the cytotoxicity of perifosine. Human Genomics, 2008, 3, 53.	1.4	11
3841	Towards a semi-automatic functional annotation tool based on decision-tree techniques. BMC Proceedings, 2008, 2, S3.	1.8	5

#	ARTICLE	IF	CITATIONS
3842	Towards structured output prediction of enzyme function. BMC Proceedings, 2008, 2, S2.	1.8	32
3843	Comparative gene expression profiling in three primary human cell lines after treatment with a novel inhibitor of Rho kinase or atorvastatin. Blood Coagulation and Fibrinolysis, 2008, 19, 709-718.	0.5	87
3844	Analysis of Protein Surface Patterns by Pocket Similarity Network. Protein and Peptide Letters, 2008, 15, 448-455.	0.4	9
3845	Computational Approaches for Predicting Causal Missense Mutations in Cancer Genome Projects. Current Bioinformatics, 2008, 3, 46-55.	0.7	6
3846	Expressed cDNAs from Embryonic and Larval Stages of the Horn Fly (Diptera: Muscidae). Journal of Medical Entomology, 2008, 45, 686-692.	0.9	10
3847	Protein Domain Annotation with Predicted Domain-Domain Interaction Networks. Protein and Peptide Letters, 2008, 15, 456-462.	0.4	3
3848	Strategies for Reliable Exploitation of Evolutionary Concepts in High Throughput Biology. Evolutionary Bioinformatics, 2008, 4, EBO.S597.	0.6	15
3849	Exploring the Evolutionary History of the Differentially Expressed Genes between Human Populations: Action of Recent Positive Selection. Evolutionary Bioinformatics, 2008, 4, EBO.S744.	0.6	1
3850	Graph-based sequence annotation using a data integration approach. Journal of Integrative Bioinformatics, 2008, 5, .	1.0	1
3851	A Bayes Random Fields Approach for Integrative Large-Scale Regulatory Network Analysis. Journal of Integrative Bioinformatics, 2008, 5, .	1.0	0
3852	Association between a Prognostic Gene Signature and Functional Gene Sets. Bioinformatics and Biology Insights, 2008, 2, BBI.S1018.	1.0	3
3853	ãfžã,ã-ãfã,ãf-ãf¼ãf¼ãf¼ã,ã@çµ±è~è\$£æž-pitfallã«é™¥ã,%ããã,ãÿã,ã«. Kagaku To Seibutsu, 2008, 46, 759-765		0
3854	Bronchoalveolar Lavage Cell Gene Expression in Acute Lung Rejection: Development of a Diagnostic Classifier. Transplantation, 2008, 85, 224-231.	0.5	41
3855	Visualizing the temporal distribution of terminologies for biological ontology development. Proceedings of SPIE, 2008, , .	0.8	0
3856	BioTDMS: a general-purpose system for integrative management of bioinformatics tools and data. International Journal of Computational Biology and Drug Design, 2008, 1, 174.	0.3	4
3857	Viral Bioinformatics: Computational Views of Host and Pathogen. Novartis Foundation Symposium, 2008, , 234-249.	1.2	6
3858	Annotating Genes of Known and Unknown Function by Large-Scale Coexpression Analysis. Plant Physiology, 2008, 147, 41-57.	2.3	162
3859	Photons, photosynthesis, and high-performance computing: challenges, progress, and promise of modeling metabolism in green algae. Journal of Physics: Conference Series, 2008, 125, 012048.	0.3	3

#	ARTICLE	IF	CITATIONS
3860	Inferring Transcription Factor interactions using a novel HV-SVM classifier. International Journal of Computational Biology and Drug Design, 2008, 1, 59.	0.3	1
3861	An integrative approach for biological data mining and visualisation. International Journal of Data Mining and Bioinformatics, 2008, 2, 54.	0.1	14
3862	Advances in molecular acute lung injury/acute respiratory distress syndrome and ventilator-induced lung injury: the role of genomics, proteomics, bioinformatics and translational biology. Current Opinion in Critical Care, 2008, 14, 3-10.	1.6	11
3863	Role of coxsackievirus and adenovirus receptor in the pathogenesis of dilated cardiomyopathy and its influencing factor. Chinese Medical Journal, 2008, 121, 1445-1449.	0.9	2
3864	Genomewide Expression Analysis Technologies. , 0, , 59-81.		0
3866	Systems Pharmacology, Biomarkers, and Biomolecular Networks. , 0, , 75-113.		0
3871	Predicting Functional Modules Using Microarray and Protein Interaction Data. , 0, , 307-329.		0
3872	APUNTES EPISTEMOLÓGICOS A LA E-CIENCIA. Revista De Filosofía (Chile), 2008, 64, .	0.1	2
3873	Biological and functional analysis of statistically significant pathways deregulated in colon cancer by using gene expression profiles. International Journal of Biological Sciences, 2008, 4, 368-378.	2.6	5
3874	Estrogen and Progesterone Control of Gene Expression in the Mouse Meibomian Gland. , 2008, 49, 1797.		76
3875	Virus Databases. , 2008, , 348-364.		2
3876	Microarray Technology: Unresolved Issues and Future Challenges from a Regulatory Perspective. Springer Series on Fluorescence, 2008, , 265-282.	0.8	3
3878	Ontologies for Bioinformatics. Bioinformatics and Biology Insights, 2008, 2, BBI.S451.	1.0	27
3879	Biomedical Ontologies in Action: Role in Knowledge Management, Data Integration and Decision Support. Yearbook of Medical Informatics, 2008, 17, 67-79.	0.8	168
3880	Candidate List of yoUr Biomarker (CLUB): A Web-based Platform to Aid Cancer Biomarker Research. Biomarker Insights, 2008, 3, BMI.S467.	1.0	9
3881	Fusion and Fission of Genes Define a Metric between Fungal Genomes. PLoS Computational Biology, 2008, 4, e1000200.	1.5	22
3882	Organization of Physical Interactomes as Uncovered by Network Schemas. PLoS Computational Biology, 2008, 4, e1000203.	1.5	16
3883	Patterns of Positive Selection in Six Mammalian Genomes. PLoS Genetics, 2008, 4, e1000144.	1.5	529

#	ARTICLE	IF	CITATIONS
3884	Improving Melanoma Classification by Integrating Genetic and Morphologic Features. <i>PLoS Medicine</i> , 2008, 5, e120.	3.9	322
3885	Genomic-Bioinformatic Analysis of Transcripts Enriched in the Third-Stage Larva of the Parasitic Nematode <i>Ascaris suum</i> . <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e246.	1.3	27
3886	Intestinal Transcriptomes of Nematodes: Comparison of the Parasites <i>Ascaris suum</i> and <i>Haemonchus contortus</i> with the Free-living <i>Caenorhabditis elegans</i> . <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e269.	1.3	42
3887	Human and Chimpanzee Gene Expression Differences Replicated in Mice Fed Different Diets. <i>PLoS ONE</i> , 2008, 3, e1504.	1.1	41
3888	Gene Expression Signature of Cigarette Smoking and Its Role in Lung Adenocarcinoma Development and Survival. <i>PLoS ONE</i> , 2008, 3, e1651.	1.1	563
3889	A New Perspective on Transcriptional System Regulation (TSR): Towards TSR Profiling. <i>PLoS ONE</i> , 2008, 3, e1656.	1.1	11
3890	Effect of Synthetic Dietary Triglycerides: A Novel Research Paradigm for Nutrigenomics. <i>PLoS ONE</i> , 2008, 3, e1681.	1.1	91
3891	Transcriptomic Analyses Reveal Novel Genes with Sexually Dimorphic Expression in the Zebrafish Gonad and Brain. <i>PLoS ONE</i> , 2008, 3, e1791.	1.1	107
3892	A Role for Gene Duplication and Natural Variation of Gene Expression in the Evolution of Metabolism. <i>PLoS ONE</i> , 2008, 3, e1838.	1.1	121
3893	De-Orphaning the Structural Proteome through Reciprocal Comparison of Evolutionarily Important Structural Features. <i>PLoS ONE</i> , 2008, 3, e2136.	1.1	21
3894	Efficient Array-Based Identification of Novel Cardiac Genes through Differentiation of Mouse ESCs. <i>PLoS ONE</i> , 2008, 3, e2176.	1.1	28
3895	Identifying Alternative Hyper-Splicing Signatures in MG-Thymoma by Exon Arrays. <i>PLoS ONE</i> , 2008, 3, e2392.	1.1	18
3896	Virus Adaptation by Manipulation of Host's Gene Expression. <i>PLoS ONE</i> , 2008, 3, e2397.	1.1	79
3897	A Meta-Analysis of Microarray Gene Expression in Mouse Stem Cells: Redefining Stemness. <i>PLoS ONE</i> , 2008, 3, e2712.	1.1	11
3898	Inferring Condition-Specific Modulation of Transcription Factor Activity in Yeast through Regulon-Based Analysis of Genomewide Expression. <i>PLoS ONE</i> , 2008, 3, e3112.	1.1	35
3899	Comparative Developmental Expression Profiling of Two <i>C. elegans</i> Isolates. <i>PLoS ONE</i> , 2008, 3, e4055.	1.1	30
3900	Molecular Subsets in the Gene Expression Signatures of Scleroderma Skin. <i>PLoS ONE</i> , 2008, 3, e2696.	1.1	334
3901	Animal trait ontology: The importance and usefulness of a unified trait vocabulary for animal species. <i>Journal of Animal Science</i> , 2008, 86, 1485-1491.	0.2	42

#	ARTICLE	IF	CITATIONS
3902	Bioinformatic Tools for Inferring Functional Information from Plant Microarray Data: Tools for the First Steps. International Journal of Plant Genomics, 2008, 2008, 1-9.	2.2	5
3903	Gene Tree Labeling Using Nonnegative Matrix Factorization on Biomedical Literature. Computational Intelligence and Neuroscience, 2008, 2008, 1-12.	1.1	9
3904	Blast2GO: A Comprehensive Suite for Functional Analysis in Plant Genomics. International Journal of Plant Genomics, 2008, 2008, 1-12.	2.2	1,866
3905	Semi-Supervised Learning for Classification of Protein Sequence Data. Scientific Programming, 2008, 16, 5-29.	0.5	7
3906	Interoperability With Moby 1.0 - It's Better Than Sharing Your Toothbrush!. Nature Precedings, 2008, , .	0.1	1
3907	Connecting Seed Lists of Mammalian Proteins Using Steiner Trees. Nature Precedings, 2008, , .	0.1	1
3908	Intra- and inter-individual genetic differences in gene expression. Nature Precedings, 2008, , .	0.1	2
3909	GO-WORDS: An Entropic Approach to Semantic Decomposition of Gene Ontology Terms. Nature Precedings, 2008, , .	0.1	0
3910	Alignment of Linear Biochemical Pathways Using Protein Structural Classification. Nature Precedings, 2008, , .	0.1	2
3911	Prediction of Functional Sites in SCOP Domains using Dynamics Perturbation Analysis. Nature Precedings, 2008, , .	0.1	1
3912	GO faster ChEBI with Reasonable Biochemistry. Nature Precedings, 2008, , .	0.1	0
3913	Polar Mapper: a computational tool for integrated visualization of protein interaction networks and mRNA expression data. Nature Precedings, 2008, , .	0.1	0
3915	From protein-disease associations to disease informatics. Frontiers in Bioscience - Landmark, 2008, Volume, 3391.	3.0	13
3916	Accessing and Integrating Data and Knowledge for Biomedical Research. Yearbook of Medical Informatics, 2008, 17, 91-101.	0.8	30
3917	Connections between ETV6-Modulated Genes: Identification of Shared Features. Cancer Informatics, 2008, 6, CIN.S556.	0.9	2
3918	CIS-REGULATORY ELEMENT BASED GENE FINDING: AN APPLICATION IN ARABIDOPSIS THALIANA. , 2008, , .		0
3919	Genomes to Proteomes. , 0, , 21-45.		1
3920	A Snapshot of the Emerging Tomato Genome Sequence. Plant Genome, 2009, 2, .	1.6	73

#	ARTICLE	IF	CITATIONS
3924	Root Development. , 2009, , .		5
3926	A Novel Information Retrieval Model for High-Throughput Molecular Medicine Modalities. <i>Cancer Informatics</i> , 2009, 8, CIN.S964.	0.9	1
3927	Parallel Pairwise Clustering. , 2009, , .		8
3928	Using Semantic Web Technologies to Annotate and Align Microarray Designs. <i>Cancer Informatics</i> , 2009, 8, CIN.S2335.	0.9	2
3929	Semantic Web-Based Integration of Cancer Pathways and Allele Frequency Data. <i>Cancer Informatics</i> , 2009, 8, CIN.S1006.	0.9	8
3930	An online conserved SSR discovery through cross-species comparison. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2009, 2, 23.	1.6	7
3931	Gene Set Enrichment Analyses Revealed Differences in Gene Expression Patterns between Males and Females. <i>In Silico Biology</i> , 2009, 9, 55-63.	0.4	22
3932	Automatic Acquisition of Synonym Resources and Assessment of their Impact on the Enhanced Search in EHRs. <i>Methods of Information in Medicine</i> , 2009, 48, 149-154.	0.7	6
3933	Comparative Analysis of Gene Regulation by the Transcription Factor PPAR α between Mouse and Human. <i>PLoS ONE</i> , 2009, 4, e6796.	1.1	245
3934	Integrated Assessment of Genomic Correlates of Protein Evolutionary Rate. <i>PLoS Computational Biology</i> , 2009, 5, e1000413.	1.5	55
3935	SWI/SNF Associates with Nascent Pre-mRNPs and Regulates Alternative Pre-mRNA Processing. <i>PLoS Genetics</i> , 2009, 5, e1000470.	1.5	70
3936	A Genome-Wide Characterization of MicroRNA Genes in Maize. <i>PLoS Genetics</i> , 2009, 5, e1000716.	1.5	318
3937	Graded Smad2/3 Activation Is Converted Directly into Levels of Target Gene Expression in Embryonic Stem Cells. <i>PLoS ONE</i> , 2009, 4, e4268.	1.1	45
3938	Emergent Genome-Wide Control in Wildtype and Genetically Mutated Lipopolysaccharides-Stimulated Macrophages. <i>PLoS ONE</i> , 2009, 4, e4905.	1.1	45
3939	Fault Tolerance in Protein Interaction Networks: Stable Bipartite Subgraphs and Redundant Pathways. <i>PLoS ONE</i> , 2009, 4, e5364.	1.1	32
3940	Transcriptome-Wide Prediction of miRNA Targets in Human and Mouse Using FASTH. <i>PLoS ONE</i> , 2009, 4, e5745.	1.1	27
3941	A Comprehensive Analysis of the Structure-Function Relationship in Proteins Based on Local Structure Similarity. <i>PLoS ONE</i> , 2009, 4, e6266.	1.1	37
3942	Genome-Wide Profile of Pleural Mesothelioma versus Parietal and Visceral Pleura: The Emerging Gene Portrait of the Mesothelioma Phenotype. <i>PLoS ONE</i> , 2009, 4, e6554.	1.1	62

#	ARTICLE	IF	CITATIONS
3943	Induction of Epithelial Mesenchymal Transition and Vasculogenesis in the Lenses of Dbl Oncogene Transgenic Mice. PLoS ONE, 2009, 4, e7058.	1.1	3
3944	Systems Integration of Biodefense Omics Data for Analysis of Pathogen-Host Interactions and Identification of Potential Targets. PLoS ONE, 2009, 4, e7162.	1.1	18
3945	Epigenetic Features of Human Mesenchymal Stem Cells Determine Their Permissiveness for Induction of Relevant Transcriptional Changes by SYT-SSX1. PLoS ONE, 2009, 4, e7904.	1.1	40
3946	Integrated Proteomic Analysis of Human Cancer Cells and Plasma from Tumor Bearing Mice for Ovarian Cancer Biomarker Discovery. PLoS ONE, 2009, 4, e7916.	1.1	53
3947	Comparative Analysis of the Global Transcriptome of Anopheles funestus from Mali, West Africa. PLoS ONE, 2009, 4, e7976.	1.1	13
3948	Accurate and Reliable Cancer Classification Based on Probabilistic Inference of Pathway Activity. PLoS ONE, 2009, 4, e8161.	1.1	111
3949	A Biochemical Genomics Screen for Substrates of Ste20p Kinase Enables the In Silico Prediction of Novel Substrates. PLoS ONE, 2009, 4, e8279.	1.1	2
3950	Genome-Wide Analysis of Small RNA and Novel MicroRNA Discovery in Human Acute Lymphoblastic Leukemia Based on Extensive Sequencing Approach. PLoS ONE, 2009, 4, e6849.	1.1	42
3951	An evolutionary approach to Function. Nature Precedings, 2009, , .	0.1	1
3952	Metarel: An Ontology to Support the Inferencing of Semantic Web Relations within Biomedical Ontologies. Nature Precedings, 2009, , .	0.1	4
3953	Automated Annotation-Based Bio-Ontology Alignment with Structural Validation. Nature Precedings, 2009, , .	0.1	2
3954	Using the Gene Ontology to Annotate Biomedical Journal Articles. Nature Precedings, 2009, , .	0.1	1
3955	Metarel: an Ontology to support the inferencing of Semantic Web relations within Biomedical Ontologies. Nature Precedings, 2009, , .	0.1	0
3956	Developing Ontology Support for Human Malaria Control Initiatives. Nature Precedings, 2009, , .	0.1	3
3957	Towards a genome-wide transcriptogram: the Saccharomyces cerevisiae case. Nature Precedings, 2009, , .	0.1	0
3958	Transforming the Axiomisation of Ontologies: The Ontology Pre-Processor Language. Nature Precedings, 2009, , .	0.1	5
3959	Topological network alignment uncovers biological function and phylogeny. Nature Precedings, 2009, , .	0.1	7
3960	PTOMSM: A modified version of Topological Overlap Measure used for predicting Protein-Protein Interaction Network. Nature Precedings, 2009, , .	0.1	0

#	ARTICLE	IF	CITATIONS
3961	Automated Prediction of Protein Attributes and Its Impact on Biomedicine and Drug Discovery. , 0, , 97-143.		6
3962	Practical network approaches and biologic interpretations of co-expression analyses in plants. <i>Plant Biotechnology</i> , 2009, 26, 3-7.	0.5	3
3963	Integrating Biological Knowledge with Gene Expression Profiles for Survival Prediction of Cancer. <i>Journal of Computational Biology</i> , 2009, 16, 265-278.	0.8	50
3964	Bootstrapping the Interactome: Unsupervised Identification of Protein Complexes in Yeast. <i>Journal of Computational Biology</i> , 2009, 16, 971-987.	0.8	85
3965	Investigating Gene and MicroRNA Expression in Glioblastoma. , 2009, , .		0
3966	Discover significant associations of orthologous simple sequence repeat patterns with gene ontology terms. , 2009, , .		0
3967	Chapter 1 The Mitochondrial Proteome Database. <i>Methods in Enzymology</i> , 2009, 457, 3-20.	0.4	78
3968	Large-Scale Proteome Profile of the Zebrafish (<i>Danio rerio</i>) Gill for Physiological and Biomarker Discovery Studies. <i>Zebrafish</i> , 2009, 6, 229-238.	0.5	45
3969	Immunological Profiles of <i>Bos taurus</i> and <i>Bos indicus</i> Cattle Infested with the Cattle Tick, <i>Rhipicephalus</i> (<i>Boophilus</i>) <i>microplus</i> . <i>Vaccine Journal</i> , 2009, 16, 1074-1086.	3.2	86
3970	Meta-analysis of cancer microarray data reveals signaling pathway hotspots. , 2009, , .		0
3971	GO Semantic Similarity-Based False Positive Reduction of Protein-Protein Interactions. , 2009, , .		1
3972	Dynamically dysfunctional protein interactions in the development of Alzheimer's disease. , 2009, , .		7
3973	A Semantic-Based Search Engine for Traditional Medical Informatics. , 2009, , .		5
3974	Pathway-Based Microarray Analysis for Defining Statistical Significant Phenotype-Related Pathways: A Review of Common Approaches. , 2009, , .		9
3975	Predicting Co-Complexed Protein Pairs Based on Communication Model Using Diverse Biological Data. , 2009, , .		0
3976	Global Differential Gene Expression in Cancers and its Implications for Building Robust Diagnostic Classifiers. , 2009, , .		0
3977	Discovering genetic polymorphism associated with gene expression levels across the whole genome. , 2009, 2009, 5466-9.		1
3978	Functional Module Analysis of Alzheimer Disease Related Genes and MicroRNAs Based on Gene Ontology Annotation. , 2009, , .		0

#	ARTICLE	IF	CITATIONS
3979	Sub-ontology modularization for large-scale web ontologies. , 2009, , .		0
3980	Higher-Order Genomic Organization of Cellular Functions in Yeast. <i>Journal of Computational Biology</i> , 2009, 16, 303-316.	0.8	11
3981	ClueGO: a Cytoscape plug-in to decipher functionally grouped gene ontology and pathway annotation networks. <i>Bioinformatics</i> , 2009, 25, 1091-1093.	1.8	5,348
3982	Nature-inspired algorithms for the genetic analysis of epistasis in common human diseases: Theoretical assessment of wrapper vs. filter approaches. , 2009, , .		1
3983	Alignment of the UMLS semantic network with BioTop: methodology and assessment. <i>Bioinformatics</i> , 2009, 25, i69-i76.	1.8	15
3984	A topology-sharing based method for protein function prediction via analysis of protein functional association networks. , 2009, , .		2
3985	Methods for optimizing statistical analyses in pharmacogenomics research. <i>Expert Review of Clinical Pharmacology</i> , 2009, 2, 559-570.	1.3	9
3986	Analysis of Gene Sets Based on the Underlying Regulatory Network. <i>Journal of Computational Biology</i> , 2009, 16, 407-426.	0.8	106
3987	Identification of Differentially Expressed Genes Between Cloned and Zygote-Developing Zebrafish (<i>Danio rerio</i>) Embryos at the Dome Stage Using Suppression Subtractive Hybridization1. <i>Biology of Reproduction</i> , 2009, 80, 674-684.	1.2	23
3988	Ontologies for cancer nanotechnology research. , 2009, 2009, 4158-61.		5
3989	Genome-Wide Identification of Genes Required for Yeast Growth Under Imatinib Stress: Vacuolar H ⁺ -ATPase Function Is an Important Target of This Anticancer Drug. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 185-198.	1.0	19
3990	Computational approaches for understanding the evolution of DNA methylation in animals. <i>Epigenetics</i> , 2009, 4, 551-556.	1.3	55
3991	Using a Fuzzy Support Vector Machine Classifier to Predict Interactions of Membrane Protein. , 2009, , .		1
3992	GO Semantic Similarity Based Analysis for Human Protein Interactions. , 2009, , .		7
3993	Visual annotation of the gene database. , 2009, 2009, 4175-7.		0
3994	Towards Reliable Isoform Quantification Using RNA-Seq Data. , 2009, , .		2
3995	Comprehensive analysis of the impact of SNPs and CNVs on human microRNAs and their regulatory genes. <i>RNA Biology</i> , 2009, 6, 412-425.	1.5	58
3996	Genome Evolution in Malaria Parasites: I. Core Genome Components. , 2009, , .		0

#	ARTICLE	IF	CITATIONS
3997	An association analysis approach to biclustering. , 2009, , .		33
3998	Enhancing creativity in synthetic biology with Interactive Virtual Environments. , 2009, , .		7
3999	Presence of Five Conditioning Film Proteins Are Highly Associated with Early Stent Encrustation. Journal of Endourology, 2009, 23, 1437-1442.	1.1	40
4000	From Modules to Models: Advanced Analysis Methods for Large-Scale Data. , 2009, , 59-83.		0
4001	Entity/quality-based logical definitions for the human skeletal phenome using PATO. , 2009, 2009, 7069-72.		67
4002	Integrating Ontological Knowledge for Iterative Causal Discovery and Visualization. Lecture Notes in Computer Science, 2009, , 168-179.	1.0	4
4003	A Model-Based Approach to Gene Clustering with Missing Observation Reconstruction in a Markov Random Field Framework. Journal of Computational Biology, 2009, 16, 475-486.	0.8	9
4004	Allergen Atlas: a comprehensive knowledge center and analysis resource for allergen information. Bioinformatics, 2009, 25, 979-980.	1.8	11
4005	Gene expression profiling of imatinib and PD166326-resistant CML cell lines identifies Fyn as a gene associated with resistance to BCR-ABL inhibitors. Molecular Cancer Therapeutics, 2009, 8, 1924-1933.	1.9	71
4006	DNA methylation is widespread and associated with differential gene expression in castes of the honeybee, <i>Apis mellifera</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11206-11211.	3.3	303
4007	Immune Gene and Cell Enrichment Is Associated with a Good Prognosis in Ependymoma. Journal of Immunology, 2009, 183, 7428-7440.	0.4	54
4008	Clusters and superclusters of phased small RNAs in the developing inflorescence of rice. Genome Research, 2009, 19, 1429-1440.	2.4	283
4009	Elucidation of the mechanism of mitochondrial iron loading in Friedreich's ataxia by analysis of a mouse mutant. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16381-16386.	3.3	197
4010	Analyzing biological network parameters with CentiScaPe. Bioinformatics, 2009, 25, 2857-2859.	1.8	469
4011	Interrogating Type 2 Diabetes Genome-Wide Association Data Using a Biological Pathway-Based Approach. Diabetes, 2009, 58, 1463-1467.	0.3	93
4012	Changes in transcript abundance relating to colony collapse disorder in honey bees (<i>Apis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10 106, 14790-14795.	3.3	196
4013	The transcriptome of human CD34 ⁺ hematopoietic stem-progenitor cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8278-8283.	3.3	28
4014	Toward a quantitative theory of intrinsically disordered proteins and their function. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19819-19823.	3.3	92

#	ARTICLE	IF	CITATIONS
4015	TrichOME: A Comparative Omics Database for Plant Trichomes. <i>Plant Physiology</i> , 2009, 152, 44-54.	2.3	98
4016	Hippocampal and Cognitive Aging across the Lifespan: A Bioenergetic Shift Precedes and Increased Cholesterol Trafficking Parallels Memory Impairment. <i>Journal of Neuroscience</i> , 2009, 29, 1805-1816.	1.7	139
4017	Human immunodeficiency virus type 1, human protein interaction database at NCBI. <i>Nucleic Acids Research</i> , 2009, 37, D417-D422.	6.5	230
4018	GS2: an efficiently computable measure of GO-based similarity of gene sets. <i>Bioinformatics</i> , 2009, 25, 1178-1184.	1.8	40
4019	Derivation of Transcriptional Regulatory Relationships by Partial Least Squares Regression. , 2009, , .		1
4020	Incorporating domain knowledge into topic modeling via Dirichlet Forest priors. , 2009, 382, 25-32.		261
4021	Identification of Marker Genes for Lipid-Lowering Effect of a Short-Chain Fructooligosaccharide by DNA Microarray Analysis. <i>Journal of Dietary Supplements</i> , 2009, 6, 254-262.	1.4	7
4022	A single transcription factor regulates evolutionarily diverse but functionally linked metabolic pathways in response to nutrient availability. <i>Molecular Systems Biology</i> , 2009, 5, 282.	3.2	55
4023	Fast and Accurate Alignment of Multiple Protein Networks. <i>Journal of Computational Biology</i> , 2009, 16, 989-999.	0.8	57
4024	Side Effect Prediction Using Cooperative Pathways. , 2009, , .		25
4025	Search of phenotype related candidate genes using gene ontology-based semantic similarity and protein interaction information: Application to Brugada syndrome. , 2009, 2009, 7079-82.		3
4026	A Measure of Semantic Similarity between GO Terms Based on Semantic Contributions of Their Ancestors. , 2009, , .		0
4027	Evaluation Model for Breast Cancer Susceptibly Gene and its Implementation Using Cytoscape. , 2009, , .		2
4028	Exploiting Domain Knowledge to Improve Biological Significance of Biclusters with Key Missing Genes. <i>Proceedings - International Conference on Data Engineering</i> , 2009, , .	0.0	1
4029	The Receptor Tyrosine Kinase EPHB4 Has Tumor Suppressor Activities in Intestinal Tumorigenesis. <i>Cancer Research</i> , 2009, 69, 7430-7438.	0.4	58
4030	A novel algorithm for detecting differentially regulated paths based on gene set enrichment analysis. <i>Bioinformatics</i> , 2009, 25, 2787-2794.	1.8	51
4031	Pathway and network-based analysis of genome-wide association studies in multiple sclerosis. <i>Human Molecular Genetics</i> , 2009, 18, 2078-2090.	1.4	371
4032	Functional genomic analysis of amniotic fluid cell-free mRNA suggests that oxidative stress is significant in Down syndrome fetuses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9425-9429.	3.3	106

#	ARTICLE	IF	CITATIONS
4033	An Integrated Approach for Experimental Target Identification of Hypoxia-induced miR-210. <i>Journal of Biological Chemistry</i> , 2009, 284, 35134-35143.	1.6	248
4034	Purification of Nuclear Poly(A)-binding Protein Nab2 Reveals Association with the Yeast Transcriptome and a Messenger Ribonucleoprotein Core Structure. <i>Journal of Biological Chemistry</i> , 2009, 284, 34911-34917.	1.6	99
4035	AUTOMATIC MODELING OF SIGNALING PATHWAYS BY NETWORK FLOW MODEL. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 309-322.	0.3	20
4036	SNPLogic: an interactive single nucleotide polymorphism selection, annotation, and prioritization system. <i>Nucleic Acids Research</i> , 2009, 37, D803-D809.	6.5	25
4037	Identification of candidate disease genes by integrating Gene Ontologies and protein-interaction networks: case study of primary immunodeficiencies. <i>Nucleic Acids Research</i> , 2009, 37, 622-628.	6.5	90
4038	Advances in Genetics, Genomics and Control of Rice Blast Disease. , 2009, , .		41
4039	Differential roles for membrane-bound and soluble syndecan-1 (CD138) in breast cancer progression. <i>Carcinogenesis</i> , 2009, 30, 397-407.	1.3	168
4040	Complex Networks. <i>Studies in Computational Intelligence</i> , 2009, , .	0.7	9
4041	Pseudo Amino Acid Composition and its Applications in Bioinformatics, Proteomics and System Biology. <i>Current Proteomics</i> , 2009, 6, 262-274.	0.1	432
4042	Sequence Identity between the Genomes of Humans and Viruses. <i>Intervirology</i> , 2009, 52, 196-200.	1.2	5
4043	COFECO: composite function annotation enriched by protein complex data. <i>Nucleic Acids Research</i> , 2009, 37, W350-W355.	6.5	19
4044	Functional Analysis of Transcription Factors in Arabidopsis. <i>Plant and Cell Physiology</i> , 2009, 50, 1232-1248.	1.5	256
4045	Coexpression network based on natural variation in human gene expression reveals gene interactions and functions. <i>Genome Research</i> , 2009, 19, 1953-1962.	2.4	112
4046	An antagonist of the chemokine receptor CXCR4 induces mitotic catastrophe in ovarian cancer cells. <i>Molecular Cancer Therapeutics</i> , 2009, 8, 1893-1905.	1.9	64
4047	Database for exploration of functional context of genes implicated in ovarian cancer. <i>Nucleic Acids Research</i> , 2009, 37, D820-D823.	6.5	37
4048	Combining multiple positive training sets to generate confidence scores for protein-protein interactions. <i>Bioinformatics</i> , 2009, 25, 105-111.	1.8	46
4049	Variable locus length in the human genome leads to ascertainment bias in functional inference for non-coding elements. <i>Bioinformatics</i> , 2009, 25, 578-584.	1.8	22
4050	How and when should interactome-derived clusters be used to predict functional modules and protein function?. <i>Bioinformatics</i> , 2009, 25, 3143-3150.	1.8	115

#	ARTICLE	IF	CITATIONS
4051	Dr. Zompo: an online data repository for <i>Zostera marina</i> and <i>Posidonia oceanica</i> ESTs. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap009-bap009.	1.4	38
4052	Semantic Search with GoPubMed. Lecture Notes in Computer Science, 2009, , 309-342.	1.0	4
4053	PIG—the pathogen interaction gateway. Nucleic Acids Research, 2009, 37, D647-D650.	6.5	57
4054	Decoding the Large-Scale Structure of Brain Function by Classifying Mental States Across Individuals. Psychological Science, 2009, 20, 1364-1372.	1.8	236
4055	Ontology Modeling and Development for Traditional Chinese Medicine. , 2009, , .		6
4056	Proteomics and Comparative Genomic Investigations Reveal Heterogeneity in Evolutionary Rate of Male Reproductive Proteins in Mice (<i>Mus domesticus</i>). Molecular Biology and Evolution, 2009, 26, 1733-1743.	3.5	93
4057	Up-to-date catalogues of yeast protein complexes. Nucleic Acids Research, 2009, 37, 825-831.	6.5	535
4058	PID: the Pathway Interaction Database. Nucleic Acids Research, 2009, 37, D674-D679.	6.5	1,419
4059	GÃ©nolevures: protein families and synteny among complete hemiascomycetous yeast proteomes and genomes. Nucleic Acids Research, 2009, 37, D550-D554.	6.5	117
4060	Molecular interactions between HNF4a, FOXA2 and GABP identified at regulatory DNA elements through ChIP-sequencing. Nucleic Acids Research, 2009, 37, 7498-7508.	6.5	63
4061	AmiGO: online access to ontology and annotation data. Bioinformatics, 2009, 25, 288-289.	1.8	1,647
4062	Network-based multiple locus linkage analysis of expression traits. Bioinformatics, 2009, 25, 1390-1396.	1.8	15
4063	The impact of incomplete knowledge on evaluation: an experimental benchmark for protein function prediction. Bioinformatics, 2009, 25, 2404-2410.	1.8	32
4064	Relationship between gene co-expression and sharing of transcription factor binding sites in <i>Drosophila melanogaster</i> . Bioinformatics, 2009, 25, 2473-2477.	1.8	45
4065	Next generation software for functional trend analysis. Bioinformatics, 2009, 25, 3043-3044.	1.8	248
4066	Synaptogenesis in Purified Cortical Subplate Neurons. Cerebral Cortex, 2009, 19, 1723-1737.	1.6	27
4067	Long-lived <i>Indy</i> induces reduced mitochondrial reactive oxygen species production and oxidative damage. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2277-2282.	3.3	71
4068	The First Draft of the Endostatin Interaction Network. Journal of Biological Chemistry, 2009, 284, 22041-22047.	1.6	78

#	ARTICLE	IF	CITATIONS
4069	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) and Quantitative Comparison of the Membrane Proteomes of Self-renewing and Differentiating Human Embryonic Stem Cells. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 959-970.	2.5	102
4070	A Complex-based Reconstruction of the <i>Saccharomyces cerevisiae</i> Interactome. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1361-1381.	2.5	96
4071	Discovering structural cis-regulatory elements by modeling the behaviors of mRNAs. <i>Molecular Systems Biology</i> , 2009, 5, 268.	3.2	32
4072	Elucidating regulatory mechanisms downstream of a signaling pathway using informative experiments. <i>Molecular Systems Biology</i> , 2009, 5, 287.	3.2	26
4073	Positive selection for elevated gene expression noise in yeast. <i>Molecular Systems Biology</i> , 2009, 5, 299.	3.2	112
4074	Chemogenomic profiling predicts antifungal synergies. <i>Molecular Systems Biology</i> , 2009, 5, 338.	3.2	71
4075	PhyloPat: an updated version of the phylogenetic pattern database contains gene neighborhood. <i>Nucleic Acids Research</i> , 2009, 37, D731-D737.	6.5	8
4076	A Unified Mixed Effects Model for Gene Set Analysis of Time Course Microarray Experiments. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2009, 8, 1-18.	0.2	30
4077	RNAither, an automated pipeline for the statistical analysis of high-throughput RNAi screens. <i>Bioinformatics</i> , 2009, 25, 678-679.	1.8	48
4078	G-SESAME: web tools for GO-term-based gene similarity analysis and knowledge discovery. <i>Nucleic Acids Research</i> , 2009, 37, W345-W349.	6.5	79
4079	Novel Proteomics Strategy Brings Insight into the Prevalence of SUMO-2 Target Sites. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1382-1390.	2.5	77
4080	Comparative Toxicogenomics Database: a knowledgebase and discovery tool for chemical-gene-disease networks. <i>Nucleic Acids Research</i> , 2009, 37, D786-D792.	6.5	246
4081	A platform to standardize, store, and visualize proteomics experimental data. <i>Acta Biochimica Et Biophysica Sinica</i> , 2009, 41, 273-279.	0.9	6
4082	Qupe—a Rich Internet Application to take a step forward in the analysis of mass spectrometry-based quantitative proteomics experiments. <i>Bioinformatics</i> , 2009, 25, 3128-3134.	1.8	29
4083	The Proteome of Seed Development in the Model Legume <i>Lotus japonicus</i> . <i>Plant Physiology</i> , 2009, 149, 1325-1340.	2.3	76
4084	OKCAM: an ontology-based, human-centered knowledgebase for cell adhesion molecules. <i>Nucleic Acids Research</i> , 2009, 37, D251-D260.	6.5	19
4085	Prior biological knowledge-based approaches for the analysis of genome-wide expression profiles using gene sets and pathways. <i>Statistical Methods in Medical Research</i> , 2009, 18, 577-593.	0.7	45
4086	Enrichment constrained time-dependent clustering analysis for finding meaningful temporal transcription modules. <i>Bioinformatics</i> , 2009, 25, 1521-1527.	1.8	18

#	ARTICLE	IF	CITATIONS
4087	Protease Gene Duplication and Proteolytic Activity in Drosophila Female Reproductive Tracts. <i>Molecular Biology and Evolution</i> , 2009, 26, 2125-2134.	3.5	37
4088	Identifying the topology of protein complexes from affinity purification assays. <i>Bioinformatics</i> , 2009, 25, 2140-2146.	1.8	15
4089	Conserved principles of mammalian transcriptional regulation revealed by RNA half-life. <i>Nucleic Acids Research</i> , 2009, 37, e115-e115.	6.5	196
4090	Genomic determination of the glucocorticoid response reveals unexpected mechanisms of gene regulation. <i>Genome Research</i> , 2009, 19, 2163-2171.	2.4	460
4091	IsoRankN: spectral methods for global alignment of multiple protein networks. <i>Bioinformatics</i> , 2009, 25, i253-i258.	1.8	322
4092	ATTED-II provides coexpressed gene networks for Arabidopsis. <i>Nucleic Acids Research</i> , 2009, 37, D987-D991.	6.5	334
4093	Sys-BodyFluid: a systematical database for human body fluid proteome research. <i>Nucleic Acids Research</i> , 2009, 37, D907-D912.	6.5	79
4094	PathExpress update: the enzyme neighbourhood method of associating gene-expression data with metabolic pathways. <i>Nucleic Acids Research</i> , 2009, 37, W335-W339.	6.5	26
4096	Complete genome sequence of Capnocytophaga ochracea type strain (VPI 2845T). <i>Standards in Genomic Sciences</i> , 2009, 1, 101-109.	1.5	14
4097	The Unfolded Protein Response Is Necessary but Not Sufficient to Compensate for Defects in Disulfide Isomerization. <i>Journal of Biological Chemistry</i> , 2009, 284, 10400-10408.	1.6	9
4098	Slow Growth Induces Heat-Shock Resistance in Normal and Respiratory-deficient Yeast. <i>Molecular Biology of the Cell</i> , 2009, 20, 891-903.	0.9	136
4099	Scalable graph clustering using stochastic flows. , 2009, , .		159
4100	Microarray and Bioinformatics Analysis of Gene Expression in Experimental Membranous Nephropathy. <i>Nephron Experimental Nephrology</i> , 2009, 112, e43-e58.	2.4	33
4101	Automatic Parameter Learning for Multiple Local Network Alignment. <i>Journal of Computational Biology</i> , 2009, 16, 1001-1022.	0.8	66
4102	A Radiation-Derived Gene Expression Signature Predicts Clinical Outcome for Breast Cancer Patients. <i>Radiation Research</i> , 2009, 171, 141-154.	0.7	13
4103	MitoMiner, an Integrated Database for the Storage and Analysis of Mitochondrial Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1324-1337.	2.5	74
4104	Lung cancer: Developmental networks gone awry?. <i>Cancer Biology and Therapy</i> , 2009, 8, 312-318.	1.5	16
4105	Integrating Genomic Data and Topological Metrics to Obtain Reliable Protein-Protein Interactions. , 2009, , .		0

#	ARTICLE	IF	CITATIONS
4106	A Branch and Bound Algorithm to Scale Alignment of Large Ontologies. , 2009, , .		1
4107	Common Regulatory Variation Impacts Gene Expression in a Cell Type-Dependent Manner. <i>Science</i> , 2009, 325, 1246-1250.	6.0	694
4108	Microarray Analysis of Female- and Larval-Specific Gene Expression in the Horn Fly (Diptera: Muscidae). <i>Journal of Medical Entomology</i> , 2009, 46, 257-270.	0.9	9
4109	A Database of Expressed Genes From <i>Cochliomyia hominivorax</i> (Diptera: Calliphoridae). <i>Journal of Medical Entomology</i> , 2009, 46, 1109-1116.	0.9	11
4110	LITSEEK. , 2009, , .		0
4111	An Overview of Nested Genes in Eukaryotic Genomes. <i>Eukaryotic Cell</i> , 2009, 8, 1321-1329.	3.4	59
4112	Global networks of functional coupling in eukaryotes from comprehensive data integration. <i>Genome Research</i> , 2009, 19, 1107-1116.	2.4	137
4113	Comparative genomic analyses of the human fungal pathogens <i>Coccidioides</i> and their relatives. <i>Genome Research</i> , 2009, 19, 1722-1731.	2.4	295
4114	CIA2 Coordinately Up-Regulates Protein Import and Synthesis in Leaf Chloroplasts. <i>Plant Physiology</i> , 2009, 150, 879-888.	2.3	40
4115	RiceArrayNet: A Database for Correlating Gene Expression from Transcriptome Profiling, and Its Application to the Analysis of Coexpressed Genes in Rice. <i>Plant Physiology</i> , 2009, 151, 16-33.	2.3	91
4116	Influence of fatty acid diets on gene expression in rat mammary epithelial cells. <i>Physiological Genomics</i> , 2009, 38, 80-88.	1.0	15
4117	Transcriptome analysis reveals an unexpected role of a collagen tyrosine kinase receptor gene, <i>Ddr2</i> , as a regulator of ovarian function. <i>Physiological Genomics</i> , 2009, 39, 120-129.	1.0	17
4118	Effects of atherogenic diet on hepatic gene expression across mouse strains. <i>Physiological Genomics</i> , 2009, 39, 172-182.	1.0	52
4119	Pleiotropic effects of negative energy balance in the postpartum dairy cow on splenic gene expression: repercussions for innate and adaptive immunity. <i>Physiological Genomics</i> , 2009, 39, 28-37.	1.0	50
4120	Estrogen Receptor β Is Required for Optimal cAMP Production in Mouse Granulosa Cells. <i>Molecular Endocrinology</i> , 2009, 23, 955-965.	3.7	48
4121	Benefits of Structural Genomics for Drug Discovery Research. <i>Infectious Disorders - Drug Targets</i> , 2009, 9, 459-474.	0.4	26
4122	An investigation into the population abundance distribution of mRNAs, proteins, and metabolites in biological systems. <i>Bioinformatics</i> , 2009, 25, 2020-2027.	1.8	45
4123	Experience report. , 2009, , .		0

#	ARTICLE	IF	CITATIONS
4124	Ontology quality assurance through analysis of term transformations. <i>Bioinformatics</i> , 2009, 25, i77-i84.	1.8	25
4125	VisANT 3.5: multi-scale network visualization, analysis and inference based on the gene ontology. <i>Nucleic Acids Research</i> , 2009, 37, W115-W121.	6.5	170
4126	ITM Probe: analyzing information flow in protein networks. <i>Bioinformatics</i> , 2009, 25, 2447-2449.	1.8	20
4127	Support tools for literature-based information access in molecular biology. , 2009, , .		1
4128	Methods for interpreting lists of affected genes obtained in a DNA microarray experiment. <i>BMC Proceedings</i> , 2009, 3, S5.	1.8	29
4129	Perturbation of Defense Pathways by Low-Dose Arsenic Exposure in Zebrafish Embryos. <i>Environmental Health Perspectives</i> , 2009, 117, 981-987.	2.8	49
4130	Cohesive versus Flexible Evolution of Functional Modules in Eukaryotes. <i>PLoS Computational Biology</i> , 2009, 5, e1000276.	1.5	19
4131	The Modular Organization of Protein Interactions in <i>Escherichia coli</i> . <i>PLoS Computational Biology</i> , 2009, 5, e1000523.	1.5	72
4132	A Threading-Based Method for the Prediction of DNA-Binding Proteins with Application to the Human Genome. <i>PLoS Computational Biology</i> , 2009, 5, e1000567.	1.5	74
4133	Decomposition of Gene Expression State Space Trajectories. <i>PLoS Computational Biology</i> , 2009, 5, e1000626.	1.5	35
4134	Geometric De-noising of Protein-Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2009, 5, e1000454.	1.5	158
4135	Mechanical Strength of 17 134 Model Proteins and Cysteine Slipknots. <i>PLoS Computational Biology</i> , 2009, 5, e1000547.	1.5	104
4136	Discovery and Annotation of Functional Chromatin Signatures in the Human Genome. <i>PLoS Computational Biology</i> , 2009, 5, e1000566.	1.5	143
4137	Identification and Functional Characterization of N-Terminally Acetylated Proteins in <i>Drosophila melanogaster</i> . <i>PLoS Biology</i> , 2009, 7, e1000236.	2.6	149
4138	Biomedical Discovery Acceleration, with Applications to Craniofacial Development. <i>PLoS Computational Biology</i> , 2009, 5, e1000215.	1.5	57
4139	Coordinated Concentration Changes of Transcripts and Metabolites in <i>Saccharomyces cerevisiae</i> . <i>PLoS Computational Biology</i> , 2009, 5, e1000270.	1.5	93
4140	Annotation Error in Public Databases: Misannotation of Molecular Function in Enzyme Superfamilies. <i>PLoS Computational Biology</i> , 2009, 5, e1000605.	1.5	587
4141	Gene set analysis methods applied to chicken microarray expression data. <i>BMC Proceedings</i> , 2009, 3, S8.	1.8	6

#	ARTICLE	IF	CITATIONS
4142	Incorporating biological knowledge in the search for gene–gene interaction in genome-wide association studies. <i>BMC Proceedings</i> , 2009, 3, S81.	1.8	3
4143	Maximal Extraction of Biological Information from Genetic Interaction Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000347.	1.5	30
4144	The Gene Ontology's Reference Genome Project: A Unified Framework for Functional Annotation across Species. <i>PLoS Computational Biology</i> , 2009, 5, e1000431.	1.5	148
4145	Conserved Expression Patterns Predict microRNA Targets. <i>PLoS Computational Biology</i> , 2009, 5, e1000513.	1.5	49
4146	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	1.5	402
4147	Dosage Regulation of the Active X Chromosome in Human Triploid Cells. <i>PLoS Genetics</i> , 2009, 5, e1000751.	1.5	19
4148	Genome-Wide Association Data Reveal a Global Map of Genetic Interactions among Protein Complexes. <i>PLoS Genetics</i> , 2009, 5, e1000782.	1.5	52
4149	Gendoo: Functional profiling of gene and disease features using MeSH vocabulary. <i>Nucleic Acids Research</i> , 2009, 37, W166-W169.	6.5	35
4150	Differential proteomic analysis of cyclosporine A-induced toxicity in renal proximal tubule cells. <i>Nephrology Dialysis Transplantation</i> , 2009, 24, 2672-2686.	0.4	32
4151	Pathway results from the chicken data set using GOTM, Pathway Studio and Ingenuity softwares. <i>BMC Proceedings</i> , 2009, 3, S11.	1.8	35
4152	STIFDB— <i>Arabidopsis</i> Stress Responsive Transcription Factor DataBase. <i>International Journal of Plant Genomics</i> , 2009, 2009, 1-8.	2.2	67
4153	Proteomic Analysis of Microtubule-associated Proteins during Macrophage Activation. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2500-2514.	2.5	41
4154	Identification of genes involved in the same pathways using a Hidden Markov Model-based approach. <i>Bioinformatics</i> , 2009, 25, 2945-2954.	1.8	6
4155	Comparison of three microarray probe annotation pipelines: differences in strategies and their effect on downstream analysis. <i>BMC Proceedings</i> , 2009, 3, S1.	1.8	7
4156	Forging Links between Human Mental Retardation-Associated CNVs and Mouse Gene Knockout Models. <i>PLoS Genetics</i> , 2009, 5, e1000531.	1.5	40
4157	Human Gene and Protein Database (HGPD): a novel database presenting a large quantity of experiment-based results in human proteomics. <i>Nucleic Acids Research</i> , 2009, 37, D762-D766.	6.5	31
4158	OligoRAP—an Oligo Re-Annotation Pipeline to improve annotation and estimate target specificity. <i>BMC Proceedings</i> , 2009, 3, S4.	1.8	9
4159	Evolutionary Processes Acting on Candidate cis-Regulatory Regions in Humans Inferred from Patterns of Polymorphism and Divergence. <i>PLoS Genetics</i> , 2009, 5, e1000592.	1.5	123

#	ARTICLE	IF	CITATIONS
4160	Identification of the <i>Schistosoma mansoni</i> TNF-Alpha Receptor Gene and the Effect of Human TNF-Alpha on the Parasite Gene Expression Profile. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e556.	1.3	33
4161	Abundantly expressed hepatic genes and their differential expression in liver of prelaying and laying geese. <i>Poultry Science</i> , 2009, 88, 1955-1962.	1.5	11
4162	Target Genes of the MADS Transcription Factor SEPALLATA3: Integration of Developmental and Hormonal Pathways in the <i>Arabidopsis</i> Flower. <i>PLoS Biology</i> , 2009, 7, e1000090.	2.6	405
4163	A Factor Graph Nested Effects Model To Identify Networks from Genetic Perturbations. <i>PLoS Computational Biology</i> , 2009, 5, e1000274.	1.5	34
4164	The Human Transcriptome: Implications for the Understanding of Human Disease. , 2009, , 123-149.		0
4165	Application and evaluation of automated semantic annotation of gene expression experiments. <i>Bioinformatics</i> , 2009, 25, 1543-1549.	1.8	9
4166	Statistical methods for gene set co-expression analysis. <i>Bioinformatics</i> , 2009, 25, 2780-2786.	1.8	139
4167	Detection of new protein domains using co-occurrence: application to <i>Plasmodium falciparum</i> . <i>Bioinformatics</i> , 2009, 25, 3077-3083.	1.8	37
4168	Gene set-based analysis of polymorphisms: finding pathways or biological processes associated to traits in genome-wide association studies. <i>Nucleic Acids Research</i> , 2009, 37, W340-W344.	6.5	64
4169	Microarray analysis of cytoplasmic versus whole cell RNA reveals a considerable number of missed and false positive mRNAs. <i>Rna</i> , 2009, 15, 1917-1928.	1.6	29
4170	Impaired Cholesterol Biosynthesis in a Neuronal Cell Line Persistently Infected with Measles Virus. <i>Journal of Virology</i> , 2009, 83, 5495-5504.	1.5	34
4171	Comparative Analysis Reveals Conserved Protein Phosphorylation Networks Implicated in Multiple Diseases. <i>Science Signaling</i> , 2009, 2, ra39.	1.6	171
4172	FlyBase: enhancing <i>Drosophila</i> Gene Ontology annotations. <i>Nucleic Acids Research</i> , 2009, 37, D555-D559.	6.5	648
4173	Visual Analysis of Dynamic Data Streams. <i>Information Visualization</i> , 2009, 8, 212-229.	1.2	17
4174	Subontology-Based Resource Management for Web-Based e-Learning. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2009, 21, 867-880.	4.0	10
4175	Identifying document topics using the Wikipedia category network. <i>Web Intelligence and Agent Systems</i> , 2009, 7, 195-207.	0.4	49
4176	Globaltest and GOEAST: two different approaches for Gene Ontology analysis. <i>BMC Proceedings</i> , 2009, 3, S10.	1.8	122
4177	<i>Ott1</i> (<i>Rbm15</i>) Is Essential for Placental Vascular Branching Morphogenesis and Embryonic Development of the Heart and Spleen. <i>Molecular and Cellular Biology</i> , 2009, 29, 333-341.	1.1	41

#	ARTICLE	IF	CITATIONS
4178	Analysis of Gene Expression Profiles in Leaf Tissues of Cultivated Peanuts and Development of EST-SSR Markers and Gene Discovery. <i>International Journal of Plant Genomics</i> , 2009, 2009, 1-14.	2.2	41
4179	The brain expression of genes involved in inflammatory response, the ribosome, and learning and memory is altered by centrally injected lipopolysaccharide in mice. <i>Pharmacogenomics Journal</i> , 2009, 9, 116-126.	0.9	66
4180	KiPar, a tool for systematic information retrieval regarding parameters for kinetic modelling of yeast metabolic pathways. <i>Bioinformatics</i> , 2009, 25, 1404-1411.	1.8	16
4181	Comparative Proteomic Phenotyping of Cell Lines and Primary Cells to Assess Preservation of Cell Type-specific Functions. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 443-450.	2.5	426
4182	Regulation of Epidermal Growth Factor Receptor Trafficking by Lysine Deacetylase HDAC6. <i>Science Signaling</i> , 2009, 2, ra84.	1.6	140
4183	Global Functional Atlas of Escherichia coli Encompassing Previously Uncharacterized Proteins. <i>PLoS Biology</i> , 2009, 7, e1000096.	2.6	331
4184	Functional organization of the yeast proteome by a yeast interactome map. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1490-1495.	3.3	18
4185	Impaired tumor growth, metastasis, angiogenesis and wound healing in annexin A1-null mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17886-17891.	3.3	92
4186	Challenges and Rewards of Interaction Proteomics. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 3-18.	2.5	78
4187	GeneSet2miRNA: finding the signature of cooperative miRNA activities in the gene lists. <i>Nucleic Acids Research</i> , 2009, 37, W323-W328.	6.5	47
4188	LRpath: a logistic regression approach for identifying enriched biological groups in gene expression data. <i>Bioinformatics</i> , 2009, 25, 211-217.	1.8	163
4189	Evolutionarily Stable Association of Intronic snoRNAs and microRNAs with Their Host Genes. <i>Genome Biology and Evolution</i> , 2009, 1, 420-428.	1.1	42
4190	MM-align: a quick algorithm for aligning multiple-chain protein complex structures using iterative dynamic programming. <i>Nucleic Acids Research</i> , 2009, 37, e83-e83.	6.5	126
4191	From <i>Corynebacterium glutamicum</i> to <i>Mycobacterium tuberculosis</i> —towards transfers of gene regulatory networks and integrated data analyses with MycoRegNet. <i>Nucleic Acids Research</i> , 2009, 37, e97-e97.	6.5	39
4192	Age-Dependent Variability in Gene Expression in Male Fischer 344 Rat Retina. <i>Toxicological Sciences</i> , 2009, 107, 281-292.	1.4	17
4193	Microarray analysis of gene expression in mouse aorta reveals role of the calcium signaling pathway in control of atherosclerosis susceptibility. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2009, 296, H1336-H1343.	1.5	27
4194	Transcriptional Profiling of the Dose Response: A More Powerful Approach for Characterizing Drug Activities. <i>PLoS Computational Biology</i> , 2009, 5, e1000512.	1.5	35
4195	Directing Experimental Biology: A Case Study in Mitochondrial Biogenesis. <i>PLoS Computational Biology</i> , 2009, 5, e1000322.	1.5	35

#	ARTICLE	IF	CITATIONS
4196	A Human Protein Interaction Network Shows Conservation of Aging Processes between Human and Invertebrate Species. <i>PLoS Genetics</i> , 2009, 5, e1000414.	1.5	106
4197	Identifying Relationships among Genomic Disease Regions: Predicting Genes at Pathogenic SNP Associations and Rare Deletions. <i>PLoS Genetics</i> , 2009, 5, e1000534.	1.5	371
4198	A comprehensive in silico expression analysis of RNA binding proteins in normal and tumor tissue; identification of potential players in tumor formation. <i>RNA Biology</i> , 2009, 6, 426-433.	1.5	51
4199	Genomic and Transcriptional Co-Localization of Protein-Coding and Long Non-Coding RNA Pairs in the Developing Brain. <i>PLoS Genetics</i> , 2009, 5, e1000617.	1.5	354
4200	Regulation of Cellular Metabolism and Cytokines by the Medicinal Herb Feverfew in the Human Monocytic THP-1 Cells. <i>Evidence-based Complementary and Alternative Medicine</i> , 2009, 6, 91-98.	0.5	20
4201	Gene expression trends and protein features effectively complement each other in gene function prediction. <i>Bioinformatics</i> , 2009, 25, 322-330.	1.8	5
4202	Human Proteinpedia: a unified discovery resource for proteomics research. <i>Nucleic Acids Research</i> , 2009, 37, D773-D781.	6.5	75
4203	<i>Apis mellifera</i> Proteomics: Where Will the Future Bee?. <i>Current Proteomics</i> , 2009, 6, 70-83.	0.1	1
4204	Using ontology visualization to facilitate access to knowledge about human disease genes. <i>Applied Ontology</i> , 2009, 4, 35-49.	1.0	3
4205	Characterization of novel and complex genomic aberrations in glioblastoma using a 32K BAC array. <i>Neuro-Oncology</i> , 2009, 11, 803-818.	0.6	43
4206	GeneCodis: interpreting gene lists through enrichment analysis and integration of diverse biological information. <i>Nucleic Acids Research</i> , 2009, 37, W317-W322.	6.5	391
4207	Transcriptional profiling reveals a critical role for tyrosine phosphatase VEâ€PTP in regulation of VEGFR2 activity and endothelial cell morphogenesis. <i>FASEB Journal</i> , 2009, 23, 1490-1502.	0.2	98
4208	The Flannotatorâ€”a gene and protein expression annotation tool for <i>Drosophila melanogaster</i> . <i>Bioinformatics</i> , 2009, 25, 548-549.	1.8	19
4209	Properties and identification of human protein drug targets. <i>Bioinformatics</i> , 2009, 25, 451-457.	1.8	276
4210	SAFEGUI: resampling-based tests of categorical significance in gene expression data made easy. <i>Bioinformatics</i> , 2009, 25, 541-542.	1.8	4
4211	The HuRef Browser: a web resource for individual human genomics. <i>Nucleic Acids Research</i> , 2009, 37, D1018-D1024.	6.5	12
4212	Parallelogram Approach Using Rat-Human In Vitro and Rat In Vivo Toxicogenomics Predicts Acetaminophen-induced Hepatotoxicity in Humans. <i>Toxicological Sciences</i> , 2009, 107, 544-552.	1.4	53
4213	Systematic analysis of dynamic miRNA-target interactions during <i>C. elegans</i> development. <i>Development (Cambridge)</i> , 2009, 136, 3043-3055.	1.2	41

#	ARTICLE	IF	CITATIONS
4214	Moby and Moby 2: Creatures of the Deep (Web). Briefings in Bioinformatics, 2009, 10, 114-128.	3.2	21
4215	Diet-induced hepatocellular carcinoma in genetically predisposed mice. Human Molecular Genetics, 2009, 18, 2975-2988.	1.4	142
4216	SysPTM: A Systematic Resource for Proteomic Research on Post-translational Modifications. Molecular and Cellular Proteomics, 2009, 8, 1839-1849.	2.5	107
4217	ChIP-on-chip significance analysis reveals large-scale binding and regulation by human transcription factor oncogenes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 244-249.	3.3	74
4218	Saint: a lightweight integration environment for model annotation. Bioinformatics, 2009, 25, 3026-3027.	1.8	25
4219	Sparse linear discriminant analysis for simultaneous testing for the significance of a gene set/pathway and gene selection. Bioinformatics, 2009, 25, 1145-1151.	1.8	92
4220	Brugia malayi Excreted/Secreted Proteins at the Host/Parasite Interface: Stage- and Gender-Specific Proteomic Profiling. PLoS Neglected Tropical Diseases, 2009, 3, e410.	1.3	187
4221	Learning a Prior on Regulatory Potential from eQTL Data. PLoS Genetics, 2009, 5, e1000358.	1.5	177
4222	Genome-wide Association Study of Alcohol Dependence. Archives of General Psychiatry, 2009, 66, 773.	13.8	354
4223	PPISearch: a web server for searching homologous protein-protein interactions across multiple species. Nucleic Acids Research, 2009, 37, W369-W375.	6.5	34
4224	lloura,ç: a software tool for analysis, visualization and semantic querying of cellular and other spatial biological data. Bioinformatics, 2009, 25, 1208-1210.	1.8	11
4225	miRo: a miRNA knowledge base. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap008-bap008.	1.4	84
4226	Hub genes with positive feedbacks function as master switches in developmental gene regulatory networks. Bioinformatics, 2009, 25, 1898-1904.	1.8	48
4227	Suppression of Phosphoinositide 3-Kinase Prevents Cardiac Aging in Mice. Circulation, 2009, 120, 1695-1703.	1.6	123
4228	The aldehyde dehydrogenase (ALDH) gene superfamily of the moss Physcomitrella patens and the algae Chlamydomonas reinhardtii and Ostreococcus tauri. Bryologist, 2009, 112, 1-11.	0.1	60
4229	The Case for Developing Consensus Standards for Research in Microbial Pathogenesis: Bacillus anthracis Toxins as an Example. Infection and Immunity, 2009, 77, 4182-4186.	1.0	3
4230	Early Upregulation of Acute Respiratory Distress Syndrome-Associated Cytokines Promotes Lethal Disease in an Aged-Mouse Model of Severe Acute Respiratory Syndrome Coronavirus Infection. Journal of Virology, 2009, 83, 7062-7074.	1.5	156
4231	Triplet repeat length bias and variation in the human transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17095-17100.	3.3	33

#	ARTICLE	IF	CITATIONS
4232	Transcriptomic Profiling of the <i>Saccharomyces cerevisiae</i> Response to Quinine Reveals a Glucose Limitation Response Attributable to Drug-Induced Inhibition of Glucose Uptake. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 5213-5223.	1.4	21
4233	Fewer permutations, more accurate <i>P</i> -values. <i>Bioinformatics</i> , 2009, 25, i161-i168.	1.8	183
4234	INTERFEROME: the database of interferon regulated genes. <i>Nucleic Acids Research</i> , 2009, 37, D852-D857.	6.5	226
4235	Multi-dimensional correlations for gene coexpression and application to the large-scale data of <i>Arabidopsis</i> . <i>Bioinformatics</i> , 2009, 25, 2677-2684.	1.8	28
4236	Exploring the human genome with functional maps. <i>Genome Research</i> , 2009, 19, 1093-1106.	2.4	196
4237	Consistent design schematics for biological systems: standardization of representation in biological engineering. <i>Journal of the Royal Society Interface</i> , 2009, 6, S393-404.	1.5	15
4238	Polar Mapper : a computational tool for integrated visualization of protein interaction networks and mRNA expression data. <i>Journal of the Royal Society Interface</i> , 2009, 6, 881-896.	1.5	12
4239	A transcriptomic analysis of superhybrid rice <i>LYP9</i> and its parents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7695-7701.	3.3	184
4240	VisHiC--hierarchical functional enrichment analysis of microarray data. <i>Nucleic Acids Research</i> , 2009, 37, W587-W592.	6.5	7
4241	MAPU 2.0: high-accuracy proteomes mapped to genomes. <i>Nucleic Acids Research</i> , 2009, 37, D902-D906.	6.5	18
4242	HIV--host interactions: a map of viral perturbation of the host system. <i>Aids</i> , 2009, 23, 549-554.	1.0	87
4243	Functionally guided alignment of protein interaction networks for module detection. <i>Bioinformatics</i> , 2009, 25, 3166-3173.	1.8	31
4244	ERGR: An ethanol-related gene resource. <i>Nucleic Acids Research</i> , 2009, 37, D840-D845.	6.5	37
4245	The origins of apicomplexan sequence innovation. <i>Genome Research</i> , 2009, 19, 1202-1213.	2.4	63
4246	Genome-Wide Impact of Androgen Receptor Trapped clone-27 Loss on Androgen-Regulated Transcription in Prostate Cancer Cells. <i>Cancer Research</i> , 2009, 69, 3140-3147.	0.4	25
4247	Biological knowledge management: the emerging role of the Semantic Web technologies. <i>Briefings in Bioinformatics</i> , 2009, 10, 392-407.	3.2	126
4248	Common polymorphic transcript variation in human disease. <i>Genome Research</i> , 2009, 19, 567-575.	2.4	70
4249	ANNIE: integrated de novo protein sequence annotation. <i>Nucleic Acids Research</i> , 2009, 37, W435-W440.	6.5	51

#	ARTICLE	IF	CITATIONS
4250	The human protein coevolution network. <i>Genome Research</i> , 2009, 19, 1861-1871.	2.4	48
4251	SUPERFAMILYâ€”sophisticated comparative genomics, data mining, visualization and phylogeny. <i>Nucleic Acids Research</i> , 2009, 37, D380-D386.	6.5	411
4252	Biophysical annotation and representation of CellML models. <i>Bioinformatics</i> , 2009, 25, 2263-2270.	1.8	16
4253	Knowledge-guided inference of domainâ€”domain interactions from incomplete proteinâ€”protein interaction networks. <i>Bioinformatics</i> , 2009, 25, 2492-2499.	1.8	24
4254	Evolutionary Forces Act on Promoter Length: Identification of Enriched Cis-Regulatory Elements. <i>Molecular Biology and Evolution</i> , 2009, 26, 1299-1307.	3.5	53
4255	LOSS OF POST-TRANSLATIONAL MODIFICATION SITES IN DISEASE. , 2009, , 337-347.		56
4256	The protein structure initiative structural genomics knowledgebase. <i>Nucleic Acids Research</i> , 2009, 37, D365-D368.	6.5	94
4257	Genome-Wide and Organ-Specific Landscapes of Epigenetic Modifications and Their Relationships to mRNA and Small RNA Transcriptomes in Maize. <i>Plant Cell</i> , 2009, 21, 1053-1069.	3.1	291
4258	Proteome-wide Prediction of Signal Flow Direction in Protein Interaction Networks Based on Interacting Domains. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2063-2070.	2.5	28
4259	Binding Sites for ETS Family of Transcription Factors Dominate the Promoter Regions of Differentially Expressed Genes in Abdominal Aortic Aneurysms. <i>Circulation: Cardiovascular Genetics</i> , 2009, 2, 565-572.	5.1	23
4260	FINDSITE: a combined evolution/structure-based approach to protein function prediction. <i>Briefings in Bioinformatics</i> , 2009, 10, 378-391.	3.2	92
4261	Precision and recall estimates for two-hybrid screens. <i>Bioinformatics</i> , 2009, 25, 372-378.	1.8	65
4262	Sequence-Based Analysis of Protein Energy Landscapes Reveals Nonuniform Thermal Adaptation within the Proteome. <i>Molecular Biology and Evolution</i> , 2009, 26, 2217-2227.	3.5	41
4263	Gene Expression Analysis Reveals New Possible Mechanisms of Vancomycin-Induced Nephrotoxicity and Identifies Gene Markers Candidates. <i>Toxicological Sciences</i> , 2009, 107, 258-269.	1.4	93
4264	Complex discovery from weighted PPI networks. <i>Bioinformatics</i> , 2009, 25, 1891-1897.	1.8	434
4265	SENT: semantic features in text. <i>Nucleic Acids Research</i> , 2009, 37, W153-W159.	6.5	5
4266	Predicting functionality of proteinâ€”DNA interactions by integrating diverse evidence. <i>Bioinformatics</i> , 2009, 25, i137-i144.	1.8	38
4267	Proteomics Analysis of Epithelial Cells Reprogrammed in Cell-free Extract. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1401-1412.	2.5	7

#	ARTICLE	IF	CITATIONS
4268	QUBIC: a qualitative biclustering algorithm for analyses of gene expression data. <i>Nucleic Acids Research</i> , 2009, 37, e101-e101.	6.5	222
4269	Generation and analysis of expressed sequence tags from a cDNA library of <i>Moniezia expansa</i> . <i>Molecular and Biochemical Parasitology</i> , 2009, 164, 80-85.	0.5	13
4270	Control of gene expression in <i>Plasmodium falciparum</i> – Ten years on. <i>Molecular and Biochemical Parasitology</i> , 2009, 164, 9-25.	0.5	88
4271	Analysis of early hepatic stage schistosomula gene expression by subtractive expressed sequence tags library. <i>Molecular and Biochemical Parasitology</i> , 2009, 166, 62-69.	0.5	13
4272	Differential effects of ethanol in the nucleus accumbens shell of alcohol-preferring (P), alcohol-non-preferring (NP) and Wistar rats: A proteomics study. <i>Pharmacology Biochemistry and Behavior</i> , 2009, 92, 304-313.	1.3	47
4273	Gene expression changes in the nucleus accumbens of alcohol-preferring rats following chronic ethanol consumption. <i>Pharmacology Biochemistry and Behavior</i> , 2009, 94, 131-147.	1.3	106
4274	Neuroprotective effects of the complement terminal pathway during demyelination: Implications for oligodendrocyte survival. <i>Journal of Neuroimmunology</i> , 2009, 213, 3-11.	1.1	21
4275	Gene expression analysis of human endometrial endothelial cells exposed to Bisphenol A. <i>Reproductive Toxicology</i> , 2009, 28, 18-25.	1.3	33
4276	The sequence-structure relationship and protein function prediction. <i>Current Opinion in Structural Biology</i> , 2009, 19, 357-362.	2.6	99
4277	The Characterization Tool: A knowledge-based stem cell, differentiated cell, and tissue database with a web-based analysis front-end. <i>Stem Cell Research</i> , 2009, 3, 88-95.	0.3	9
4278	Incremental generation of an EST set for the analysis of scrapie pathogenesis. <i>Small Ruminant Research</i> , 2009, 81, 75-78.	0.6	0
4279	PSI-2: Structural Genomics to Cover Protein Domain Family Space. <i>Structure</i> , 2009, 17, 869-881.	1.6	120
4280	The CATH Hierarchy Revisited – Structural Divergence in Domain Superfamilies and the Continuity of Fold Space. <i>Structure</i> , 2009, 17, 1051-1062.	1.6	58
4281	Comparative DNA microarray analysis of human monocyte derived dendritic cells and MUTZ-3 cells exposed to the moderate skin sensitizer cinnamaldehyde. <i>Toxicology and Applied Pharmacology</i> , 2009, 239, 273-283.	1.3	40
4282	Protein function prediction – the power of multiplicity. <i>Trends in Biotechnology</i> , 2009, 27, 210-219.	4.9	106
4283	Convergence of biomarkers, bioinformatics and nanotechnology for individualized cancer treatment. <i>Trends in Biotechnology</i> , 2009, 27, 350-358.	4.9	83
4284	The W, X, Y and Z of sex-chromosome dosage compensation. <i>Trends in Genetics</i> , 2009, 25, 226-233.	2.9	145
4285	Effects of simulated light regimes on gene expression in Antarctic krill (<i>Euphausia superba</i> Dana). <i>Journal of Experimental Marine Biology and Ecology</i> , 2009, 381, 57-64.	0.7	29

#	ARTICLE	IF	CITATIONS
4286	POINeT: protein interactome with sub-network analysis and hub prioritization. BMC Bioinformatics, 2009, 10, 114.	1.2	47
4287	Incorporating functional inter-relationships into protein function prediction algorithms. BMC Bioinformatics, 2009, 10, 142.	1.2	68
4288	The High Throughput Sequence Annotation Service (HT-SAS) – the shortcut from sequence to true Medline words. BMC Bioinformatics, 2009, 10, 148.	1.2	4
4289	Orymold: ontology based gene expression data integration and analysis tool applied to rice.. BMC Bioinformatics, 2009, 10, 158.	1.2	3
4290	Predicting genetic interactions with random walks on biological networks. BMC Bioinformatics, 2009, 10, 17.	1.2	58
4291	Incorporating pathway information into boosting estimation of high-dimensional risk prediction models. BMC Bioinformatics, 2009, 10, 18.	1.2	64
4292	Construction and use of gene expression covariation matrix. BMC Bioinformatics, 2009, 10, 214.	1.2	2
4293	Transcriptional programs: Modelling higher order structure in transcriptional control. BMC Bioinformatics, 2009, 10, 218.	1.2	3
4294	Semi-automated curation of protein subcellular localization: a text mining-based approach to Gene Ontology (GO) Cellular Component curation. BMC Bioinformatics, 2009, 10, 228.	1.2	51
4295	CLEAN: CLustering Enrichment ANALysis. BMC Bioinformatics, 2009, 10, 234.	1.2	65
4296	Identification of novel DNA repair proteins via primary sequence, secondary structure, and homology. BMC Bioinformatics, 2009, 10, 25.	1.2	23
4297	dictyExpress: a Dictyostelium discoideum gene expression database with an explorative data analysis web-based interface. BMC Bioinformatics, 2009, 10, 265.	1.2	63
4298	Correlating gene and protein expression data using Correlated Factor Analysis. BMC Bioinformatics, 2009, 10, 272.	1.2	13
4299	MultiLoc2: integrating phylogeny and Gene Ontology terms improves subcellular protein localization prediction. BMC Bioinformatics, 2009, 10, 274.	1.2	264
4300	Usefulness and limitations of dK random graph models to predict interactions and functional homogeneity in biological networks under a pseudo-likelihood parameter estimation approach. BMC Bioinformatics, 2009, 10, 277.	1.2	1
4301	Biomedical word sense disambiguation with ontologies and metadata: automation meets accuracy. BMC Bioinformatics, 2009, 10, 28.	1.2	23
4302	Context-driven discovery of gene cassettes in mobile integrons using a computational grammar. BMC Bioinformatics, 2009, 10, 281.	1.2	17
4303	RRW: repeated random walks on genome-scale protein networks for local cluster discovery. BMC Bioinformatics, 2009, 10, 283.	1.2	158

#	ARTICLE	IF	CITATIONS
4304	Exploratory and inferential analysis of gene cluster neighborhood graphs. BMC Bioinformatics, 2009, 10, 288.	1.2	5
4305	A methodology for the analysis of differential coexpression across the human lifespan. BMC Bioinformatics, 2009, 10, 306.	1.2	18
4306	Robust extraction of functional signals from gene set analysis using a generalized threshold free scoring function. BMC Bioinformatics, 2009, 10, 307.	1.2	35
4307	STAR NET 2: a web-based tool for accelerating discovery of gene regulatory networks using microarray co-expression data. BMC Bioinformatics, 2009, 10, 332.	1.2	55
4308	GIFtS: annotation landscape analysis with GeneCards. BMC Bioinformatics, 2009, 10, 348.	1.2	41
4309	Construction of an annotated corpus to support biomedical information extraction. BMC Bioinformatics, 2009, 10, 349.	1.2	73
4310	The Genome Reverse Compiler: an explorative annotation tool. BMC Bioinformatics, 2009, 10, 35.	1.2	14
4311	ArrayMining: a modular web-application for microarray analysis combining ensemble and consensus methods with cross-study normalization. BMC Bioinformatics, 2009, 10, 358.	1.2	85
4312	Phylogeny-guided interaction mapping in seven eukaryotes. BMC Bioinformatics, 2009, 10, 393.	1.2	15
4313	Inferring protein function by domain context similarities in protein-protein interaction networks. BMC Bioinformatics, 2009, 10, 395.	1.2	22
4314	Graphle: Interactive exploration of large, dense graphs. BMC Bioinformatics, 2009, 10, 417.	1.2	15
4315	TransportTP: A two-phase classification approach for membrane transporter prediction and characterization. BMC Bioinformatics, 2009, 10, 418.	1.2	53
4316	Critical assessment of sequence-based protein-protein interaction prediction methods that do not require homologous protein sequences. BMC Bioinformatics, 2009, 10, 419.	1.2	46
4317	Quantitative comparison of microarray experiments with published leukemia related gene expression signatures. BMC Bioinformatics, 2009, 10, 422.	1.2	40
4318	WebCARMA: a web application for the functional and taxonomic classification of unassembled metagenomic reads. BMC Bioinformatics, 2009, 10, 430.	1.2	78
4319	The Medicago truncatula gene expression atlas web server. BMC Bioinformatics, 2009, 10, 441.	1.2	175
4320	Next generation transcriptomes for next generation genomes using est2assembly. BMC Bioinformatics, 2009, 10, 447.	1.2	54
4321	Predicting functional upstream open reading frames in Saccharomyces cerevisiae. BMC Bioinformatics, 2009, 10, 451.	1.2	10

#	ARTICLE	IF	CITATIONS
4322	A general modular framework for gene set enrichment analysis. BMC Bioinformatics, 2009, 10, 47.	1.2	300
4323	GORilla: a tool for discovery and visualization of enriched GO terms in ranked gene lists. BMC Bioinformatics, 2009, 10, 48.	1.2	3,032
4324	ContDist: a tool for the analysis of quantitative gene and promoter properties. BMC Bioinformatics, 2009, 10, 7.	1.2	8
4325	RGG: A general GUI Framework for R scripts. BMC Bioinformatics, 2009, 10, 74.	1.2	5
4326	Modeling genomic data with type attributes, balancing stability and maintainability. BMC Bioinformatics, 2009, 10, 97.	1.2	6
4327	Methods for comparative metagenomics. BMC Bioinformatics, 2009, 10, S12.	1.2	96
4328	Principal component tests: applied to temporal gene expression data. BMC Bioinformatics, 2009, 10, S26.	1.2	5
4329	Transcriptional interaction-assisted identification of dynamic nucleosome positioning. BMC Bioinformatics, 2009, 10, S31.	1.2	3
4330	Prediction of amyloid fibril-forming segments based on a support vector machine. BMC Bioinformatics, 2009, 10, S45.	1.2	81
4331	Mutual information estimation reveals global associations between stimuli and biological processes. BMC Bioinformatics, 2009, 10, S52.	1.2	79
4332	Human gene expression sensitivity according to large scale meta-analysis. BMC Bioinformatics, 2009, 10, S56.	1.2	10
4333	Comparison of automated candidate gene prediction systems using genes implicated in type 2 diabetes by genome-wide association studies. BMC Bioinformatics, 2009, 10, S69.	1.2	16
4334	OGO: an ontological approach for integrating knowledge about orthology. BMC Bioinformatics, 2009, 10, S13.	1.2	15
4335	GoWeb: a semantic search engine for the life science web. BMC Bioinformatics, 2009, 10, S7.	1.2	35
4336	Bio-jETI: a framework for semantics-based service composition. BMC Bioinformatics, 2009, 10, S8.	1.2	56
4337	Integrating phenotype and gene expression data for predicting gene function. BMC Bioinformatics, 2009, 10, S20.	1.2	7
4338	Structural and functional-annotation of an equine whole genome oligoarray. BMC Bioinformatics, 2009, 10, S8.	1.2	21
4339	Protopia: a protein-protein interaction tool. BMC Bioinformatics, 2009, 10, S17.	1.2	9

#	ARTICLE	IF	CITATIONS
4340	The Human EST Ontology Explorer: a tissue-oriented visualization system for ontologies distribution in human EST collections. BMC Bioinformatics, 2009, 10, S2.	1.2	1
4341	A comprehensive assessment of N-terminal signal peptides prediction methods. BMC Bioinformatics, 2009, 10, S2.	1.2	58
4342	Leveraging existing biological knowledge in the identification of candidate genes for facial dysmorphology. BMC Bioinformatics, 2009, 10, S12.	1.2	14
4343	Ontology driven integration platform for clinical and translational research. BMC Bioinformatics, 2009, 10, S2.	1.2	16
4344	Identification of temporal association rules from time-series microarray data sets. BMC Bioinformatics, 2009, 10, S6.	1.2	22
4345	Assessing reliability of protein-protein interactions by integrative analysis of data in model organisms. BMC Bioinformatics, 2009, 10, S5.	1.2	16
4346	Issues in learning an ontology from text. BMC Bioinformatics, 2009, 10, S1.	1.2	11
4347	Practical application of ontologies to annotate and analyse large scale raw mouse phenotype data. BMC Bioinformatics, 2009, 10, S2.	1.2	39
4348	Inferring novel disease indications for known drugs by semantically linking drug action and disease mechanism relationships. BMC Bioinformatics, 2009, 10, S4.	1.2	58
4349	BOWiki: an ontology-based wiki for annotation of data and integration of knowledge in biology. BMC Bioinformatics, 2009, 10, S5.	1.2	13
4350	Open Biomedical Ontology-based Medline exploration. BMC Bioinformatics, 2009, 10, S6.	1.2	10
4351	DoOPSearch: a web-based tool for finding and analysing common conserved motifs in the promoter regions of different chordate and plant genes. BMC Bioinformatics, 2009, 10, S6.	1.2	5
4352	Functional assessment of time course microarray data. BMC Bioinformatics, 2009, 10, S9.	1.2	19
4353	Improved mutation tagging with gene identifiers applied to membrane protein stability prediction. BMC Bioinformatics, 2009, 10, S3.	1.2	16
4354	Knowledge-based variable selection for learning rules from proteomic data. BMC Bioinformatics, 2009, 10, S16.	1.2	6
4355	Genomic signatures of local directional selection in a high gene flow marine organism; the Atlantic cod (<i>Gadus morhua</i>). BMC Evolutionary Biology, 2009, 9, 276.	3.2	198
4356	An integrated approach for the systematic identification and characterization of heart-enriched genes with unknown functions. BMC Genomics, 2009, 10, 100.	1.2	17
4357	Discovering genes associated with dormancy in the monogonont rotifer <i>Brachionus plicatilis</i> . BMC Genomics, 2009, 10, 108.	1.2	84

#	ARTICLE	IF	CITATIONS
4358	Prediction of disease-related mutations affecting protein localization. BMC Genomics, 2009, 10, 122.	1.2	63
4359	Comparative expression pathway analysis of human and canine mammary tumors. BMC Genomics, 2009, 10, 135.	1.2	141
4360	Comparative analysis indicates that alternative splicing in plants has a limited role in functional expansion of the proteome. BMC Genomics, 2009, 10, 154.	1.2	50
4361	Gene expression profiling to characterize sediment toxicity – a pilot study using <i>Caenorhabditis elegans</i> whole genome microarrays. BMC Genomics, 2009, 10, 160.	1.2	68
4362	Evolution of alternative and constitutive regions of mammalian 5'UTRs. BMC Genomics, 2009, 10, 162.	1.2	62
4363	Genome wide signatures of positive selection: The comparison of independent samples and the identification of regions associated to traits. BMC Genomics, 2009, 10, 178.	1.2	85
4364	QTL global meta-analysis: are trait determining genes clustered?. BMC Genomics, 2009, 10, 184.	1.2	27
4365	Gene set internal coherence in the context of functional profiling. BMC Genomics, 2009, 10, 197.	1.2	28
4366	Next-generation pyrosequencing of gonad transcriptomes in the polyploid lake sturgeon (<i>Acipenser</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 2009, 10, 203.	1.2	131
4367	Transcriptomic analysis of the entomopathogenic nematode <i>Heterorhabditis bacteriophora</i> TTO1. BMC Genomics, 2009, 10, 205.	1.2	20
4368	Identifying genes related to choriogenesis in insect panoistic ovaries by Suppression Subtractive Hybridization. BMC Genomics, 2009, 10, 206.	1.2	47
4369	Identification and target prediction of miRNAs specifically expressed in rat neural tissue. BMC Genomics, 2009, 10, 214.	1.2	66
4370	Sequencing and de novo analysis of a coral larval transcriptome using 454 GSFlx. BMC Genomics, 2009, 10, 219.	1.2	405
4371	Organization and evolution of two SIDER retroposon subfamilies and their impact on the <i>Leishmania</i> genome. BMC Genomics, 2009, 10, 240.	1.2	40
4372	A White Champion (<i>Silene latifolia</i>) floral expressed sequence tag (EST) library: annotation, EST-SSR characterization, transferability, and utility for comparative mapping. BMC Genomics, 2009, 10, 243.	1.2	45
4373	Gene expression profiling within the spleen of <i>Clostridium perfringens</i> -challenged Broilers fed antibiotic-medicated and non-medicated diets. BMC Genomics, 2009, 10, 260.	1.2	32
4374	Transcriptomes and pathways associated with infectivity, survival and immunogenicity in <i>Brugia malayi</i> L3. BMC Genomics, 2009, 10, 267.	1.2	35
4375	Analysis of salivary transcripts and antigens of the sand fly <i>Phlebotomus arabicus</i> . BMC Genomics, 2009, 10, 282.	1.2	79

#	ARTICLE	IF	CITATIONS
4376	Expressed sequence tags from larval gut of the European corn borer (<i>Ostrinia nubilalis</i>): Exploring candidate genes potentially involved in <i>Bacillus thuringiensis</i> toxicity and resistance. <i>BMC Genomics</i> , 2009, 10, 286.	1.2	42
4377	Predicting protein-protein interactions in <i>Arabidopsis thaliana</i> through integration of orthology, gene ontology and co-expression. <i>BMC Genomics</i> , 2009, 10, 288.	1.2	120
4378	Characterization of the <i>Zoarces viviparus</i> liver transcriptome using massively parallel pyrosequencing. <i>BMC Genomics</i> , 2009, 10, 345.	1.2	65
4379	A proposed syntax for Minimotif Semantics, version 1. <i>BMC Genomics</i> , 2009, 10, 360.	1.2	16
4380	Correlations between RNA and protein expression profiles in 23 human cell lines. <i>BMC Genomics</i> , 2009, 10, 365.	1.2	422
4381	MicroPC (¼PC): A comprehensive resource for predicting and comparing plant microRNAs. <i>BMC Genomics</i> , 2009, 10, 366.	1.2	32
4382	Generation, annotation, and analysis of ESTs from midgut tissue of adult female <i>Anopheles stephensi</i> mosquitoes. <i>BMC Genomics</i> , 2009, 10, 386.	1.2	8
4383	Extending the models for iron and sulfur oxidation in the extreme Acidophile <i>Acidithiobacillus ferrooxidans</i> . <i>BMC Genomics</i> , 2009, 10, 394.	1.2	309
4384	Comparative 454 pyrosequencing of transcripts from two olive genotypes during fruit development. <i>BMC Genomics</i> , 2009, 10, 399.	1.2	227
4385	An expressed sequence tag (EST) library for <i>Drosophila serrata</i> , a model system for sexual selection and climatic adaptation studies. <i>BMC Genomics</i> , 2009, 10, 40.	1.2	26
4386	<i>Streptococcus pneumoniae</i> nasopharyngeal colonization induces type I interferons and interferon-induced gene expression. <i>BMC Genomics</i> , 2009, 10, 404.	1.2	42
4387	UFO: a web server for ultra-fast functional profiling of whole genome protein sequences. <i>BMC Genomics</i> , 2009, 10, 409.	1.2	15
4388	GEM-TREND: a web tool for gene expression data mining toward relevant network discovery. <i>BMC Genomics</i> , 2009, 10, 411.	1.2	30
4389	Reciprocal regulation of microRNA and mRNA profiles in neuronal development and synapse formation. <i>BMC Genomics</i> , 2009, 10, 419.	1.2	32
4390	Comparative EST transcript profiling of peach fruits under different post-harvest conditions reveals candidate genes associated with peach fruit quality. <i>BMC Genomics</i> , 2009, 10, 423.	1.2	63
4391	Global characterization of <i>Artemisia annua</i> glandular trichome transcriptome using 454 pyrosequencing. <i>BMC Genomics</i> , 2009, 10, 465.	1.2	197
4392	Characterization of full-length sequenced cDNA inserts (FLics) from Atlantic salmon (<i>Salmo salar</i>). <i>BMC Genomics</i> , 2009, 10, 502.	1.2	29
4393	Analysis of expressed sequence tags and identification of genes encoding cell-wall-degrading enzymes from the fungivorous nematode <i>Aphelenchus avenae</i> . <i>BMC Genomics</i> , 2009, 10, 525.	1.2	32

#	ARTICLE	IF	CITATIONS
4394	Combinatorial effects of environmental parameters on transcriptional regulation in <i>Saccharomyces cerevisiae</i> : A quantitative analysis of a compendium of chemostat-based transcriptome data. <i>BMC Genomics</i> , 2009, 10, 53.	1.2	55
4395	Comparative transcripts profiling reveals new insight into molecular processes regulating lycopene accumulation in a sweet orange (<i>Citrus sinensis</i>) red-flesh mutant. <i>BMC Genomics</i> , 2009, 10, 540.	1.2	69
4396	A transcriptome analysis identifies molecular effectors of unconjugated bilirubin in human neuroblastoma SH-SY5Y cells. <i>BMC Genomics</i> , 2009, 10, 543.	1.2	26
4397	Ligand-specific sequential regulation of transcription factors for differentiation of MCF-7 cells. <i>BMC Genomics</i> , 2009, 10, 545.	1.2	45
4398	Genome-wide analysis of chimpanzee genes with premature termination codons. <i>BMC Genomics</i> , 2009, 10, 56.	1.2	12
4399	The salivary gland transcriptome of the neotropical malaria vector <i>Anopheles darlingi</i> reveals accelerated evolution of genes relevant to hematophagy. <i>BMC Genomics</i> , 2009, 10, 57.	1.2	71
4400	454 pyrosequencing based transcriptome analysis of <i>Zygaena filipendulae</i> with focus on genes involved in biosynthesis of cyanogenic glucosides. <i>BMC Genomics</i> , 2009, 10, 574.	1.2	61
4401	The other side of comparative genomics: genes with no orthologs between the cow and other mammalian species. <i>BMC Genomics</i> , 2009, 10, 604.	1.2	8
4402	Transcriptional profiling of trait deterioration in the insect pathogenic nematode <i>Heterorhabditis bacteriophora</i> . <i>BMC Genomics</i> , 2009, 10, 609.	1.2	23
4403	The expansion of amino-acid repeats is not associated to adaptive evolution in mammalian genes. <i>BMC Genomics</i> , 2009, 10, 619.	1.2	6
4404	Genome-wide profiling of <i>Populus</i> small RNAs. <i>BMC Genomics</i> , 2009, 10, 620.	1.2	90
4405	Identification of genes differentially expressed as result of adenovirus type 5- and adenovirus type 12-transformation. <i>BMC Genomics</i> , 2009, 10, 67.	1.2	6
4406	Desiccation survival in an Antarctic nematode: molecular analysis using expressed sequenced tags. <i>BMC Genomics</i> , 2009, 10, 69.	1.2	76
4407	MytiBase: a knowledgebase of mussel (<i>M. galloprovincialis</i>) transcribed sequences. <i>BMC Genomics</i> , 2009, 10, 72.	1.2	102
4408	Asymmetrical distribution of non-conserved regulatory sequences at PHOX2B is reflected at the ENCODE loci and illuminates a possible genome-wide trend. <i>BMC Genomics</i> , 2009, 10, 8.	1.2	22
4409	Somatic, germline and sex hierarchy regulated gene expression during <i>Drosophila</i> metamorphosis. <i>BMC Genomics</i> , 2009, 10, 80.	1.2	49
4410	Comprehensive splicing graph analysis of alternative splicing patterns in chicken, compared to human and mouse. <i>BMC Genomics</i> , 2009, 10, S5.	1.2	27
4411	Annotating the human genome with Disease Ontology. <i>BMC Genomics</i> , 2009, 10, S6.	1.2	204

#	ARTICLE	IF	CITATIONS
4412	Genome-wide analysis of alternative splicing in cow: implications in bovine as a model for human diseases. <i>BMC Genomics</i> , 2009, 10, S11.	1.2	31
4413	Measuring similarity between gene expression profiles: a Bayesian approach. <i>BMC Genomics</i> , 2009, 10, S14.	1.2	11
4414	MINER: exploratory analysis of gene interaction networks by machine learning from expression data. <i>BMC Genomics</i> , 2009, 10, S17.	1.2	5
4415	PutidaNET: Interactome database service and network analysis of <i>Pseudomonas putida</i> KT2440. <i>BMC Genomics</i> , 2009, 10, S18.	1.2	19
4416	MitoInteractome: Mitochondrial protein interactome database, and its application in 'aging network' analysis. <i>BMC Genomics</i> , 2009, 10, S20.	1.2	30
4417	DNA-binding residues and binding mode prediction with binding-mechanism concerned models. <i>BMC Genomics</i> , 2009, 10, S23.	1.2	9
4418	Immunome Knowledge Base (IKB): An integrated service for immunome research. <i>BMC Immunology</i> , 2009, 10, 3.	0.9	33
4419	The Plant-Associated Microbe Gene Ontology (PAMGO) Consortium: community development of new Gene Ontology terms describing biological processes involved in microbe-host interactions. <i>BMC Microbiology</i> , 2009, 9, S1.	1.3	55
4420	Common and contrasting themes in host cell-targeted effectors from bacterial, fungal, oomycete and nematode plant symbionts described using the Gene Ontology. <i>BMC Microbiology</i> , 2009, 9, S3.	1.3	38
4421	Gene Ontology annotation highlights shared and divergent pathogenic strategies of type III effector proteins deployed by the plant pathogen <i>Pseudomonas syringae</i> pv tomato DC3000 and animal pathogenic <i>Escherichia coli</i> strains. <i>BMC Microbiology</i> , 2009, 9, S4.	1.3	24
4422	Gene Ontology annotation of the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>BMC Microbiology</i> , 2009, 9, S8.	1.3	17
4423	Transcript and proteomic analysis of developing white lupin (<i>Lupinus albus</i> L.) roots. <i>BMC Plant Biology</i> , 2009, 9, 1.	1.6	182
4424	TRUNCATULIX - a data warehouse for the legume community. <i>BMC Plant Biology</i> , 2009, 9, 19.	1.6	11
4425	Identification, characterization and utilization of unigene derived microsatellite markers in tea (<i>Camellia sinensis</i> L.). <i>BMC Plant Biology</i> , 2009, 9, 53.	1.6	104
4426	Ontology-oriented retrieval of putative microRNAs in <i>Vitis vinifera</i> via GrapeMiRNA: a web database of de novo predicted grape microRNAs. <i>BMC Plant Biology</i> , 2009, 9, 82.	1.6	8
4427	Sequence diversity in three tomato species: SNPs, markers, and molecular evolution. <i>BMC Plant Biology</i> , 2009, 9, 85.	1.6	44
4428	DDEC: Dragon database of genes implicated in esophageal cancer. <i>BMC Cancer</i> , 2009, 9, 219.	1.1	24
4429	BioDEAL: community generation of biological annotations. <i>BMC Medical Informatics and Decision Making</i> , 2009, 9, S5.	1.5	2

#	ARTICLE	IF	CITATIONS
4430	How to identify essential genes from molecular networks?. BMC Systems Biology, 2009, 3, 102.	3.0	79
4431	Human synthetic lethal inference as potential anti-cancer target gene detection. BMC Systems Biology, 2009, 3, 116.	3.0	45
4432	Using cell fate attractors to uncover transcriptional regulation of HL60 neutrophil differentiation. BMC Systems Biology, 2009, 3, 20.	3.0	29
4433	Protein-protein interaction as a predictor of subcellular location. BMC Systems Biology, 2009, 3, 28.	3.0	63
4434	Version control of pathway models using XML patches. BMC Systems Biology, 2009, 3, 34.	3.0	7
4435	BowTieBuilder: modeling signal transduction pathways. BMC Systems Biology, 2009, 3, 67.	3.0	42
4436	An editor for pathway drawing and data visualization in the Biopathways Workbench. BMC Systems Biology, 2009, 3, 99.	3.0	21
4437	Computing Consistency Between Microarray Data and Known Gene Regulation Relationships. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 1075-1082.	3.6	2
4438	Counter-regulation by atorvastatin of gene modulations induced by L-NAME hypertension is associated with vascular protection. Vascular Pharmacology, 2009, 51, 253-261.	1.0	9
4439	Allergen databases and allergen semantics. Regulatory Toxicology and Pharmacology, 2009, 54, S7-S10.	1.3	16
4440	Creating an Ontology-Based Human Phenotyping System: The Rockefeller University Bleeding History Experience. Clinical and Translational Science, 2009, 2, 382-385.	1.5	9
4441	Unique Early Gene Expression Patterns in Human Adult-to-Adult Living Donor Liver Grafts Compared to Deceased Donor Grafts. American Journal of Transplantation, 2009, 9, 758-772.	2.6	41
4442	Criteria for the selection of single nucleotide polymorphisms in pathway pharmacogenetics: TNF inhibitors as a case study. Drug Discovery Today, 2009, 14, 837-844.	3.2	9
4443	The yeast lysosome-like vacuole: Endpoint and crossroads. Biochimica Et Biophysica Acta - Molecular Cell Research, 2009, 1793, 650-663.	1.9	337
4444	Advanced in silico analysis of expressed sequence tag (EST) data for parasitic nematodes of major socio-economic importance – Fundamental insights toward biotechnological outcomes. Biotechnology Advances, 2009, 27, 439-448.	6.0	29
4445	Formulating and testing hypotheses in functional genomics. Artificial Intelligence in Medicine, 2009, 45, 97-107.	3.8	21
4446	Computational intelligence and machine learning in bioinformatics. Artificial Intelligence in Medicine, 2009, 45, 91-96.	3.8	17
4447	Genome-wide validation of <i>Magnaporthe grisea</i> gene structures based on transcription evidence. FEBS Letters, 2009, 583, 797-800.	1.3	3

#	ARTICLE	IF	CITATIONS
4448	Bioinformatics analysis of mass spectrometry-based proteomics data sets. <i>FEBS Letters</i> , 2009, 583, 1703-1712.	1.3	147
4449	MicroRNA expression changes during human leukemic HL-60 cell differentiation induced by 4-hydroxynonenal, a product of lipid peroxidation. <i>Free Radical Biology and Medicine</i> , 2009, 46, 282-288.	1.3	55
4450	A model-driven approach for representing clinical archetypes for Semantic Web environments. <i>Journal of Biomedical Informatics</i> , 2009, 42, 150-164.	2.5	63
4451	Fuzzy c-means clustering with prior biological knowledge. <i>Journal of Biomedical Informatics</i> , 2009, 42, 74-81.	2.5	80
4452	Onto-clust-A methodology for combining clustering analysis and ontological methods for identifying groups of comorbidities for developmental disorders. <i>Journal of Biomedical Informatics</i> , 2009, 42, 165-175.	2.5	10
4453	The caBIG terminology review process. <i>Journal of Biomedical Informatics</i> , 2009, 42, 571-580.	2.5	28
4454	Applying evolutionary terminology auditing to the Gene Ontology. <i>Journal of Biomedical Informatics</i> , 2009, 42, 518-529.	2.5	23
4455	Discovery of functional miRNA-mRNA regulatory modules with computational methods. <i>Journal of Biomedical Informatics</i> , 2009, 42, 685-691.	2.5	54
4456	Text-mining approach to evaluate terms for ontology development. <i>Journal of Biomedical Informatics</i> , 2009, 42, 824-830.	2.5	15
4457	Integrative and genomics approaches to uncover the mechanistic bases of fish behavior and its diversity. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2009, 152, 9-21.	0.8	15
4458	MDM2-Dependent Downregulation of p21 and hnRNP K Provides a Switch between Apoptosis and Growth Arrest Induced by Pharmacologically Activated p53. <i>Cancer Cell</i> , 2009, 15, 171-183.	7.7	159
4459	A specific transcriptional response of yeast cells to camptothecin dependent on the Swi4 and Mbp1 factors. <i>European Journal of Pharmacology</i> , 2009, 603, 29-36.	1.7	8
4460	Developments in Genomics to Improve Understanding, Diagnosis and Management of Aneurysms and Peripheral Artery Disease. <i>European Journal of Vascular and Endovascular Surgery</i> , 2009, 38, 676-682.	0.8	26
4461	Genome-wide system analysis reveals stable yet flexible network dynamics in yeast. <i>IET Systems Biology</i> , 2009, 3, 219-228.	0.8	10
4462	Identifying differentially expressed pathways via a mixed integer linear programming model. <i>IET Systems Biology</i> , 2009, 3, 475-486.	0.8	26
4463	Scalable learning of large networks. <i>IET Systems Biology</i> , 2009, 3, 404-413.	0.8	0
4464	Integrating BioPAX pathway knowledge with SBML models. <i>IET Systems Biology</i> , 2009, 3, 317-328.	0.8	29
4465	Chemical Genomics Based on Yeast Genetics. , 0, , 223-238.		0

#	ARTICLE	IF	CITATIONS
4467	Somatic mutation databases as tools for molecular epidemiology and molecular pathology of cancer: Proposed guidelines for improving data collection, distribution, and integration. <i>Human Mutation</i> , 2009, 30, 275-282.	1.1	14
4468	Functional annotations improve the predictive score of human disease-related mutations in proteins. <i>Human Mutation</i> , 2009, 30, 1237-1244.	1.1	552
4469	Downregulations of B-cell lymphoma 2 and myeloid cell leukemia sequence 1 by microRNA 153 induce apoptosis in a glioblastoma cell line DBTRG-G05MG. <i>International Journal of Cancer</i> , 2010, 126, 1029-1035.	2.3	104
4470	Distribution and neuronal expression of phosphatidylinositol phosphate kinase II β in the mouse brain. <i>Journal of Comparative Neurology</i> , 2009, 517, 296-312.	0.9	48
4471	A versatile platform for comprehensive chip-based explorative cytometry. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2009, 75A, 362-370.	1.1	76
4472	Analysis of Rex1 (zfp42) function in embryonic stem cell differentiation. <i>Developmental Dynamics</i> , 2009, 238, 1863-1877.	0.8	61
4473	A proteomic workflow for discovery of serum carrier protein-bound biomarker candidates of alcohol abuse using LC-MS/MS. <i>Electrophoresis</i> , 2009, 30, 2207-2214.	1.3	29
4474	Improvement of gel-separated protein identification by DMF-assisted digestion and peptide recovery after electroblotting. <i>Electrophoresis</i> , 2009, 30, 3626-3635.	1.3	18
4475	Analysis of integral membrane proteins by heat gel-embedding combined with improved in-gel digestions. <i>Electrophoresis</i> , 2009, 30, 4109-4117.	1.3	11
4476	PPAR β nuclear receptor controls multiple regulatory pathways of osteoblast differentiation from marrow mesenchymal stem cells. <i>Journal of Cellular Biochemistry</i> , 2009, 106, 232-246.	1.2	156
4477	Prediction of interactiveness between small molecules and enzymes by combining gene ontology and compound similarity. <i>Journal of Computational Chemistry</i> , 2010, 31, 1766-1776.	1.5	13
4478	Human cytomegalovirus productively infects adrenocortical cells and induces an early cortisol response. <i>Journal of Cellular Physiology</i> , 2009, 221, 629-641.	2.0	14
4479	Hematopoietic immortalizing function of the NKL subclass homeobox gene <i>TLX1</i> . <i>Genes Chromosomes and Cancer</i> , 2010, 49, 119-131.	1.5	2
4480	Uncovering genetic regulatory network divergence between duplicate genes using yeast eQTL landscape. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2009, 312B, 722-733.	0.6	9
4481	Shotgun proteomic analysis of the microsomal fraction of eukaryotic cells using a two-dimensional reversed-phase-ion-pair reversed-phase HPLC setup. <i>Journal of Separation Science</i> , 2009, 32, 1165-1174.	1.3	5
4482	Combined usage of cascade affinity fractionation and LC-MS/MS for the proteomics of adult mouse testis. <i>Journal of Separation Science</i> , 2009, 32, 3871-3879.	1.3	5
4483	Exploiting corpus-related ontologies for conceptualizing document corpora. <i>Journal of the Association for Information Science and Technology</i> , 2009, 60, 2287-2299.	2.6	0
4484	Microarray-based gene expression analysis as a process characterization tool to establish comparability of complex biological products: Scale-up of a whole-cell immunotherapy product. <i>Biotechnology and Bioengineering</i> , 2009, 104, 796-808.	1.7	5

#	ARTICLE	IF	CITATIONS
4485	DATE analysis: A general theory of biological change applied to microarray data. <i>Biotechnology Progress</i> , 2009, 25, 1275-1288.	1.3	2
4486	Dynamic culture of droplet-confined cell arrays. <i>Biotechnology Progress</i> , 2010, 26, 220-231.	1.3	6
4487	Use of microarray hybridization to identify <i>Brugia</i> genes involved in mosquito infectivity. <i>Parasitology Research</i> , 2009, 106, 227-235.	0.6	9
4488	Isolation and characterization of conserved non-coding sequences among rice (<i>Oryza sativa</i> L.) paralogous regions. <i>Molecular Genetics and Genomics</i> , 2009, 281, 11-18.	1.0	9
4489	Analysis and comparison of a set of expressed sequence tags of the parthenogenetic water flea <i>Daphnia carinata</i> . <i>Molecular Genetics and Genomics</i> , 2009, 282, 197-203.	1.0	25
4490	Identification of common genetic variants that account for transcript isoform variation between human populations. <i>Human Genetics</i> , 2009, 125, 81-93.	1.8	75
4491	Strategies and issues in the detection of pathway enrichment in genome-wide association studies. <i>Human Genetics</i> , 2009, 126, 289-301.	1.8	112
4492	Analytical methods for inferring functional effects of single base pair substitutions in human cancers. <i>Human Genetics</i> , 2009, 126, 481-498.	1.8	19
4493	In vitro multipotent differentiation and barrier function of a human mammary epithelium. <i>Cell and Tissue Research</i> , 2009, 335, 383-395.	1.5	29
4494	Functional Annotation and Analysis of Expressed Sequence Tags from the Hepatopancreas of Mitten Crab (<i>Eriocheir sinensis</i>). <i>Marine Biotechnology</i> , 2009, 11, 317-326.	1.1	68
4495	Identification of Genes Involved in Immune Response, Microsatellite, and SNP Markers from Expressed Sequence Tags Generated from Hemocytes of Freshwater Pearl Mussel (<i>Hyriopsis cumingii</i>). <i>Marine Biotechnology</i> , 2009, 11, 520-530.	1.1	38
4496	Stress-related genes define essential steps in the response of maize seedlings to smoke-water. <i>Functional and Integrative Genomics</i> , 2009, 9, 231-242.	1.4	29
4497	Membrane transporters and carbon metabolism implicated in chloride homeostasis differentiate salt stress responses in tolerant and sensitive Citrus rootstocks. <i>Functional and Integrative Genomics</i> , 2009, 9, 293-309.	1.4	80
4498	Transcriptome pathways unique to dehydration tolerant relatives of modern wheat. <i>Functional and Integrative Genomics</i> , 2009, 9, 377-396.	1.4	130
4499	Aligning the proteome and genome of the silkworm, <i>Bombyx mori</i> . <i>Functional and Integrative Genomics</i> , 2009, 9, 447-454.	1.4	1
4500	Porcine muscle sensory attributes associate with major changes in gene networks involving CAPZB, ANKRD1, and CTBP2. <i>Functional and Integrative Genomics</i> , 2009, 9, 455-471.	1.4	39
4501	Identifying protein interactions with metal-modified DNA using microarray technology. <i>Journal of Biological Inorganic Chemistry</i> , 2009, 14, 193-199.	1.1	10
4502	Full-Length Enriched cDNA Library Construction from Tissues Related to Energy Metabolism in Pigs. <i>Molecules and Cells</i> , 2009, 28, 529-536.	1.0	7

#	ARTICLE	IF	CITATIONS
4503	Variation in host specificity and gene content in strains from genetically isolated lineages of the ectomycorrhizal fungus <i>Paxillus involutus</i> s. lat.. <i>Mycorrhiza</i> , 2009, 19, 549-558.	1.3	14
4504	Gene expression profile in colon cancer cells with respect to XIAP expression status. <i>International Journal of Colorectal Disease</i> , 2009, 24, 245-260.	1.0	11
4505	Analysis of expression pathways alterations of <i>Arabidopsis thaliana</i> induced by a Necrosis- and Ethylene-inducing protein. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009, 388, 4515-4522.	1.2	0
4506	Mechanisms of cytotoxicity of nickel ions based on gene expression profiles. <i>Biomaterials</i> , 2009, 30, 141-148.	5.7	166
4507	Efficient mining of multilevel gene association rules from microarray and gene ontology. <i>Information Systems Frontiers</i> , 2009, 11, 433-447.	4.1	10
4508	Integrative connectionist learning systems inspired by nature: current models, future trends and challenges. <i>Natural Computing</i> , 2009, 8, 199-218.	1.8	30
4509	An in silico strategy identified the target gene candidates regulated by dehydration responsive element binding proteins (DREBs) in <i>Arabidopsis</i> genome. <i>Plant Molecular Biology</i> , 2009, 69, 167-178.	2.0	7
4510	Genome-wide targeted prediction of ABA responsive genes in rice based on over-represented cis-motif in co-expressed genes. <i>Plant Molecular Biology</i> , 2009, 69, 261-271.	2.0	48
4511	Improved prediction of malaria degradomes by supervised learning with SVM and profile kernel. <i>Genetica</i> , 2009, 136, 189-209.	0.5	31
4512	Microarray analysis of altered gene expression in ER α -overexpressing HEK293 cells. <i>Endocrine</i> , 2009, 36, 224-232.	1.1	23
4513	Differential gene expression in the developing human macula: microarray analysis using rare tissue samples. <i>Journal of Ocular Biology, Diseases, and Informatics</i> , 2009, 2, 176-189.	0.2	8
4514	Transcriptional profiling of hematopoietic stem cells by high-throughput sequencing. <i>International Journal of Hematology</i> , 2009, 89, 24-33.	0.7	8
4515	Differential proteomic analysis of developmental stages of <i>Acca sellowiana</i> somatic embryos. <i>Acta Physiologiae Plantarum</i> , 2009, 31, 501-514.	1.0	20
4516	The effect of trans-10, cis-12 conjugated linoleic acid on gene expression profiles related to lipid metabolism in human intestinal-like Caco-2 cells. <i>Genes and Nutrition</i> , 2009, 4, 103-112.	1.2	8
4517	Effect of the quality of the interaction data on predicting protein function from protein-protein interactions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2009, 1, 40-45.	2.2	2
4518	Towards a proteome signature for invasive ductal breast carcinoma derived from label-free nanoscale LC-MS protein expression profiling of tumorous and glandular tissue. <i>Analytical and Bioanalytical Chemistry</i> , 2009, 395, 2443-2456.	1.9	31
4519	Mouse, man, and meaning: bridging the semantics of mouse phenotype and human disease. <i>Mammalian Genome</i> , 2009, 20, 457-461.	1.0	21
4520	ANEXdb: an integrated animal ANnotation and microarray EXpression database. <i>Mammalian Genome</i> , 2009, 20, 768-777.	1.0	28

#	ARTICLE	IF	CITATIONS
4521	The Contribution of Transposable Elements to Expressed Coding Sequence in <i>Arabidopsis thaliana</i> . <i>Journal of Molecular Evolution</i> , 2009, 68, 80-89.	0.8	68
4522	Low Contents of Carbon and Nitrogen in Highly Abundant Proteins: Evidence of Selection for the Economy of Atomic Composition. <i>Journal of Molecular Evolution</i> , 2009, 68, 248-255.	0.8	15
4523	Comprehensive and quantitative analysis of yeast deletion mutants defective in apical and isotropic bud growth. <i>Current Genetics</i> , 2009, 55, 365-380.	0.8	50
4524	PPF: Automated prediction of gene ontology functional annotations with confidence scores using protein sequence data. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 566-582.	1.5	105
4525	Cell cycle kinases predicted from conserved biophysical properties. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 655-668.	1.5	2
4526	Assessment of ligand binding residue predictions in CASP8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 138-146.	1.5	36
4527	Differentiation of a Highly Tumorigenic Basal Cell Compartment in Urothelial Carcinoma. <i>Stem Cells</i> , 2009, 27, 1487-1495.	1.4	117
4528	Kidney modeling and systems physiology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2009, 1, 172-190.	6.6	26
4529	Comparative proteomic analysis of <i>Rhodosporidium toruloides</i> during lipid accumulation. <i>Yeast</i> , 2009, 26, 553-566.	0.8	72
4530	Investigating sample pooling strategies for DIGE experiments to address biological variability. <i>Proteomics</i> , 2009, 9, 388-397.	1.3	127
4531	Dissecting the human plasma proteome and inflammatory response biomarkers. <i>Proteomics</i> , 2009, 9, 470-484.	1.3	20
4532	Recent developments in public proteomic MS repositories and pipelines. <i>Proteomics</i> , 2009, 9, 861-881.	1.3	42
4533	PPI spider: A tool for the interpretation of proteomics data in the context of protein-protein interaction networks. <i>Proteomics</i> , 2009, 9, 2740-2749.	1.3	63
4534	Nanozeolite-driven approach for enrichment of secretory proteins in human hepatocellular carcinoma cells. <i>Proteomics</i> , 2009, 9, 4881-4888.	1.3	20
4535	Quantitative analysis of phosphopeptides in search of the disease biomarker from the hepatocellular carcinoma specimen. <i>Proteomics</i> , 2009, 9, 3395-3408.	1.3	53
4536	The properties of hub proteins in a yeast aggregated cell cycle network and its phase sub-networks. <i>Proteomics</i> , 2009, 9, 4812-4824.	1.3	10
4537	Proteomic analysis of mitochondria from <i>Caenorhabditis elegans</i> . <i>Proteomics</i> , 2009, 9, 4539-4553.	1.3	57
4538	Proteomics data repositories. <i>Proteomics</i> , 2009, 9, 4653-4663.	1.3	39

#	ARTICLE	IF	CITATIONS
4539	Systematic prediction of human membrane receptor interactions. <i>Proteomics</i> , 2009, 9, 5243-5255.	1.3	22
4540	Towards the mammalian interactome: Inference of a core mammalian interaction set in mouse. <i>Proteomics</i> , 2009, 9, 5256-5266.	1.3	17
4541	Identification and characterization of novel ERCC55 interacting proteins: Evidence for the existence of several ERCC55 splicing variants; including the cytosolic ERCC55. <i>Proteomics</i> , 2009, 9, 5267-5287.	1.3	16
4542	Gram-positive bacteria produce membrane vesicles: Proteomics-based characterization of <i>Staphylococcus aureus</i> -derived membrane vesicles. <i>Proteomics</i> , 2009, 9, 5425-5436.	1.3	532
4543	Localized network centrality and essentiality in the yeast protein interaction network. <i>Proteomics</i> , 2009, 9, 5143-5154.	1.3	36
4544	Cholinergic switch associated with morphological differentiation in neuroblastoma. <i>Journal of Pathology</i> , 2009, 219, 463-472.	2.1	26
4545	Proteomics analysis of liver pathological calcification suggests a role for the IQ motif containing GTPase activating protein 1 in myofibroblast function. <i>Proteomics - Clinical Applications</i> , 2009, 3, 307-321.	0.8	3
4546	The proteome of the human breast cancer cell line MDA-MB-231: Analysis by LTQ-Orbitrap mass spectrometry. <i>Proteomics - Clinical Applications</i> , 2009, 3, 41-50.	0.8	11
4547	Comparative proteomic analysis of differentially expressed proteins in an <i>in vitro</i> cellular carcinogenesis model of oral squamous cell carcinoma. <i>Proteomics - Clinical Applications</i> , 2009, 3, 322-337.	0.8	7
4548	Quantitative proteomic analysis of ovarian cancer cells identified mitochondrial proteins associated with paclitaxel resistance. <i>Proteomics - Clinical Applications</i> , 2009, 3, 1288-1295.	0.8	21
4549	Structure and function of <i>Pseudomonas aeruginosa</i> protein PA1324 (21kDa). <i>Protein Science</i> , 2009, 18, 606-618.	3.1	13
4550	Identification of secreted glycoproteins of human prostate and bladder stromal cells by comparative quantitative proteomics. <i>Prostate</i> , 2009, 69, 49-61.	1.2	24
4551	Construction of an adult barnacle (<i>Balanus amphitrite</i>) cDNA library and selection of reference genes for quantitative RT-PCR studies. <i>BMC Molecular Biology</i> , 2009, 10, 62.	3.0	30
4552	Mapping the human membrane proteome: a majority of the human membrane proteins can be classified according to function and evolutionary origin. <i>BMC Biology</i> , 2009, 7, 50.	1.7	497
4553	GRIP: A web-based system for constructing Gold Standard datasets for protein-protein interaction prediction. <i>Source Code for Biology and Medicine</i> , 2009, 4, 2.	1.7	24
4554	HAMSTER: visualizing microarray experiments as a set of minimum spanning trees. <i>Source Code for Biology and Medicine</i> , 2009, 4, 8.	1.7	0
4555	Correlation of microRNA levels during hypoxia with predicted target mRNAs through genome-wide microarray analysis. <i>BMC Medical Genomics</i> , 2009, 2, 15.	0.7	65
4556	Integrated analysis of DNA methylation and gene expression reveals specific signaling pathways associated with platinum resistance in ovarian cancer. <i>BMC Medical Genomics</i> , 2009, 2, 34.	0.7	192

#	ARTICLE	IF	CITATIONS
4557	Muscle Research and Gene Ontology: New standards for improved data integration. BMC Medical Genomics, 2009, 2, 6.	0.7	16
4558	Identifying significant genetic regulatory networks in the prostate cancer from microarray data based on transcription factor analysis and conditional independency. BMC Medical Genomics, 2009, 2, 70.	0.7	41
4559	3PFDB - A database of Best Representative PSSM Profiles (BRPs) of Protein Families generated using a novel data mining approach. BioData Mining, 2009, 2, 8.	2.2	8
4560	Sequencing over 13â€Œ000 expressed sequence tags from six subtractive cDNA libraries of wild and modern wheats following slow drought stress. Plant, Cell and Environment, 2009, 32, 220-236.	2.8	86
4561	Differential Gene Expression in CD45 ⁺ Cells at Paraâ€œortic Foci Stage of Chicken Haematopoiesis. Scandinavian Journal of Immunology, 2009, 70, 288-294.	1.3	7
4562	Hormonal regulation of temperatureâ€œinduced growth in Arabidopsis. Plant Journal, 2009, 60, 589-601.	2.8	271
4563	The <i>Aedes aegypti</i> larval transcriptome: a comparative perspective with emphasis on trypsins and the domain structure of peritrophins. Insect Molecular Biology, 2009, 18, 33-44.	1.0	65
4564	Transcriptional profiling of the sperm storage organs of <i>Drosophila melanogaster</i> . Insect Molecular Biology, 2009, 18, 465-475.	1.0	70
4565	Shotgun proteomics approach to characterizing the embryonic proteome of the silkworm, <i>Bombyx mori</i> , at labrum appearance stage. Insect Molecular Biology, 2009, 18, 649-660.	1.0	20
4566	Sugar sweet springtails: on the transcriptional response of <i>Folsomia candida</i> (Collembola) to desiccation stress. Insect Molecular Biology, 2009, 18, 737-746.	1.0	34
4567	Back to basics â€œ how the evolution of the extracellular matrix underpinned vertebrate evolution. International Journal of Experimental Pathology, 2009, 90, 95-100.	0.6	24
4568	A pilot study to evaluate gene expression profiles in peripheral blood mononuclear cells (PBMCs) from children with GH deficiency and Turner syndrome in response to GH treatment. Clinical Endocrinology, 2009, 70, 429-434.	1.2	24
4569	Genomic reaction norms: using integrative biology to understand molecular mechanisms of phenotypic plasticity. Molecular Ecology, 2009, 18, 3763-3780.	2.0	297
4570	<i>Cryptococcus neoformans</i> Siteâ€œ2 protease is required for virulence and survival in the presence of azole drugs. Molecular Microbiology, 2009, 74, 672-690.	1.2	56
4571	Functional annotation of expressed sequence tags as a tool to understand the molecular mechanism controlling flower bud development in tree peony. Physiologia Plantarum, 2009, 135, 436-449.	2.6	20
4572	Retroviral vector integration in post-transplant hematopoiesis in mice conditioned with either submyeloablative or ablative irradiation. Gene Therapy, 2009, 16, 1452-1464.	2.3	9
4573	All dosage compensation is local: Gene-by-gene regulation of sex-biased expression on the chicken Z chromosome. Heredity, 2009, 102, 312-320.	1.2	125
4574	Body size in <i>Drosophila</i> : genetic architecture, allometries and sexual dimorphism. Heredity, 2009, 102, 246-256.	1.2	31

#	ARTICLE	IF	CITATIONS
4575	Hypoxia response and VEGF-A expression in human proximal tubular epithelial cells in stable and progressive renal disease. <i>Laboratory Investigation</i> , 2009, 89, 337-346.	1.7	95
4576	Sepsis induces extensive autophagic vacuolization in hepatocytes: a clinical and laboratory-based study. <i>Laboratory Investigation</i> , 2009, 89, 549-561.	1.7	128
4577	Proteome-wide cellular protein concentrations of the human pathogen <i>Leptospira interrogans</i> . <i>Nature</i> , 2009, 460, 762-765.	13.7	402
4578	Dynamic modularity in protein interaction networks predicts breast cancer outcome. <i>Nature Biotechnology</i> , 2009, 27, 199-204.	9.4	654
4579	How to visually interpret biological data using networks. <i>Nature Biotechnology</i> , 2009, 27, 921-924.	9.4	93
4580	Missing in action: enzyme functional annotations in biological databases. <i>Nature Chemical Biology</i> , 2009, 5, 521-525.	3.9	53
4581	Gene expression divergence in yeast is coupled to evolution of DNA-encoded nucleosome organization. <i>Nature Genetics</i> , 2009, 41, 438-445.	9.4	132
4582	Validation of candidate causal genes for obesity that affect shared metabolic pathways and networks. <i>Nature Genetics</i> , 2009, 41, 415-423.	9.4	257
4583	RNAiCut: automated detection of significant genes from functional genomic screens. <i>Nature Methods</i> , 2009, 6, 476-477.	9.0	24
4584	A general pipeline for quality and statistical assessment of protein interaction data using R and Bioconductor. <i>Nature Protocols</i> , 2009, 4, 535-546.	5.5	15
4585	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <i>Nature Protocols</i> , 2009, 4, 698-705.	5.5	769
4586	Polycomb group proteins: navigators of lineage pathways led astray in cancer. <i>Nature Reviews Cancer</i> , 2009, 9, 773-784.	12.8	537
4587	Genotype-phenotype databases: challenges and solutions for the post-genomic era. <i>Nature Reviews Genetics</i> , 2009, 10, 9-18.	7.7	87
4588	A census of human transcription factors: function, expression and evolution. <i>Nature Reviews Genetics</i> , 2009, 10, 252-263.	7.7	1,357
4589	ChIP-seq: advantages and challenges of a maturing technology. <i>Nature Reviews Genetics</i> , 2009, 10, 669-680.	7.7	1,728
4590	Individualized therapy in non-small-cell lung cancer: future versus current clinical practice. <i>Oncogene</i> , 2009, 28, S38-S45.	2.6	28
4591	Nonparametric Testing for DNA Copy Number Induced Differential mRNA Gene Expression. <i>Biometrics</i> , 2009, 65, 19-29.	0.8	43
4592	Computational and experimental approaches to chart the <i>Escherichia coli</i> cell-envelope-associated proteome and interactome. <i>FEMS Microbiology Reviews</i> , 2009, 33, 66-97.	3.9	53

#	ARTICLE	IF	CITATIONS
4593	Genome-scale models of bacterial metabolism: reconstruction and applications. <i>FEMS Microbiology Reviews</i> , 2009, 33, 164-190.	3.9	268
4594	Hypoxia induces erythroid-specific 5-aminolevulinic synthase expression in human erythroid cells through transforming growth factor- β^2 signaling. <i>FEBS Journal</i> , 2009, 276, 1370-1382.	2.2	13
4595	Mutation of epidermal growth factor receptor is associated with MIG6 expression. <i>FEBS Journal</i> , 2009, 276, 5239-5251.	2.2	24
4596	Dynamics of global gene expression changes during brain metastasis formation. <i>Neuropathology</i> , 2009, 29, 389-397.	0.7	5
4597	HP05- $\frac{1}{2}$ *THE PROTEOME OF MESENTERIC LYMPH DURING ACUTE PANCREATITIS AND IMPLICATIONS FOR TREATMENT. <i>ANZ Journal of Surgery</i> , 2009, 79, A39-A40.	0.3	9
4598	Immunogenic males: a genome-wide analysis of reproduction and the cost of mating in <i>Drosophila melanogaster</i> females. <i>Journal of Evolutionary Biology</i> , 2009, 22, 964-973.	0.8	73
4599	Fenton chemistry and oxidative stress mediate the toxicity of the β^2 -amyloid peptide in a <i>Drosophila</i> model of Alzheimer's disease. <i>European Journal of Neuroscience</i> , 2009, 29, 1335-1347.	1.2	159
4600	Proteomics-inferred genome typing (PIGT) demonstrates inter-population recombination as a strategy for environmental adaptation. <i>Environmental Microbiology</i> , 2009, 11, 313-325.	1.8	59
4601	Ranking Genes by Their Co-expression to Subsets of Pathway Members. <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 1-13.	1.8	11
4602	A Probabilistic Graph-Theoretic Approach to Integrate Multiple Predictions for the Protein-Protein Subnetwork Prediction Challenge. <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 224-233.	1.8	20
4603	Gene Expression Profiling Related to Anti-inflammatory Properties of Curcumin in K562 Leukemia Cells. <i>Annals of the New York Academy of Sciences</i> , 2009, 1171, 391-398.	1.8	37
4604	Analysis of Gene Expression in Parkinson's Disease: Possible Involvement of Neurotrophic Support and Axon Guidance in Dopaminergic Cell Death. <i>Brain Pathology</i> , 2009, 19, 91-107.	2.1	159
4605	Gene Expression Analysis of Tuberous Sclerosis Complex Cortical Tubers Reveals Increased Expression of Adhesion and Inflammatory Factors. <i>Brain Pathology</i> , 2010, 20, 704-719.	2.1	132
4606	The Human Ageing Genomic Resources: online databases and tools for biogerontologists. <i>Aging Cell</i> , 2009, 8, 65-72.	3.0	173
4607	Transcriptome analysis of <i>Medicago truncatula</i> leaf senescence: similarities and differences in metabolic and transcriptional regulations as compared with <i>Arabidopsis</i> , nodule senescence and nitric oxide signalling. <i>New Phytologist</i> , 2009, 181, 563-575.	3.5	52
4608	The <i>Populus</i> Genome Integrative Explorer (PopGenIE): a new resource for exploring the <i>Populus</i> genome. <i>New Phytologist</i> , 2009, 182, 1013-1025.	3.5	208
4609	A combined database related and de novo MS-identification of yeast mannose-1-phosphate guanyltransferase PSA1 interaction partners at different phases of batch cultivation. <i>International Journal of Mass Spectrometry</i> , 2009, 281, 126-133.	0.7	2
4610	Comparison of dorsal root ganglion gene expression in rat models of traumatic and HIV-associated neuropathic pain. <i>European Journal of Pain</i> , 2009, 13, 387-398.	1.4	83

#	ARTICLE	IF	CITATIONS
4611	Ontology driven semantic profiling and retrieval in medical information systems. <i>Web Semantics</i> , 2009, 7, 317-331.	2.2	39
4612	A 454 sequencing approach for large scale phylogenomic analysis of the common emperor scorpion (<i>Pandinus imperator</i>). <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 826-834.	1.2	87
4613	Impact of environmental and genetic factors on expression of maize gene classes: Relevance to grain composition. <i>Journal of Food Composition and Analysis</i> , 2009, 22, 158-164.	1.9	4
4614	Learning decision trees with taxonomy of propositionalized attributes. <i>Pattern Recognition</i> , 2009, 42, 84-92.	5.1	16
4616	A portal for rhizobial genomes: RhizoGATE integrates a <i>Sinorhizobium meliloti</i> genome annotation update with postgenome data. <i>Journal of Biotechnology</i> , 2009, 140, 45-50.	1.9	38
4617	The Sequence Analysis and Management System "SAMS-2.0: Data management and sequence analysis adapted to changing requirements from traditional sanger sequencing to ultrafast sequencing technologies. <i>Journal of Biotechnology</i> , 2009, 140, 3-12.	1.9	37
4618	Low temperature restoring effect on F508del-CFTR misprocessing: A proteomic approach. <i>Journal of Proteomics</i> , 2009, 73, 218-230.	1.2	29
4619	Basic networks: Definition and applications. <i>Journal of Theoretical Biology</i> , 2009, 258, 53-59.	0.8	1
4620	Robust ANOVA for microarray data. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2009, 98, 38-44.	1.8	14
4621	Profiling of molecular pathways regulated by microRNA 601. <i>Computational Biology and Chemistry</i> , 2009, 33, 429-433.	1.1	25
4622	PCHM: A bioinformatic resource for high-throughput human mitochondrial proteome searching and comparison. <i>Computers in Biology and Medicine</i> , 2009, 39, 689-696.	3.9	3
4623	Evaluation of two cell surface modification methods for proteomic analysis of plasma membrane from isolated mouse hepatocytes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 32-41.	1.1	14
4624	Know your limits: Assumptions, constraints and interpretation in systems biology. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 1280-1287.	1.1	7
4625	Modelling with knowledge: A review of emerging semantic approaches to environmental modelling. <i>Environmental Modelling and Software</i> , 2009, 24, 577-587.	1.9	109
4626	An expert system to identify transcription factor binding target genes by phylogenetic footprinting. <i>Expert Systems With Applications</i> , 2009, 36, 4923-4928.	4.4	0
4627	The Phagosomal Proteome in Interferon- γ -Activated Macrophages. <i>Immunity</i> , 2009, 30, 143-154.	6.6	206
4628	Exploiting noun phrases and semantic relationships for text document clustering. <i>Information Sciences</i> , 2009, 179, 2249-2262.	4.0	74
4629	Predicting protein subnuclear localization using CO-amino-acid composition features. <i>BioSystems</i> , 2009, 98, 73-79.	0.9	34

#	ARTICLE	IF	CITATIONS
4630	Identification of proteases and their types. <i>Analytical Biochemistry</i> , 2009, 385, 153-160.	1.1	66
4631	Proteome analysis of a single zebrafish embryo using three different digestion strategies coupled with liquid chromatography-tandem mass spectrometry. <i>Analytical Biochemistry</i> , 2009, 394, 177-185.	1.1	25
4632	A top-down approach to enhance the power of predicting human protein subcellular localization: Hum-mPloc 2.0. <i>Analytical Biochemistry</i> , 2009, 394, 269-274.	1.1	158
4633	Recovering context-specific gene network modules from expression data: A brief review. <i>Frontiers of Biology in China: Selected Publications From Chinese Universities</i> , 2009, 4, 414-418.	0.2	1
4634	Differential gene expression profiling in mucus glands of honey bee (<i>Apis mellifera</i>) drones during sexual maturation. <i>Apidologie</i> , 2009, 40, 481-495.	0.9	17
4635	Meta-analysis of age-related gene expression profiles identifies common signatures of aging. <i>Bioinformatics</i> , 2009, 25, 875-881.	1.8	651
4636	Systems-level approaches for identifying and analyzing genetic interaction networks in <i>Escherichia coli</i> and extensions to other prokaryotes. <i>Molecular BioSystems</i> , 2009, 5, 1439.	2.9	29
4637	Sampling the Waterhemp (<i>Amaranthus tuberculatus</i>) Genome Using Pyrosequencing Technology. <i>Weed Science</i> , 2009, 57, 463-469.	0.8	53
4638	Mechanism of Auxin-Regulated Gene Expression in Plants. <i>Annual Review of Genetics</i> , 2009, 43, 265-285.	3.2	602
4639	Integrating Proteomic, Transcriptional, and Interactome Data Reveals Hidden Components of Signaling and Regulatory Networks. <i>Science Signaling</i> , 2009, 2, ra40.	1.6	161
4640	System-Wide Changes to SUMO Modifications in Response to Heat Shock. <i>Science Signaling</i> , 2009, 2, ra24.	1.6	415
4641	Strategic Reading, Ontologies, and the Future of Scientific Publishing. <i>Science</i> , 2009, 325, 828-832.	6.0	142
4642	Functional Profiling Methods in Cancer. <i>Methods in Molecular Biology</i> , 2009, 576, 363-374.	0.4	2
4643	Improving detection of differentially expressed gene sets by applying cluster enrichment analysis to Gene Ontology. <i>BMC Bioinformatics</i> , 2009, 10, 240.	1.2	13
4644	The Silkworm Z Chromosome Is Enriched in Testis-Specific Genes. <i>Genetics</i> , 2009, 182, 493-501.	1.2	90
4645	A Genome-wide Survey of the Prevalence and Evolutionary Forces Acting on Human Nonsense SNPs. <i>American Journal of Human Genetics</i> , 2009, 84, 224-234.	2.6	69
4646	Diverse Genome-wide Association Studies Associate the IL12/IL23 Pathway with Crohn Disease. <i>American Journal of Human Genetics</i> , 2009, 84, 399-405.	2.6	246
4647	Clinical Diagnostics in Human Genetics with Semantic Similarity Searches in Ontologies. <i>American Journal of Human Genetics</i> , 2009, 85, 457-464.	2.6	444

#	ARTICLE	IF	CITATIONS
4648	The Biological Coherence of Human Phenome Databases. American Journal of Human Genetics, 2009, 85, 801-808.	2.6	37
4649	Prediction of functionally related proteins by comparative genomics in silico. Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry, 2009, 3, 323-334.	0.2	1
4650	The interactome: Predicting the protein-protein interactions in cells. Cellular and Molecular Biology Letters, 2009, 14, 1-22.	2.7	36
4651	Plant developmental genetics: Integrating data from different experiments in databases. Russian Journal of Genetics, 2009, 45, 1302-1316.	0.2	0
4652	Exploration of homodimer receptor: homodimer protein interactions. International Journal of Bioinformatics Research and Applications, 2009, 5, 447.	0.1	2
4653	Improved Membrane Proteomics Coverage of Human Embryonic Stem Cells by Peptide IPG-IEF. Journal of Proteome Research, 2009, 8, 5642-5649.	1.8	30
4654	NOPdb: Nucleolar Proteome Database--2008 update. Nucleic Acids Research, 2009, 37, D181-D184.	6.5	243
4655	Stable Isotope Labeling and Label-Free Proteomics of <i>Drosophila parkin</i> Null Mutants. Journal of Proteome Research, 2009, 8, 4500-4510.	1.8	17
4656	Proteomic and Bioinformatic Analysis on Endocrine Organs of Domesticated Silkworm, <i>Bombyx mori</i> L. for a Comprehensive Understanding of Their Roles and Relations. Journal of Proteome Research, 2009, 8, 2620-2632.	1.8	36
4657	Next-generation tag sequencing for cancer gene expression profiling. Genome Research, 2009, 19, 1825-1835.	2.4	306
4658	Notice of Violation of IEEE Publication Principles - Systematically Identifying Genes and Pathways in Multiple Cancer Types Using HGD & PSO-SVM. , 2009, , .		2
4659	Large-Scale Analysis of Thermostable, Mammalian Proteins Provides Insights into the Intrinsically Disordered Proteome. Journal of Proteome Research, 2009, 8, 211-226.	1.8	76
4660	Comparative Interactomics: Analysis of <i>Arabidopsis</i> 14-3-3 Complexes Reveals Highly Conserved 14-3-3 Interactions between Humans and Plants. Journal of Proteome Research, 2009, 8, 1913-1924.	1.8	38
4661	Proteomic Study of Human Glioblastoma Multiforme Tissue Employing Complementary Two-Dimensional Liquid Chromatography- and Mass Spectrometry-Based Approaches. Journal of Proteome Research, 2009, 8, 4604-4614.	1.8	28
4662	A dependency graph approach for the analysis of differential gene expression profiles. Molecular BioSystems, 2009, 5, 1720.	2.9	27
4663	Insight into the Sialome of the Black Fly, <i>Simulium vittatum</i> . Journal of Proteome Research, 2009, 8, 1474-1488.	1.8	49
4664	MUI: A New Functional Similarity Measure for Gene Products Based on Gene Ontology. , 2009, , .		0
4665	Ligand Prediction for Orphan Targets Using Support Vector Machines and Various Target-Ligand Kernels Is Dominated by Nearest Neighbor Effects. Journal of Chemical Information and Modeling, 2009, 49, 2155-2167.	2.5	63

#	ARTICLE	IF	CITATIONS
4666	The Bologna Annotation Resource: a Non Hierarchical Method for the Functional and Structural Annotation of Protein Sequences Relying on a Comparative Large-Scale Genome Analysis. <i>Journal of Proteome Research</i> , 2009, 8, 4362-4371.	1.8	9
4667	Identification of candidate genes affecting δ^9 -tetrahydrocannabinol biosynthesis in <i>Cannabis sativa</i> . <i>Journal of Experimental Botany</i> , 2009, 60, 3715-3726.	2.4	130
4668	Proteomic Analysis of Naphthalene-Induced Airway Epithelial Injury and Repair in a Cystic Fibrosis Mouse Model. <i>Journal of Proteome Research</i> , 2009, 8, 3606-3616.	1.8	24
4669	Fishing the Target of Antitubercular Compounds: <i>In Silico</i> Target Deconvolution Model Development and Validation. <i>Journal of Proteome Research</i> , 2009, 8, 2788-2798.	1.8	27
4670	Identifying Protein Complexes Using Hybrid Properties. <i>Journal of Proteome Research</i> , 2009, 8, 5212-5218.	1.8	27
4671	Large Quasi-Tree Drawing: A Neighborhood Based Approach. , 2009, , .		2
4672	Constructing Yeast Phenotypic Gene Network Using Morphological Inclusion Relations. , 2009, , .		0
4673	PLIPS, an Automatically Collected Database of Protein Lists Reported by Proteomics Studies. <i>Journal of Proteome Research</i> , 2009, 8, 1193-1197.	1.8	10
4674	Classification of Information Fusion Methods in Systems Biology. <i>In Silico Biology</i> , 2009, 9, 65-76.	0.4	8
4675	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
4676	Essential Core of Protein-Protein Interaction Network in <i>Escherichia coli</i> . <i>Journal of Proteome Research</i> , 2009, 8, 1925-1931.	1.8	30
4677	RDF, Jena, SparQL and the 'Semantic Web'. , 2009, , .		28
4678	Computer Networks. <i>Communications in Computer and Information Science</i> , 2009, , .	0.4	0
4679	Metadata and Semantic Research. <i>Communications in Computer and Information Science</i> , 2009, , .	0.4	0
4680	Uncovering the evolutionary history of innate immunity: The simple metazoan <i>Hydra</i> uses epithelial cells for host defence. <i>Developmental and Comparative Immunology</i> , 2009, 33, 559-569.	1.0	195
4681	A Yeast Killer Toxin Screen Provides Insights into A/B Toxin Entry, Trafficking, and Killing Mechanisms. <i>Developmental Cell</i> , 2009, 17, 552-560.	3.1	68
4682	Annotation of stress-response proteins in the aspergilli. <i>Fungal Genetics and Biology</i> , 2009, 46, S105-S120.	0.9	76
4683	The 2008 update of the <i>Aspergillus nidulans</i> genome annotation: A community effort. <i>Fungal Genetics and Biology</i> , 2009, 46, S2-S13.	0.9	99

#	ARTICLE	IF	CITATIONS
4684	ReproArrayGTS: A cDNA microarray for identification of reproduction-related genes in the giant tiger shrimp <i>Penaeus monodon</i> and characterization of a novel nuclear autoantigenic sperm protein (NASP) gene. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 90-99.	0.4	29
4685	Bioinformatic analysis of expressed sequence tags from grass shrimp <i>Palaemonetes pugio</i> exposed to environmental stressors. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 187-195.	0.4	11
4686	Gene expression profile of grass shrimp <i>Palaemonetes pugio</i> exposed to chronic hypoxia. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 196-208.	0.4	26
4687	Chasing relationships between nutrition and reproduction: A comparative transcriptome analysis of hepatopancreas and testis from <i>Eriocheir sinensis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 227-234.	0.4	42
4688	Quantitative Proteomics Reveals the Function of Unconventional Ubiquitin Chains in Proteasomal Degradation. <i>Cell</i> , 2009, 137, 133-145.	13.5	948
4690	Profiling the Human Protein-DNA Interactome Reveals ERK2 as a Transcriptional Repressor of Interferon Signaling. <i>Cell</i> , 2009, 139, 610-622.	13.5	352
4691	The IFITM Proteins Mediate Cellular Resistance to Influenza A H1N1 Virus, West Nile Virus, and Dengue Virus. <i>Cell</i> , 2009, 139, 1243-1254.	13.5	1,111
4692	A Physical and Regulatory Map of Host-Influenza Interactions Reveals Pathways in H1N1 Infection. <i>Cell</i> , 2009, 139, 1255-1267.	13.5	593
4693	Proteome Differences between Brown and White Fat Mitochondria Reveal Specialized Metabolic Functions. <i>Cell Metabolism</i> , 2009, 10, 324-335.	7.2	205
4694	LOX-1 dependent overexpression of immunoglobulins in cardiomyocytes in response to angiotensin II. <i>Biochemical and Biophysical Research Communications</i> , 2009, 379, 395-399.	1.0	25
4695	Prediction of functionally important sites from protein sequences using sparse kernel least squares classifiers. <i>Biochemical and Biophysical Research Communications</i> , 2009, 384, 155-159.	1.0	6
4696	A graph model based study on regulatory impacts of transcription factors of <i>Drosophila melanogaster</i> and comparison across species. <i>Biochemical and Biophysical Research Communications</i> , 2009, 386, 559-562.	1.0	0
4697	Identification of gene networks associated with erythroid differentiation. <i>Blood Cells, Molecules, and Diseases</i> , 2009, 43, 74-80.	0.6	13
4698	Differential expression of genes encoding anti-oxidant enzymes in Sydney rock oysters, <i>Saccostrea glomerata</i> (Gould) selected for disease resistance. <i>Fish and Shellfish Immunology</i> , 2009, 26, 799-810.	1.6	60
4699	Identification of immune related genes in Atlantic halibut (<i>Hippoglossus hippoglossus</i> L.) following in vivo antigenic and in vitro mitogenic stimulation. <i>Fish and Shellfish Immunology</i> , 2009, 27, 729-738.	1.6	17
4700	Repetitive DNA elements, nucleosome binding and human gene expression. <i>Gene</i> , 2009, 436, 12-22.	1.0	32
4701	More radical amino acid replacements in primates than in rodents: Support for the evolutionary role of effective population size. <i>Gene</i> , 2009, 440, 50-56.	1.0	22
4702	Identification of expressed transposable element insertions in the sequenced genome of <i>Drosophila melanogaster</i> . <i>Gene</i> , 2009, 439, 55-62.	1.0	19

#	ARTICLE	IF	CITATIONS
4703	Gene Ontology for type III effectors: capturing processes at the host-pathogen interface. Trends in Microbiology, 2009, 17, 304-311.	3.5	11
4704	Controlled vocabularies for microbial virulence factors. Trends in Microbiology, 2009, 17, 279-285.	3.5	14
4705	Applying the Gene Ontology in microbial annotation. Trends in Microbiology, 2009, 17, 262-268.	3.5	17
4706	What we can learn about Escherichia coli through application of Gene Ontology. Trends in Microbiology, 2009, 17, 269-278.	3.5	16
4707	Functional annotations for the Saccharomyces cerevisiae genome: the knowns and the known unknowns. Trends in Microbiology, 2009, 17, 286-294.	3.5	49
4708	Describing commonalities in microbial effector delivery using the Gene Ontology. Trends in Microbiology, 2009, 17, 312-319.	3.5	5
4709	Viewing the microbial world through the lens of the Gene Ontology. Trends in Microbiology, 2009, 17, 259-261.	3.5	8
4710	Infection strategies of filamentous microbes described with the Gene Ontology. Trends in Microbiology, 2009, 17, 320-327.	3.5	9
4711	The spontaneously hypertensive rat model of ADHD – The importance of selecting the appropriate reference strain. Neuropharmacology, 2009, 57, 619-626.	2.0	176
4712	Epileptogenesis alters gene expression pattern in rats subjected to amygdala-dependent emotional learning. Neuroscience, 2009, 159, 468-482.	1.1	2
4713	Challenges in phenotype definition in the whole-genome era: multivariate models of memory and intelligence. Neuroscience, 2009, 164, 88-107.	1.1	51
4714	Regulation of mouse embryonic stem cell neural differentiation by retinoic acid. Developmental Biology, 2009, 328, 456-471.	0.9	82
4715	Evolution of early embryogenesis in rhabditid nematodes. Developmental Biology, 2009, 335, 253-262.	0.9	51
4716	Comparative analyses of distributions and functions of Z-DNA in Arabidopsis and rice. Genomics, 2009, 93, 383-391.	1.3	5
4717	Contrast features of CpG islands in the promoter and other regions in the dog genome. Genomics, 2009, 94, 117-124.	1.3	21
4718	Finding disease-specific coordinated functions by multi-function genes: Insight into the coordination mechanisms in diseases. Genomics, 2009, 94, 94-100.	1.3	17
4719	Expression levels of NF-Y target genes changed by CDKN1B correlate with clinical prognosis in multiple cancers. Genomics, 2009, 94, 219-227.	1.3	19
4720	Ontological discovery environment: A system for integrating gene-phenotype associations. Genomics, 2009, 94, 377-387.	1.3	35

#	ARTICLE	IF	CITATIONS
4721	High-resolution mapping of the protein interaction network for the human transcription machinery and affinity purification of RNA polymerase II-associated complexes. <i>Methods</i> , 2009, 48, 381-386.	1.9	77
4722	Integration of genetic and genomic methods for identification of genes and gene variants encoding QTLs in the nonhuman primate. <i>Methods</i> , 2009, 49, 63-69.	1.9	9
4723	Phenotypic expression of maternally inherited deafness is affected by RNA modification and cytoplasmic ribosomal proteins. <i>Molecular Genetics and Metabolism</i> , 2009, 97, 297-304.	0.5	9
4724	Dosage analysis of Z chromosome genes using microarray in silkworm, <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 315-321.	1.2	88
4725	The salivary transcriptome of <i>Anopheles gambiae</i> (Diptera: Culicidae) larvae: A microarray-based analysis. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 382-394.	1.2	29
4726	Proteomic analysis of <i>Drosophila mojavensis</i> male accessory glands suggests novel classes of seminal fluid proteins. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 366-371.	1.2	50
4727	An insight into the transcriptome and proteome of the salivary gland of the stable fly, <i>Stomoxys calcitrans</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 607-614.	1.2	31
4728	Expanded CAG repeats in the murine Huntington's disease gene increases neuronal differentiation of embryonic and neural stem cells. <i>Molecular and Cellular Neurosciences</i> , 2009, 40, 1-13.	1.0	24
4729	Identification of neuronal target genes for CCAAT/Enhancer Binding Proteins. <i>Molecular and Cellular Neurosciences</i> , 2009, 40, 313-327.	1.0	40
4730	Exploring transcriptional conservation between <i>Ancylostoma caninum</i> and <i>Haemonchus contortus</i> by oligonucleotide microarray and bioinformatic analyses. <i>Molecular and Cellular Probes</i> , 2009, 23, 1-9.	0.9	11
4731	Bioinformatic analysis of abundant, gender-enriched transcripts of adult <i>Ascaris suum</i> (Nematoda) using a semi-automated workflow platform. <i>Molecular and Cellular Probes</i> , 2009, 23, 205-217.	0.9	16
4732	A systems biology perspective on cholangiocellular carcinoma development: Focus on MAPK-signaling and the extracellular environment. <i>Journal of Hepatology</i> , 2009, 50, 1122-1131.	1.8	18
4733	Domain-Based and Family-Specific Sequence Identity Thresholds Increase the Levels of Reliable Protein Function Transfer. <i>Journal of Molecular Biology</i> , 2009, 387, 416-430.	2.0	98
4734	Identification of DNA-binding Proteins Using Structural, Electrostatic and Evolutionary Features. <i>Journal of Molecular Biology</i> , 2009, 387, 1040-1053.	2.0	75
4735	Structure and in Vivo Requirement of the Yeast Spt6 SH2 Domain. <i>Journal of Molecular Biology</i> , 2009, 389, 211-225.	2.0	47
4736	A Computationally Guided Protein-Interaction Screen Uncovers Coiled-Coil Interactions Involved in Vesicular Trafficking. <i>Journal of Molecular Biology</i> , 2009, 392, 228-241.	2.0	16
4737	Alternative to Homo-oligomerisation: The Creation of Local Symmetry in Proteins by Internal Amplification. <i>Journal of Molecular Biology</i> , 2009, 394, 522-534.	2.0	19
4738	Early kinetics of the transcriptional response of human leukocytes to staphylococcal superantigenic enterotoxins A and G. <i>Microbial Pathogenesis</i> , 2009, 47, 171-176.	1.3	9

#	ARTICLE	IF	CITATIONS
4739	Significant modulation of mitochondrial electron transport system by nicotine in various rat brain regions. <i>Mitochondrion</i> , 2009, 9, 186-195.	1.6	20
4740	Revealing Global Regulatory Perturbations across Human Cancers. <i>Molecular Cell</i> , 2009, 36, 900-911.	4.5	193
4741	Analysis of expressed sequence tags from body wall, intestine and respiratory tree of sea cucumber (<i>Apostichopus japonicus</i>). <i>Aquaculture</i> , 2009, 296, 193-199.	1.7	42
4742	The genomic transcriptional response of female fathead minnows (<i>Pimephales promelas</i>) to an acute exposure to the androgen, 17 β -trenbolone. <i>Aquatic Toxicology</i> , 2009, 91, 44-53.	1.9	43
4743	Animal Systems Biology: Towards a Systems View of Development in <i>C. Elegans</i> . , 0, , 137-165.		0
4744	Approaching <i>Drosophila</i> development through proteomic tools and databases: At the hub of the post-genomic era. <i>Mechanisms of Development</i> , 2009, 126, 761-770.	1.7	4
4745	Identification of Src tyrosine kinase substrates in platelet-derived growth factor receptor signaling. <i>Molecular Oncology</i> , 2009, 3, 439-450.	2.1	65
4746	Incorporating Biological Knowledge into Density-Based Clustering Analysis of Gene Expression Data. , 2009, , .		3
4747	Genomic Analyses of the Microsporidian <i>Nosema ceranae</i> , an Emergent Pathogen of Honey Bees. <i>PLoS Pathogens</i> , 2009, 5, e1000466.	2.1	194
4748	Proteomic Analysis of an $\alpha 7$ Nicotinic Acetylcholine Receptor Interactome. <i>Journal of Proteome Research</i> , 2009, 8, 1849-1858.	1.8	82
4749	Searching the Mouse Genome Informatics (MGI) Resources for Information on Mouse Biology from Genotype to Phenotype. <i>Current Protocols in Bioinformatics</i> , 2009, 25, Unit1.7.	25.8	21
4750	Online Tools for Predicting Integral Membrane Proteins. <i>Methods in Molecular Biology</i> , 2009, 528, 3-23.	0.4	8
4751	GeneDecks: Paralog Hunting and Gene-Set Distillation with GeneCards Annotation. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 477-487.	1.0	74
4752	BRNI: Modular analysis of transcriptional regulatory programs. <i>BMC Bioinformatics</i> , 2009, 10, 155.	1.2	6
4753	Knowledge driven decomposition of tumor expression profiles. <i>BMC Bioinformatics</i> , 2009, 10, S20.	1.2	2
4754	Interactive visualization of clusters in microarray data: an efficient tool for improved metabolic analysis of <i>E. coli</i> . <i>Microbial Cell Factories</i> , 2009, 8, 37.	1.9	5
4755	Open access to sequence: Browsing the <i>Pichia pastoris</i> genome. <i>Microbial Cell Factories</i> , 2009, 8, 53.	1.9	55
4756	Comprehensive proteomic analysis of human cervical-vaginal fluid using colposcopy samples. <i>Proteome Science</i> , 2009, 7, 17.	0.7	84

#	ARTICLE	IF	CITATIONS
4757	Mitochondrial proteomics on human fibroblasts for identification of metabolic imbalance and cellular stress. <i>Proteome Science</i> , 2009, 7, 20.	0.7	37
4758	GO Explorer: A gene-ontology tool to aid in the interpretation of shotgun proteomics data. <i>Proteome Science</i> , 2009, 7, 6.	0.7	35
4759	In vitro nuclear interactome of the HIV-1 Tat protein. <i>Retrovirology</i> , 2009, 6, 47.	0.9	86
4760	Rare peptide segments are found significantly more often in proto-oncoproteins than control proteins: implications for immunology and oncology. <i>Journal of the Royal Society Interface</i> , 2009, 6, 123-127.	1.5	7
4761	Genome and proteome annotation: organization, interpretation and integration. <i>Journal of the Royal Society Interface</i> , 2009, 6, 129-147.	1.5	45
4763	Application of Ontologies in Bioinformatics. , 2009, , 735-756.		10
4764	Knowledge Standardization in Evolutionary Biology: The Comparative Data Analysis Ontology. , 2009, , 195-214.		2
4765	Protein Networks and Pathway Analysis. <i>Methods in Molecular Biology</i> , 2009, 563, v-vii.	0.4	33
4766	From Protein Structure to Function with Bioinformatics. , 2009, , .		29
4767	The Functional Annotation of Mammalian Genomes: The Challenge of Phenotyping. <i>Annual Review of Genetics</i> , 2009, 43, 305-333.	3.2	60
4768	The Automation of Science. <i>Science</i> , 2009, 324, 85-89.	6.0	458
4769	Array MAPPIT: High-Throughput Interactome Analysis in Mammalian Cells. <i>Journal of Proteome Research</i> , 2009, 8, 877-886.	1.8	53
4770	Computational Systems Biology. <i>Methods in Molecular Biology</i> , 2009, , .	0.4	5
4771	Enzyme Function Prediction with Interpretable Models. <i>Methods in Molecular Biology</i> , 2009, 541, 373-420.	0.4	24
4772	Gene set enrichment analysis made simple. <i>Statistical Methods in Medical Research</i> , 2009, 18, 565-575.	0.7	166
4773	Bacterial Genome Sequencing. <i>Methods in Molecular Biology</i> , 2009, 551, 231-247.	0.4	19
4774	Apple Functional Genomics. , 2009, , 121-142.		3
4775	Formal Concept Analysis. <i>Lecture Notes in Computer Science</i> , 2009, , .	1.0	8

#	ARTICLE	IF	CITATIONS
4777	Modular Ontologies. Lecture Notes in Computer Science, 2009, , .	1.0	62
4781	Bioinformatics: A Concept-Based Introduction. , 2009, , .		2
4782	GoPubMed: Exploring PubMed with Ontological Background Knowledge. , 2009, , 385-399.		16
4784	REVIEW : Recent advances in developing web-servers for predicting protein attributes. Natural Science, 2009, 01, 63-92.	0.2	222
4785	Differential Regulation of Immune Responses and Macrophage/Neuron Interactions in the Dorsal Root Ganglion in Young and Adult Rats following Nerve Injury. Molecular Pain, 2009, 5, 1744-8069-5-70.	1.0	104
4786	Gene expression profiling of the tumor microenvironment during breast cancer progression. Breast Cancer Research, 2009, 11, R7.	2.2	547
4787	Tandem repeats modify the structure of human genes hosted in segmental duplications. Genome Biology, 2009, 10, R137.	13.9	32
4788	Towards accurate imputation of quantitative genetic interactions. Genome Biology, 2009, 10, R140.	13.9	24
4789	Catalogues of mammalian long noncoding RNAs: modest conservation and incompleteness. Genome Biology, 2009, 10, R124.	13.9	232
4790	Expansion of the human mitochondrial proteome by intra- and inter-compartmental protein duplication. Genome Biology, 2009, 10, R135.	13.9	23
4791	Motif composition, conservation and condition-specificity of single and alternative transcription start sites in the Drosophila genome. Genome Biology, 2009, 10, R73.	13.9	86
4792	Developmental roles of 21 Drosophila transcription factors are determined by quantitative differences in binding to an overlapping set of thousands of genomic regions. Genome Biology, 2009, 10, R80.	13.9	313
4793	Global expression analysis of the brown alga Ectocarpus siliculosus (Phaeophyceae) reveals large-scale reprogramming of the transcriptome in response to abiotic stress. Genome Biology, 2009, 10, R66.	13.9	138
4794	The Cell Cycle Ontology: An application ontology for the representation and integrated analysis of the cell cycle process. Genome Biology, 2009, 10, R58.	13.9	38
4795	Evolutionary rates and centrality in the yeast gene regulatory network. Genome Biology, 2009, 10, R35.	13.9	64
4796	TFCat: the curated catalog of mouse and human transcription factors. Genome Biology, 2009, 10, R29.	13.9	193
4797	Protein function annotation by homology-based inference. Genome Biology, 2009, 10, 207.	13.9	182
4798	Sequence-based feature prediction and annotation of proteins. Genome Biology, 2009, 10, 206.	13.9	53

#	ARTICLE	IF	CITATIONS
4799	Linking genes to diseases: it's all in the data. <i>Genome Medicine</i> , 2009, 1, 77.	3.6	46
4800	Using prior knowledge and genome-wide association to identify pathways involved in multiple sclerosis. <i>Genome Medicine</i> , 2009, 1, 65.	3.6	21
4801	Man-Machine Interactions. <i>Advances in Intelligent and Soft Computing</i> , 2009, , .	0.2	4
4802	Utility of mass spectrometry for proteome analysis: part II. Ion-activation methods, statistics, bioinformatics and annotation. <i>Expert Review of Proteomics</i> , 2009, 6, 171-197.	1.3	16
4803	Bacteriophages. <i>Methods in Molecular Biology</i> , 2009, , .	0.4	35
4804	Software Tool for Researching Annotations of Proteins: Open-Source Protein Annotation Software with Data Visualization. <i>Analytical Chemistry</i> , 2009, 81, 9819-9823.	3.2	207
4805	Databases and Data Mining. , 2009, , 659-672.		0
4806	Expression of Wnt receptors in adult spiral ganglion neurons: frizzled 9 localization at growth cones of regenerating neurites. <i>Neuroscience</i> , 2009, 164, 478-487.	1.1	27
4807	Transcriptional response in the peripheral blood of patients infected with <i>Salmonella enterica</i> serovar Typhi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22433-22438.	3.3	76
4808	Algorithms in Bioinformatics. <i>Lecture Notes in Computer Science</i> , 2009, , .	1.0	2
4810	A Hybrid Approach for Biomedical Entity Name Recognition. , 2009, , .		5
4811	PlasmoDB: a functional genomic database for malaria parasites. <i>Nucleic Acids Research</i> , 2009, 37, D539-D543.	6.5	1,030
4812	Next generation tools for the annotation of human SNPs. <i>Briefings in Bioinformatics</i> , 2009, 10, 35-52.	3.2	101
4813	A Primary Xenograft Model of Small-Cell Lung Cancer Reveals Irreversible Changes in Gene Expression Imposed by Culture <i>in vitro</i> . <i>Cancer Research</i> , 2009, 69, 3364-3373.	0.4	406
4814	An integrated comparative phosphoproteomic and bioinformatic approach reveals a novel class of MPM-2 motifs upregulated in EGFRvIII-expressing glioblastoma cells. <i>Molecular BioSystems</i> , 2009, 5, 59-67.	2.9	27
4815	Transcriptome Analysis and Identification of Genes Related to Immune Function in Skin of the Chinese Brown Frog. <i>Zoological Science</i> , 2009, 26, 80.	0.3	25
4816	Lipoprotein ontology as a functional knowledge base. , 2009, , .		1
4817	JBrowse: A next-generation genome browser. <i>Genome Research</i> , 2009, 19, 1630-1638.	2.4	724

#	ARTICLE	IF	CITATIONS
4818	Spatial Encoding Scheme for Protein Supporting Structure Discovery. , 2009, , .		0
4819	Notice of Violation of IEEE Publication Principles: PathMapper-an integrative approach for oncogene pathway identification. , 2009, , .		1
4820	Research on data integration of bioinformatics database based on web services. , 2009, , .		0
4821	Predicting gene function with positive and unlabeled examples. , 2009, , .		0
4822	Semantics of Multimodal Network Models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 271-280.	1.9	18
4823	Metadata-driven software for clinical trials. , 2009, , .		11
4824	A Semiautomatic Method to Achieve Independent and Intact Gene Ontology Slim (InitGO) and its Cytoscape Plugin Implementation. , 2009, , .		0
4825	Dynamic network topology changes in functional modules predict responses to oxidative stress in yeast. Molecular BioSystems, 2009, 5, 276.	2.9	12
4826	Gene prioritization using a probabilistic knowledge model. , 2009, , .		2
4827	Global Changes in Processing of mRNA 3' Untranslated Regions Characterize Clinically Distinct Cancer Subtypes. Cancer Research, 2009, 69, 9422-9430.	0.4	136
4828	Computational and Systems Biology. Molecular BioSystems, 2009, 5, 1391.	2.9	1
4829	An automatic gene ontology software tool for bicluster and cluster comparisons. , 2009, , .		1
4830	Mechanisms underlying methotrexate-induced pulmonary toxicity. Expert Opinion on Drug Safety, 2009, 8, 451-458.	1.0	40
4831	Adaptive response in embryogenesis: VI. Comparative microarray analysis of gene expressions in mouse fetuses. International Journal of Radiation Biology, 2009, 85, 70-86.	1.0	12
4832	Communication interception of human signal transduction pathways by Human Immunodeficiency Virus-1. , 2009, , .		0
4833	Applying fuzzy support vector machine to predict membrane protein interactions with different representations. , 2009, , .		0
4834	Revealing Biological Modules via Graph Summarization. Journal of Computational Biology, 2009, 16, 253-264.	0.8	47
4835	Clustering incorporating shortest paths identifies relevant modules in functional interaction networks. , 2009, , .		1

#	ARTICLE	IF	CITATIONS
4836	Improvements to cardiovascular Gene Ontology. <i>Atherosclerosis</i> , 2009, 205, 9-14.	0.4	15
4837	Pro-atherogenic effects of probucol in apo E-KO mice may be mediated through alterations in immune system: Parallel alterations in gene expression in the aorta and liver. <i>Atherosclerosis</i> , 2009, 206, 427-433.	0.4	4
4838	Generation of Gene Ontology benchmark datasets with various types of positive signal. <i>BMC Bioinformatics</i> , 2009, 10, 319.	1.2	5
4839	Automated Database Mediation Using Ontological Metadata Mappings. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2009, 16, 723-737.	2.2	9
4840	Expression of Cyclophilin B is Associated with Malignant Progression and Regulation of Genes Implicated in the Pathogenesis of Breast Cancer. <i>American Journal of Pathology</i> , 2009, 174, 297-308.	1.9	69
4841	Relationships between Deficits in Tissue Mass and Transcriptional Programs after Partial Hepatectomy in Mice. <i>American Journal of Pathology</i> , 2009, 175, 947-957.	1.9	22
4842	Transcriptional neoteny in the human brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5743-5748.	3.3	347
4843	Role of Horizontal Gene Transfer in the Evolution of Plant Parasitism Among Nematodes. <i>Methods in Molecular Biology</i> , 2009, 532, 517-535.	0.4	54
4844	Comprehensive Proteomic Analysis of Human Endometrial Fluid Aspirate. <i>Journal of Proteome Research</i> , 2009, 8, 4622-4632.	1.8	107
4845	3D Genome Tuner: Compare Multiple Circular Genomes in a 3D Context. <i>Genomics, Proteomics and Bioinformatics</i> , 2009, 7, 143-146.	3.0	1
4846	An atlas of chaperoneâ€“protein interactions in <i>Saccharomyces cerevisiae</i> : implications to protein folding pathways in the cell. <i>Molecular Systems Biology</i> , 2009, 5, 275.	3.2	202
4847	Discovering Biological Networks from Diverse Functional Genomic Data. <i>Methods in Molecular Biology</i> , 2009, 563, 157-175.	0.4	18
4848	Manipulating Large-Scale Arabidopsis Microarray Expression Data: Identifying Dominant Expression Patterns and Biological Process Enrichment. <i>Methods in Molecular Biology</i> , 2009, 553, 57-77.	0.4	42
4849	A Hierarchical Classification Ant Colony Algorithm for Predicting Gene Ontology Terms. <i>Lecture Notes in Computer Science</i> , 2009, , 68-79.	1.0	20
4850	Expression Profiling of the Ovarian Surface Kinome Reveals Candidate Genes for Early Neoplastic Changes. <i>Translational Oncology</i> , 2009, 2, 341-IN4.	1.7	28
4851	T1829 The Proteome of Mesenteric Lymph During Acute Pancreatitis and Implications for Treatment. <i>Gastroenterology</i> , 2009, 136, A-588.	0.6	0
4852	Pathway databases and tools for their exploitation: benefits, current limitations and challenges. <i>Molecular Systems Biology</i> , 2009, 5, 290.	3.2	173
4853	A pharmacogene database enhanced by the 1000 Genomes Project. <i>Pharmacogenetics and Genomics</i> , 2009, 19, 829-832.	0.7	18

#	ARTICLE	IF	CITATIONS
4854	Progression-Free Survival Is Simply a Measure of a Drug's Effect While Administered and Is Not a Surrogate for Overall Survival. <i>Cancer Journal (Sudbury, Mass)</i> , 2009, 15, 379-385.	1.0	57
4855	An Identification Method of Data-Specific GO Terms from a Microarray Data Set. <i>IEICE Transactions on Information and Systems</i> , 2009, E92-D, 1093-1102.	0.4	2
4856	Bioinformatic Strategies for cDNA-Microarray Data Processing. , 0, , 61-74.		1
4858	Study of the Relationship between Mus musculus Protein Sequences and Their Biological Functions. , 2009, , .		2
4859	Gene Expression Differences in Infected and Noninfected Middle Ear Complementary DNA Libraries. <i>JAMA Otolaryngology</i> , 2009, 135, 33.	1.5	12
4860	Calling International Rescue: knowledge lost in literature and data landslide!. <i>Biochemical Journal</i> , 2009, 424, 317-333.	1.7	56
4861	Decreased sigmoidal ABCB1 (P-glycoprotein) expression in ulcerative colitis is associated with disease activity. <i>Pharmacogenomics</i> , 2009, 10, 1941-1953.	0.6	44
4862	The evolution of protein functions and networks: a family-centric approach. <i>Biochemical Society Transactions</i> , 2009, 37, 745-750.	1.6	3
4863	The proteomic signature of NPM/ALK reveals deregulation of multiple cellular pathways. <i>Blood</i> , 2009, 114, 1585-1595.	0.6	55
4864	Gene expression-based classification and regulatory networks of pediatric acute lymphoblastic leukemia. <i>Blood</i> , 2009, 114, 4486-4493.	0.6	41
4865	Relationship of differential gene expression profiles in CD34+ myelodysplastic syndrome marrow cells to disease subtype and progression. <i>Blood</i> , 2009, 114, 4847-4858.	0.6	68
4866	Transcription Regulatory Networks Analysis Using CAGE. , 2009, , 153-168.		0
4867	Gene-Expression Ontologies and Tag-Based Expression Profiling. , 2009, , 169-178.		0
4868	Studying Root Development Using a Genomic Approach. , 0, , 325-351.		3
4870	Modeling a Regulatory Network Using Temporal Gene Expression Data: Why and How?. , 0, , 69-96.		1
4871	Comparative Analysis of Expression Profiles in Shoots and Roots of Tomato Systemically Infected by Tomato spotted wilt virus Reveals Organ-Specific Transcriptional Responses. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1504-1513.	1.4	64
4872	Oncogenes and pathway identification using filter-based approaches between various carcinoma types in lung. <i>International Journal of Computational Biology and Drug Design</i> , 2009, 2, 236.	0.3	2
4873	A cube framework for incorporating inter-gene information into biological data mining. <i>International Journal of Data Mining and Bioinformatics</i> , 2009, 3, 3.	0.1	4

#	ARTICLE	IF	CITATIONS
4874	Study of microarray time series data based on Forward-Backward Linear Prediction and Singular Value Decomposition. <i>International Journal of Data Mining and Bioinformatics</i> , 2009, 3, 145.	0.1	6
4875	Clustering sequences by overlap. <i>International Journal of Data Mining and Bioinformatics</i> , 2009, 3, 260.	0.1	4
4878	Global sequence properties for superfamily prediction: a machine learning approach. <i>Journal of Integrative Bioinformatics</i> , 2009, 6, .	1.0	1
4879	Exploring the relationship between polymorphic (TG/CA) n repeats in intron 1 regions and gene expression. <i>Human Genomics</i> , 2009, 3, 236-45.	1.4	10
4880	Protein-protein interaction databases: keeping up with growing interactomes. <i>Human Genomics</i> , 2009, 3, 291-7.	1.4	128
4881	Use of pathway information in molecular epidemiology. <i>Human Genomics</i> , 2009, 4, 21.	1.4	42
4882	Complete genome sequence of <i>Halorhabdus utahensis</i> type strain (AX-2T). <i>Standards in Genomic Sciences</i> , 2009, 1, 218-225.	1.5	22
4883	COMPARATIVE ANALYSIS OF AEROBIC AND ANAEROBIC PROKARYOTES TO IDENTIFY CORRELATION BETWEEN OXYGEN REQUIREMENT AND GENE-GENE FUNCTIONAL ASSOCIATION PATTERNS. , 2009, , .		1
4884	Complete genome sequence of <i>Methanoculleus marisnigri</i> Romesser et al. 1981 type strain JR1. <i>Standards in Genomic Sciences</i> , 2009, 1, 189-196.	1.5	34
4885	Complete genome sequence of <i>Beutenbergia cavernae</i> type strain (HKI 0122T). <i>Standards in Genomic Sciences</i> , 2009, 1, 21-28.	1.5	12
4886	Complete genome sequence of <i>Cryptobacterium curtum</i> type strain (12-3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 93-100.	1.5	17
4887	Complete genome sequence of <i>Desulfomicrobium baculatum</i> type strain (XT). <i>Standards in Genomic Sciences</i> , 2009, 1, 29-37.	1.5	36
4888	Complete genome sequence of <i>Acidimicrobium ferrooxidans</i> type strain (ICPT). <i>Standards in Genomic Sciences</i> , 2009, 1, 38-45.	1.5	32
4889	Complete genome sequence of <i>Sanguibacter keddieii</i> type strain (ST-74T). <i>Standards in Genomic Sciences</i> , 2009, 1, 110-118.	1.5	16
4890	Complete genome sequence of <i>Catenulispora acidiphila</i> type strain (ID 139908T). <i>Standards in Genomic Sciences</i> , 2009, 1, 119-125.	1.5	24
4891	Complete genome sequence of <i>Leptotrichia buccalis</i> type strain (C-1013-bT). <i>Standards in Genomic Sciences</i> , 2009, 1, 126-132.	1.5	24
4892	Complete genome sequence of <i>Saccharomonospora viridis</i> type strain (P101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 141-149.	1.5	24
4893	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 46-53.	1.5	38

#	ARTICLE	IF	CITATIONS
4894	Complete genome sequence of <i>Pedobacter heparinus</i> type strain (HIM 762-3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 54-62.	1.5	25
4895	Complete genome sequence of <i>Halogeometricum borinquense</i> type strain (PR3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 150-158.	1.5	23
4896	Complete genome sequence of <i>Anaerococcus prevotii</i> type strain (PC1T). <i>Standards in Genomic Sciences</i> , 2009, 1, 159-165.	1.5	25
4897	Complete genome sequence of <i>Atopobium parvulum</i> type strain (IPP 1246T). <i>Standards in Genomic Sciences</i> , 2009, 1, 166-173.	1.5	30
4898	Complete genome sequence of <i>Staphylothermus marinus</i> Stetter and Fiala 1986 type strain F1. <i>Standards in Genomic Sciences</i> , 2009, 1, 183-188.	1.5	8
4899	Complete genome sequence of <i>Eggerthella lenta</i> type strain (VPI 0255T). <i>Standards in Genomic Sciences</i> , 2009, 1, 174-182.	1.5	37
4900	Complete genome sequence of <i>Kangiella koreensis</i> type strain (SW-125T). <i>Standards in Genomic Sciences</i> , 2009, 1, 226-233.	1.5	28
4901	Complete genome sequence of <i>Jonesia denitrificans</i> type strain (Prevot 55134T). <i>Standards in Genomic Sciences</i> , 2009, 1, 262-269.	1.5	14
4902	Complete genome sequence of <i>Halomicrobium mukohataei</i> type strain (arg-2T). <i>Standards in Genomic Sciences</i> , 2009, 1, 270-277.	1.5	31
4903	Complete genome sequence of <i>Rhodothermus marinus</i> type strain (R-10T). <i>Standards in Genomic Sciences</i> , 2009, 1, 283-290.	1.5	45
4904	Complete genome sequence of <i>Streptobacillus moniliformis</i> type strain (9901T). <i>Standards in Genomic Sciences</i> , 2009, 1, 300-307.	1.5	21
4905	Complete genome sequence of <i>Brachybacterium faecium</i> type strain (Schefferle 6-10T). <i>Standards in Genomic Sciences</i> , 2009, 1, 3-11.	1.5	25
4906	Complete genome sequence of <i>Pirellula staleyi</i> type strain (ATCC 27377T). <i>Standards in Genomic Sciences</i> , 2009, 1, 308-316.	1.5	34
4907	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541T). <i>Standards in Genomic Sciences</i> , 2009, 1, 12-20.	1.5	100
4908	Gpos-mPLoc: A Top-Down Approach to Improve the Quality of Predicting Subcellular Localization of Gram-Positive Bacterial Proteins. <i>Protein and Peptide Letters</i> , 2009, 16, 1478-1484.	0.4	100
4909	Complete genome sequence of <i>Dyadobacter fermentans</i> type strain (NS114T). <i>Standards in Genomic Sciences</i> , 2009, 1, 133-140.	1.5	25
4910	Complete genome sequence of <i>Thermanaerovibrio acidaminovorans</i> type strain (Su883T). <i>Standards in Genomic Sciences</i> , 2009, 1, 254-261.	1.5	23
4911	Novel Insights into Adipogenesis from Omics Data. <i>Current Medicinal Chemistry</i> , 2009, 16, 2952-2964.	1.2	35

#	ARTICLE	IF	CITATIONS
4912	Bayesian Analysis of Biological Networks: Clusters, Motifs, Cross-Species Correlations. , 2009, , 65-83.		2
4913	Complete genome sequence of <i>Slackia heliotrinireducens</i> type strain (RHS 1T). Standards in Genomic Sciences, 2009, 1, 234-241.	1.5	20
4914	Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575T). Standards in Genomic Sciences, 2009, 1, 242-253.	1.5	35
4915	Complete genome sequence of <i>Stackebrandtia nassauensis</i> type strain (LLR-40K-21T). Standards in Genomic Sciences, 2009, 1, 292-299.	1.5	23
4916	A Conditional Suite of Tests for Identifying Differentially Expressed Genes in a DNA Microarray Experiment with Little Replication. Statistics in Biopharmaceutical Research, 2009, 1, 26-38.	0.6	5
4917	Construction of Engineering Domain Ontology through Extraction of Knowledge from Domain Handbooks. , 2009, , .		6
4918	A systems biology network model for genetic association studies of nicotine addiction and treatment. Pharmacogenetics and Genomics, 2009, 19, 538-551.	0.7	22
4919	Constitutive Secretion in <i>Tetrahymena thermophila</i> . Eukaryotic Cell, 2010, 9, 674-681.	3.4	20
4920	Effect of Therapeutic Mild Hypothermia on the Genomics of the Hippocampus After Moderate Traumatic Brain Injury in Rats. Neurosurgery, 2010, 67, 730-742.	0.6	36
4921	Fast Revelation of the Motif Mode for a Yeast Protein Interaction Network Through Intelligent Agent-Based Distributed Computing. Protein and Peptide Letters, 2010, 17, 1091-1101.	0.4	1
4922	The Nature of Protein Domain Evolution: Shaping the Interaction Network. Current Genomics, 2010, 11, 368-376.	0.7	46
4923	Gene Duplication and Environmental Adaptation within Yeast Populations. Genome Biology and Evolution, 2010, 2, 591-601.	1.1	44
4924	Complete genome sequence of <i>Planctomyces limnophilus</i> type strain (M ¹ /4 290T). Standards in Genomic Sciences, 2010, 3, 47-56.	1.5	31
4925	Permanent draft genome sequence of <i>Dethiosulfovibrio peptidovorans</i> type strain (SEBR 4207T). Standards in Genomic Sciences, 2010, 3, 85-92.	1.5	9
4926	Complete genome sequence of <i>Ferrimonas balearica</i> type strain (PATT). Standards in Genomic Sciences, 2010, 3, 174-182.	1.5	14
4927	Metagenomes and metatranscriptomes from the L4 long-term coastal monitoring station in the Western English Channel. Standards in Genomic Sciences, 2010, 3, 183-193.	1.5	28
4928	Non-contiguous finished genome sequence of <i>Aminomonas paucivorans</i> type strain (GLU-3T). Standards in Genomic Sciences, 2010, 3, 285-293.	1.5	9
4929	Complete genome sequence of <i>Ilyobacter polytropus</i> type strain (CuHbu1T). Standards in Genomic Sciences, 2010, 3, 304-314.	1.5	10

#	ARTICLE	IF	CITATIONS
4930	Complete genome sequence of <i>Nocardiopsis dassonvillei</i> type strain (IMRU 509T). <i>Standards in Genomic Sciences</i> , 2010, 3, 325-336.	1.5	32
4931	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3T). <i>Standards in Genomic Sciences</i> , 2010, 2, 57-65.	1.5	44
4932	Quantifying Protein Function Specificity in the Gene Ontology. <i>Standards in Genomic Sciences</i> , 2010, 2, 238-244.	1.5	7
4933	Complete genome sequence of <i>Kribbella flavida</i> type strain (IFO 14399T). <i>Standards in Genomic Sciences</i> , 2010, 2, 185-192.	1.5	11
4934	Complete genome sequence of <i>Conexibacter woesei</i> type strain (ID131577T). <i>Standards in Genomic Sciences</i> , 2010, 2, 212-219.	1.5	24
4935	Complete genome sequence of <i>Thermocrinis albus</i> type strain (HI 11/12T). <i>Standards in Genomic Sciences</i> , 2010, 2, 194-202.	1.5	18
4936	Complete genome sequence of <i>Meiothermus silvanus</i> type strain (VI-R2T). <i>Standards in Genomic Sciences</i> , 2010, 3, 37-46.	1.5	19
4937	Complete genome sequence of <i>Olsenella uli</i> type strain (VPI D76D-27CT). <i>Standards in Genomic Sciences</i> , 2010, 3, 76-84.	1.5	43
4938	Complete genome sequence of <i>Acidaminococcus fermentans</i> type strain (VR4T). <i>Standards in Genomic Sciences</i> , 2010, 3, 1-14.	1.5	31
4939	Complete genome sequence of <i>Meiothermus ruber</i> type strain (21T). <i>Standards in Genomic Sciences</i> , 2010, 3, 26-36.	1.5	33
4940	Complete genome sequence of <i>Acetohalobium arabaticum</i> type strain (Z-7288T). <i>Standards in Genomic Sciences</i> , 2010, 3, 57-65.	1.5	24
4941	Complete genome sequence of <i>Ignisphaera aggregans</i> type strain (AQ1.S1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 66-75.	1.5	15
4942	Complete genome sequence of <i>Candidatus Ruthia magnifica</i> . <i>Standards in Genomic Sciences</i> , 2010, 3, 163-173.	1.5	18
4943	Complete genome sequence of <i>Vulcanisaeta distributa</i> type strain (IC-017T). <i>Standards in Genomic Sciences</i> , 2010, 3, 117-125.	1.5	10
4944	Complete genome sequence of <i>Arcanobacterium haemolyticum</i> type strain (11018T). <i>Standards in Genomic Sciences</i> , 2010, 3, 126-135.	1.5	8
4945	Complete genome sequence of <i>Thermosediminibacter oceani</i> type strain (JW/IW-1228PT). <i>Standards in Genomic Sciences</i> , 2010, 3, 108-116.	1.5	12
4946	Complete genome sequence of <i>Spirochaeta smaragdinae</i> type strain (SEBR 4228T). <i>Standards in Genomic Sciences</i> , 2010, 3, 1-9.	1.5	18
4947	Complete genome sequence of <i>Thermobaculum terrenum</i> ™ type strain (YNP1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 153-162.	1.5	11

#	ARTICLE	IF	CITATIONS
4948	Complete genome sequence of Syntrophothermus lipocalidus type strain (TGB-C1T). Standards in Genomic Sciences, 2010, 3, 268-275.	1.5	13
4949	Complete genome sequence of Desulfarculus baarsii type strain (2st14T). Standards in Genomic Sciences, 2010, 3, 276-284.	1.5	37
4950	Complete genome sequence of Intrasporangium calvum type strain (7 KIPT). Standards in Genomic Sciences, 2010, 3, 294-303.	1.5	7
4951	Complete genome sequence of Methanothermus fervidus type strain (V24ST). Standards in Genomic Sciences, 2010, 3, 315-324.	1.5	17
4952	Complete genome sequence of Thermaerobacter marianensis type strain (7p75aT). Standards in Genomic Sciences, 2010, 3, 337-345.	1.5	10
4953	Complete genome sequence of the Medicago microsymbiont Ensifer (Sinorhizobium) medicae strain WSM419. Standards in Genomic Sciences, 2010, 2, 77-86.	1.5	100
4954	Complete genome sequence of Rhizobium leguminosarum bv trifolii strain WSM2304, an effective microsymbiont of the South American clover Trifolium polymorphum.. Standards in Genomic Sciences, 2010, 2, 66-76.	1.5	60
4955	Complete genome sequence of Xylanimonas cellulositytica type strain (XIL07T). Standards in Genomic Sciences, 2010, 2, 1-8.	1.5	10
4956	Complete genome sequence of Alicyclobacillus acidocaldarius type strain (104-IAT). Standards in Genomic Sciences, 2010, 2, 9-18.	1.5	24
4957	Complete genome sequence of Sphaerobacter thermophilus type strain (S 6022T). Standards in Genomic Sciences, 2010, 2, 49-56.	1.5	27
4958	Complete genome sequence of Streptosporangium roseum type strain (NI 9100T). Standards in Genomic Sciences, 2010, 2, 29-37.	1.5	27
4959	The JCVI standard operating procedure for annotating prokaryotic metagenomic shotgun sequencing data. Standards in Genomic Sciences, 2010, 2, 229-237.	1.5	55
4960	Complete genome sequence of Chitinophaga pinensis type strain (UQM 2034T). Standards in Genomic Sciences, 2010, 2, 87-95.	1.5	74
4961	Complete genome sequence of Sulfurospirillum deleyianum type strain (5175T). Standards in Genomic Sciences, 2010, 2, 149-157.	1.5	29
4962	Complete genome sequence of Haloterrigena turkmenica type strain (4kT). Standards in Genomic Sciences, 2010, 2, 107-116.	1.5	32
4963	Complete genome sequence of Haliangium ochraceum type strain (SMP-2T). Standards in Genomic Sciences, 2010, 2, 96-106.	1.5	70
4964	Complete genome sequence of Geodermatophilus obscurus type strain (G-20T). Standards in Genomic Sciences, 2010, 2, 158-167.	1.5	56
4965	Complete genome sequence of Nakamurella multipartita type strain (Y-104T). Standards in Genomic Sciences, 2010, 2, 168-175.	1.5	35

#	ARTICLE	IF	CITATIONS
4966	Complete genome sequence of Spirosoma linguale type strain (1T). Standards in Genomic Sciences, 2010, 2, 176-184.	1.5	40
4967	Complete genome sequence of Segniliparus rotundus type strain (CDC 1076T). Standards in Genomic Sciences, 2010, 2, 203-211.	1.5	10
4968	Complete genome sequence of Sebaldella termitidis type strain (NCTC 11300T). Standards in Genomic Sciences, 2010, 2, 220-227.	1.5	34
4969	Complete genome sequence of Thermosphaera aggregans type strain (M11TLT). Standards in Genomic Sciences, 2010, 2, 245-259.	1.5	14
4970	Complete genome sequence of Brachyspira murdochii type strain (56-150T). Standards in Genomic Sciences, 2010, 2, 260-269.	1.5	20
4971	Complete genome sequence of Aminobacterium colombiense type strain (ALA-1T). Standards in Genomic Sciences, 2010, 2, 280-289.	1.5	32
4972	Complete genome sequence of Arcobacter nitrofigilis type strain (CIT). Standards in Genomic Sciences, 2010, 2, 300-308.	1.5	40
4973	Complete genome sequence of Coraliomargarita akajimensis type strain (04OKA010-24T). Standards in Genomic Sciences, 2010, 2, 290-299.	1.5	28
4974	Complete genome sequence of Thermobispora bispora type strain (R51T). Standards in Genomic Sciences, 2010, 2, 318-326.	1.5	23
4975	Proteins: Sequence to Structure and Function – Current Status. Current Protein and Peptide Science, 2010, 11, 498-514.	0.7	55
4976	Complete genome sequence of Desulfohalobium retbaense type strain (HR100T). Standards in Genomic Sciences, 2010, 2, 38-48.	1.5	22
4977	Complete genome sequence of Archaeoglobus profundus type strain (AV18T). Standards in Genomic Sciences, 2010, 2, 327-346.	1.5	26
4978	Using Compound Similarity and Functional Domain Composition for Prediction of Drug-Target Interaction Networks. Medicinal Chemistry, 2010, 6, 388-395.	0.7	10
4979	Nuclear magnetic resonance in conjunction with functional genomics suggests mitochondrial dysfunction in a murine model of cancer cachexia. International Journal of Molecular Medicine, 2011, 27, 15-24.	1.8	70
4980	Evolution of Neuronal and Endothelial Transcriptomes in Primates. Genome Biology and Evolution, 2010, 2, 284-292.	1.1	14
4981	Maternal protein restriction with or without folic acid supplementation during pregnancy alters the hepatic transcriptome in adult male rats. British Journal of Nutrition, 2010, 103, 1711-1719.	1.2	77
4982	Complete genome sequence of Denitrovibrio acetiphilus type strain (N2460T). Standards in Genomic Sciences, 2010, 2, 270-279.	1.5	16
4983	Genome-wide functional annotation by integrating multiple microarray datasets using meta-analysis. International Journal of Data Mining and Bioinformatics, 2010, 4, 357.	0.1	10

#	ARTICLE	IF	CITATIONS
4984	Evolutionary Dynamics of Complete <i>Campylobacter</i> Pan-Genomes and the Bacterial Species Concept. <i>Genome Biology and Evolution</i> , 2010, 2, 646-655.	1.1	98
4985	Quality improvement of rule-based gene group descriptions using information about GO terms importance occurring in premises of determined rules. <i>International Journal of Applied Mathematics and Computer Science</i> , 2010, 20, 555-570.	1.5	5
4986	Review of QSAR Models for Enzyme Classes of Drug Targets: Theoretical Background and Applications in Parasites, Hosts and Other Organisms. <i>Current Pharmaceutical Design</i> , 2010, 16, 2710-2723.	0.9	47
4987	Exploration of Potential Tumor Markers for Lung Adenocarcinomas by Two-Dimensional Gel Electrophoresis Coupled with Nano-LC/MS/MS. <i>Journal of the Chinese Chemical Society</i> , 2010, 57, 180-188.	0.8	4
4988	Artificial Intelligence Techniques for Colorectal Cancer Drug Metabolism: Ontologies and Complex Networks. <i>Current Drug Metabolism</i> , 2010, 11, 347-368.	0.7	59
4989	Transcriptional Effects of S100B on Neuroblastoma Cells: Perturbation of Cholesterol Homeostasis and Interference on the Cell Cycle. <i>Gene Expression</i> , 2010, 14, 345-359.	0.5	14
4990	Shotgun Proteomics and Network Analysis between Plasma Membrane and Extracellular Matrix Proteins from Rat Olfactory Ensheathing Cells. <i>Cell Transplantation</i> , 2010, 19, 133-146.	1.2	27
4991	Deregulated Genes in Sporadic Vestibular Schwannomas. <i>Otology and Neurotology</i> , 2010, 31, 256-266.	0.7	34
4992	CHANGES IN THE MESENTERIC LYMPH PROTEOME INDUCED BY HEMORRHAGIC SHOCK. <i>Shock</i> , 2010, 34, 140-149.	1.0	28
4993	Genetic mapping of EST-SSRs, SSR and InDels to improve saturation of genomic regions in a previously developed sunflower map. <i>Electronic Journal of Biotechnology</i> , 2010, 13, 0-0.	1.2	16
4994	A human B-cell interactome identifies MYB and FOXM1 as master regulators of proliferation in germinal centers. <i>Molecular Systems Biology</i> , 2010, 6, 377.	3.2	336
4995	An introduction to effective use of enrichment analysis software. <i>Human Genomics</i> , 2010, 4, 202.	1.4	60
4996	Automated identification of pathways from quantitative genetic interaction data. <i>Molecular Systems Biology</i> , 2010, 6, 379.	3.2	70
4997	A general lack of compensation for gene dosage in yeast. <i>Molecular Systems Biology</i> , 2010, 6, 368.	3.2	118
5000	Reconstruction and Use of Microbial Metabolic Networks: the Core <i>Escherichia coli</i> Metabolic Model as an Educational Guide. <i>EcoSal Plus</i> , 2010, 4, .	2.1	195
5002	An integrated model for visualizing biclusters from gene expression data and PPI networks. , 2010, , .		0
5003	Gene expression of the liver in response to chronic hypoxia. <i>Physiological Genomics</i> , 2010, 41, 275-288.	1.0	51
5005	Dynamic CRM occupancy reflects a temporal map of developmental progression. <i>Molecular Systems Biology</i> , 2010, 6, 383.	3.2	44

#	ARTICLE	IF	CITATIONS
5006	Complete genome sequence of <i>Gordonia bronchialis</i> type strain (3410T). <i>Standards in Genomic Sciences</i> , 2010, 2, 19-28.	1.5	26
5007	Ranking relations using analogies in biological and information networks. <i>Annals of Applied Statistics</i> , 2010, 4, 615-644.	0.5	3
5008	Steroid Pretreatment of Organ Donors to Prevent Postischemic Renal Allograft Failure. <i>Annals of Internal Medicine</i> , 2010, 153, 222.	2.0	66
5009	SATB1 dictates expression of multiple genes including IL-5 involved in human T helper cell differentiation. <i>Blood</i> , 2010, 116, 1443-1453.	0.6	62
5010	EZH2-mediated epigenetic silencing in germinal center B cells contributes to proliferation and lymphomagenesis. <i>Blood</i> , 2010, 116, 5247-5255.	0.6	262
5011	Deep sequencing of the small RNA transcriptome of normal and malignant human B cells identifies hundreds of novel microRNAs. <i>Blood</i> , 2010, 116, e118-e127.	0.6	188
5012	Deterministic graph-theoretic algorithm for detecting modules in biological interaction networks. <i>International Journal of Bioinformatics Research and Applications</i> , 2010, 6, 101.	0.1	3
5013	Scaling alignment of large ontologies. <i>International Journal of Bioinformatics Research and Applications</i> , 2010, 6, 384.	0.1	4
5014	Assessing gene length biases in gene set analysis of Genome-Wide Association Studies. <i>International Journal of Computational Biology and Drug Design</i> , 2010, 3, 297.	0.3	9
5015	Meta analysis algorithms for microarray gene expression data using Gene Regulatory Networks. <i>International Journal of Data Mining and Bioinformatics</i> , 2010, 4, 487.	0.1	3
5016	Resource descriptions, ontology, and resource discovery. <i>International Journal of Metadata, Semantics and Ontologies</i> , 2010, 5, 194.	0.2	10
5017	Dependencies between ontology design parameters. <i>International Journal of Metadata, Semantics and Ontologies</i> , 2010, 5, 265.	0.2	6
5018	Noise tolerance of Multiple Classifier Systems in data integration-based gene function prediction. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, 346-362.	1.0	0
5019	On solvability, regularity, and locality of the problem of genome annotation. <i>Pattern Recognition and Image Analysis</i> , 2010, 20, 386-395.	0.6	16
5020	Gene expression profiling of the endophytic fungus <i>Neotyphodium loliin</i> association with its host plant perennial ryegrass. <i>Australasian Plant Pathology</i> , 2010, 39, 467.	0.5	16
5021	Representing ontogeny through ontology: A developmental biologist's guide to the gene ontology. <i>Molecular Reproduction and Development</i> , 2010, 77, 314-329.	1.0	19
5022	Prioritizing GWAS Results: A Review of Statistical Methods and Recommendations for Their Application. <i>American Journal of Human Genetics</i> , 2010, 86, 6-22.	2.6	531
5023	Integrating Pathway Analysis and Genetics of Gene Expression for Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2010, 86, 581-591.	2.6	224

#	ARTICLE	IF	CITATIONS
5024	Gene Expression and Genetic Variation in Response to Endoplasmic Reticulum Stress in Human Cells. American Journal of Human Genetics, 2010, 86, 719-729.	2.6	91
5025	Insights into Colon Cancer Etiology via a Regularized Approach to Gene Set Analysis of GWAS Data. American Journal of Human Genetics, 2010, 86, 860-871.	2.6	130
5026	Powerful SNP-Set Analysis for Case-Control Genome-wide Association Studies. American Journal of Human Genetics, 2010, 86, 929-942.	2.6	541
5027	A microarray analysis of early activated pathways in concanavalin A-induced hepatitis. Journal of Zhejiang University: Science B, 2010, 11, 366-377.	1.3	10
5028	A Gross Anatomy Ontology for Hymenoptera. PLoS ONE, 2010, 5, e15991.	1.1	250
5029	The use of network analyses for elucidating mechanisms in cardiovascular disease. Molecular BioSystems, 2010, 6, 289-304.	2.9	81
5030	DNA microarrays to define and search for genes associated with obesity. Biotechnology Journal, 2010, 5, 99-112.	1.8	33
5031	Hepatoprotective effect of oleuropein in mice: Mechanisms uncovered by gene expression profiling. Biotechnology Journal, 2010, 5, 950-960.	1.8	40
5032	Studying Plant-Pathogen Interactions in the Genomics Era: Beyond Molecular Koch's Postulates to Systems Biology. Annual Review of Phytopathology, 2010, 48, 457-479.	3.5	57
5033	Generation of Functional Hepatocytes From Mouse Germ Line Cell-Derived Pluripotent Stem Cells In Vitro. Stem Cells and Development, 2010, 19, 1183-1194.	1.1	21
5034	Ontological technologies for user modelling. International Journal of Metadata, Semantics and Ontologies, 2010, 5, 32.	0.2	70
5035	Current Progress in Static and Dynamic Modeling of Biological Networks. Systems Biology, 2010, , 13-73.	0.1	4
5037	Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPAR δ . Cellular and Molecular Life Sciences, 2010, 67, 4049-4064.	2.4	38
5038	Correlation between parental transcriptome and field data for the characterization of heterosis in Zea mays L. Theoretical and Applied Genetics, 2010, 120, 401-413.	1.8	79
5039	Near-isogenic cotton germplasm lines that differ in fiber-bundle strength have temporal differences in fiber gene expression patterns as revealed by comparative high-throughput profiling. Theoretical and Applied Genetics, 2010, 120, 1347-1366.	1.8	48
5040	Diet-induced gene expression of isolated pancreatic islets from a polygenic mouse model of the metabolic syndrome. Diabetologia, 2010, 53, 309-320.	2.9	44
5041	Gene expression profiles in the brain of the neonate mouse perinatally exposed to methylmercury and/or polychlorinated biphenyls. Archives of Toxicology, 2010, 84, 271-286.	1.9	18
5042	Sensitivity and resistance towards isoliquiritigenin, doxorubicin and methotrexate in T cell acute lymphoblastic leukaemia cell lines by pharmacogenomics. Naunyn-Schmiedeberg's Archives of Pharmacology, 2010, 382, 221-234.	1.4	20

#	ARTICLE	IF	CITATIONS
5043	Optimization of parameters for coverage of low molecular weight proteins. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 398, 2867-2881.	1.9	43
5044	New evidence for habitat-specific selection in Wadden Sea <i>Zostera marina</i> populations revealed by genome scanning using SNP and microsatellite markers. <i>Marine Biology</i> , 2010, 157, 81-89.	0.7	34
5045	Accelerated Evolutionary Rate of Housekeeping Genes in Tunicates. <i>Journal of Molecular Evolution</i> , 2010, 71, 153-167.	0.8	40
5046	Genes Devoid of Full-Length Transposable Element Insertions are Involved in Development and in the Regulation of Transcription in Human and Closely Related Species. <i>Journal of Molecular Evolution</i> , 2010, 71, 180-191.	0.8	11
5047	Variable Numbers of Tandem Repeats in <i>Plasmodium falciparum</i> Genes. <i>Journal of Molecular Evolution</i> , 2010, 71, 268-278.	0.8	24
5048	Retrotransposon expression in ethanol-stressed <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2010, 87, 1447-1454.	1.7	16
5049	Allucin-induced global gene expression profile of <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 219-229.	1.7	24
5050	EST analysis and annotation of transcripts derived from a trichome-specific cDNA library from <i>Salvia fruticosa</i> . <i>Plant Cell Reports</i> , 2010, 29, 523-534.	2.8	33
5051	Analysis of expressed sequence tags from the <i>Ulva prolifera</i> (Chlorophyta). <i>Chinese Journal of Oceanology and Limnology</i> , 2010, 28, 26-36.	0.7	9
5052	Integrating Genomic Signatures for Immunologic Discovery. <i>Immunity</i> , 2010, 32, 152-161.	6.6	52
5053	Alterations in gene expression of human vascular endothelial cells associated with nanotopographic cues. <i>Biomaterials</i> , 2010, 31, 8882-8888.	5.7	66
5054	A semi-dependent decomposition approach to learn hierarchical classifiers. <i>Pattern Recognition</i> , 2010, 43, 3795-3804.	5.1	5
5055	Using Gene Ontology annotations in exploratory microarray clustering to understand cancer etiology. <i>Pattern Recognition Letters</i> , 2010, 31, 2138-2146.	2.6	16
5056	Dividing protein interaction networks for modular network comparative analysis. <i>Pattern Recognition Letters</i> , 2010, 31, 2083-2096.	2.6	9
5057	The tetratricopeptide repeats (TPR)-like superfamily of proteins in <i>Leishmania</i> spp., as revealed by multi-relational data mining. <i>Pattern Recognition Letters</i> , 2010, 31, 2178-2189.	2.6	5
5058	Essential molecular functions associated with the circular code evolution. <i>Journal of Theoretical Biology</i> , 2010, 264, 613-622.	0.8	39
5059	The annotation of full zinc proteomes. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 1071-1078.	1.1	27
5060	Ecological functions and differentially expressed transcripts of translucent bracts in an alpine glasshouse™ plant <i>Rheum nobile</i> (Polygonaceae). <i>Planta</i> , 2010, 231, 1505-1511.	1.6	20

#	ARTICLE	IF	CITATIONS
5061	A MOD(ern) perspective on literature curation. <i>Molecular Genetics and Genomics</i> , 2010, 283, 415-425.	1.0	22
5062	An approach based on a genome-wide association study reveals candidate loci for narcolepsy. <i>Human Genetics</i> , 2010, 128, 433-441.	1.8	41
5063	The Effects of Immunostimulation Through Dietary Manipulation in the Rainbow Trout; Evaluation of Mucosal Immunity. <i>Marine Biotechnology</i> , 2010, 12, 88-99.	1.1	28
5064	Effect of Early Introduction of Microencapsulated Diet to Larval Atlantic Halibut, <i>Hippoglossus hippoglossus</i> L. Assessed by Microarray Analysis. <i>Marine Biotechnology</i> , 2010, 12, 214-229.	1.1	21
5065	Identification of Immune Genes of the Agamaki Clam (<i>Sinonovacula constricta</i>) by Sequencing and Bioinformatic Analysis of ESTs. <i>Marine Biotechnology</i> , 2010, 12, 282-291.	1.1	35
5066	Expression of Sex and Reproduction-Related Genes in <i>Marsupenaeus japonicus</i> . <i>Marine Biotechnology</i> , 2010, 12, 664-677.	1.1	13
5067	TaNf-YC11, one of the light-upregulated NF-YC members in <i>Triticum aestivum</i> , is co-regulated with photosynthesis-related genes. <i>Functional and Integrative Genomics</i> , 2010, 10, 265-276.	1.4	38
5068	Wheat defense genes in fungal (<i>Puccinia striiformis</i>) infection. <i>Functional and Integrative Genomics</i> , 2010, 10, 227-239.	1.4	37
5069	The transcript repeat element: the human Alu sequence as a component of gene networks influencing cancer. <i>Functional and Integrative Genomics</i> , 2010, 10, 307-319.	1.4	28
5070	Coexpression landscape in ATTED-II: usage of gene list and gene network for various types of pathways. <i>Journal of Plant Research</i> , 2010, 123, 311-319.	1.2	58
5071	Microarray analysis of p-anisaldehyde-induced transcriptome of <i>Saccharomyces cerevisiae</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2010, 37, 313-322.	1.4	23
5072	Ins and Outs of Systems Biology vis-à-vis Molecular Biology: Continuation or Clear Cut?. <i>Acta Biotheoretica</i> , 2010, 58, 15-49.	0.7	21
5073	Interaction networks as a tool to investigate the mechanisms of aging. <i>Biogerontology</i> , 2010, 11, 463-473.	2.0	14
5074	Prediction of mitochondrial proteins of malaria parasite using split amino acid composition and PSSM profile. <i>Amino Acids</i> , 2010, 39, 101-110.	1.2	54
5075	The Micronutrient Genomics Project: a community-driven knowledge base for micronutrient research. <i>Genes and Nutrition</i> , 2010, 5, 285-296.	1.2	47
5076	A hierarchical multi-label classification ant colony algorithm for protein function prediction. <i>Memetic Computing</i> , 2010, 2, 165-181.	2.7	43
5077	A Serial Analysis of Gene Expression Profile of the Alzheimer's Disease Tg2576 Mouse Model. <i>Neurotoxicity Research</i> , 2010, 17, 360-379.	1.3	54
5078	OsCAS: a comprehensive web-based annotation platform for rice microarray data. <i>Biochip Journal</i> , 2010, 4, 9-15.	2.5	0

#	ARTICLE	IF	CITATIONS
5079	Computational identification of seed-specific transcription factors involved in anthocyanin production in black rice. <i>Biochip Journal</i> , 2010, 4, 247-255.	2.5	25
5080	Array2GO: a simple web-based tool to search gene ontology for analysis of multi genes expression. <i>Biochip Journal</i> , 2010, 4, 329-335.	2.5	2
5081	Quantitative proteomic analysis of S-nitrosated proteins in diabetic mouse liver with ICAT switch method. <i>Protein and Cell</i> , 2010, 1, 675-687.	4.8	22
5082	Gene expression profiling in the human keratinocyte cell line, hacat exposed to urushiol isolated from sap of korean lacquer tree (<i>Rhus verniciflua</i> Stokes). <i>Molecular and Cellular Toxicology</i> , 2010, 6, 79-86.	0.8	1
5083	Power training and postmenopausal hormone therapy affect transcriptional control of specific co-regulated gene clusters in skeletal muscle. <i>Age</i> , 2010, 32, 347-363.	3.0	32
5084	Understanding the "Horizontal Dimension" of Molecular Evolution to Annotate, Classify, and Discover Proteins with Functional Domains. <i>Journal of Computer Science and Technology</i> , 2010, 25, 82-94.	0.9	0
5085	A linear programming model based on network flow for pathway inference. <i>Journal of Systems Science and Complexity</i> , 2010, 23, 971-977.	1.6	0
5086	Generation and analysis of expressed sequence tags from the medicinal plant <i>Salvia miltiorrhiza</i> . <i>Science China Life Sciences</i> , 2010, 53, 273-285.	2.3	33
5087	Computational RNomics: Structure identification and functional prediction of non-coding RNAs in silico. <i>Science China Life Sciences</i> , 2010, 53, 548-562.	2.3	7
5088	A web-based platform for rice microarray annotation and data analysis. <i>Science China Life Sciences</i> , 2010, 53, 1467-1473.	2.3	0
5089	ModuleNet: An R package on regulatory network building. <i>Science Bulletin</i> , 2010, 55, 3430-3435.	1.7	1
5090	Genome-wide identification and annotation of HIF-1 α binding sites in two cell lines using massively parallel sequencing. <i>The HUGO Journal</i> , 2010, 4, 35-48.	4.1	43
5091	Follicle-stimulating hormone regulation of microRNA expression on progesterone production in cultured rat granulosa cells. <i>Endocrine</i> , 2010, 38, 158-166.	1.1	87
5092	A microarray analysis of the effects of moderate hypothermia and rewarming on gene expression by human hepatocytes (HepG2). <i>Cell Stress and Chaperones</i> , 2010, 15, 687-702.	1.2	18
5093	Adipocyte Accumulation of Long-Chain Fatty Acids in Obesity is Multifactorial, Resulting from Increased Fatty Acid Uptake and Decreased Activity of Genes Involved in Fat Utilization. <i>Obesity Surgery</i> , 2010, 20, 93-107.	1.1	54
5094	Ontological evaluation of transcriptional differences between sperm of infertile males and fertile donors using microarray analysis. <i>Journal of Assisted Reproduction and Genetics</i> , 2010, 27, 111-120.	1.2	21
5095	"Just one animal among many?" Existential phenomenology, ethics, and stem cell research. <i>Theoretical Medicine and Bioethics</i> , 2010, 31, 197-224.	0.4	1
5096	Generation and gene ontology based analysis of expressed sequence tags (EST) from a <i>Panax ginseng</i> C. A. Meyer roots. <i>Molecular Biology Reports</i> , 2010, 37, 3465-3472.	1.0	54

#	ARTICLE	IF	CITATIONS
5097	MYBBP1A: a new Ipr1™s binding protein in mice. <i>Molecular Biology Reports</i> , 2010, 37, 3863-3868.	1.0	13
5098	Rootstock-regulated gene expression patterns in apple tree scions. <i>Tree Genetics and Genomes</i> , 2010, 6, 57-72.	0.6	79
5099	Initial changes in the transcriptome of <i>Euphorbia esula</i> seeds induced to germinate with a combination of constant and diurnal alternating temperatures. <i>Plant Molecular Biology</i> , 2010, 73, 131-142.	2.0	30
5100	Characterising functionally important and ecologically meaningful genetic diversity using a candidate gene approach. <i>Genetica</i> , 2010, 138, 419-432.	0.5	32
5101	Discovery and evaluation of candidate sex-determining genes and xenobiotics in the gonads of lake sturgeon (<i>Acipenser fulvescens</i>). <i>Genetica</i> , 2010, 138, 745-756.	0.5	72
5102	Belief Propagation Estimation of Protein and Domain Interactions Using the Sum-Product Algorithm. <i>IEEE Transactions on Information Theory</i> , 2010, 56, 742-755.	1.5	6
5103	Gene Function Prediction With Gene Interaction Networks: A Context Graph Kernel Approach. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2010, 14, 119-128.	3.6	23
5104	Transcriptional response to heat stress in the Antarctic bivalve <i>Laternula elliptica</i> . <i>Journal of Experimental Marine Biology and Ecology</i> , 2010, 391, 65-72.	0.7	50
5105	Construction and preliminary analysis of a normalized cDNA library from <i>Locusta migratoria manilensis</i> topically infected with <i>Metarhizium anisopliae</i> var. <i>acidum</i> . <i>Journal of Insect Physiology</i> , 2010, 56, 998-1002.	0.9	7
5106	Identification of immediate response genes dominantly expressed in juvenile resistant and susceptible <i>Biomphalaria glabrata</i> snails upon exposure to <i>Schistosoma mansoni</i> . <i>Molecular and Biochemical Parasitology</i> , 2010, 169, 27-39.	0.5	59
5107	Integration of heterogeneous data sources for gene function prediction using decision templates and ensembles of learning machines. <i>Neurocomputing</i> , 2010, 73, 1533-1537.	3.5	20
5108	Effect of high-fat feeding on expression of genes controlling availability of dopamine in mouse hypothalamus. <i>Nutrition</i> , 2010, 26, 411-422.	1.1	79
5109	Transcriptional profiling of skeletal muscle reveals factors that are necessary to maintain satellite cell integrity during ageing. <i>Mechanisms of Ageing and Development</i> , 2010, 131, 9-20.	2.2	37
5110	Insights into aging through measurements of the <i>Drosophila</i> proteome as a function of temperature. <i>Mechanisms of Ageing and Development</i> , 2010, 131, 584-590.	2.2	7
5111	Systematic analysis and prediction of longevity genes in <i>Caenorhabditis elegans</i> . <i>Mechanisms of Ageing and Development</i> , 2010, 131, 700-709.	2.2	25
5112	Elevating the perspective on human stress genomics. <i>Psychoneuroendocrinology</i> , 2010, 35, 955-962.	1.3	105
5113	PlasmoPredict: a gene function prediction website for <i>Plasmodium falciparum</i> . <i>Trends in Parasitology</i> , 2010, 26, 107-110.	1.5	3
5114	Protein annotation in the era of personal genomics. <i>Current Opinion in Structural Biology</i> , 2010, 20, 335-341.	2.6	1

#	ARTICLE	IF	CITATIONS
5115	MoDEL (Molecular Dynamics Extended Library): A Database of Atomistic Molecular Dynamics Trajectories. <i>Structure</i> , 2010, 18, 1399-1409.	1.6	123
5116	Detailed Analysis of Function Divergence in a Large and Diverse Domain Superfamily: Toward a Refined Protocol of Function Classification. <i>Structure</i> , 2010, 18, 1522-1535.	1.6	33
5117	The pursuit of susceptibility genes for Alzheimer's disease: progress and prospects. <i>Trends in Genetics</i> , 2010, 26, 84-93.	2.9	122
5118	Increased sequence conservation of domain repeats in prokaryotic proteins. <i>Trends in Genetics</i> , 2010, 26, 383-387.	2.9	8
5119	Critical reasoning on causal inference in genome-wide linkage and association studies. <i>Trends in Genetics</i> , 2010, 26, 493-498.	2.9	59
5120	Word add-in for ontology recognition: semantic enrichment of scientific literature. <i>BMC Bioinformatics</i> , 2010, 11, 103.	1.2	13
5121	SCPS: a fast implementation of a spectral method for detecting protein families on a genome-wide scale. <i>BMC Bioinformatics</i> , 2010, 11, 120.	1.2	54
5122	Mayday - integrative analytics for expression data. <i>BMC Bioinformatics</i> , 2010, 11, 121.	1.2	102
5123	Integrating gene expression and GO classification for PCA by preclustering. <i>BMC Bioinformatics</i> , 2010, 11, 158.	1.2	15
5124	ProbFAST: Probabilistic Functional Analysis System Tool. <i>BMC Bioinformatics</i> , 2010, 11, 161.	1.2	2
5125	GeneMesh: a web-based microarray analysis tool for relating differentially expressed genes to MeSH terms. <i>BMC Bioinformatics</i> , 2010, 11, 166.	1.2	12
5126	Response network analysis of differential gene expression in human epithelial lung cells during avian influenza infections. <i>BMC Bioinformatics</i> , 2010, 11, 170.	1.2	18
5127	JISTIC: Identification of Significant Targets in Cancer. <i>BMC Bioinformatics</i> , 2010, 11, 189.	1.2	41
5128	Modelling p-value distributions to improve theme-driven survival analysis of cancer transcriptome datasets. <i>BMC Bioinformatics</i> , 2010, 11, 19.	1.2	7
5129	Properties and identification of antibiotic drug targets. <i>BMC Bioinformatics</i> , 2010, 11, 195.	1.2	39
5130	Missing value imputation for epistatic MAPs. <i>BMC Bioinformatics</i> , 2010, 11, 197.	1.2	20
5131	Predicting gene function using hierarchical multi-label decision tree ensembles. <i>BMC Bioinformatics</i> , 2010, 11, 2.	1.2	143
5132	Structural fragment clustering reveals novel structural and functional motifs in α -helical transmembrane proteins. <i>BMC Bioinformatics</i> , 2010, 11, 204.	1.2	13

#	ARTICLE	IF	CITATIONS
5133	GOAL: A software tool for assessing biological significance of genes groups. BMC Bioinformatics, 2010, 11, 229.	1.2	27
5134	ChIPpeakAnno: a Bioconductor package to annotate ChIP-seq and ChIP-chip data. BMC Bioinformatics, 2010, 11, 237.	1.2	963
5135	Gene bi-targeting by viral and human miRNAs. BMC Bioinformatics, 2010, 11, 249.	1.2	27
5136	PhenoFam-gene set enrichment analysis through protein structural information. BMC Bioinformatics, 2010, 11, 254.	1.2	6
5137	Detecting disease associated modules and prioritizing active genes based on high throughput data. BMC Bioinformatics, 2010, 11, 26.	1.2	70
5138	The Yeast Resource Center Public Image Repository: A large database of fluorescence microscopy images. BMC Bioinformatics, 2010, 11, 263.	1.2	34
5139	Prediction of breast cancer prognosis using gene set statistics provides signature stability and biological context. BMC Bioinformatics, 2010, 11, 277.	1.2	87
5140	Gene prioritization and clustering by multi-view text mining. BMC Bioinformatics, 2010, 11, 28.	1.2	33
5141	A comparison of probe-level and probeset models for small-sample gene expression data. BMC Bioinformatics, 2010, 11, 281.	1.2	8
5142	Revealing and avoiding bias in semantic similarity scores for protein pairs. BMC Bioinformatics, 2010, 11, 290.	1.2	38
5143	Super-sparse principal component analyses for high-throughput genomic data. BMC Bioinformatics, 2010, 11, 296.	1.2	35
5144	Saliva Ontology: An ontology-based framework for a Salivaomics Knowledge Base. BMC Bioinformatics, 2010, 11, 302.	1.2	52
5145	Accessing the SEED Genome Databases via Web Services API: Tools for Programmers. BMC Bioinformatics, 2010, 11, 319.	1.2	122
5146	PCA2GO: a new multivariate statistics based method to identify highly expressed GO-Terms. BMC Bioinformatics, 2010, 11, 336.	1.2	4
5147	A factor model to analyze heterogeneity in gene expression. BMC Bioinformatics, 2010, 11, 368.	1.2	15
5148	GeneBrowser 2: an application to explore and identify common biological traits in a set of genes. BMC Bioinformatics, 2010, 11, 389.	1.2	5
5149	Compartmentalization of the Edinburgh Human Metabolic Network. BMC Bioinformatics, 2010, 11, 393.	1.2	92
5150	Ranked retrieval of Computational Biology models. BMC Bioinformatics, 2010, 11, 423.	1.2	24

#	ARTICLE	IF	CITATIONS
5151	CircuitsDB: a database of mixed microRNA/transcription factor feed-forward regulatory circuits in human and mouse. BMC Bioinformatics, 2010, 11, 435.	1.2	129
5152	An exploratory data analysis method to reveal modular latent structures in high-throughput data. BMC Bioinformatics, 2010, 11, 440.	1.2	10
5153	Relations as patterns: bridging the gap between OBO and OWL. BMC Bioinformatics, 2010, 11, 441.	1.2	44
5154	The Neural/Immune Gene Ontology: clipping the Gene Ontology for neurological and immunological systems. BMC Bioinformatics, 2010, 11, 458.	1.2	23
5155	Investigating the validity of current network analysis on static conglomerate networks by protein network stratification. BMC Bioinformatics, 2010, 11, 466.	1.2	8
5156	BSSF: a fingerprint based ultrafast binding site similarity search and function analysis server. BMC Bioinformatics, 2010, 11, 47.	1.2	27
5157	Trees on networks: resolving statistical patterns of phylogenetic similarities among interacting proteins. BMC Bioinformatics, 2010, 11, 470.	1.2	3
5158	PeptideMine - A webserver for the design of peptides for protein-peptide binding studies derived from protein-protein interactomes. BMC Bioinformatics, 2010, 11, 473.	1.2	8
5159	FragViz: visualization of fragmented networks. BMC Bioinformatics, 2010, 11, 475.	1.2	2
5160	A bi-ordering approach to linking gene expression with clinical annotations in gastric cancer. BMC Bioinformatics, 2010, 11, 477.	1.2	3
5161	MCL-CAw: a refinement of MCL for detecting yeast complexes from weighted PPI networks by incorporating core-attachment structure. BMC Bioinformatics, 2010, 11, 504.	1.2	63
5162	Booly: a new data integration platform. BMC Bioinformatics, 2010, 11, 513.	1.2	9
5163	solQTL: a tool for QTL analysis, visualization and linking to genomes at SGN database. BMC Bioinformatics, 2010, 11, 525.	1.2	19
5164	Global screening of potential <i>Candida albicans</i> biofilm-related transcription factors via network comparison. BMC Bioinformatics, 2010, 11, 53.	1.2	29
5165	Formalization of taxon-based constraints to detect inconsistencies in annotation and ontology development. BMC Bioinformatics, 2010, 11, 530.	1.2	48
5166	Incorporating significant amino acid pairs to identify O-linked glycosylation sites on transmembrane proteins and non-transmembrane proteins. BMC Bioinformatics, 2010, 11, 536.	1.2	34
5167	Biana: a software framework for compiling biological interactions and analyzing networks. BMC Bioinformatics, 2010, 11, 56.	1.2	85
5168	An improved method for scoring protein-protein interactions using semantic similarity within the gene ontology. BMC Bioinformatics, 2010, 11, 562.	1.2	153

#	ARTICLE	IF	CITATIONS
5169	Systematic integration of experimental data and models in systems biology. BMC Bioinformatics, 2010, 11, 582.	1.2	28
5170	IntelliGO: a new vector-based semantic similarity measure including annotation origin. BMC Bioinformatics, 2010, 11, 588.	1.2	80
5171	PETALS: Proteomic Evaluation and Topological Analysis of a mutated Locus' Signaling. BMC Bioinformatics, 2010, 11, 596.	1.2	11
5172	A temporal precedence based clustering method for gene expression microarray data. BMC Bioinformatics, 2010, 11, 68.	1.2	9
5173	Extracting consistent knowledge from highly inconsistent cancer gene data sources. BMC Bioinformatics, 2010, 11, 76.	1.2	46
5174	Enrichment of homologs in insignificant BLAST hits by co-complex network alignment. BMC Bioinformatics, 2010, 11, 86.	1.2	8
5175	HDAPD: a web tool for searching the disease-associated protein structures. BMC Bioinformatics, 2010, 11, 88.	1.2	1
5176	BisoGenet: a new tool for gene network building, visualization and analysis. BMC Bioinformatics, 2010, 11, 91.	1.2	294
5177	Short clones or long clones? A simulation study on the use of paired reads in metagenomics. BMC Bioinformatics, 2010, 11, S12.	1.2	11
5178	A hub-attachment based method to detect functional modules from confidence-scored protein interactions and expression profiles. BMC Bioinformatics, 2010, 11, S25.	1.2	40
5179	Functional characterization and topological modularity of molecular interaction networks. BMC Bioinformatics, 2010, 11, S35.	1.2	13
5180	Predicting protein functions by relaxation labelling protein interaction network. BMC Bioinformatics, 2010, 11, S64.	1.2	16
5181	Knowledge-based analysis of microarrays for the discovery of transcriptional regulation relationships. BMC Bioinformatics, 2010, 11, S8.	1.2	12
5182	Association of tissue lineage and gene expression: conservatively and differentially expressed genes define common and special functions of tissues. BMC Bioinformatics, 2010, 11, S1.	1.2	27
5183	Sorting out inherent features of head-to-head gene pairs by evolutionary conservation. BMC Bioinformatics, 2010, 11, S16.	1.2	11
5184	IPRStats: visualization of the functional potential of an InterProScan run. BMC Bioinformatics, 2010, 11, S13.	1.2	12
5185	Quail Genomics: a knowledgebase for Northern bobwhite. BMC Bioinformatics, 2010, 11, S13.	1.2	14
5186	Discovering gene functional relationships using FAUN (Feature Annotation Using Nonnegative matrix) Tj ETQq1 1 0,784314 rgBT /Overl 1.2 12	1.2	12

#	ARTICLE	IF	CITATIONS
5187	Next generation models for storage and representation of microbial biological annotation. BMC Bioinformatics, 2010, 11, S15.	1.2	9
5188	GOModeler- A tool for hypothesis-testing of functional genomics datasets. BMC Bioinformatics, 2010, 11, S29.	1.2	11
5189	Identification of diagnostic subnetwork markers for cancer in human protein-protein interaction network. BMC Bioinformatics, 2010, 11, S8.	1.2	58
5190	DODO: an efficient orthologous genes assignment tool based on domain architectures. Domain based ortholog detection. BMC Bioinformatics, 2010, 11, S6.	1.2	13
5191	Network analysis of human protein location. BMC Bioinformatics, 2010, 11, S9.	1.2	12
5192	Positive selection of HIV host factors and the evolution of lentivirus genes. BMC Evolutionary Biology, 2010, 10, 186.	3.2	15
5193	Suppression subtractive hybridization analysis reveals expression of conserved and novel genes in male accessory glands of the ant <i>Leptothorax gredleri</i> . BMC Evolutionary Biology, 2010, 10, 273.	3.2	6
5194	Human functional genetic studies are biased against the medically most relevant primate-specific genes. BMC Evolutionary Biology, 2010, 10, 316.	3.2	16
5195	Schizophrenia and vitamin D related genes could have been subject to latitude-driven adaptation. BMC Evolutionary Biology, 2010, 10, 351.	3.2	32
5196	Analysis of a normalised expressed sequence tag (EST) library from a key pollinator, the bumblebee <i>Bombus terrestris</i> . BMC Genomics, 2010, 11, 110.	1.2	15
5197	Transcriptomic changes arising during light-induced sporulation in <i>Physarum polycephalum</i> . BMC Genomics, 2010, 11, 115.	1.2	23
5198	Whole genome analysis of p38 SAPK-mediated gene expression upon stress. BMC Genomics, 2010, 11, 144.	1.2	55
5199	Transcriptome analysis of reproductive tissue and intrauterine developmental stages of the tsetse fly (<i>Glossina morsitans morsitans</i>). BMC Genomics, 2010, 11, 160.	1.2	23
5200	TC-motifs at the TATA-box expected position in plant genes: a novel class of motifs involved in the transcription regulation. BMC Genomics, 2010, 11, 166.	1.2	70
5201	Systematic discovery of regulatory motifs in <i>Fusarium graminearum</i> by comparing four <i>Fusarium</i> genomes. BMC Genomics, 2010, 11, 208.	1.2	16
5202	An insight into the sialome of <i>Glossina morsitans morsitans</i> . BMC Genomics, 2010, 11, 213.	1.2	76
5203	Intronic microRNAs support their host genes by mediating synergistic and antagonistic regulatory effects. BMC Genomics, 2010, 11, 224.	1.2	126
5204	Genome-wide comparison between IL-17 and combined TNF-alpha/IL-17 induced genes in primary murine hepatocytes. BMC Genomics, 2010, 11, 226.	1.2	50

#	ARTICLE	IF	CITATIONS
5205	Whole transcriptome analysis of the hippocampus: toward a molecular portrait of epileptogenesis. BMC Genomics, 2010, 11, 230.	1.2	92
5206	Signal pathways JNK and NF- κ B, identified by global gene expression profiling, are involved in regulation of TNF α -induced mPGES-1 and COX-2 expression in gingival fibroblasts. BMC Genomics, 2010, 11, 241.	1.2	48
5207	Discovery and comparative profiling of microRNAs in a sweet orange red-flesh mutant and its wild type. BMC Genomics, 2010, 11, 246.	1.2	120
5208	Genomics Portals: integrative web-platform for mining genomics data. BMC Genomics, 2010, 11, 27.	1.2	13
5209	An EST resource for tilapia based on 17 normalized libraries and assembly of 116,899 sequence tags. BMC Genomics, 2010, 11, 278.	1.2	39
5210	Salmo salar and Esox lucius full-length cDNA sequences reveal changes in evolutionary pressures on a post-tetraploidization genome. BMC Genomics, 2010, 11, 279.	1.2	163
5211	Touring Ensembl: A practical guide to genome browsing. BMC Genomics, 2010, 11, 295.	1.2	33
5212	Massively parallel pyrosequencing-based transcriptome analyses of small brown planthopper (Laodelphax striatellus), a vector insect transmitting rice stripe virus (RSV). BMC Genomics, 2010, 11, 303.	1.2	115
5213	Genome-wide expression links the electron transfer pathway of Shewanella oneidensis to chemotaxis. BMC Genomics, 2010, 11, 319.	1.2	12
5214	Classifying genes to the correct Gene Ontology Slim term in Saccharomyces cerevisiae using neighbouring genes with classification learning. BMC Genomics, 2010, 11, 340.	1.2	5
5215	Germline-dependent gene expression in distant non-gonadal somatic tissues of Drosophila. BMC Genomics, 2010, 11, 346.	1.2	31
5216	Development of an oligo DNA microarray for the European sea bass and its application to expression profiling of jaw deformity. BMC Genomics, 2010, 11, 354.	1.2	37
5217	Functional genomics of human bronchial epithelial cells directly interacting with conidia of Aspergillus fumigatus. BMC Genomics, 2010, 11, 358.	1.2	61
5218	Insights into shell deposition in the Antarctic bivalve Laternula elliptica: gene discovery in the mantle transcriptome using 454 pyrosequencing. BMC Genomics, 2010, 11, 362.	1.2	160
5219	The expression of genes coding for distinct types of glycine-rich proteins varies according to the biology of three metastriate ticks, Rhipicephalus (Boophilus) microplus, Rhipicephalus sanguineus and Amblyomma cajennense. BMC Genomics, 2010, 11, 363.	1.2	60
5220	Proteome-wide survey of phosphorylation patterns affected by nuclear DNA polymorphisms in Arabidopsis thaliana. BMC Genomics, 2010, 11, 411.	1.2	21
5221	Orthology confers intron position conservation. BMC Genomics, 2010, 11, 412.	1.2	29
5222	Comparative analysis of secreted protein evolution using expressed sequence tags from four poplar leaf rusts (Melampsora spp.). BMC Genomics, 2010, 11, 422.	1.2	59

#	ARTICLE	IF	CITATIONS
5223	An insight into the sialotranscriptome of the brown dog tick, <i>Rhipicephalus sanguineus</i> . BMC Genomics, 2010, 11, 450.	1.2	91
5224	Genome mapping and characterization of the <i>Anopheles gambiae</i> heterochromatin. BMC Genomics, 2010, 11, 459.	1.2	44
5225	Expression profiling of prospero in the <i>Drosophila</i> larval chemosensory organ: Between growth and outgrowth. BMC Genomics, 2010, 11, 47.	1.2	10
5226	Gill transcriptome response to changes in environmental calcium in the green spotted puffer fish. BMC Genomics, 2010, 11, 476.	1.2	39
5227	An insight into the sialotranscriptome of the West Nile mosquito vector, <i>Culex tarsalis</i> . BMC Genomics, 2010, 11, 51.	1.2	37
5228	A potential role for intragenic miRNAs on their hosts' interactome. BMC Genomics, 2010, 11, 533.	1.2	142
5229	Aberrant host immune response induced by highly virulent PRRSV identified by digital gene expression tag profiling. BMC Genomics, 2010, 11, 544.	1.2	78
5230	High-throughput sequencing and analysis of the gill tissue transcriptome from the deep-sea hydrothermal vent mussel <i>Bathymodiolus azoricus</i> . BMC Genomics, 2010, 11, 559.	1.2	114
5231	Genome-wide computational prediction of tandem gene arrays: application in yeasts. BMC Genomics, 2010, 11, 56.	1.2	13
5232	Heading Down the Wrong Pathway: on the Influence of Correlation within Gene Sets. BMC Genomics, 2010, 11, 574.	1.2	69
5233	Differential gene expression during the moult cycle of Antarctic krill (<i>Euphausia superba</i>). BMC Genomics, 2010, 11, 582.	1.2	43
5234	Genetic diversity and striatal gene networks: focus on the heterogeneous stock-collaborative cross (HS-CC) mouse. BMC Genomics, 2010, 11, 585.	1.2	58
5235	Gene duplications in prokaryotes can be associated with environmental adaptation. BMC Genomics, 2010, 11, 588.	1.2	102
5236	A transcriptomic analysis of gene expression in the venom gland of the snake <i>Bothrops alternatus</i> (urutu). BMC Genomics, 2010, 11, 605.	1.2	55
5237	Transcriptome and proteome analysis of <i>Pinctada margaritifera</i> calcifying mantle and shell: focus on biomineralization. BMC Genomics, 2010, 11, 613.	1.2	208
5238	Genes optimized by evolution for accurate and fast translation encode in Archaea and Bacteria a broad and characteristic spectrum of protein functions. BMC Genomics, 2010, 11, 617.	1.2	7
5239	Insights into metazoan evolution from <i>alvinella pompejana</i> cDNAs. BMC Genomics, 2010, 11, 634.	1.2	46
5240	Bioinformatic analysis of ESTs collected by Sanger and pyrosequencing methods for a keystone forest tree species: oak. BMC Genomics, 2010, 11, 650.	1.2	82

#	ARTICLE	IF	CITATIONS
5241	LAB-Secretome: a genome-scale comparative analysis of the predicted extracellular and surface-associated proteins of Lactic Acid Bacteria. BMC Genomics, 2010, 11, 651.	1.2	79
5242	Skeletal muscle gene expression in response to resistance exercise: sex specific regulation. BMC Genomics, 2010, 11, 659.	1.2	91
5243	Comparative transcriptome profiling analyses during the lag phase uncover YAP1, PDR1, PDR3, RPN4, and HSF1 as key regulatory genes in genomic adaptation to the lignocellulose derived inhibitor HMF for <i>Saccharomyces cerevisiae</i> . BMC Genomics, 2010, 11, 660.	1.2	146
5244	A genome-wide study of PDZ-domain interactions in <i>C. elegans</i> reveals a high frequency of non-canonical binding. BMC Genomics, 2010, 11, 671.	1.2	39
5245	Apoplast proteome reveals that extracellular matrix contributes to multistress response in poplar. BMC Genomics, 2010, 11, 674.	1.2	70
5246	Deep sequencing of New World screw-worm transcripts to discover genes involved in insecticide resistance. BMC Genomics, 2010, 11, 695.	1.2	31
5247	Relationship between operon preference and functional properties of persistent genes in bacterial genomes. BMC Genomics, 2010, 11, 71.	1.2	24
5248	Combining modularity, conservation, and interactions of proteins significantly increases precision and coverage of protein function prediction. BMC Genomics, 2010, 11, 717.	1.2	12
5249	Gene prioritization in Type 2 Diabetes using domain interactions and network analysis. BMC Genomics, 2010, 11, 84.	1.2	24
5250	Data integration and exploration for the identification of molecular mechanisms in tumor-immune cells interaction. BMC Genomics, 2010, 11, S7.	1.2	16
5251	Predicting gene function using few positive examples and unlabeled ones. BMC Genomics, 2010, 11, S11.	1.2	2
5252	Generation, analysis and functional annotation of expressed sequence tags from the sheepshead minnow (<i>Cyprinodon variegatus</i>). BMC Genomics, 2010, 11, S4.	1.2	3
5253	Core genome components and lineage specific expansions in malaria parasites <i>Plasmodium</i> . BMC Genomics, 2010, 11, S13.	1.2	8
5254	Investigation gene and microRNA expression in glioblastoma. BMC Genomics, 2010, 11, S16.	1.2	36
5255	A new approach to construct pathway connected networks and its application in dose responsive gene expression profiles of rat liver regulated by 2,4DNT. BMC Genomics, 2010, 11, S4.	1.2	5
5256	Qualitative reasoning of dynamic gene regulatory interactions from gene expression data. BMC Genomics, 2010, 11, S14.	1.2	10
5257	Advancing standards for bioinformatics activities: persistence, reproducibility, disambiguation and Minimum Information About a Bioinformatics investigation (MIABi). BMC Genomics, 2010, 11, S27.	1.2	29
5258	In planta gene expression analysis of <i>Xanthomonas oryzae</i> pathovar <i>oryzae</i> , African strain MAI1. BMC Microbiology, 2010, 10, 170.	1.3	26

#	ARTICLE	IF	CITATIONS
5259	New structural and functional defects in polyphosphate deficient bacteria: A cellular and proteomic study. <i>BMC Microbiology</i> , 2010, 10, 7.	1.3	35
5260	SoyDB: a knowledge database of soybean transcription factors. <i>BMC Plant Biology</i> , 2010, 10, 14.	1.6	104
5261	Pathway analysis of the transcriptome and metabolome of salt sensitive and tolerant poplar species reveals evolutionary adaption of stress tolerance mechanisms. <i>BMC Plant Biology</i> , 2010, 10, 150.	1.6	141
5262	RoBuST: an integrated genomics resource for the root and bulb crop families Apiaceae and Alliaceae. <i>BMC Plant Biology</i> , 2010, 10, 161.	1.6	14
5263	Transcriptome changes in grapevine (<i>Vitis vinifera</i> L.) cv. Malbec leaves induced by ultraviolet-B radiation. <i>BMC Plant Biology</i> , 2010, 10, 224.	1.6	120
5264	Transcriptome analysis of germinating maize kernels exposed to smoke-water and the active compound KAR1. <i>BMC Plant Biology</i> , 2010, 10, 236.	1.6	43
5265	Structure and expression of the maize (<i>Zea mays</i> L.) SUN-domain protein gene family: evidence for the existence of two divergent classes of SUN proteins in plants. <i>BMC Plant Biology</i> , 2010, 10, 269.	1.6	70
5266	Complementary genetic and genomic approaches help characterize the linkage group I seed protein QTL in soybean. <i>BMC Plant Biology</i> , 2010, 10, 41.	1.6	96
5267	Large impact of the apoplast on somatic embryogenesis in <i>Cyclamen persicum</i> offers possibilities for improved developmental control in vitro. <i>BMC Plant Biology</i> , 2010, 10, 77.	1.6	30
5268	Uncovering the evolutionary origin of plant molecular processes: comparison of Coleochaete (<i>Coleochaetales</i>) and Spirogyra (<i>Zygnematales</i>) transcriptomes. <i>BMC Plant Biology</i> , 2010, 10, 96.	1.6	91
5269	The RNA binding protein HuR differentially regulates unique subsets of mRNAs in estrogen receptor negative and estrogen receptor positive breast cancer. <i>BMC Cancer</i> , 2010, 10, 126.	1.1	53
5270	Growth delay of human bladder cancer cells by Prostate Stem Cell Antigen downregulation is associated with activation of immune signaling pathways. <i>BMC Cancer</i> , 2010, 10, 129.	1.1	32
5271	Onconase responsive genes in human mesothelioma cells: implications for an RNA damaging therapeutic agent. <i>BMC Cancer</i> , 2010, 10, 34.	1.1	29
5272	Merging transcriptomics and metabolomics - advances in breast cancer profiling. <i>BMC Cancer</i> , 2010, 10, 628.	1.1	101
5273	Determining correspondences between high-frequency MedDRA concepts and SNOMED: a case study. <i>BMC Medical Informatics and Decision Making</i> , 2010, 10, 66.	1.5	20
5274	Investigation of PARP-1, PARP-2, and PARG interactomes by affinity-purification mass spectrometry. <i>Proteome Science</i> , 2010, 8, 22.	0.7	133
5275	Cellular and molecular evidence for a role of tumor necrosis factor alpha in the ovulatory mechanism of trout. <i>Reproductive Biology and Endocrinology</i> , 2010, 8, 34.	1.4	34
5276	ReCGiP, a database of reproduction candidate genes in pigs based on bibliomics. <i>Reproductive Biology and Endocrinology</i> , 2010, 8, 96.	1.4	7

#	ARTICLE	IF	CITATIONS
5277	A genomics-informed, SNP association study reveals FBLN1 and FABP4 as contributing to resistance to fleece rot in Australian Merino sheep. <i>BMC Veterinary Research</i> , 2010, 6, 27.	0.7	25
5278	Snazer: the simulations and networks analyzer. <i>BMC Systems Biology</i> , 2010, 4, 1.	3.0	175
5279	The function of communities in protein interaction networks at multiple scales. <i>BMC Systems Biology</i> , 2010, 4, 100.	3.0	79
5280	Molecular mechanistic associations of human diseases. <i>BMC Systems Biology</i> , 2010, 4, 124.	3.0	11
5281	A yeast's eye view of mammalian reproduction: cross-species gene co-expression in meiotic prophase. <i>BMC Systems Biology</i> , 2010, 4, 125.	3.0	6
5282	Protein complex prediction based on k-connected subgraphs in protein interaction network. <i>BMC Systems Biology</i> , 2010, 4, 129.	3.0	37
5283	Statistical inference of the time-varying structure of gene-regulation networks. <i>BMC Systems Biology</i> , 2010, 4, 130.	3.0	135
5284	Regulatory network modelling of iron acquisition by a fungal pathogen in contact with epithelial cells. <i>BMC Systems Biology</i> , 2010, 4, 148.	3.0	31
5285	Multi-level reproducibility of signature hubs in human interactome for breast cancer metastasis. <i>BMC Systems Biology</i> , 2010, 4, 151.	3.0	30
5286	Patterns of human gene expression variance show strong associations with signaling network hierarchy. <i>BMC Systems Biology</i> , 2010, 4, 154.	3.0	24
5287	Regulation patterns in signaling networks of cancer. <i>BMC Systems Biology</i> , 2010, 4, 162.	3.0	38
5288	Features analysis for identification of date and party hubs in protein interaction network of <i>Saccharomyces Cerevisiae</i> . <i>BMC Systems Biology</i> , 2010, 4, 172.	3.0	13
5289	Understanding protein evolutionary rate by integrating gene co-expression with protein interactions. <i>BMC Systems Biology</i> , 2010, 4, 179.	3.0	12
5290	Integrated cellular network of transcription regulations and protein-protein interactions. <i>BMC Systems Biology</i> , 2010, 4, 20.	3.0	57
5291	Searching for functional gene modules with interaction component models. <i>BMC Systems Biology</i> , 2010, 4, 4.	3.0	23
5292	Low-complexity regions within protein sequences have position-dependent roles. <i>BMC Systems Biology</i> , 2010, 4, 43.	3.0	181
5293	Identification of responsive gene modules by network-based gene clustering and extending: application to inflammation and angiogenesis. <i>BMC Systems Biology</i> , 2010, 4, 47.	3.0	56
5294	An information-flow-based model with dissipation, saturation and direction for active pathway inference. <i>BMC Systems Biology</i> , 2010, 4, 72.	3.0	5

#	ARTICLE	IF	CITATIONS
5295	Network properties of human disease genes with pleiotropic effects. <i>BMC Systems Biology</i> , 2010, 4, 78.	3.0	81
5296	Composite functional module inference: detecting cooperation between transcriptional regulation and protein interaction by mantel test. <i>BMC Systems Biology</i> , 2010, 4, 82.	3.0	6
5297	A collection of bioconductor methods to visualize gene-list annotations. <i>BMC Research Notes</i> , 2010, 3, 10.	0.6	47
5298	OntoFox: web-based support for ontology reuse. <i>BMC Research Notes</i> , 2010, 3, 175.	0.6	145
5299	Predicted sub-populations in a marine shrimp proteome as revealed by combined EST and cDNA data from multiple <i>Penaeus</i> species. <i>BMC Research Notes</i> , 2010, 3, 295.	0.6	10
5300	Applying the functional abnormality ontology pattern to anatomical functions. <i>Journal of Biomedical Semantics</i> , 2010, 1, 4.	0.9	12
5301	An evolutionary approach to Function. <i>Journal of Biomedical Semantics</i> , 2010, 1, S4.	0.9	3
5302	Modeling biomedical experimental processes with OBI. <i>Journal of Biomedical Semantics</i> , 2010, 1, S7.	0.9	207
5303	Transcriptomic underpinning of toxicant-mediated physiological function alterations in three terrestrial invertebrate taxa: A review. <i>Environmental Pollution</i> , 2010, 158, 2793-2808.	3.7	66
5304	The molecular basis for sonographic cervical shortening at term: identification of differentially expressed genes and the epithelial-mesenchymal transition as a function of cervical length. <i>American Journal of Obstetrics and Gynecology</i> , 2010, 203, 472.e1-472.e14.	0.7	29
5305	Semantic SenseLab: Implementing the vision of the Semantic Web in neuroscience. <i>Artificial Intelligence in Medicine</i> , 2010, 48, 21-28.	3.8	7
5306	A knowledge-driven approach to biomedical document conceptualization. <i>Artificial Intelligence in Medicine</i> , 2010, 49, 67-78.	3.8	12
5307	Dynamic composition of medical support services in the ICU: Platform and algorithm design details. <i>Computer Methods and Programs in Biomedicine</i> , 2010, 100, 248-264.	2.6	15
5308	A Cellular Memory of Developmental History Generates Phenotypic Diversity in <i>C. elegans</i> . <i>Current Biology</i> , 2010, 20, 149-155.	1.8	111
5309	Rapid Expansion and Functional Divergence of Subtelomeric Gene Families in Yeasts. <i>Current Biology</i> , 2010, 20, 895-903.	1.8	323
5310	A Gene-Specific Requirement of RNA Polymerase II CTD Phosphorylation for Sexual Differentiation in <i>S. pombe</i> . <i>Current Biology</i> , 2010, 20, 1053-1064.	1.8	67
5311	Visualizing the drug target landscape. <i>Drug Discovery Today</i> , 2010, 15, 3-15.	3.2	50
5312	Heteronemin, a spongian sesterterpene, inhibits TNF α -induced NF- κ B activation through proteasome inhibition and induces apoptotic cell death. <i>Biochemical Pharmacology</i> , 2010, 79, 610-622.	2.0	85

#	ARTICLE	IF	CITATIONS
5313	Positive selection on apoptosis related genes. FEBS Letters, 2010, 584, 469-476.	1.3	38
5314	Modulation of gene expression by α -tocopherol and α -tocopheryl phosphate in THP-1 monocytes. Free Radical Biology and Medicine, 2010, 49, 1989-2000.	1.3	48
5315	Brevetoxin-2 induces an inflammatory response in an alveolar macrophage cell line. International Journal of Hygiene and Environmental Health, 2010, 213, 352-358.	2.1	12
5316	Tick-susceptible <i>Bos taurus</i> cattle display an increased cellular response at the site of larval <i>Rhipicephalus (Boophilus) microplus</i> attachment, compared with tick-resistant <i>Bos indicus</i> cattle. International Journal for Parasitology, 2010, 40, 431-441.	1.3	61
5317	SoFoCles: Feature filtering for microarray classification based on Gene Ontology. Journal of Biomedical Informatics, 2010, 43, 1-14.	2.5	22
5318	GOClonto: An ontological clustering approach for conceptualizing PubMed abstracts. Journal of Biomedical Informatics, 2010, 43, 31-40.	2.5	13
5319	CelOWS: An ontology based framework for the provision of semantic web services related to biological models. Journal of Biomedical Informatics, 2010, 43, 125-136.	2.5	30
5320	Average correlation clustering algorithm (ACCA) for grouping of co-regulated genes with similar pattern of variation in their expression values. Journal of Biomedical Informatics, 2010, 43, 560-568.	2.5	20
5321	Protein interaction network underpins concordant prognosis among heterogeneous breast cancer signatures. Journal of Biomedical Informatics, 2010, 43, 385-396.	2.5	49
5322	Transcriptional networks characterize ventricular dysfunction after myocardial infarction: A proof-of-concept investigation. Journal of Biomedical Informatics, 2010, 43, 812-819.	2.5	13
5323	Epigenetic modifications induced by RGC-32 in colon cancer. Experimental and Molecular Pathology, 2010, 88, 67-76.	0.9	41
5324	Toxicogenomics and cancer risk assessment: A framework for key event analysis and dose-response assessment for nongenotoxic carcinogens. Regulatory Toxicology and Pharmacology, 2010, 58, 369-381.	1.3	31
5325	Machine learning approach identifies new pathways associated with demyelination in a viral model of multiple sclerosis. Journal of Cellular and Molecular Medicine, 2010, 14, 434-448.	1.6	53
5326	The Need for Even Further Clarity About Cleary. Industrial and Organizational Psychology, 2010, 3, 206-209.	0.5	1
5327	Establishment of mice expressing EGFP in the placode-derived inner ear sensory cell lineage and FACS array analysis focused on the regional specificity of the otocyst. Journal of Comparative Neurology, 2010, 518, 4702-4722.	0.9	3
5328	Pathway-based analysis for genome-wide association studies using supervised principal components. Genetic Epidemiology, 2010, 34, 716-724.	0.6	48
5329	Comparative gene expression profiling of olfactory ensheathing cells from olfactory bulb and olfactory mucosa. Glia, 2010, 58, 1570-1580.	2.5	62
5330	Global changes in gene regulation demonstrate that unconjugated bilirubin is able to upregulate and activate select components of the endoplasmic reticulum stress response pathway. Journal of Biochemical and Molecular Toxicology, 2010, 24, 73-88.	1.4	9

#	ARTICLE	IF	CITATIONS
5331	Communicating subcellular distributions. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2010, 77A, 686-692.	1.1	26
5332	Evaluation and optimization of removal of an acid-insoluble surfactant for shotgun analysis of membrane proteome. <i>Electrophoresis</i> , 2010, 31, 2705-2713.	1.3	47
5333	Dried polyacrylamide gel absorption: A method for efficient elimination of the interferences from SDS-solubilized protein samples in mass spectrometry-based proteome analysis. <i>Electrophoresis</i> , 2010, 31, 3816-3822.	1.3	10
5336	Microarray data classification using inductive logic programming and gene ontology background information. <i>Journal of Chemometrics</i> , 2010, 24, 231-240.	0.7	5
5337	Functional Features, Biological Pathways, and Protein Interaction Networks of Addiction-Related Genes. <i>Chemistry and Biodiversity</i> , 2010, 7, 1153-1162.	1.0	16
5338	Scientific data repositories on the Web: An initial survey. <i>Journal of the Association for Information Science and Technology</i> , 2010, 61, 2029-2048.	2.6	70
5339	Concepts and semantic relations in information science. <i>Journal of the Association for Information Science and Technology</i> , 2010, 61, 1951-1969.	2.6	35
5340	Dynamic network rewiring determines temporal regulatory functions in <i>Drosophila melanogaster</i> development processes. <i>BioEssays</i> , 2010, 32, 505-513.	1.2	16
5341	Subcellular phosphoproteomics. <i>Mass Spectrometry Reviews</i> , 2010, 29, 962-990.	2.8	36
5342	Bootstrapping location relations from text. <i>Proceedings of the American Society for Information Science and Technology</i> , 2010, 47, 1-9.	0.2	1
5343	Rescue of F508del-CFTR by RXR motif inactivation triggers proteome modulation associated with the unfolded protein response. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 856-865.	1.1	31
5344	Using ontologies for querying and analysing protein-protein interaction data. <i>Procedia Computer Science</i> , 2010, 1, 997-1004.	1.2	17
5345	MIB: Using mutual information for biclustering gene expression data. <i>Pattern Recognition</i> , 2010, 43, 2692-2697.	5.1	33
5346	Meta sequence analysis of human blood peptides and their parent proteins. <i>Journal of Proteomics</i> , 2010, 73, 1163-1175.	1.2	25
5347	Development of a new magnetic beads-based immunoprecipitation strategy for proteomics analysis. <i>Journal of Proteomics</i> , 2010, 73, 1491-1501.	1.2	6
5348	It's the machine that matters: Predicting gene function and phenotype from protein networks. <i>Journal of Proteomics</i> , 2010, 73, 2277-2289.	1.2	111
5349	Bioinformatics algorithm development for Grid environments. <i>Journal of Systems and Software</i> , 2010, 83, 1249-1257.	3.3	3
5350	Gneg-mPLoc: A top-down strategy to enhance the quality of predicting subcellular localization of Gram-negative bacterial proteins. <i>Journal of Theoretical Biology</i> , 2010, 264, 326-333.	0.8	163

#	ARTICLE	IF	CITATIONS
5351	Community detection in graphs. <i>Physics Reports</i> , 2010, 486, 75-174.	10.3	8,128
5352	Analysis of expressed sequence tags from a NaHCO ₃ -treated alkali-tolerant plant, <i>Chloris virgata</i> . <i>Plant Physiology and Biochemistry</i> , 2010, 48, 247-255.	2.8	18
5353	Advances in Nutrigenomics research: Novel and future analytical approaches to investigate the biological activity of natural compounds and food functions. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2010, 51, 290-304.	1.4	92
5354	Query performance evaluation of an architecture for fine-grained integration of heterogeneous grid data sources. <i>Future Generation Computer Systems</i> , 2010, 26, 1073-1091.	4.9	2
5355	Clustering of tag-induced subgraphs in complex networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010, 389, 5887-5894.	1.2	2
5356	A repertoire of the dominant transcripts from the salivary glands of the blood-sucking bug, <i>Triatoma dimidiata</i> , a vector of Chagas disease. <i>Infection, Genetics and Evolution</i> , 2010, 10, 184-191.	1.0	40
5357	Assessment of protein domain fusions in human protein interaction networks prediction: Application to the human kinetochore model. <i>New Biotechnology</i> , 2010, 27, 755-765.	2.4	9
5358	Integration of Gene Ontology-based similarities for supporting analysis of protein-protein interaction networks. <i>Pattern Recognition Letters</i> , 2010, 31, 2073-2082.	2.6	12
5359	High density gene expression microarrays and gene ontology analysis for identifying processes in implanted tissue engineering constructs. <i>Biomaterials</i> , 2010, 31, 8299-8312.	5.7	19
5360	An integrative pathway-based clinical-genomic model for cancer survival prediction. <i>Statistics and Probability Letters</i> , 2010, 80, 1313-1319.	0.4	20
5361	Proteomic analysis of embryonic <i>Fasciola hepatica</i> : Characterization and antigenic potential of a developmentally regulated heat shock protein. <i>Veterinary Parasitology</i> , 2010, 169, 62-75.	0.7	27
5362	Semantic Web and Social Web heading towards Living Documents in the Life Sciences. <i>Web Semantics</i> , 2010, 8, 155-162.	2.2	20
5363	Gel absorption-based sample preparation for the analysis of membrane proteome by mass spectrometry. <i>Analytical Biochemistry</i> , 2010, 404, 204-210.	1.1	19
5364	Effects of moderate drinking during pregnancy on placental gene expression. <i>Alcohol</i> , 2010, 44, 673-690.	0.8	52
5365	Changes in gene expression in regions of the extended amygdala of alcohol-preferring rats after binge-like alcohol drinking. <i>Alcohol</i> , 2010, 44, 171-183.	0.8	61
5366	Proteomic analysis of primary porcine endothelial cells after infection by classical swine fever virus. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 1882-1888.	1.1	15
5367	Intra- and inter-omic fusion of metabolic profiling data in a systems biology framework. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2010, 104, 121-131.	1.8	51
5368	Towards an ontology for psychosis. <i>Cognitive Systems Research</i> , 2010, 11, 42-52.	1.9	5

#	ARTICLE	IF	CITATIONS
5369	Natural immunity to cancer in humans. <i>Current Opinion in Immunology</i> , 2010, 22, 215-222.	2.4	153
5370	An elastic network model to identify characteristic stress response genes. <i>Computational Biology and Chemistry</i> , 2010, 34, 193-202.	1.1	1
5371	Functional characterization of plant small RNAs based on next-generation sequencing data. <i>Computational Biology and Chemistry</i> , 2010, 34, 308-312.	1.1	11
5372	A knowledge-driven probabilistic framework for the prediction of protein-protein interaction networks. <i>Computers in Biology and Medicine</i> , 2010, 40, 306-317.	3.9	16
5373	Utilizing shared interacting domain patterns and Gene Ontology information to improve protein-protein interaction prediction. <i>Computers in Biology and Medicine</i> , 2010, 40, 555-564.	3.9	11
5374	Relationship between periodic dinucleotides and the nucleosome structure revealed by alpha shape modeling. <i>Chemical Physics Letters</i> , 2010, 489, 225-228.	1.2	14
5375	Management of evolving semantic grid metadata within a collaborative platform. <i>Information Sciences</i> , 2010, 180, 1837-1849.	4.0	4
5376	Towards reliable isoform quantification using RNA-SEQ data. <i>BMC Bioinformatics</i> , 2010, 11, S6.	1.2	32
5377	Gene expression following induction of regeneration in <i>Drosophila</i> wing imaginal discs. Expression profile of regenerating wing discs. <i>BMC Developmental Biology</i> , 2010, 10, 94.	2.1	56
5378	Global transcriptional profiles of beating clusters derived from human induced pluripotent stem cells and embryonic stem cells are highly similar. <i>BMC Developmental Biology</i> , 2010, 10, 98.	2.1	76
5379	Tracking the transcriptional host response from the acute to the regenerative phase of experimental pneumococcal meningitis. <i>BMC Infectious Diseases</i> , 2010, 10, 176.	1.3	16
5380	Inflammation gene variants and susceptibility to albuminuria in the U.S. population: analysis in the Third National Health and Nutrition Examination Survey (NHANES III), 1991-1994. <i>BMC Medical Genetics</i> , 2010, 11, 155.	2.1	14
5381	Senescent vs. non-senescent cells in the human annulus in vivo: Cell harvest with laser capture microdissection and gene expression studies with microarray analysis. <i>BMC Biotechnology</i> , 2010, 10, 5.	1.7	31
5382	Identification of recurring protein structure microenvironments and discovery of novel functional sites around CYS residues. <i>BMC Structural Biology</i> , 2010, 10, 4.	2.3	21
5383	Structural interpretation of protein-protein interaction network. <i>BMC Structural Biology</i> , 2010, 10, S4.	2.3	10
5384	Nutrient control of eukaryote cell growth: a systems biology study in yeast. <i>BMC Biology</i> , 2010, 8, 68.	1.7	89
5385	The evolution and functional repertoire of translation proteins following the origin of life. <i>Biology Direct</i> , 2010, 5, 15.	1.9	41
5386	Bioinformatics analysis of <i>Brucella</i> vaccines and vaccine targets using VIOLIN. <i>Immunome Research</i> , 2010, 6, S5.	0.1	46

#	ARTICLE	IF	CITATIONS
5387	Curating the innate immunity interactome. <i>BMC Systems Biology</i> , 2010, 4, 117.	3.0	68
5388	Antimalarial drug targets in <i>Plasmodium falciparum</i> predicted by stage-specific metabolic network analysis. <i>BMC Systems Biology</i> , 2010, 4, 120.	3.0	101
5389	BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models. <i>BMC Systems Biology</i> , 2010, 4, 92.	3.0	467
5390	Identifying dysfunctional crosstalk of pathways in various regions of Alzheimer's disease brains. <i>BMC Systems Biology</i> , 2010, 4, S11.	3.0	80
5391	Shrunken methodology to genome-wide SNPs selection and construction of SNPs networks. <i>BMC Systems Biology</i> , 2010, 4, S5.	3.0	8
5392	Predicting environmental chemical factors associated with disease-related gene expression data. <i>BMC Medical Genomics</i> , 2010, 3, 17.	0.7	24
5393	LNCaP Atlas: Gene expression associated with in vivoprogression to castration-recurrent prostate cancer. <i>BMC Medical Genomics</i> , 2010, 3, 43.	0.7	73
5394	Literature-based discovery of diabetes- and ROS-related targets. <i>BMC Medical Genomics</i> , 2010, 3, 49.	0.7	29
5395	A reference guide for tree analysis and visualization. <i>BioData Mining</i> , 2010, 3, 1.	2.2	81
5396	Applications and methods utilizing the Simple Semantic Web Architecture and Protocol (SSWAP) for bioinformatics resource discovery and disparate data and service integration. <i>BioData Mining</i> , 2010, 3, 3.	2.2	11
5397	ATHENA: A knowledge-based hybrid backpropagation-grammatical evolution neural network algorithm for discovering epistasis among quantitative trait Loci. <i>BioData Mining</i> , 2010, 3, 5.	2.2	43
5398	Comparative proteomic analysis of differentially expressed proteins in primary retinoblastoma tumors. <i>Proteomics - Clinical Applications</i> , 2010, 4, 449-463.	0.8	34
5399	Shotgun proteomics identifies proteins specific for acute renal transplant rejection. <i>Proteomics - Clinical Applications</i> , 2010, 4, 32-47.	0.8	105
5400	Proteomic analysis of endoscopically (endoscopic pancreatic function test) collected gastroduodenal fluid using inâ€gel tryptic digestion followed by LCâ€MS/MS. <i>Proteomics - Clinical Applications</i> , 2010, 4, 715-725.	0.8	22
5401	Global analysis of the rat and human platelet proteome â€ the molecular blueprint for illustrating multiâ€functional platelets and crossâ€species function evolution. <i>Proteomics</i> , 2010, 10, 2444-2457.	1.3	33
5402	From proteome lists to biological impactâ€ tools and strategies for the analysis of large MS data sets. <i>Proteomics</i> , 2010, 10, 1270-1283.	1.3	54
5403	Data management and functional annotation of the Korean reference plasma proteome. <i>Proteomics</i> , 2010, 10, 1250-1255.	1.3	8
5404	Pathway analysis of dilated cardiomyopathy using global proteomic profiling and enrichment maps. <i>Proteomics</i> , 2010, 10, 1316-1327.	1.3	55

#	ARTICLE	IF	CITATIONS
5405	Differential proteomic analysis of lymphatic, venous, and arterial endothelial cells extracted from bovine mesenteric vessels. <i>Proteomics</i> , 2010, 10, 1658-1672.	1.3	13
5406	Pathway Palette: A rich internet application for peptide, protein and network oriented analysis of MS data. <i>Proteomics</i> , 2010, 10, 1880-1885.	1.3	21
5407	A domain level interaction network of amyloid precursor protein and A β of Alzheimer's disease. <i>Proteomics</i> , 2010, 10, 2377-2395.	1.3	41
5408	Proteome profile of the developing maize (<i>Zea mays</i> L.) rachis. <i>Proteomics</i> , 2010, 10, 3051-3055.	1.3	19
5409	MASPECTRAS 2: An integration and analysis platform for proteomic data. <i>Proteomics</i> , 2010, 10, 2719-2722.	1.3	20
5410	Protein Information and Knowledge Extractor: Discovering biological information from proteomics data. <i>Proteomics</i> , 2010, 10, 3262-3271.	1.3	7
5411	Prediction of subcellular locations of proteins: Where to proceed?. <i>Proteomics</i> , 2010, 10, 3970-3983.	1.3	81
5412	Modularity of intrinsic disorder in the human proteome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 212-221.	1.5	98
5413	Large scale analysis of secondary structure changes in proteins suggests a role for disorder to order transitions in nucleotide binding proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 236-248.	1.5	15
5414	Identification, analysis, and prediction of protein ubiquitination sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 365-380.	1.5	513
5415	Comparison of structure based and threading based approaches to protein functional annotation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 18-134.	1.5	27
5416	Quantifying the evolutionary divergence of protein structures: The role of function change and function conservation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 181-196.	1.5	34
5417	Current status of membrane protein structure classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1760-1773.	1.5	22
5418	Algorithmic and analytical methods in network biology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 277-292.	6.6	28
5419	<i>In silico</i> models of cancer. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 438-459.	6.6	103
5420	Toward a complete <i>in silico</i> , multi-layered embryonic stem cell regulatory network. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 708-733.	6.6	21
5421	Discovery of complex pathways from observational data. <i>Statistics in Medicine</i> , 2010, 29, 1998-2011.	0.8	27
5422	Molecular signaling in zebrafish development and the vertebrate phylotypic period. <i>Evolution & Development</i> , 2010, 12, 144-156.	1.1	33

#	ARTICLE	IF	CITATIONS
5423	Programed cell death shapes the expression of horns within and between species of horned beetles. <i>Evolution & Development</i> , 2010, 12, 449-458.	1.1	38
5424	Human Variation in Alcohol Response Is Influenced by Variation in Neuronal Signaling Genes. <i>Alcoholism: Clinical and Experimental Research</i> , 2010, 34, 800-812.	1.4	87
5425	Ethanol Alters the Osteogenic Differentiation of Amniotic Fluid-Derived Stem Cells. <i>Alcoholism: Clinical and Experimental Research</i> , 2010, 34, 1714-1722.	1.4	11
5426	Detecting Gene Duplications in the Human Lineage. <i>Annals of Human Genetics</i> , 2010, 74, 555-565.	0.3	6
5427	Comparative ecophysiology and genomics of the toxic unicellular alga <i>Fibrocapsa japonica</i> . <i>New Phytologist</i> , 2010, 185, 446-458.	3.5	7
5428	Evidence of aberrant lipid metabolism in hepatitis C and hepatocellular carcinoma. <i>Hpb</i> , 2010, 12, 625-636.	0.1	60
5429	Incorporating Predictor Network in Penalized Regression with Application to Microarray Data. <i>Biometrics</i> , 2010, 66, 474-484.	0.8	91
5430	Distance-responsive genes found in dancing honey bees. <i>Genes, Brain and Behavior</i> , 2010, 9, 825-830.	1.1	24
5431	Global gene profiling and comprehensive bioinformatics analysis of a 46,XY female with pericentric inversion of the Y chromosome. <i>Congenital Anomalies (discontinued)</i> , 2010, 50, 40-51.	0.3	3
5432	Comparison of membrane fraction proteomic profiles of normal and cancerous human colorectal tissues with gel-assisted digestion and iTRAQ labeling mass spectrometry. <i>FEBS Journal</i> , 2010, 277, 3028-3038.	2.2	63
5433	Discovery of host defence genes in the Japanese scallop <i>Mizuhopecten yessoensis</i> Jay by expressed sequence tag analysis of kidney tissue. <i>Aquaculture Research</i> , 2010, 41, 1602-1613.	0.9	18
5434	Analysis of the salt-stress response at cell-type resolution. <i>Plant, Cell and Environment</i> , 2010, 33, 543-551.	2.8	34
5435	Analysis of <i>Rickettsia typhi</i> -infected and uninfected cat flea (<i>Ctenocephalides felis</i>) midgut cDNA libraries: deciphering molecular pathways involved in host response to <i>R. typhi</i> infection. <i>Insect Molecular Biology</i> , 2010, 19, 229-241.	1.0	30
5436	Bowman's Birk inhibitor affects pathways associated with energy metabolism in <i>Drosophila melanogaster</i> . <i>Insect Molecular Biology</i> , 2010, 19, 303-313.	1.0	14
5437	Variation in gene expression of <i>Andropogon gerardii</i> in response to altered environmental conditions associated with climate change. <i>Journal of Ecology</i> , 2010, 98, 374-383.	1.9	29
5438	Rapid evolution and selection inferred from the transcriptomes of sympatric crater lake cichlid fishes. <i>Molecular Ecology</i> , 2010, 19, 197-211.	2.0	203
5439	Changes in reproductive roles are associated with changes in gene expression in fire ant queens. <i>Molecular Ecology</i> , 2010, 19, 1200-1211.	2.0	35
5440	Six quantitative trait loci influence task thresholds for hygienic behaviour in honeybees (<i>Apis</i>) Tj ETQq1 1 0.784314 rgBT /Qglocke 10	2.0	98

#	ARTICLE	IF	CITATIONS
5441	Current therapeutic approaches for patients with myelodysplastic syndromes. <i>British Journal of Haematology</i> , 2010, 150, 131-143.	1.2	29
5442	A conserved activation element in BMP signaling during <i>Drosophila</i> development. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 69-76.	3.6	88
5443	Systematic identification of fragile sites via genome-wide location analysis of γ -H2AX. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 299-305.	3.6	167
5444	Adipose tissue pathways involved in weight loss of cancer cachexia. <i>British Journal of Cancer</i> , 2010, 102, 1541-1548.	2.9	114
5445	Mutated genes, pathways and processes in tumours. <i>EMBO Reports</i> , 2010, 11, 805-810.	2.0	31
5446	Sustainable digital infrastructure. <i>EMBO Reports</i> , 2010, 11, 730-734.	2.0	43
5447	Uncovering new substrates for Aurora A kinase. <i>EMBO Reports</i> , 2010, 11, 977-984.	2.0	59
5448	Correlation analysis between genome-wide expression profiles and cytoarchitectural abnormalities in the prefrontal cortex of psychiatric disorders. <i>Molecular Psychiatry</i> , 2010, 15, 326-336.	4.1	118
5449	SZGR: a comprehensive schizophrenia gene resource. <i>Molecular Psychiatry</i> , 2010, 15, 453-462.	4.1	84
5450	The transcriptional network for mesenchymal transformation of brain tumours. <i>Nature</i> , 2010, 463, 318-325.	13.7	1,114
5451	Long non-coding RNA HOTAIR reprograms chromatin state to promote cancer metastasis. <i>Nature</i> , 2010, 464, 1071-1076.	13.7	4,648
5452	Genome-wide measurement of RNA secondary structure in yeast. <i>Nature</i> , 2010, 467, 103-107.	13.7	713
5453	GREAT improves functional interpretation of cis-regulatory regions. <i>Nature Biotechnology</i> , 2010, 28, 495-501.	9.4	3,789
5454	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	9.4	490
5455	Chemical genetics screen for enhancers of rapamycin identifies a specific inhibitor of an SCF family E3 ubiquitin ligase. <i>Nature Biotechnology</i> , 2010, 28, 738-742.	9.4	132
5456	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	9.4	613
5457	Ontology engineering. <i>Nature Biotechnology</i> , 2010, 28, 128-130.	9.4	113
5458	Functional analysis of multiple genomic signatures demonstrates that classification algorithms choose phenotype-related genes. <i>Pharmacogenomics Journal</i> , 2010, 10, 310-323.	0.9	41

#	ARTICLE	IF	CITATIONS
5459	GO-Ata€Š:in silicoprediction of gene function inArabidopsis thalianaby combining heterogeneous data. Plant Journal, 2010, 61, 713-721.	2.8	17
5460	AFLP-based transcript profiling for cassava genome-wide expression analysis in the onset of storage root formation. Physiologia Plantarum, 2010, 140, 189-298.	2.6	29
5461	Proteome analysis of chloroplasts from the moss Physcomitrella patens (Hedw.) B.S.G.. Biochemistry (Moscow), 2010, 75, 1470-1483.	0.7	8
5462	Applicability of coexpression networks analysis to anticancer drug targets discovery. Molecular Biology, 2010, 44, 326-333.	0.4	1
5463	Automatic policing of biochemical annotations using genomic correlations. Nature Chemical Biology, 2010, 6, 34-40.	3.9	28
5464	ChIP-Seq identification of weakly conserved heart enhancers. Nature Genetics, 2010, 42, 806-810.	9.4	395
5465	Whole-genome sequencing and comprehensive variant analysis of a Japanese individual using massively parallel sequencing. Nature Genetics, 2010, 42, 931-936.	9.4	106
5466	A protocol for generating a high-quality genome-scale metabolic reconstruction. Nature Protocols, 2010, 5, 93-121.	5.5	1,568
5467	Expander: from expression microarrays to networks and functions. Nature Protocols, 2010, 5, 303-322.	5.5	183
5468	I-TASSER: a unified platform for automated protein structure and function prediction. Nature Protocols, 2010, 5, 725-738.	5.5	5,594
5469	Gene function analysis in complex data sets using ErmineJ. Nature Protocols, 2010, 5, 1148-1159.	5.5	113
5470	Next-generation genomics: an integrative approach. Nature Reviews Genetics, 2010, 11, 476-486.	7.7	554
5471	Statistical analysis strategies for association studies involving rare variants. Nature Reviews Genetics, 2010, 11, 773-785.	7.7	426
5472	Analysing biological pathways in genome-wide association studies. Nature Reviews Genetics, 2010, 11, 843-854.	7.7	722
5473	Decoding signalling networks by mass spectrometry-based proteomics. Nature Reviews Molecular Cell Biology, 2010, 11, 427-439.	16.1	534
5474	Transient Peripheral Immune Response and Central Nervous System Leaky Compartmentalization in a Viral Model for Multiple Sclerosis. Brain Pathology, 2010, 20, 890-901.	2.1	20
5475	Generation and analysis of 10 000 ESTs from the halfâ€smooth tongue sole <i>Cynoglossus semilaevis</i> and identification of microsatellite and SNP markers. Journal of Fish Biology, 2010, 76, 1190-1204.	0.7	27
5476	Network-based genomic discovery: application and comparison of Markov random-field models. Journal of the Royal Statistical Society Series C: Applied Statistics, 2010, 59, 105-125.	0.5	19

#	ARTICLE	IF	CITATIONS
5477	Impaired metabolism in donor kidney grafts after steroid pretreatment. <i>Transplant International</i> , 2010, 23, 796-804.	0.8	7
5478	The Human Phenotype Ontology. <i>Clinical Genetics</i> , 2010, 77, 525-534.	1.0	267
5479	Analysis of expressed sequence tags from the <i>Huperzia serrata</i> leaf for gene discovery in the areas of secondary metabolite biosynthesis and development regulation. <i>Physiologia Plantarum</i> , 2010, 139, 1-12.	2.6	40
5480	An EST-based genome scan using 454 sequencing in the marine snail <i>Littorina saxatilis</i> . <i>Journal of Evolutionary Biology</i> , 2010, 23, 2004-2016.	0.8	71
5481	Distributed Biomedical Terminology Development: From Experiments to Open Process. <i>Yearbook of Medical Informatics</i> , 2010, 19, 58-63.	0.8	1
5482	Imaging Informatics: Toward Capturing and Processing Semantic Information in Radiology Images. <i>Yearbook of Medical Informatics</i> , 2010, 19, 34-42.	0.8	8
5483	A stem-cell ageing hypothesis on the origin of Parkinson's disease. <i>Nature Precedings</i> , 2010, , .	0.1	0
5484	Global Network Alignment. <i>Nature Precedings</i> , 2010, , .	0.1	0
5485	The Cognitive Atlas: Employing Interaction Design Processes to Facilitate Collaborative Ontology Creation. <i>Nature Precedings</i> , 2010, , .	0.1	8
5486	Expression profile reveals novel prognostic biomarkers in hepatocellular carcinoma. <i>Frontiers in Bioscience - Elite</i> , 2010, E2, 829-840.	0.9	15
5487	System biology analysis of cell cycle pathway involved in hepatocellular carcinoma. <i>Frontiers in Bioscience - Scholar</i> , 2010, S2, 1127-1144.	0.8	8
5492	A MODEL PLANT GENOME RESOURCE AND COMPARATIVE GENOMICS. <i>Acta Horticulturae</i> , 2010, , 31-41.	0.1	0
5493	Current Trends and New Challenges of Databases and Web Applications for Systems Driven Biological Research. <i>Frontiers in Physiology</i> , 2010, 1, 147.	1.3	12
5494	Periodicity Detection Method for Small-Sample Time Series Datasets. <i>Bioinformatics and Biology Insights</i> , 2010, 4, BBI.S5983.	1.0	7
5495	Protein Bioinformatics Infrastructure for the Integration and Analysis of Multiple High-Throughput <i>omics</i> Data. <i>Advances in Bioinformatics</i> , 2010, 2010, 1-19.	5.7	19
5496	Complementarity of network and sequence information in homologous proteins. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, 275-289.	1.0	20
5497	Allelic Selection of Amplicons in Glioblastoma Revealed by Combining Somatic and Germline Analysis. <i>PLoS Genetics</i> , 2010, 6, e1001086.	1.5	27
5498	Molecular Signatures of Quiescent, Mobilized and Leukemia-Initiating Hematopoietic Stem Cells. <i>PLoS ONE</i> , 2010, 5, e8785.	1.1	114

#	ARTICLE	IF	CITATIONS
5499	Bayesian Markov Random Field Analysis for Protein Function Prediction Based on Network Data. PLoS ONE, 2010, 5, e9293.	1.1	81
5500	Evaluation of a Prediction Protocol to Identify Potential Targets of Epigenetic Reprogramming by the Cancer Associated Epstein Barr Virus. PLoS ONE, 2010, 5, e9443.	1.1	7
5501	High-Content, Image-Based Screening for Drug Targets in Yeast. PLoS ONE, 2010, 5, e10177.	1.1	48
5502	Multidimensional Gene Set Analysis of Genomic Data. PLoS ONE, 2010, 5, e10348.	1.1	75
5503	Phenex: Ontological Annotation of Phenotypic Diversity. PLoS ONE, 2010, 5, e10500.	1.1	78
5504	Genome Landscape and Evolutionary Plasticity of Chromosomes in Malaria Mosquitoes. PLoS ONE, 2010, 5, e10592.	1.1	35
5505	Re-Annotation Is an Essential Step in Systems Biology Modeling of Functional Genomics Data. PLoS ONE, 2010, 5, e10642.	1.1	21
5506	Reconstruction and Validation of RefRec: A Global Model for the Yeast Molecular Interaction Network. PLoS ONE, 2010, 5, e10662.	1.1	12
5507	Sequencing, Analysis, and Annotation of Expressed Sequence Tags for Camelus dromedarius. PLoS ONE, 2010, 5, e10720.	1.1	40
5508	A Chemical Genetic Screen for Modulators of Asymmetrical 2,2-Dimeric Naphthoquinones Cytotoxicity in Yeast. PLoS ONE, 2010, 5, e10846.	1.1	19
5509	Heterozygosity for Pten Promotes Tumorigenesis in a Mouse Model of Medulloblastoma. PLoS ONE, 2010, 5, e10849.	1.1	40
5510	Statistical Tests for Associations between Two Directed Acyclic Graphs. PLoS ONE, 2010, 5, e10996.	1.1	3
5511	The Gene Expression Profile in the Synovium as a Predictor of the Clinical Response to Infliximab Treatment in Rheumatoid Arthritis. PLoS ONE, 2010, 5, e11310.	1.1	96
5512	Activated Notch1 Target Genes during Embryonic Cell Differentiation Depend on the Cellular Context and Include Lineage Determinants and Inhibitors. PLoS ONE, 2010, 5, e11481.	1.1	84
5513	Gene Expression Analysis of Forskolin Treated Basilar Papillae Identifies MicroRNA181a as a Mediator of Proliferation. PLoS ONE, 2010, 5, e11502.	1.1	18
5514	A Combined Transcriptomics and Lipidomics Analysis of Subcutaneous, Epididymal and Mesenteric Adipose Tissue Reveals Marked Functional Differences. PLoS ONE, 2010, 5, e11525.	1.1	79
5515	Identification and Characterization of Full-Length cDNAs in Channel Catfish (<i>Ictalurus punctatus</i>) and Blue Catfish (<i>Ictalurus furcatus</i>). PLoS ONE, 2010, 5, e11546.	1.1	40
5516	Gene Expression Profiling of the Local Cecal Response of Genetic Chicken Lines That Differ in Their Susceptibility to <i>Campylobacter jejuni</i> Colonization. PLoS ONE, 2010, 5, e11827.	1.1	69

#	ARTICLE	IF	CITATIONS
5517	The Human-Bacterial Pathogen Protein Interaction Networks of <i>Bacillus anthracis</i> , <i>Francisella tularensis</i> , and <i>Yersinia pestis</i> . <i>PLoS ONE</i> , 2010, 5, e12089.	1.1	131
5518	Partitioning of Minimotifs Based on Function with Improved Prediction Accuracy. <i>PLoS ONE</i> , 2010, 5, e12276.	1.1	7
5519	Identifying Molecular Effects of Diet through Systems Biology: Influence of Herring Diet on Sterol Metabolism and Protein Turnover in Mice. <i>PLoS ONE</i> , 2010, 5, e12361.	1.1	17
5520	Analysis of Human and Mouse Reprogramming of Somatic Cells to Induced Pluripotent Stem Cells. What Is in the Plate?. <i>PLoS ONE</i> , 2010, 5, e12664.	1.1	47
5521	Finding New Genes for Non-Syndromic Hearing Loss through an In Silico Prioritization Study. <i>PLoS ONE</i> , 2010, 5, e12742.	1.1	10
5522	Enrichment Map: A Network-Based Method for Gene-Set Enrichment Visualization and Interpretation. <i>PLoS ONE</i> , 2010, 5, e13984.	1.1	1,883
5523	De Novo Transcriptome Sequencing in <i>Anopheles funestus</i> Using Illumina RNA-Seq Technology. <i>PLoS ONE</i> , 2010, 5, e14202.	1.1	132
5524	The Transcriptional Response in Human Umbilical Vein Endothelial Cells Exposed to Insulin: A Dynamic Gene Expression Approach. <i>PLoS ONE</i> , 2010, 5, e14390.	1.1	8
5525	Analysis of Kinase Gene Expression Patterns across 5681 Human Tissue Samples Reveals Functional Genomic Taxonomy of the Kinome. <i>PLoS ONE</i> , 2010, 5, e15068.	1.1	44
5526	Therapeutic Implications of GIPC1 Silencing in Cancer. <i>PLoS ONE</i> , 2010, 5, e15581.	1.1	22
5527	Male-biased genes of <i>Drosophila melanogaster</i> that are conserved in mammalian testis. <i>Frontiers in Bioscience - Elite</i> , 2010, E2, 668.	0.9	0
5528	Insights into Protein Sequence and Structure-Derived Features Mediating 3D Domain Swapping Mechanism using Support Vector Machine Based Approach. <i>Bioinformatics and Biology Insights</i> , 2010, 4, BBI.S4464.	1.0	13
5529	Computational identification and analysis of protein short linear motifs. <i>Frontiers in Bioscience - Landmark</i> , 2010, 15, 801.	3.0	34
5530	The Human Transcriptome. , 2010, , 89-103.		2
5531	Expression of immune genes during metamorphosis of <i>Xenopus</i> : a survey. <i>Frontiers in Bioscience - Landmark</i> , 2010, 15, 348.	3.0	5
5532	Urinary proteomics evaluation in interstitial cystitis/painful bladder syndrome: a pilot study. <i>International Braz J Urol: Official Journal of the Brazilian Society of Urology</i> , 2010, 36, 464-479.	0.7	31
5533	Prostaglandin E2receptor subtype EP2- and EP4-regulated gene expression profiling in human ciliary smooth muscle cells. <i>Physiological Genomics</i> , 2010, 42, 348-360.	1.0	7
5534	A Computer Scientist's Guide to the Regulatory Genome. <i>Fundamenta Informaticae</i> , 2010, 103, 323-332.	0.3	2

#	ARTICLE	IF	CITATIONS
5536	Integration of Relational and Textual Biomedical Sources. <i>Methods of Information in Medicine</i> , 2010, 49, 337-348.	0.7	9
5537	Optimal Network Alignment with Graphlet Degree Vectors. <i>Cancer Informatics</i> , 2010, 9, CIN.S4744.	0.9	149
5538	An Ontology for Description of Drug Discovery Investigations. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	13
5539	Identification of Gene Expression Signature in Estrogen Receptor Positive Breast Carcinoma. <i>Biomarkers in Cancer</i> , 2010, 2, BIC.S3793.	3.6	34
5540	Transcriptional and physiological responses to chronic ACTH treatment by the mouse kidney. <i>Physiological Genomics</i> , 2010, 40, 158-166.	1.0	21
5541	On the Classification of Epistatic Interactions. <i>Genetics</i> , 2010, 184, 827-837.	1.2	33
5542	Identification of Stage Biomarkers for Human African Trypanosomiasis. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 82, 983-990.	0.6	38
5543	Genome-wide misexpression of X-linked versus autosomal genes associated with hybrid male sterility. <i>Genome Research</i> , 2010, 20, 1097-1102.	2.4	38
5544	The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. <i>Nucleic Acids Research</i> , 2010, 38, D473-D479.	6.5	403
5545	Probing the Reproducibility of Leaf Growth and Molecular Phenotypes: A Comparison of Three <i>Arabidopsis</i> Accessions Cultivated in Ten Laboratories. <i>Plant Physiology</i> , 2010, 152, 2142-2157.	2.3	137
5546	Conserved elements associated with ribosomal genes and their trans-splice acceptor sites in <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2010, 38, 2990-3004.	6.5	5
5547	PTMScout, a Web Resource for Analysis of High Throughput Post-translational Proteomics Studies. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2558-2570.	2.5	39
5548	dbDEPC: a database of Differentially Expressed Proteins in human Cancers. <i>Nucleic Acids Research</i> , 2010, 38, D658-D664.	6.5	19
5549	Predicting Meiotic Pathways in Human Fetal Oogenesis1. <i>Biology of Reproduction</i> , 2010, 82, 543-551.	1.2	11
5550	A High-Throughput Data Mining of Single Nucleotide Polymorphisms in <i>Coffea</i> Species Expressed Sequence Tags Suggests Differential Homeologous Gene Expression in the Allotetraploid <i>Coffea arabica</i> . <i>Plant Physiology</i> , 2010, 154, 1053-1066.	2.3	61
5551	Associating Genes and Protein Complexes with Disease via Network Propagation. <i>PLoS Computational Biology</i> , 2010, 6, e1000641.	1.5	758
5552	Involvement of Vacuolar Sequestration and Active Transport in Tolerance of <i>Saccharomyces cerevisiae</i> to Hop Iso- α -Acids. <i>Applied and Environmental Microbiology</i> , 2010, 76, 318-328.	1.4	40
5553	Dual coding in alternative reading frames correlates with intrinsic protein disorder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5429-5434.	3.3	92

#	ARTICLE	IF	CITATIONS
5554	Molecular and Physiological Analysis of Drought Stress in Arabidopsis Reveals Early Responses Leading to Acclimation in Plant Growth. <i>Plant Physiology</i> , 2010, 154, 1254-1271.	2.3	580
5555	MGMT modulates glioblastoma angiogenesis and response to the tyrosine kinase inhibitor sunitinib. <i>Neuro-Oncology</i> , 2010, 12, 822-833.	0.6	74
5556	Gene expression profiling of genetically determined growth variation in bivalve larvae (<i>Crassostrea gigas</i>). <i>Journal of Experimental Biology</i> , 2010, 213, 749-758.	0.8	64
5557	Ontogenomic study of the relationship between number of gene splice variants and GO categorization. <i>Bioinformatics</i> , 2010, 26, 1945-1949.	1.8	2
5558	Novel sequence feature variant type analysis of the HLA genetic association in systemic sclerosis. <i>Human Molecular Genetics</i> , 2010, 19, 707-719.	1.4	37
5559	hPDI: a database of experimental human protein-DNA interactions. <i>Bioinformatics</i> , 2010, 26, 287-289.	1.8	86
5560	SPICi: a fast clustering algorithm for large biological networks. <i>Bioinformatics</i> , 2010, 26, 1105-1111.	1.8	210
5561	Temporal waves of coherent gene expression during <i>Drosophila</i> embryogenesis. <i>Bioinformatics</i> , 2010, 26, 2731-2736.	1.8	11
5562	Hypoxia stimulates CXCR4 signalling in ileal carcinoids. <i>Endocrine-Related Cancer</i> , 2010, 17, 303-316.	1.6	35
5563	Genome-wide assessment of differential roles for p300 and CBP in transcription regulation. <i>Nucleic Acids Research</i> , 2010, 38, 5396-5408.	6.5	133
5564	In-depth Qualitative and Quantitative Profiling of Tyrosine Phosphorylation Using a Combination of Phosphopeptide Immunoaffinity Purification and Stable Isotope Dimethyl Labeling. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 84-99.	2.5	155
5565	A ChIP-seq defined genome-wide map of vitamin D receptor binding: Associations with disease and evolution. <i>Genome Research</i> , 2010, 20, 1352-1360.	2.4	737
5566	Faster-Z Evolution Is Predominantly Due to Genetic Drift. <i>Molecular Biology and Evolution</i> , 2010, 27, 661-670.	3.5	114
5567	Role of microRNA-23b in flow-regulation of Rb phosphorylation and endothelial cell growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3234-3239.	3.3	160
5568	An Insight into the Sialotranscriptome of <i>Simulium nigricornum</i> , a Black Fly Associated with Fogo Selvagem in South America. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 82, 1060-1075.	0.6	36
5569	GO-Bayes: Gene Ontology-based overrepresentation analysis using a Bayesian approach. <i>Bioinformatics</i> , 2010, 26, 905-911.	1.8	29
5570	ConceptGen: a gene set enrichment and gene set relation mapping tool. <i>Bioinformatics</i> , 2010, 26, 456-463.	1.8	134
5571	The RFX Protein RfxA Is an Essential Regulator of Growth and Morphogenesis in <i>Penicillium marneffei</i> . <i>Eukaryotic Cell</i> , 2010, 9, 578-591.	3.4	26

#	ARTICLE	IF	CITATIONS
5572	Gene3D: merging structure and function for a Thousand genomes. <i>Nucleic Acids Research</i> , 2010, 38, D296-D300.	6.5	50
5573	Molecular modeling of the bifunctional enzyme UDP-GlcNAc 2-epimerase/ManNAc kinase and predictions of structural effects of mutations associated with HIBM and sialuria. <i>Glycobiology</i> , 2010, 20, 322-337.	1.3	22
5574	The comprehensive microbial resource. <i>Nucleic Acids Research</i> , 2010, 38, D340-D345.	6.5	241
5576	PCFamily: a web server for searching homologous protein complexes. <i>Nucleic Acids Research</i> , 2010, 38, W516-W522.	6.5	12
5577	What can whole genome expression data tell us about the ecology and evolution of personality?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 4001-4012.	1.8	95
5578	Systems-level cancer gene identification from protein interaction network topology applied to melanogenesis-related functional genomics data. <i>Journal of the Royal Society Interface</i> , 2010, 7, 423-437.	1.5	95
5579	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. <i>Nucleic Acids Research</i> , 2010, 38, e171-e171.	6.5	62
5580	Transcriptome Analysis Indicates an Enhanced Activation of Adaptive and Innate Immunity by <i>Chlamydia</i> -Infected Murine Epithelial Cells Treated with Interferon β . <i>Journal of Infectious Diseases</i> , 2010, 202, 1405-1414.	1.9	12
5581	Novel Metastasis-Related Gene CIM Functions in the Regulation of Multiple Cellular Stress-Response Pathways. <i>Cancer Research</i> , 2010, 70, 9949-9958.	0.4	23
5582	Quantifying the biological significance of gene ontology biological processes—implications for the analysis of systems-wide data. <i>Bioinformatics</i> , 2010, 26, 378-384.	1.8	80
5583	Culture, immortalization, and characterization of human Meibomian gland epithelial cells. , 2010, 51, 3993.		93
5584	Selenium-Responsive Proteins in the Sera of Selenium-Enriched Yeast-Supplemented Healthy African American and Caucasian Men. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 2332-2340.	1.1	13
5585	Cyclosporin-A Induced Toxicity in Rat Renal Collecting Duct Cells: Interference with Enhanced Hypertonicity Induced Apoptosis. <i>Cellular Physiology and Biochemistry</i> , 2010, 26, 887-900.	1.1	11
5586	HIERARCHICAL CLASSIFICATION OF GENE ONTOLOGY TERMS USING THE GOstruct METHOD. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 357-376.	0.3	62
5587	Transcriptomic responses to heat stress in invasive and native blue mussels (genus <i>Mytilus</i>): molecular correlates of invasive success. <i>Journal of Experimental Biology</i> , 2010, 213, 3548-3558.	0.8	220
5588	Noncanonical transcript forms in yeast and their regulation during environmental stress. <i>Rna</i> , 2010, 16, 1256-1267.	1.6	72
5589	Defining the transcriptome and proteome in three functionally different human cell lines. <i>Molecular Systems Biology</i> , 2010, 6, 450.	3.2	324
5590	Cross-species chemogenomic profiling reveals evolutionarily conserved drug mode of action. <i>Molecular Systems Biology</i> , 2010, 6, 451.	3.2	143

#	ARTICLE	IF	CITATIONS
5591	A genome-wide map of human genetic interactions inferred from radiation hybrid genotypes. <i>Genome Research</i> , 2010, 20, 1122-1132.	2.4	85
5592	Assessing the effect of the CLPG mutation on the microRNA catalog of skeletal muscle using high-throughput sequencing. <i>Genome Research</i> , 2010, 20, 1651-1662.	2.4	38
5593	Posttranslational regulation impacts the fate of duplicated genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2967-2971.	3.3	65
5594	High-throughput method for analyzing methylation of CpGs in targeted genomic regions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12587-12592.	3.3	34
5595	Parkinson Disease-associated DJ-1 Is Required for the Expression of the Glial Cell Line-derived Neurotrophic Factor Receptor RET in Human Neuroblastoma Cells. <i>Journal of Biological Chemistry</i> , 2010, 285, 18565-18574.	1.6	37
5596	Integration of General Amino Acid Control and Target of Rapamycin (TOR) Regulatory Pathways in Nitrogen Assimilation in Yeast. <i>Journal of Biological Chemistry</i> , 2010, 285, 16893-16911.	1.6	107
5597	Computational Tools for the Interactive Exploration of Proteomic and Structural Data. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1703-1715.	2.5	9
5598	PANTHER version 7: improved phylogenetic trees, orthologs and collaboration with the Gene Ontology Consortium. <i>Nucleic Acids Research</i> , 2010, 38, D204-D210.	6.5	553
5599	Chimeric tRNAs as tools to induce proteome damage and identify components of stress responses. <i>Nucleic Acids Research</i> , 2010, 38, e30-e30.	6.5	38
5600	UTRdb and UTRsite (RELEASE 2010): a collection of sequences and regulatory motifs of the untranslated regions of eukaryotic mRNAs. <i>Nucleic Acids Research</i> , 2010, 38, D75-D80.	6.5	285
5601	CORUM: the comprehensive resource of mammalian protein complexesâ€”2009. <i>Nucleic Acids Research</i> , 2010, 38, D497-D501.	6.5	898
5602	Tissue-specific transcript annotation and expression profiling with complementary next-generation sequencing technologies. <i>Nucleic Acids Research</i> , 2010, 38, e165-e165.	6.5	32
5603	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
5604	Modularity and directionality in genetic interaction maps. <i>Bioinformatics</i> , 2010, 26, i228-i236.	1.8	27
5605	Assessing the functional coherence of gene sets with metrics based on the Gene Ontology graph. <i>Bioinformatics</i> , 2010, 26, i79-i87.	1.8	22
5606	Identifying informative subsets of the Gene Ontology with information bottleneck methods. <i>Bioinformatics</i> , 2010, 26, 2445-2451.	1.8	18
5607	Ontological realism: A methodology for coordinated evolution of scientific ontologies. <i>Applied Ontology</i> , 2010, 5, 139-188.	1.0	188
5608	PANDITplus: toward better integration of evolutionary view on molecular sequences with supplementary bioinformatics resources. <i>Trends in Evolutionary Biology</i> , 2010, 2, 1.	0.4	6

#	ARTICLE	IF	CITATIONS
5609	Multilevel Legal Ontologies. Lecture Notes in Computer Science, 2010, , 136-154.	1.0	5
5610	Functional analysis of tenocytes gene expression in tendon fascicles subjected to cyclic tensile strain. Connective Tissue Research, 2010, 51, 434-444.	1.1	27
5611	PI3K(p110 α) Protects Against Myocardial Infarction-Induced Heart Failure. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 724-732.	1.1	160
5612	PathText: a text mining integrator for biological pathway visualizations. Bioinformatics, 2010, 26, i374-i381.	1.8	47
5613	Network-based Identification of Novel Cancer Genes. Molecular and Cellular Proteomics, 2010, 9, 648-655.	2.5	54
5614	Gene function prediction using semantic similarity clustering and enrichment analysis in the malaria parasite <i>Plasmodium falciparum</i> . Bioinformatics, 2010, 26, 2431-2437.	1.8	17
5615	Assigning roles to DNA regulatory motifs using comparative genomics. Bioinformatics, 2010, 26, 860-866.	1.8	155
5616	High-throughput sequence analysis of <i>Ciona intestinalis</i> SL trans-spliced mRNAs: Alternative expression modes and gene function correlates. Genome Research, 2010, 20, 636-645.	2.4	40
5617	Gene function prediction from synthetic lethality networks via ranking on demand. Bioinformatics, 2010, 26, 912-918.	1.8	23
5618	Global gene expression analysis for evaluation and design of biomaterials. Science and Technology of Advanced Materials, 2010, 11, 013001.	2.8	3
5619	The annotation and the usage of scientific databases could be improved with public issue tracker software. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq035.	1.4	5
5621	Biomedical Informatics for Cancer Research. , 2010, , .		13
5622	EuroDia: a beta-cell gene expression resource. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq024-baq024.	1.4	9
5623	Iterated Local Search for Biclustering of Microarray Data. Lecture Notes in Computer Science, 2010, , 219-229.	1.0	7
5624	Genomic repertoires of DNA-binding transcription factors across the tree of life. Nucleic Acids Research, 2010, 38, 7364-7377.	6.5	140
5625	The EMBRACE web service collection. Nucleic Acids Research, 2010, 38, W683-W688.	6.5	40
5626	The microRNA miR-124 controls gene expression in the sensory nervous system of <i>Caenorhabditis elegans</i> . Nucleic Acids Research, 2010, 38, 3780-3793.	6.5	91
5627	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM1325, an effective microsymbiont of annual Mediterranean clovers.. Standards in Genomic Sciences, 2010, 2, 347-356.	1.5	53

#	ARTICLE	IF	CITATIONS
5628	DNA Repair and the Accumulation of Oxidatively Damaged DNA Are Affected by Fruit Intake in Mice. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2010, 65A, 1300-1311.	1.7	9
5629	Separation and identification of mouse liver membrane proteins using a gel-based approach in combination with 2DnanoLC-Q-TOF-MS/MS. <i>Journal of Family Business Management</i> , 2010, 1, 015015.	2.6	2
5630	Of mice and men: comparative proteomics of bronchoalveolar fluid. <i>European Respiratory Journal</i> , 2010, 35, 1388-1395.	3.1	43
5631	The Human Oral Microbiome Database: a web accessible resource for investigating oral microbe taxonomic and genomic information. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq013-baq013.	1.4	874
5632	Meta-Analysis of Genome-Wide Gene Expression Differences in Onset and Maintenance Phases of Genetic Hypertension. <i>Hypertension</i> , 2010, 56, 319-324.	1.3	56
5633	Non-redundant patent sequence databases with value-added annotations at two levels. <i>Nucleic Acids Research</i> , 2010, 38, D52-D56.	6.5	11
5635	CLIC: clustering analysis of large microarray datasets with individual dimension-based clustering. <i>Nucleic Acids Research</i> , 2010, 38, W246-W253.	6.5	13
5636	Network Enrichment Analysis in Complex Experiments. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010, 9, Article22.	0.2	56
5637	Genome Sequence of the Cellulosome-Producing Mesophilic Organism <i>Clostridium cellulovorans</i> 743B. <i>Journal of Bacteriology</i> , 2010, 192, 901-902.	1.0	68
5638	Ensembl's 10th year. <i>Nucleic Acids Research</i> , 2010, 38, D557-D562.	6.5	251
5639	Unifying Themes in Microbial Associations with Animal and Plant Hosts Described Using the Gene Ontology. <i>Microbiology and Molecular Biology Reviews</i> , 2010, 74, 479-503.	2.9	46
5640	i-GSEA4GWAS: a web server for identification of pathways/gene sets associated with traits by applying an improved gene set enrichment analysis to genome-wide association study. <i>Nucleic Acids Research</i> , 2010, 38, W90-W95.	6.5	166
5641	Robust and accurate data enrichment statistics via distribution function of sum of weights. <i>Bioinformatics</i> , 2010, 26, 2752-2759.	1.8	18
5642	Introducing Knowledge into Differential Expression Analysis. <i>Journal of Computational Biology</i> , 2010, 17, 953-967.	0.8	9
5643	Delineation and interpretation of gene networks towards their effect in cellular physiology- A reverse engineering approach for the identification of critical molecular players, through the use of ontologies. , 2010, 2010, 6709-12.		4
5644	A systems-biology approach to modular genetic complexity. <i>Chaos</i> , 2010, 20, 026102.	1.0	14
5645	Operon prediction based on quadratic discriminant analysis in <i>Escherichia coli</i> genome. , 2010, , .		0
5646	Decomposing PPI networks for complex discovery. , 2010, , .		2

#	ARTICLE	IF	CITATIONS
5647	GOGA: GO-driven Genetic Algorithm-based fuzzy clustering of gene expression data. , 2010, , .		4
5648	A novel method for mining temporally dependent association rules in three-dimensional microarray datasets. , 2010, , .		7
5649	Tracking, tuning, and terminating microbial physiology using synthetic riboregulators. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15898-15903.	3.3	166
5650	Classification of genome-wide copy number variations and their associated SNP and gene networks analysis. , 2010, , .		0
5651	An Online System for Functional Relationship Analysis of Genome-Wide Gene Products. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	1
5652	MicroRNA, mRNA, and protein expression link development and aging in human and macaque brain. Genome Research, 2010, 20, 1207-1218.	2.4	283
5653	Regulatory and metabolic rewiring during laboratory evolution of ethanol tolerance in <i>E. coli</i> . Molecular Systems Biology, 2010, 6, 378.	3.2	141
5654	The Protein Interaction Network of the Human Transcription Machinery Reveals a Role for the Conserved GTPase RPA4/GPN1 and Microtubule Assembly in Nuclear Import and Biogenesis of RNA Polymerase II. Molecular and Cellular Proteomics, 2010, 9, 2827-2839.	2.5	96
5655	The construction of protein-protein interaction network based on machine learning method. , 2010, , .		1
5656	Gene Ontology Rewritten for Computing Gene Functional Similarity. , 2010, , .		1
5657	Ontology in a Wiki collaboratively authoring ontologies the simple way. , 2010, , .		0
5658	Gene ontology classification: Building high-level knowledge using genetic algorithms. , 2010, , .		7
5659	Gene ontology fuzzy-enrichment analysis to investigate drug mode-of-action. , 2010, , .		0
5660	Recursive expectation-maximization clustering: A method for identifying buffering mechanisms composed of phenomic modules. Chaos, 2010, 20, 026103.	1.0	10
5661	An information theory-based tool for characterizing the interaction environment of a protein. , 2010, 2010, 5529-32.		1
5662	Mining osmotic stress response genes from Arabidopsis genome. , 2010, , .		0
5663	Topological network alignment uncovers biological function and phylogeny. Journal of the Royal Society Interface, 2010, 7, 1341-1354.	1.5	281
5664	Using Direct and Indirect Neighbours to Predict Protein Function in GO-Evaluated PPI Data Set. , 2010, , .		1

#	ARTICLE	IF	CITATIONS
5665	Testicular postgenomics: targeting the regulation of spermatogenesis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 1481-1500.	1.8	36
5666	Microarray Analysis and Draft Genomes of Two <i>Escherichia coli</i> O157:H7 Lineage II Cattle Isolates FRIK966 and FRIK2000 Investigating Lack of Shiga Toxin Expression. <i>Foodborne Pathogens and Disease</i> , 2010, 7, 763-773.	0.8	15
5667	A dictionary on microRNAs and their putative target pathways. <i>Nucleic Acids Research</i> , 2010, 38, 4476-4486.	6.5	88
5668	Reinforcement Learning Method for BioAgents. , 2010, , .		4
5669	Fuzzy concept lattices: Examples using the Gene Ontology. , 2010, , .		3
5670	The <i>Aspergillus</i> Genome Database, a curated comparative genomics resource for gene, protein and sequence information for the <i>Aspergillus</i> research community. <i>Nucleic Acids Research</i> , 2010, 38, D420-D427.	6.5	111
5671	Trinucleotide repeats in human genome and exome. <i>Nucleic Acids Research</i> , 2010, 38, 4027-4039.	6.5	124
5672	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
5673	Pattern Recognition in Bioinformatics. <i>Lecture Notes in Computer Science</i> , 2010, , .	1.0	1
5674	LEARNING WITH GENE ONTOLOGY ANNOTATION USING FEATURE SELECTION AND CONSTRUCTION. <i>Applied Artificial Intelligence</i> , 2010, 24, 5-38.	2.0	2
5675	Dynamics of the Skeletal Muscle Secretome during Myoblast Differentiation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2482-2496.	2.5	248
5676	Towards Improved Assessment of Functional Similarity in Large-Scale Screens: A Study on Indel Length. <i>Journal of Computational Biology</i> , 2010, 17, 1-20.	0.8	15
5677	Considering Personal Organization: Metadata Practices of Scientists. <i>Journal of Library Metadata</i> , 2010, 10, 156-172.	0.6	10
5678	Detection of Locally Over-Represented GO Terms in Protein-Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2010, 17, 443-457.	0.8	12
5679	Growth Factor Regulation of Prostaglandin-Endoperoxide Synthase 2 (Ptgs2) Expression in Colonic Mesenchymal Stem Cells. <i>Journal of Biological Chemistry</i> , 2010, 285, 5026-5039.	1.6	33
5680	Amacrine Cell Gene Expression and Survival Signaling: Differences from Neighboring Retinal Ganglion Cells. , 2010, 51, 3800.		21
5681	Polygenic and directional regulatory evolution across pathways in <i>Saccharomyces</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5058-5063.	3.3	93
5682	SCAN: SNP and copy number annotation. <i>Bioinformatics</i> , 2010, 26, 259-262.	1.8	214

#	ARTICLE	IF	CITATIONS
5683	Decision support based on genomics: integration of data- and knowledge-driven reasoning. International Journal of Biomedical Engineering and Technology, 2010, 3, 287.	0.2	3
5684	Eukaryotic genes of archaeobacterial origin are more important than the more numerous eubacterial genes, irrespective of function. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17252-17255.	3.3	74
5685	Ergatis: a web interface and scalable software system for bioinformatics workflows. Bioinformatics, 2010, 26, 1488-1492.	1.8	83
5686	Site-specific Phosphorylation Dynamics of the Nuclear Proteome during the DNA Damage Response. Molecular and Cellular Proteomics, 2010, 9, 1314-1323.	2.5	225
5687	Systematic Interpretation of Comutated Genes in Large-Scale Cancer Mutation Profiles. Molecular Cancer Therapeutics, 2010, 9, 2186-2195.	1.9	12
5688	Mass spectrometry-based proteomics in biomedical research: emerging technologies and future strategies. Expert Reviews in Molecular Medicine, 2010, 12, e30.	1.6	27
5689	Prognostic and Predictive Gene Signature for Adjuvant Chemotherapy in Resected Non-“Small-Cell Lung Cancer. Journal of Clinical Oncology, 2010, 28, 4417-4424.	0.8	405
5690	Advances in translational bioinformatics: computational approaches for the hunting of disease genes. Briefings in Bioinformatics, 2010, 11, 96-110.	3.2	83
5691	Canonical and alternate functions of the microRNA biogenesis machinery. Genes and Development, 2010, 24, 1951-1960.	2.7	203
5692	Dynamic Landscapes of Four Histone Modifications during Deetiolation in <i>Arabidopsis</i> . Plant Cell, 2010, 21, 3732-3748.	3.1	212
5693	Unraveling human complexity and disease with systems biology and personalized medicine. Personalized Medicine, 2010, 7, 275-289.	0.8	50
5694	Improving disease gene prioritization using the semantic similarity of Gene Ontology terms. Bioinformatics, 2010, 26, i561-i567.	1.8	104
5695	ISOFORM ABUNDANCE INFERENCE PROVIDES A MORE ACCURATE ESTIMATION OF GENE EXPRESSION LEVELS IN RNA-SEQ. Journal of Bioinformatics and Computational Biology, 2010, 08, 177-192.	0.3	33
5696	Genomic predictors of prostate cancer therapy outcomes. Expert Review of Molecular Diagnostics, 2010, 10, 619-636.	1.5	4
5697	Ubiquitin accumulation in autophagy-deficient mice is dependent on the Nrf2-mediated stress response pathway: a potential role for protein aggregation in autophagic substrate selection. Journal of Cell Biology, 2010, 191, 537-552.	2.3	156
5698	A MULTI-STRATEGY APPROACH TO INFORMATIVE GENE IDENTIFICATION FROM GENE EXPRESSION DATA. Journal of Bioinformatics and Computational Biology, 2010, 08, 19-38.	0.3	10
5699	PROTEIN SUBCELLULAR MULTI-LOCALIZATION PREDICTION USING A MIN-MAX MODULAR SUPPORT VECTOR MACHINE. International Journal of Neural Systems, 2010, 20, 13-28.	3.2	33
5700	Integration of functional information of genes in fuzzy clustering of short time series gene expression data. , 2010, , .		0

#	ARTICLE	IF	CITATIONS
5701	Biclustering of Expression Microarray Data with Topic Models. , 2010, , .		23
5702	Comprehensive Mapping of the Human Kinome to Epidermal Growth Factor Receptor Signaling. Journal of Biological Chemistry, 2010, 285, 21134-21142.	1.6	39
5703	Aging-Related Gene Expression in Hippocampus Proper Compared with Dentate Gyrus Is Selectively Associated with Metabolic Syndrome Variables in Rhesus Monkeys. Journal of Neuroscience, 2010, 30, 6058-6071.	1.7	53
5704	Early Transcriptional Events During Osteogenic Differentiation of Human Bone Marrow Stromal Cells Induced by Lim Mineralization Protein 3. Gene Expression, 2010, 15, 27-42.	0.5	18
5705	A Protein Involved in the Assembly of an Extracellular Calcium Storage Matrix. Journal of Biological Chemistry, 2010, 285, 12831-12839.	1.6	42
5706	The DEAD-box RNA helicase-like Utp25 is an SSU processome component. Rna, 2010, 16, 2156-2169.	1.6	39
5707	Adaptations of Candida albicans for Growth in the Mammalian Intestinal Tract. Eukaryotic Cell, 2010, 9, 1075-1086.	3.4	131
5708	Regulation of hematopoietic stem cells by their mature progeny. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21689-21694.	3.3	65
5709	Longitudinal shift in diabetic wound microbiota correlates with prolonged skin defense response. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14799-14804.	3.3	189
5710	TGF- β 1 Accelerates Dendritic Cell Differentiation from Common Dendritic Cell Progenitors and Directs Subset Specification toward Conventional Dendritic Cells. Journal of Immunology, 2010, 185, 5326-5335.	0.4	50
5711	Negative Regulation of Meiotic Gene Expression by the Nuclear Poly(a)-binding Protein in Fission Yeast*. Journal of Biological Chemistry, 2010, 285, 27859-27868.	1.6	72
5712	c-Myb Promotes the Survival of CD4+CD8+ Double-Positive Thymocytes through Upregulation of Bcl-xL. Journal of Immunology, 2010, 184, 2793-2804.	0.4	46
5713	Diversification in the genetic architecture of gene expression and transcriptional networks in organ differentiation of Populus. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8492-8497.	3.3	63
5714	MicroRNA Expression Differentiates Histology and Predicts Survival of Lung Cancer. Clinical Cancer Research, 2010, 16, 430-441.	3.2	316
5715	Increased Mutation Frequency in Redox-Impaired <i>Escherichia coli</i> Due to RelA- and RpoS-Mediated Repression of DNA Repair. Applied and Environmental Microbiology, 2010, 76, 5463-5470.	1.4	6
5716	Global modeling of transcriptional responses in interaction networks. Bioinformatics, 2010, 26, 2713-2720.	1.8	8
5717	Sperm Proteomics Reveals Intensified Selection on Mouse Sperm Membrane and Acrosome Genes. Molecular Biology and Evolution, 2010, 27, 1235-1246.	3.5	95
5718	Fast integration of heterogeneous data sources for predicting gene function with limited annotation. Bioinformatics, 2010, 26, 1759-1765.	1.8	124

#	ARTICLE	IF	CITATIONS
5719	Interactive and functional centrality in transcriptional co-expression networks. <i>Bioinformatics</i> , 2010, 26, 3083-3089.	1.8	32
5720	Pandora, a PATHway and Network DiscOveRy Approach based on common biological evidence. <i>Bioinformatics</i> , 2010, 26, 529-535.	1.8	9
5721	Inference of combinatorial Boolean rules of synergistic gene sets from cancer microarray datasets. <i>Bioinformatics</i> , 2010, 26, 1506-1512.	1.8	12
5722	The Gene Wiki: community intelligence applied to human gene annotation. <i>Nucleic Acids Research</i> , 2010, 38, D633-D639.	6.5	67
5723	The Early Whole-Blood Transcriptional Signature of Dengue Virus and Features Associated with Progression to Dengue Shock Syndrome in Vietnamese Children and Young Adults. <i>Journal of Virology</i> , 2010, 84, 12982-12994.	1.5	108
5724	The Negatome database: a reference set of non-interacting protein pairs. <i>Nucleic Acids Research</i> , 2010, 38, D540-D544.	6.5	114
5725	TopoGSA: network topological gene set analysis. <i>Bioinformatics</i> , 2010, 26, 1271-1272.	1.8	58
5726	Sex-specific and lineage-specific alternative splicing in primates. <i>Genome Research</i> , 2010, 20, 180-189.	2.4	239
5727	TreeHugger: A New Test for Enrichment of Gene Ontology Terms. <i>INFORMS Journal on Computing</i> , 2010, 22, 210-221.	1.0	4
5728	Selection upon Genome Architecture: Conservation of Functional Neighborhoods with Changing Genes. <i>PLoS Computational Biology</i> , 2010, 6, e1000953.	1.5	53
5729	FunSimMat update: new features for exploring functional similarity. <i>Nucleic Acids Research</i> , 2010, 38, D244-D248.	6.5	25
5730	PSiFR: an integrated resource for prediction of protein structure and function. <i>Bioinformatics</i> , 2010, 26, 687-688.	1.8	13
5731	Deep SAGE analysis of the <i>Caenorhabditis elegans</i> transcriptome. <i>Nucleic Acids Research</i> , 2010, 38, 3252-3262.	6.5	16
5732	PhenoHM: human-mouse comparative phenome genome server. <i>Nucleic Acids Research</i> , 2010, 38, W165-W174.	6.5	19
5733	ExpressionView—an interactive viewer for modules identified in gene expression data. <i>Bioinformatics</i> , 2010, 26, 2062-2063.	1.8	6
5734	Gene-oriented ortholog database: a functional comparison platform for orthologous loci. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq002-baq002.	1.4	7
5735	Cre-loxP DNA recombination is possible with only minimal unspecific transcriptional changes and without cardiomyopathy in Tg(I±MHC-MerCreMer) mice. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2010, 299, H1671-H1678.	1.5	34
5736	Common genetic variation in the sex hormone metabolic pathway and endometrial cancer risk: pathway-based evaluation of candidate genes. <i>Carcinogenesis</i> , 2010, 31, 827-833.	1.3	42

#	ARTICLE	IF	CITATIONS
5737	The Relationship among Gene Expression, the Evolution of Gene Dosage, and the Rate of Protein Evolution. <i>PLoS Genetics</i> , 2010, 6, e1000944.	1.5	189
5738	How to Understand the Cell by Breaking It: Network Analysis of Gene Perturbation Screens. <i>PLoS Computational Biology</i> , 2010, 6, e1000655.	1.5	51
5739	A Quick Guide to Large-Scale Genomic Data Mining. <i>PLoS Computational Biology</i> , 2010, 6, e1000779.	1.5	34
5740	Deciphering Diseases and Biological Targets for Environmental Chemicals using Toxicogenomics Networks. <i>PLoS Computational Biology</i> , 2010, 6, e1000788.	1.5	43
5741	Intergenic and Repeat Transcription in Human, Chimpanzee and Macaque Brains Measured by RNA-Seq. <i>PLoS Computational Biology</i> , 2010, 6, e1000843.	1.5	62
5742	Use of Data-Biased Random Walks on Graphs for the Retrieval of Context-Specific Networks from Genomic Data. <i>PLoS Computational Biology</i> , 2010, 6, e1000889.	1.5	79
5743	Genome-Wide Analysis Reveals Novel Genes Essential for Heme Homeostasis in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2010, 6, e1001044.	1.5	32
5744	An Integration of Genome-Wide Association Study and Gene Expression Profiling to Prioritize the Discovery of Novel Susceptibility Loci for Osteoporosis-Related Traits. <i>PLoS Genetics</i> , 2010, 6, e1000977.	1.5	191
5745	Angiotensin II-regulated transcription regulatory genes in adrenal steroidogenesis. <i>Physiological Genomics</i> , 2010, 42A, 259-266.	1.0	19
5746	A Population Genetic Hidden Markov Model for Detecting Genomic Regions Under Selection. <i>Molecular Biology and Evolution</i> , 2010, 27, 1673-1685.	3.5	19
5747	Pathema: a clade-specific bioinformatics resource center for pathogen research. <i>Nucleic Acids Research</i> , 2010, 38, D408-D414.	6.5	18
5748	Capture Compound Mass Spectrometry Sheds Light on the Molecular Mechanisms of Liver Toxicity of Two Parkinson Drugs. <i>Toxicological Sciences</i> , 2010, 113, 243-253.	1.4	34
5749	Analyses of an Expressed Sequence Tag Library from <i>Taenia solium</i> , <i>Cysticercus</i> . <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e919.	1.3	12
5750	Molecular mechanisms mediating preconditioning following chronic ischemia differ from those in classical second window. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2010, 299, H752-H762.	1.5	36
5751	Comparative transcriptome analysis of green/white variegated sectors in <i>Arabidopsis thaliana</i> variegated2: responses to oxidative and other stresses in white sectors. <i>Journal of Experimental Botany</i> , 2010, 61, 2433-2445.	2.4	46
5752	Protein Interaction Networks—More Than Mere Modules. <i>PLoS Computational Biology</i> , 2010, 6, e1000659.	1.5	57
5753	Ameliorative Effects of Mulberry (<i>Morus alba</i> L.) Leaves on Hyperlipidemia in Rats Fed a High-Fat Diet: Induction of Fatty Acid Oxidation, Inhibition of Lipogenesis, and Suppression of Oxidative Stress. <i>Bioscience, Biotechnology and Biochemistry</i> , 2010, 74, 2385-2395.	0.6	79
5754	Functional Characterization of Transcription Factor Motifs Using Cross-species Comparison across Large Evolutionary Distances. <i>PLoS Computational Biology</i> , 2010, 6, e1000652.	1.5	28

#	ARTICLE	IF	CITATIONS
5755	Getting Started in Gene Orthology and Functional Analysis. <i>PLoS Computational Biology</i> , 2010, 6, e1000703.	1.5	100
5756	Characterizing the Metabolism of Dehalococcoides with a Constraint-Based Model. <i>PLoS Computational Biology</i> , 2010, 6, e1000887.	1.5	46
5757	Simultaneous Genome-Wide Inference of Physical, Genetic, Regulatory, and Functional Pathway Components. <i>PLoS Computational Biology</i> , 2010, 6, e1001009.	1.5	20
5758	Mapping Dynamic Histone Acetylation Patterns to Gene Expression in Nanog-Depleted Murine Embryonic Stem Cells. <i>PLoS Computational Biology</i> , 2010, 6, e1001034.	1.5	23
5759	Translational Selection Is Ubiquitous in Prokaryotes. <i>PLoS Genetics</i> , 2010, 6, e1001004.	1.5	76
5760	Common Inherited Variation in Mitochondrial Genes Is Not Enriched for Associations with Type 2 Diabetes or Related Glycemic Traits. <i>PLoS Genetics</i> , 2010, 6, e1001058.	1.5	429
5761	G1 arrest and differentiation can occur independently of Rb family function. <i>Journal of Cell Biology</i> , 2010, 191, 809-825.	2.3	30
5762	FuncBase : a resource for quantitative gene function annotation. <i>Bioinformatics</i> , 2010, 26, 1806-1807.	1.8	14
5763	Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. <i>Nucleic Acids Research</i> , 2010, 38, W210-W213.	6.5	283
5764	AltAnalyze and DomainGraph: analyzing and visualizing exon expression data. <i>Nucleic Acids Research</i> , 2010, 38, W755-W762.	6.5	310
5765	The Teleost Anatomy Ontology: Anatomical Representation for the Genomics Age. <i>Systematic Biology</i> , 2010, 59, 369-383.	2.7	76
5766	Ontogenetic Complexity of Sexual Dimorphism and Sex-Specific Selection. <i>Molecular Biology and Evolution</i> , 2010, 27, 1570-1578.	3.5	99
5767	Detecting subtle functional differences in ketopantoate reductase and related enzymes using a rule-based approach with sequence-structure homology recognition scores. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 859-869.	1.0	1
5768	A Computational Approach to Analyze the Mechanism of Action of the Kinase Inhibitor Bafetinib. <i>PLoS Computational Biology</i> , 2010, 6, e1001001.	1.5	23
5769	Prediction of human functional genetic networks from heterogeneous data using RVM-based ensemble learning. <i>Bioinformatics</i> , 2010, 26, 807-813.	1.8	28
5770	BioXSD: the common data-exchange format for everyday bioinformatics web services. <i>Bioinformatics</i> , 2010, 26, i540-i546.	1.8	20
5771	FlyTF: improved annotation and enhanced functionality of the Drosophila transcription factor database. <i>Nucleic Acids Research</i> , 2010, 38, D443-D447.	6.5	70
5772	Genome-Wide Analysis of Light- and Temperature-Entrained Circadian Transcripts in <i>Caenorhabditis elegans</i> . <i>PLoS Biology</i> , 2010, 8, e1000503.	2.6	60

#	ARTICLE	IF	CITATIONS
5773	Polymorphic Cis- and Trans-Regulation of Human Gene Expression. <i>PLoS Biology</i> , 2010, 8, e1000480.	2.6	142
5774	Network Modeling Identifies Molecular Functions Targeted by miR-204 to Suppress Head and Neck Tumor Metastasis. <i>PLoS Computational Biology</i> , 2010, 6, e1000730.	1.5	140
5775	The Cellular Robustness by Genetic Redundancy in Budding Yeast. <i>PLoS Genetics</i> , 2010, 6, e1001187.	1.5	58
5776	Practical Application of Toxicogenomics for Profiling Toxicant-Induced Biological Perturbations. <i>International Journal of Molecular Sciences</i> , 2010, 11, 3397-3412.	1.8	21
5777	Smed454 dataset: unravelling the transcriptome of <i>Schmidtea mediterranea</i> . <i>BMC Genomics</i> , 2010, 11, 731.	1.2	48
5778	An Integrative -omics Approach to Identify Functional Sub-Networks in Human Colorectal Cancer. <i>PLoS Computational Biology</i> , 2010, 6, e1000639.	1.5	140
5779	Finding the "Dark Matter" in Human and Yeast Protein Network Prediction and Modelling. <i>PLoS Computational Biology</i> , 2010, 6, e1000945.	1.5	21
5780	Functional Genomics Complements Quantitative Genetics in Identifying Disease-Gene Associations. <i>PLoS Computational Biology</i> , 2010, 6, e1000991.	1.5	55
5781	A Scalable Approach for Discovering Conserved Active Subnetworks across Species. <i>PLoS Computational Biology</i> , 2010, 6, e1001028.	1.5	17
5782	Quantitative Comparison of Catalytic Mechanisms and Overall Reactions in Convergently Evolved Enzymes: Implications for Classification of Enzyme Function. <i>PLoS Computational Biology</i> , 2010, 6, e1000700.	1.5	33
5783	Integrated functional networks of process, tissue, and developmental stage specific interactions in <i>Arabidopsis thaliana</i> . <i>BMC Systems Biology</i> , 2010, 4, 180.	3.0	21
5784	A novel approach to analyze gene expression data demonstrates that the F508 mutation in CFTR downregulates the antigen presentation pathway. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2010, 298, L473-L482.	1.3	21
5785	Homotypic clusters of transcription factor binding sites are a key component of human promoters and enhancers. <i>Genome Research</i> , 2010, 20, 565-577.	2.4	203
5786	Empowering 21st Century Biology. <i>BioScience</i> , 2010, 60, 923-930.	2.2	24
5787	Meeting report: a workshop on Best Practices in Genome Annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq001-baq001.	1.4	18
5788	Genomic Similarity and Kernel Methods II: Methods for Genomic Information. <i>Human Heredity</i> , 2010, 70, 132-140.	0.4	67
5789	A multi-tier data mining workflow to analyze the age related shift from diglycosylated- to tetra-glycosylated-FSH secretion by the anterior pituitary. , 2010, , .		1
5790	Biochemical network matching and composition. , 2010, , .		3

#	ARTICLE	IF	CITATIONS
5791	Quantitative Proteomics Discloses MET Expression in Mitochondria as a Direct Target of MET Kinase Inhibitor in Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2629-2641.	2.5	22
5792	A Large-scale genetic association study of esophageal adenocarcinoma risk. <i>Carcinogenesis</i> , 2010, 31, 1259-1263.	1.3	46
5793	Population differentiation as a test for selective sweeps. <i>Genome Research</i> , 2010, 20, 393-402.	2.4	600
5794	Practical Applications of the Gene Ontology Resource. , 2010, , 319-339.		0
5795	Combinatorial Optimization and Applications. <i>Lecture Notes in Computer Science</i> , 2010, , .	1.0	5
5796	Simultaneous Clustering of Multiple Gene Expression and Physical Interaction Datasets. <i>PLoS Computational Biology</i> , 2010, 6, e1000742.	1.5	35
5797	Patterns of HIV-1 Protein Interaction Identify Perturbed Host-Cellular Subsystems. <i>PLoS Computational Biology</i> , 2010, 6, e1000863.	1.5	57
5798	Transcriptional responses to thermal acclimation in the eurythermal fish <i>Gillichthys mirabilis</i> (Cooper 1864). <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2010, 299, R843-R852.	0.9	62
5799	Disease and phenotype gene set analysis of disease-based gene expression in mouse and human. <i>Physiological Genomics</i> , 2010, 42A, 162-167.	1.0	17
5800	Development and Application of Bovine and Porcine Oligonucleotide Arrays with Protein-Based Annotation. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-11.	3.0	7
5801	Identification of Multiple Hypoxia Signatures in Neuroblastoma Cell Lines by l1-l2Regularization and Data Reduction. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-11.	3.0	10
5802	Interoperability between phenotype and anatomy ontologies. <i>Bioinformatics</i> , 2010, 26, 3112-3118.	1.8	40
5803	GeneCards Version 3: the human gene integrator. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq020-baq020.	1.4	1,257
5804	GOing Bayesian: model-based gene set analysis of genome-scale data. <i>Nucleic Acids Research</i> , 2010, 38, 3523-3532.	6.5	190
5805	Endothelial pro-atherosclerotic response to extracellular diabetic-like environment: Possible role of thioredoxin-interacting protein. <i>Nephrology Dialysis Transplantation</i> , 2010, 25, 2141-2149.	0.4	28
5806	Multi-relational factorizations for cancer subclassification. , 2010, , .		2
5807	RB-pathway disruption in breast cancer. <i>Cell Cycle</i> , 2010, 9, 4153-4163.	1.3	163
5808	Complete genome sequence of <i>Cellulomonas flavigena</i> type strain (134T). <i>Standards in Genomic Sciences</i> , 2010, 3, 15-25.	1.5	38

#	ARTICLE	IF	CITATIONS
5809	Semi-automated ontology generation within OBO-Edit. <i>Bioinformatics</i> , 2010, 26, i88-i96.	1.8	28
5810	Human Variation in Short Regions Predisposed to Deep Evolutionary Conservation. <i>Molecular Biology and Evolution</i> , 2010, 27, 1279-1288.	3.5	7
5811	The IntAct molecular interaction database in 2010. <i>Nucleic Acids Research</i> , 2010, 38, D525-D531.	6.5	574
5812	VirtualPlant: A Software Platform to Support Systems Biology Research. <i>Plant Physiology</i> , 2010, 152, 500-515.	2.3	254
5813	The Association of Multiple Interacting Genes with Specific Phenotypes in Rice Using Gene Coexpression Networks. <i>Plant Physiology</i> , 2010, 154, 13-24.	2.3	93
5814	Computational Methods for the Prediction of Protein-Protein Interactions. <i>Protein and Peptide Letters</i> , 2010, 17, 1069-1078.	0.4	23
5815	Both Noncoding and Protein-Coding RNAs Contribute to Gene Expression Evolution in the Primate Brain. <i>Genome Biology and Evolution</i> , 2010, 2, 67-79.	1.1	103
5816	The Salivary Gland Transcriptome of the Eastern Tree Hole Mosquito, <i>Ochlerotatus triseriatus</i> . <i>Journal of Medical Entomology</i> , 2010, 47, 376-386.	0.9	17
5817	A New Measure Based on Gene Ontology for Semantic Similarity of Genes. , 2010, , .		6
5818	Extracting multi-function features for cancer genes. , 2010, , .		0
5819	Sensitivity Analysis for the Cross-Match Test, With Applications in Genomics. <i>Journal of the American Statistical Association</i> , 2010, 105, 1005-1013.	1.8	10
5820	Scalable discovery of best clusters on large graphs. <i>Proceedings of the VLDB Endowment</i> , 2010, 3, 693-702.	2.1	43
5821	Emergence and Evolution of Modern Molecular Functions Inferred from Phylogenomic Analysis of Ontological Data. <i>Molecular Biology and Evolution</i> , 2010, 27, 1710-1733.	3.5	43
5822	Cooperation between myogenic regulatory factors and SIX family transcription factors is important for myoblast differentiation. <i>Nucleic Acids Research</i> , 2010, 38, 6857-6871.	6.5	96
5823	Efficient query evaluation for DAG-shaped hierarchies. , 2010, , .		0
5824	Prognostic Gene Expression Signature for Squamous Cell Carcinoma of Lung. <i>Clinical Cancer Research</i> , 2010, 16, 5038-5047.	3.2	31
5825	Aurora kinase A as a rational target for therapy in glioblastoma. <i>Journal of Neurosurgery: Pediatrics</i> , 2010, 6, 98-105.	0.8	39
5826	Gene Set Analysis of Lung Samples Provides Insight into Pathogenesis of Progressive, Fibrotic Pulmonary Sarcoidosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2010, 181, 1367-1375.	2.5	76

#	ARTICLE	IF	CITATIONS
5827	Noncoding Sequences Near Duplicated Genes Evolve Rapidly. <i>Genome Biology and Evolution</i> , 2010, 2, 518-533.	1.1	20
5828	7-aa Peptide Mimic from HVR1 of HCV Protects Hepatic Injury in Rats by Reduced Expression of Key Pro-Inflammatory Factors. <i>Inflammation and Allergy: Drug Targets</i> , 2010, 9, 135-145.	1.8	8
5829	Negative correlations in collaboration. , 2010, , .		5
5830	Gene set analysis using principal components. , 2010, , .		0
5831	The Salivary Gland Transcriptome of the Eastern Tree Hole Mosquito, <i>Ochlerotatus triseriatus</i> . <i>Journal of Medical Entomology</i> , 2010, 47, 376-386.	0.9	12
5832	Increased Expression of Angiogenic Genes in the Brains of Mouse Meg3-Null Embryos. <i>Endocrinology</i> , 2010, 151, 2443-2452.	1.4	148
5833	Gene Expression Profiling of Mouse Embryos with Microarrays. <i>Methods in Enzymology</i> , 2010, 477, 511-541.	0.4	5
5834	The Antiproliferative Effects of Progestins in T47D Breast Cancer Cells Are Tempered by Progestin Induction of the ETS Transcription Factor E1f5. <i>Molecular Endocrinology</i> , 2010, 24, 1380-1392.	3.7	16
5835	Functional Conservation of DNA Methylation in the Pea Aphid and the Honeybee. <i>Genome Biology and Evolution</i> , 2010, 2, 719-728.	1.1	109
5836	Defining Cell Identity by Comprehensive Gene Expression Profiling. <i>Current Medicinal Chemistry</i> , 2010, 17, 3245-3252.	1.2	4
5837	GOVis, A Gene Ontology Visualization Tool Based on Multi-Dimensional Values. <i>Protein and Peptide Letters</i> , 2010, 17, 675-680.	0.4	2
5838	Generation and Analysis of ESTs from the Grass Carp, <i>Ctenopharyngodon idellus</i> . <i>Animal Biotechnology</i> , 2010, 21, 217-225.	0.7	5
5839	Fragile regions and not functional constraints predominate in shaping gene organization in the genus <i>Drosophila</i> . <i>Genome Research</i> , 2010, 20, 1084-1096.	2.4	56
5840	From raw materials to validated system: the construction of a genomic library and microarray to interpret systemic perturbations in Northern bobwhite. <i>Physiological Genomics</i> , 2010, 42, 219-235.	1.0	55
5841	Highly conserved transcriptional responses to mechanical ventilation of the lung. <i>Physiological Genomics</i> , 2010, 42, 384-396.	1.0	20
5842	The FLIGHT <i>Drosophila</i> RNAi database. <i>Fly</i> , 2010, 4, 344-348.	0.9	4
5843	The hot research topics and the research fronts in the field of web data mining(WDM) based on Web of Science. , 2010, , .		2
5844	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912

#	ARTICLE	IF	CITATIONS
5845	Toward Quantitative Proteomics of Organ Substructures: Implications for Renal Physiology. <i>Seminars in Nephrology</i> , 2010, 30, 487-499.	0.6	10
5846	Integrative Analysis of -Omics Data and Histologic Scoring in Renal Disease and Transplantation: Renal Histogenomics. <i>Seminars in Nephrology</i> , 2010, 30, 520-530.	0.6	15
5847	Integrative Systems Biology for Data-Driven Knowledge Discovery. <i>Seminars in Nephrology</i> , 2010, 30, 443-454.	0.6	20
5848	PREDICTION OF REGULATORY TRANSCRIPTION FACTORS IN T HELPER CELL DIFFERENTIATION AND MAINTENANCE. , 2010, , .		2
5849	Pathways and Promoter Networks Analysis Provides Systems Topology for Systems Biology Approaches. <i>Seminars in Nephrology</i> , 2010, 30, 477-486.	0.6	4
5850	Impact of the 1000 Genomes Project on the next wave of pharmacogenomic discovery. <i>Pharmacogenomics</i> , 2010, 11, 249-256.	0.6	43
5851	Computational Challenges in Systems Biology. , 2010, , 175-223.		3
5852	The Effects of Two Different <i>Ganoderma</i> Species (<i>Lingzhi</i>) on Gene Expression in Human Monocytic THP-1 Cells. <i>Nutrition and Cancer</i> , 2010, 62, 648-658.	0.9	11
5853	Finding explained groups of time-course gene expression profiles with predictive clustering trees. <i>Molecular BioSystems</i> , 2010, 6, 729.	2.9	30
5854	Analyzing Shotgun Proteomic Data with PatternLab for Proteomics. <i>Current Protocols in Bioinformatics</i> , 2010, 30, Unit 13.13.1-15.	25.8	24
5855	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. <i>Science Signaling</i> , 2010, 3, ra3.	1.6	1,319
5856	Long-term genome-wide blood RNA expression profiles yield novel molecular response candidates for IFN- β treatment in relapsing remitting MS. <i>Pharmacogenomics</i> , 2010, 11, 147-161.	0.6	42
5857	ACLAME: A CLAssification of Mobile genetic Elements, update 2010. <i>Nucleic Acids Research</i> , 2010, 38, D57-D61.	6.5	289
5858	Transcriptional Profiling of Human Embryonic Stem Cells Differentiating to Definitive and Primitive Endoderm and Further Toward the Hepatic Lineage. <i>Stem Cells and Development</i> , 2010, 19, 961-978.	1.1	17
5859	Using the DFCI Gene Index Databases for Biological Discovery. <i>Current Protocols in Bioinformatics</i> , 2010, 29, Unit1.6.1-36.	25.8	12
5860	Automating Mathematical Modeling of Biochemical Reaction Networks. <i>Systems Biology</i> , 2010, , 159-205.	0.1	4
5862	<i>S</i> -Alkylating Labeling Strategy for Site-Specific Identification of the <i>S</i> -Nitrosoproteome. <i>Journal of Proteome Research</i> , 2010, 9, 6417-6439.	1.8	64
5863	Statistical Methods for Integrating Multiple Types of High-Throughput Data. <i>Methods in Molecular Biology</i> , 2010, 620, 511-529.	0.4	5

#	ARTICLE	IF	CITATIONS
5869	Liverbase: A Comprehensive View of Human Liver Biology. <i>Journal of Proteome Research</i> , 2010, 9, 50-58.	1.8	41
5870	Owlifier: Creating OWL-DL ontologies from simple spreadsheet-based knowledge descriptions. <i>Ecological Informatics</i> , 2010, 5, 19-25.	2.3	10
5871	Application of genetic/genomic approaches to allergic disorders. <i>Journal of Allergy and Clinical Immunology</i> , 2010, 126, 425-436.	1.5	20
5872	Tissue factor pathway inhibitor-2 is induced by fluid shear stress in vascular smooth muscle cells and affects cell proliferation and survival. <i>Journal of Vascular Surgery</i> , 2010, 52, 167-175.	0.6	36
5873	Malignant pleural mesothelioma: Genome-wide expression patterns reflecting general resistance mechanisms and a proposal of novel targets. <i>Lung Cancer</i> , 2010, 67, 57-68.	0.9	62
5874	Transcription profiling of acute temperature stress in the Antarctic plunderfish <i>Harpagifer antarcticus</i> . <i>Marine Genomics</i> , 2010, 3, 35-44.	0.4	58
5875	AmphiEST: Enabling comparative analysis of ESTs from five developmental stages of amphioxus. <i>Marine Genomics</i> , 2010, 3, 151-155.	0.4	6
5876	Gilthead sea bream (<i>Sparus auratus</i>) and European sea bass (<i>Dicentrarchus labrax</i>) expressed sequence tags: Characterization, tissue-specific expression and gene markers. <i>Marine Genomics</i> , 2010, 3, 179-191.	0.4	25
5877	Annulus cells from more degenerated human discs show modified gene expression in 3D culture compared with expression in cells from healthier discs. <i>Spine Journal</i> , 2010, 10, 721-727.	0.6	28
5878	From RNA-seq reads to differential expression results. <i>Genome Biology</i> , 2010, 11, 220.	13.9	603
5879	Mechanistic Toxicity Assessment of Nanomaterials by Whole-Cell-Array Stress Genes Expression Analysis. <i>Environmental Science & Technology</i> , 2010, 44, 5964-5970.	4.6	160
5880	Gene association analysis: a survey of frequent pattern mining from gene expression data. <i>Briefings in Bioinformatics</i> , 2010, 11, 210-224.	3.2	70
5881	Prediction of protease substrates using sequence and structure features. <i>Bioinformatics</i> , 2010, 26, 1714-1722.	1.8	61
5882	Contrasts between adaptive coding and noncoding changes during human evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7853-7857.	3.3	102
5883	The ascorbic acid content of tomato fruits is associated with the expression of genes involved in pectin degradation. <i>BMC Plant Biology</i> , 2010, 10, 163.	1.6	103
5884	Transcriptome analysis of monocyte-HIV interactions. <i>Retrovirology</i> , 2010, 7, 53.	0.9	52
5885	Proteome changes of lungs artificially infected with H-PRRSV and N-PRRSV by two-dimensional fluorescence difference gel electrophoresis. <i>Virology Journal</i> , 2010, 7, 107.	1.4	18
5886	Structural similarity-based predictions of protein interactions between HIV-1 and <i>Homo sapiens</i> . <i>Virology Journal</i> , 2010, 7, 82.	1.4	70

#	ARTICLE	IF	CITATIONS
5887	A novel paradigm for cell and molecule interaction ontology: from the CMM model to IMGT-ONTOLOGY. Immunome Research, 2010, 6, 1.	0.1	23
5888	Further developments towards a genome-scale metabolic model of yeast. BMC Systems Biology, 2010, 4, 145.	3.0	95
5889	Genetic Risk Factors for Hepatopulmonary Syndrome in Patients With Advanced Liver Disease. Gastroenterology, 2010, 139, 130-139.e24.	0.6	78
5890	Novel Application of Electrostatic Repulsion-Hydrophilic Interaction Chromatography (ERLIC) in Shotgun Proteomics: Comprehensive Profiling of Rat Kidney Proteome. Journal of Proteome Research, 2010, 9, 3520-3526.	1.8	84
5891	Inductive Databases and Constraint-Based Data Mining. , 2010, , .		6
5892	Biclustering of DNA microarray data using artificial immune system. , 2010, , .		3
5893	An Informatics-assisted Label-free Quantitation Strategy that Depicts Phosphoproteomic Profiles in Lung Cancer Cell Invasion. Journal of Proteome Research, 2010, 9, 5582-5597.	1.8	57
5894	Antiproliferative Mechanisms of the Flavonoids 2,2- Dihydroxychalcone and Fisetin in Human Prostate Cancer Cells. Nutrition and Cancer, 2010, 62, 668-681.	0.9	33
5895	Gene expression atlas for human embryogenesis. FASEB Journal, 2010, 24, 3341-3350.	0.2	45
5896	Genome-wide pathway analysis implicates intracellular transmembrane protein transport in Alzheimer disease. Journal of Human Genetics, 2010, 55, 707-709.	1.1	50
5897	Protein annotation and modelling servers at University College London. Nucleic Acids Research, 2010, 38, W563-W568.	6.5	316
5898	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
5899	Proteome Profiling and Functional Classification of Intracellular Proteins from Conidia of the Human-Pathogenic Mold <i>Aspergillus fumigatus</i> . Journal of Proteome Research, 2010, 9, 3427-3442.	1.8	86
5900	microRNA-122 as a regulator of mitochondrial metabolic gene network in hepatocellular carcinoma. Molecular Systems Biology, 2010, 6, 402.	3.2	169
5901	First Insight into the Human Liver Proteome from PROTEOME ^{SKY} -LIVER ^{Hu} 1.0, a Publicly Available Database. Journal of Proteome Research, 2010, 9, 79-94.	1.8	40
5903	Frequent subgraph discovery in dynamic networks. , 2010, , .		35
5904	Topology-Free Querying of Protein Interaction Networks. Journal of Computational Biology, 2010, 17, 237-252.	0.8	99
5905	Modeling sequence and function similarity between proteins for protein functional annotation. , 2010, 2010, 499-502.		6

#	ARTICLE	IF	CITATIONS
5906	Mapping Mental Function to Brain Structure: How Can Cognitive Neuroimaging Succeed?. Perspectives on Psychological Science, 2010, 5, 753-761.	5.2	195
5907	Population Proteomics of the European Hake (<i>Merluccius merluccius</i>). Journal of Proteome Research, 2010, 9, 6392-6404.	1.8	21
5908	Systems Analysis of Protein Modification and Cellular Responses Induced by Electrophile Stress. Accounts of Chemical Research, 2010, 43, 673-683.	7.6	198
5909	Ontology and the Future of Dental Research Informatics. Journal of the American Dental Association, 2010, 141, 1173-1175.	0.7	8
5910	A new method for measuring the semantic similarity on gene ontology. , 2010, , .		11
5911	Insight into the Sialome of the Bed Bug, <i>Cimex lectularius</i> . Journal of Proteome Research, 2010, 9, 3820-3831.	1.8	65
5912	High-Throughput Virtual Screening of Proteins Using GRID Molecular Interaction Fields. Journal of Chemical Information and Modeling, 2010, 50, 155-169.	2.5	75
5913	Pocket Similarity: Are $\hat{\pm}$ Carbons Enough?. Journal of Chemical Information and Modeling, 2010, 50, 1466-1475.	2.5	43
5914	Simple Method for Quantitative Analysis of N-Linked Glycoproteins in Hepatocellular Carcinoma Specimens. Journal of Proteome Research, 2010, 9, 308-318.	1.8	43
5915	Development Approach for e-Science Ontology: A Case Study in Biological Domain. , 2010, , .		1
5916	An Introduction to Microarray Data Analysis and Visualization. Methods in Enzymology, 2010, 470, 19-50.	0.4	12
5917	Reconstructing Gene Histories in Ascomycota Fungi. Methods in Enzymology, 2010, 470, 447-485.	0.4	3
5918	PLAZA: A Comparative Genomics Resource to Study Gene and Genome Evolution in Plants. Plant Cell, 2010, 21, 3718-3731.	3.1	243
5919	The effect of tert-butyl hydroperoxide on hepatic transcriptome expression patterns in the striped sea bream (<i>Lithognathus mormyrus</i> ; <i>Teleostei</i>). Free Radical Research, 2010, 44, 991-1003.	1.5	2
5920	Human Adipose-Derived Mesenchymal Stem Cells: Direction to a Phenotype Sharing Similarities with the Disc, Gene Expression Profiling, and Coculture with Human Annulus Cells. Tissue Engineering - Part A, 2010, 16, 2843-2860.	1.6	55
5921	Developmental regulation and individual differences of neuronal H3K4me3 epigenomes in the prefrontal cortex. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8824-8829.	3.3	218
5922	Transcriptome profiling of zebrafish infected with <i>Streptococcus suis</i> . Microbial Pathogenesis, 2010, 48, 178-187.	1.3	63
5923	Genome-wide Dissection of MicroRNA Functions and Cotargeting Networks Using Gene Set Signatures. Molecular Cell, 2010, 38, 140-153.	4.5	212

#	ARTICLE	IF	CITATIONS
5924	A Consensus of Core Protein Complex Compositions for <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , 2010, 38, 916-928.	4.5	91
5925	â€˜Rejectedâ€™ vs. â€˜rejectingâ€™ transcriptomes in allogeneic challenged colonial urochordates. <i>Molecular Immunology</i> , 2010, 47, 2083-2093.	1.0	6
5926	Ontology management and evolution for business intelligence. <i>International Journal of Information Management</i> , 2010, 30, 559-566.	10.5	52
5927	Study of anti-inflammatory activities of the pure compounds from <i>Andrographis paniculata</i> (burm.f.) Nees and their effects on gene expression. <i>International Immunopharmacology</i> , 2010, 10, 1361-1373.	1.7	84
5928	Transcriptional profiling of ESTs responsive to <i>Rhizobium vitis</i> from â€˜Tamnaraâ€™ grapevines (<i>Vitis</i> sp.). <i>Journal of Plant Physiology</i> , 2010, 167, 1084-1092.	1.6	6
5929	Evolutionary Trace Annotation of Protein Function in the Structural Proteome. <i>Journal of Molecular Biology</i> , 2010, 396, 1451-1473.	2.0	38
5930	Global Network Analysis of Lipid-Raft-Related Proteins Reveals Their Centrality in the Network and Their Roles in Multiple Biological Processes. <i>Journal of Molecular Biology</i> , 2010, 402, 761-773.	2.0	6
5931	Transcriptional effects of progesterone receptor antagonist in rat granulosa cells. <i>Molecular and Cellular Endocrinology</i> , 2010, 315, 121-130.	1.6	10
5932	Identification of genes differentially expressed in hemocytes of <i>Scylla paramamosain</i> in response to lipopolysaccharide. <i>Fish and Shellfish Immunology</i> , 2010, 28, 167-177.	1.6	59
5933	Searching for immunomodulatory sequences in sea bass (<i>Dicentrarchus labrax</i> L.): Transcripts analysis from thymus. <i>Fish and Shellfish Immunology</i> , 2010, 29, 571-578.	1.6	15
5934	Microarray analysis of gene expression in eastern oyster (<i>Crassostrea virginica</i>) reveals a novel combination of antimicrobial and oxidative stress host responses after dermo (<i>Perkinsus marinus</i>) challenge. <i>Fish and Shellfish Immunology</i> , 2010, 29, 921-929.	1.6	66
5935	Osteo-transcriptomics of human mesenchymal stem cells: Accelerated gene expression and osteoblast differentiation induced by vitamin D reveals c-MYC as an enhancer of BMP2-induced osteogenesis. <i>Bone</i> , 2010, 46, 613-627.	1.4	88
5936	Hunting for robust gene signature from cancer profiling data: Sources of variability, different interpretations, and recent methodological developments. <i>Cancer Letters</i> , 2010, 296, 9-16.	3.2	30
5937	Expression of cytokine genes in the aorta is altered by the deficiency in MCP-1: Effect of a high-fat, high-cholesterol diet. <i>Cytokine</i> , 2010, 50, 121-128.	1.4	20
5938	A Simple Method for Gene Expression and Chromatin Profiling of Individual Cell Types within a Tissue. <i>Developmental Cell</i> , 2010, 18, 1030-1040.	3.1	360
5939	Role of NFKB2 on the early myeloid differentiation of CD34+ hematopoietic stem/progenitor cells. <i>Differentiation</i> , 2010, 80, 195-203.	1.0	18
5940	The use of neuroproteomics in drug abuse research. <i>Drug and Alcohol Dependence</i> , 2010, 107, 11-22.	1.6	17
5941	Prediction of protein subcellular localization by weighted gene ontology terms. <i>Biochemical and Biophysical Research Communications</i> , 2010, 399, 402-405.	1.0	18

#	ARTICLE	IF	CITATIONS
5942	Understanding gene essentiality by finely characterizing hubs in the yeast protein interaction network. <i>Biochemical and Biophysical Research Communications</i> , 2010, 401, 112-116.	1.0	17
5943	Teasing apart a three-way symbiosis: Transcriptome analyses of <i>Curvularia protuberata</i> in response to viral infection and heat stress. <i>Biochemical and Biophysical Research Communications</i> , 2010, 401, 225-230.	1.0	59
5944	Prediction of midbody, centrosome and kinetochore proteins based on gene ontology information. <i>Biochemical and Biophysical Research Communications</i> , 2010, 401, 382-384.	1.0	33
5945	Aberrant gene expression profile in a mouse model of endometriosis mirrors that observed in women. <i>Fertility and Sterility</i> , 2010, 93, 1615-1627.e18.	0.5	51
5946	Venomics of the spider <i>Ornithoctonus huwena</i> based on transcriptomic versus proteomic analysis. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 81-88.	0.4	22
5947	Identification of immune-relevant genes by expressed sequence tag analysis of head kidney from grass carp (<i>Ctenopharyngodon idella</i>). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 116-123.	0.4	11
5948	The transcriptome of the early life history stages of the California Sea Hare <i>Aplysia californica</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 165-170.	0.4	28
5949	Multi-transcript expression patterns in the gastrolith disk and the hypodermis of the crayfish <i>Cherax quadricarinatus</i> at premolt. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 171-177.	0.4	11
5950	Analysis and functional annotation of expressed sequence tags from in vitro cell lines of elasmobranchs: Spiny dogfish shark (<i>Squalus acanthias</i>) and little skate (<i>Leucoraja erinacea</i>). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 199-206.	0.4	11
5951	Generation and analysis of expressed sequence tags from adductor muscle of Japanese scallop <i>Mizuhopecten yessoensis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 288-294.	0.4	6
5952	Ligand-Specific c-Fos Expression Emerges from the Spatiotemporal Control of ErbB Network Dynamics. <i>Cell</i> , 2010, 141, 884-896.	13.5	217
5953	Chromatin-Remodeling Components of the BAF Complex Facilitate Reprogramming. <i>Cell</i> , 2010, 141, 943-955.	13.5	357
5954	Functional Overlap and Regulatory Links Shape Genetic Interactions between Signaling Pathways. <i>Cell</i> , 2010, 143, 991-1004.	13.5	123
5955	A Tissue-Specific Atlas of Mouse Protein Phosphorylation and Expression. <i>Cell</i> , 2010, 143, 1174-1189.	13.5	1,564
5956	Neurocognitive Phenotypes and Genetic Dissection of Disorders of Brain and Behavior. <i>Neuron</i> , 2010, 68, 218-230.	3.8	20
5957	A cross-laboratory comparison of expression profiling data from normal human postmortem brain. <i>Neuroscience</i> , 2010, 167, 384-395.	1.1	27
5958	Cognitive neuroscience 2.0: building a cumulative science of human brain function. <i>Trends in Cognitive Sciences</i> , 2010, 14, 489-496.	4.0	173
5959	Arsenite exposure in human lymphoblastoid cell lines induces autophagy and coordinated induction of lysosomal genes. <i>Toxicology Letters</i> , 2010, 199, 153-159.	0.4	38

#	ARTICLE	IF	CITATIONS
5960	Identification of immunologically relevant genes in mare and foal dendritic cells responding to infection by <i>Rhodococcus equi</i> . <i>Veterinary Immunology and Immunopathology</i> , 2010, 136, 144-150.	0.5	9
5961	Developmental gene regulation in the era of genomics. <i>Developmental Biology</i> , 2010, 339, 230-239.	0.9	43
5962	ATX expression and LPA signalling are vital for the development of the nervous system. <i>Developmental Biology</i> , 2010, 339, 451-464.	0.9	133
5963	Protein kinase A regulates GDNF/RET-dependent but not GDNF/Ret-independent ureteric bud outgrowth from the Wolffian duct. <i>Developmental Biology</i> , 2010, 347, 337-347.	0.9	14
5964	Conservation and regulatory associations of a wide affinity range of mouse transcription factor binding sites. <i>Genomics</i> , 2010, 95, 185-195.	1.3	44
5965	Investigation of low-dose ritonavir on human peripheral blood mononuclear cells using gene expression whole genome microarrays. <i>Genomics</i> , 2010, 96, 57-65.	1.3	8
5966	Curcumin Extends Life Span, Improves Health Span, and Modulates the Expression of Age-Associated Aging Genes in <i>Drosophila melanogaster</i> . <i>Rejuvenation Research</i> , 2010, 13, 561-570.	0.9	195
5967	Computational analysis of microRNA function in heart development. <i>Acta Biochimica Et Biophysica Sinica</i> , 2010, 42, 662-670.	0.9	17
5968	A novel role for cardiac ankyrin repeat protein Ankrd1/CARP as a co-activator of the p53 tumor suppressor protein. <i>Archives of Biochemistry and Biophysics</i> , 2010, 502, 60-67.	1.4	58
5969	Mass spectrometry-based proteomics in cell biology. <i>Journal of Cell Biology</i> , 2010, 190, 491-500.	2.3	348
5970	The power of protein interaction networks for associating genes with diseases. <i>Bioinformatics</i> , 2010, 26, 1057-1063.	1.8	314
5971	Towards an Ontology of Cognitive Control. <i>Topics in Cognitive Science</i> , 2010, 2, 678-692.	1.1	122
5972	The <i>Chlorella variabilis</i> NC64A Genome Reveals Adaptation to Photosymbiosis, Coevolution with Viruses, and Cryptic Sex. <i>Plant Cell</i> , 2010, 22, 2943-2955.	3.1	441
5973	A gene family-based method for interspecies comparisons of sequencing-based transcriptomes and its use in environmental adaptation analysis. <i>Journal of Genetics and Genomics</i> , 2010, 37, 205-218.	1.7	3
5974	Remarkably ancient balanced polymorphisms in a multi-locus gene network. <i>Nature</i> , 2010, 464, 54-58.	13.7	147
5975	Bioinformatic and Computational Analysis for Genomic Medicine. , 2010, , 111-130.		0
5976	Mapping of long-range associations throughout the fission yeast genome reveals global genome organization linked to transcriptional regulation. <i>Nucleic Acids Research</i> , 2010, 38, 8164-8177.	6.5	228
5977	Statistical Methods for Pathway Analysis of Genome-Wide Data for Association with Complex Genetic Traits. <i>Advances in Genetics</i> , 2010, 72, 141-179.	0.8	86

#	ARTICLE	IF	CITATIONS
5978	Estrogen Receptor $\hat{\pm}$ Controls a Gene Network in Luminal-Like Breast Cancer Cells Comprising Multiple Transcription Factors and MicroRNAs. <i>American Journal of Pathology</i> , 2010, 176, 2113-2130.	1.9	151
5979	agriGO: a GO analysis toolkit for the agricultural community. <i>Nucleic Acids Research</i> , 2010, 38, W64-W70.	6.5	2,289
5980	MiDReG: A method of mining developmentally regulated genes using Boolean implications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5732-5737.	3.3	57
5981	A Novel Computational Method for Predicting Disease Genes Based on Functional Similarity. <i>Lecture Notes in Computer Science</i> , 2010, , 42-51.	1.0	1
5982	Bioinformatics Predictions of Localization and Targeting. <i>Methods in Molecular Biology</i> , 2010, 619, 285-305.	0.4	10
5983	Genetics and Genomics of Populus. , 2010, , .		28
5984	Statistical Methods in Molecular Biology. <i>Methods in Molecular Biology</i> , 2010, , .	0.4	16
5985	An Omics Perspective on Cancer Research. , 2010, , .		20
5986	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
5987	A Hybrid Cluster-Lift Method for the Analysis of Research Activities. <i>Lecture Notes in Computer Science</i> , 2010, , 152-161.	1.0	1
5989	Bioinformatics for LC-MS/MS-Based Proteomics. <i>Methods in Molecular Biology</i> , 2010, 658, 61-91.	0.4	22
5990	Advances in Computational Biology. <i>Advances in Experimental Medicine and Biology</i> , 2010, , .	0.8	2
5992	Statistical Modelling and Regression Structures. , 2010, , .		13
5993	Knowledge Engineering and Management by the Masses. <i>Lecture Notes in Computer Science</i> , 2010, , .	1.0	3
5994	Knowledge Science, Engineering and Management. <i>Lecture Notes in Computer Science</i> , 2010, , .	1.0	1
5995	Systematic analysis of regulation and functions of co-expressed microRNAs in humans. <i>Molecular BioSystems</i> , 2010, 6, 1863.	2.9	2
5996	Circadian Control of Global Gene Expression Patterns. <i>Annual Review of Genetics</i> , 2010, 44, 419-444.	3.2	274
5997	Methodologies and Results in Grapevine Research. , 2010, , .		20

#	ARTICLE	IF	CITATIONS
5998	Hybrid Artificial Intelligence Systems. Lecture Notes in Computer Science, 2010, , .	1.0	2
5999	Human Milk Proteins: An Interactomics and Updated Functional Overview. Journal of Proteome Research, 2010, 9, 3339-3373.	1.8	103
6000	Multiple Classifier Systems. Lecture Notes in Computer Science, 2010, , .	1.0	2
6001	CONSTRUCTING AN YEAST PHENOTYPIC GENE NETWORK USING MORPHOLOGICAL INCLUSION RELATIONS. International Journal on Artificial Intelligence Tools, 2010, 19, 235-250.	0.7	1
6005	Introduction to Marine Genomics. , 2010, , .		6
6006	An Approach to Exploring Description Logic Knowledge Bases. Lecture Notes in Computer Science, 2010, , 209-224.	1.0	14
6007	Novel genes exhibit distinct patterns of function acquisition and network integration. Genome Biology, 2010, 11, R127.	13.9	71
6008	Constructing a fish metabolic network model. Genome Biology, 2010, 11, R115.	13.9	47
6009	A standard variation file format for human genome sequences. Genome Biology, 2010, 11, R88.	13.9	79
6010	A human functional protein interaction network and its application to cancer data analysis. Genome Biology, 2010, 11, R53.	13.9	591
6011	Phylogenetic detection of numerous gene duplications shared by animals, fungi and plants. Genome Biology, 2010, 11, R38.	13.9	20
6012	Inferring the functions of longevity genes with modular subnetwork biomarkers of Caenorhabditis elegans aging. Genome Biology, 2010, 11, R13.	13.9	50
6013	Gene ontology analysis for RNA-seq: accounting for selection bias. Genome Biology, 2010, 11, R14.	13.9	5,824
6014	Integrating phenotype ontologies across multiple species. Genome Biology, 2010, 11, R2.	13.9	232
6015	PhenomiR: a knowledgebase for microRNA expression in diseases and biological processes. Genome Biology, 2010, 11, R6.	13.9	247
6016	Novel proteins associated with risk for coronary heart disease or stroke among postmenopausal women identified by in-depth plasma proteome profiling. Genome Medicine, 2010, 2, 48.	3.6	66
6017	Integration of microRNA changes in vivo identifies novel molecular features of muscle insulin resistance in type 2 diabetes. Genome Medicine, 2010, 2, 9.	3.6	225
6018	Using transcriptomics to identify and validate novel biomarkers of human skeletal muscle cancer cachexia. Genome Medicine, 2010, 2, 1.	3.6	124

#	ARTICLE	IF	CITATIONS
6021	Theory and Applications of Ontology: Computer Applications. , 2010, , .		77
6022	Bioinformatics Methods in Clinical Research. Methods in Molecular Biology, 2010, , .	0.4	15
6023	Probabilistic topic modeling for genomic data interpretation. , 2010, , .		40
6024	Horizon for Scientific Practice: Scientific Discovery and Progress. International Studies in the Philosophy of Science, 2010, 24, 187-215.	0.2	2
6025	False Discovery Rate Control With Groups. Journal of the American Statistical Association, 2010, 105, 1215-1227.	1.8	107
6026	Gene-disease prioritization through biomedical networks. , 2010, , .		1
6027	Living the high life: high-altitude adaptation. Genome Biology, 2010, 11, 133.	13.9	83
6028	Analyzing genetic factors involved in recombinant protein expression enhancement. , 2010, , .		0
6029	An electronic warfare meta-model for network centric systems. , 2010, , .		1
6030	Network based analysis of hepatitis C virus Core and NS4B protein interactions. Molecular BioSystems, 2010, 6, 2539.	2.9	44
6031	Virus-mPLOC: A Fusion Classifier for Viral Protein Subcellular Location Prediction by Incorporating Multiple Sites. Journal of Biomolecular Structure and Dynamics, 2010, 28, 175-186.	2.0	130
6032	Identification of Genes Potentially Involved in Pearl Formation by Expressed Sequence Tag Analysis of Mantle from Freshwater Pearl Mussel(Hyriopsis Cumingii Lea). Journal of Shellfish Research, 2010, 29, 527-534.	0.3	8
6033	Enforcing Conceptual Modeling to improve the understanding of human genome. , 2010, , .		18
6034	Coccidian Merozoite Transcriptome Analysis from Eimeria maxima in Comparison to Eimeria tenella and Eimeria acervulina. Journal of Parasitology, 2010, 96, 49-57.	0.3	18
6035	Molecular Function Prediction Using Neighborhood Features. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 208-217.	1.9	60
6036	Inference of patient-specific pathway activities from multi-dimensional cancer genomics data using PARADIGM. Bioinformatics, 2010, 26, i237-i245.	1.8	681
6037	Site-Specific Proteomics Approach for Study Protein S-Nitrosylation. Analytical Chemistry, 2010, 82, 7160-7168.	3.2	61
6038	IDENTIFYING CO-REGULATING MICRORNA GROUPS. Journal of Bioinformatics and Computational Biology, 2010, 08, 99-115.	0.3	20

#	ARTICLE	IF	CITATIONS
6039	A sparse regulatory network of copy-number driven expression reveals putative breast cancer oncogenes. , 2010, , .		2
6040	PODD - Towards an Extensible, Domain-Agnostic Scientific Data Management System. , 2010, , .		6
6041	Towards a methodology for Lipoprotein Ontology. , 2010, , .		1
6042	Curve Profiling Feature: Novel Compact Representation for Drosophila Embryonic Gene Expression Pattern Mining. , 2010, , .		1
6043	Leveraging Gene Ontology Annotations to Improve a Memory-Based Language Understanding System. , 2010, , .		2
6044	Integration of biological knowledge in the mixture-of-Gaussians analysis of genomic clustering. , 2010, , .		4
6045	Comparative Gene Expression Analysis of Susceptible and Resistant Near-Isogenic Lines in Common Wheat Infected by Puccinia triticina. DNA Research, 2010, 17, 211-222.	1.5	59
6046	Gene Set Analysis with Covariates. , 2010, , .		0
6047	Dynamism in gene expression across multiple studies. Physiological Genomics, 2010, 40, 128-140.	1.0	12
6048	Variation in anonymous and EST-microsatellites suggests adaptive population divergence in turbot. Marine Ecology - Progress Series, 2010, 420, 231-239.	0.9	45
6049	Translation efficiency in humans: tissue specificity, global optimization and differences between developmental stages. Nucleic Acids Research, 2010, 38, 2964-2974.	6.5	69
6050	Analysis of Gene Expression Data Based on Density and Biological Knowledge. , 2010, , .		2
6051	A Hidden Markov Model Approach to Testing Multiple Hypotheses on a Tree-Transformed Gene Ontology Graph. Journal of the American Statistical Association, 2010, 105, 1444-1454.	1.8	21
6052	Smoothing Gene Expression Using Biological Networks. , 2010, , .		1
6053	Mining protein lists from proteomics studies: applications for drug discovery. Expert Opinion on Drug Discovery, 2010, 5, 323-331.	2.5	1
6054	Approximate Ontology Matching Based on Structure Quantization. , 2010, , .		0
6055	Data-Fusion in Clustering Microarray Data: Balancing Discovery and Interpretability. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 50-63.	1.9	18
6056	Hierarchical order of gene expression levels. , 2010, , .		0

#	ARTICLE	IF	CITATIONS
6057	The iFly tracking system for an automated locomotor and behavioural analysis of <i>Drosophila melanogaster</i> . <i>Integrative Biology (United Kingdom)</i> , 2011, 3, 755.	0.6	30
6058	A Max-Flow-Based Approach to the Identification of Protein Complexes Using Protein Interaction and Microarray Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 621-634.	1.9	46
6059	Improving Prediction Accuracy of Protein-DNA Docking with GPU Computing. , 2011, , .		0
6060	Microarray-based target identification using drug hypersensitive fission yeast expressing ORFeome. <i>Molecular BioSystems</i> , 2011, 7, 1463.	2.9	21
6061	Comparison of Two Methods for Finding Biomedical Categories in Medline. , 2011, , .		1
6062	Lasso logistic regression based approach for extracting plants coregenes responding to abiotic stresses. , 2011, , .		3
6063	Detecting coherent local patterns from time series gene expression data by a temporal biclustering method. , 2011, , .		2
6064	An Efficient Mining Algorithm to Predict Transcription Factor DNA Binding Preferences. , 2011, , .		0
6065	Searching for Coexpressed Genes in Three-Color cDNA Microarray Data Using a Probabilistic Model-Based Hough Transform. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1093-1107.	1.9	6
6066	DOPCA: A New Method for Calculating Ontology-Based Semantic Similarity. , 2011, , .		4
6067	The synthetic genetic interaction network reveals small molecules that target specific pathways in <i>Saccharomyces cerevisiae</i> . <i>Molecular BioSystems</i> , 2011, 7, 2019.	2.9	8
6068	NAViGaTOR: Large Scalable and Interactive Navigation and Analysis of Large Graphs. <i>Internet Mathematics</i> , 2011, 7, 314-347.	0.7	13
6069	What does biologically meaningful mean? A perspective on gene regulatory network validation. <i>Genome Biology</i> , 2011, 12, 109.	13.9	54
6070	Transcriptome-Wide Studies of Merkel Cell Carcinoma and Validation of Intratumoral CD8+ Lymphocyte Invasion As an Independent Predictor of Survival. <i>Journal of Clinical Oncology</i> , 2011, 29, 1539-1546.	0.8	272
6071	RATT: Rapid Annotation Transfer Tool. <i>Nucleic Acids Research</i> , 2011, 39, e57-e57.	6.5	291
6072	An enhanced graph-oriented approach for change management in distributed biomedical ontologies and linked data. , 2011, , .		3
6073	OrchidBase: A Collection of Sequences of the Transcriptome Derived from Orchids. <i>Plant and Cell Physiology</i> , 2011, 52, 238-243.	1.5	78
6074	An experiential analysis of microarray time series data of cancer metastasis using XMAS. , 2011, , .		0

#	ARTICLE	IF	CITATIONS
6075	MicroRNA expression analysis reveals significant biological pathways in human prostate cancer. , 2011, , .		1
6076	Employing Weighted Biological Network Structure for Finding Disease Genetic Markers in SNP Association Studies. , 2011, , .		2
6077	TCLUST: A Fast Method for Clustering Genome-Scale Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 808-818.	1.9	14
6078	The bovine milk proteome: cherishing, nourishing and fostering molecular complexity. An interactomics and functional overview. Molecular BioSystems, 2011, 7, 579-597.	2.9	83
6079	Synthetic lethal hubs associated with vincristine resistant neuroblastoma. Molecular BioSystems, 2011, 7, 200-214.	2.9	9
6080	Quantitative analysis of the secretion of the MCP family of chemokines by muscle cells. Molecular BioSystems, 2011, 7, 311-321.	2.9	41
6081	Context-specific miRNA regulation network predicts cancer prognosis. , 2011, , .		2
6082	The preservation of bidirectional promoter architecture in Eukaryotes - Functional or co-regulation constraint?. , 2011, , .		0
6083	Early gene response of human brain microvascular endothelial cells to <i>Listeria monocytogenes</i> infection. Canadian Journal of Microbiology, 2011, 57, 441-446.	0.8	5
6084	Retrieval of Patent Documents from Heterogeneous Sources Using Ontologies and Similarity Analysis. , 2011, , .		6
6085	Topology Improves Phylogenetic Motif Functional Site Predictions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 226-233.	1.9	5
6086	Computational gene identification for colon cancer using Digital Gene Expression Displayer. , 2011, , .		0
6087	Bottom-up ontology development reusing semi-structured life sciences diagrams. , 2011, , .		0
6088	Identifying gene-disease associations using word proximity and similarity of Gene Ontology terms. , 2011, , .		1
6089	Identifying modular function via edge annotation in gene correlation networks using Gene Ontology search. , 2011, , .		4
6090	A ranking-based method to predict protein function in terms of gene ontology. , 2011, , .		0
6091	ProKinO: A Framework for Protein Kinase Ontology. , 2011, , .		4
6092	Associating gene functional groups with multiple clinical conditions using Jaccard similarity. , 2011, , .		2

#	ARTICLE	IF	CITATIONS
6093	GOREvenge: A Novel Generic Reverse Engineering Method for the Identification of Critical Molecular Players, Through the Use of Ontologies. IEEE Transactions on Biomedical Engineering, 2011, 58, 3522-3527.	2.5	24
6094	Asymmetric Comparison and Querying of Biological Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 876-889.	1.9	18
6095	Two-Phase Resolution of Polyploidy in the <i>Arabidopsis</i> Metabolic Network Gives Rise to Relative and Absolute Dosage Constraints. Plant Cell, 2011, 23, 1719-1728.	3.1	137
6096	OryzaExpress: An Integrated Database of Gene Expression Networks and Omics Annotations in Rice. Plant and Cell Physiology, 2011, 52, 220-229.	1.5	108
6097	Augmented Transitive Relationships in Direct Protein-Protein Interaction Prediction. , 2011, , .		0
6098	From Sequences to Papers: An Information Retrieval Exercise. , 2011, , .		1
6099	The BRENDA Tissue Ontology (BTO): the first all-integrating ontology of all organisms for enzyme sources. Nucleic Acids Research, 2011, 39, D507-D513.	6.5	153
6100	Hierarchical multi-label classification for protein function prediction: A local approach based on neural networks. , 2011, , .		15
6101	Multiscale Mathematical Modeling to Support Drug Development. IEEE Transactions on Biomedical Engineering, 2011, 58, 3508-3512.	2.5	15
6102	Topology-based scoring method for identification of responsive protein-protein interaction subnetwork. , 2011, , .		1
6103	Mining of EL-GCIs. , 2011, , .		2
6104	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
6105	The Antiproliferative Effect of Dietary Fiber Phenolic Compounds Ferulic Acid and <i>p</i> -Coumaric Acid on the Cell Cycle of Caco-2 Cells. Nutrition and Cancer, 2011, 63, 611-622.	0.9	148
6106	The Comparative Toxicogenomics Database: update 2011. Nucleic Acids Research, 2011, 39, D1067-D1072.	6.5	220
6107	Mapping the Subcellular Protein Distribution in Three Human Cell Lines. Journal of Proteome Research, 2011, 10, 3766-3777.	1.8	37
6108	True Path Rule Hierarchical Ensembles for Genome-Wide Gene Function Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 832-847.	1.9	104
6109	RNA-sequence analysis of human B-cells. Genome Research, 2011, 21, 991-998.	2.4	126
6110	Fuzzy concept lattice construction: A basis for building fuzzy ontologies. , 2011, , .		10

#	ARTICLE	IF	CITATIONS
6111	iSMART: An Integrated Cloud Computing Web Server for Traditional Chinese Medicine for Online Virtual Screening, <i>de novo</i> Evolution and Drug Design. Journal of Biomolecular Structure and Dynamics, 2011, 29, 243-250.	2.0	59
6112	LINKING PHARMGKB TO PHENOTYPE STUDIES AND ANIMAL MODELS OF DISEASE FOR DRUG REPURPOSING. , 2011, , .		9
6113	Quantitative Proteomic Analysis of Dystrophic Dog Muscle. Journal of Proteome Research, 2011, 10, 2465-2478.	1.8	72
6114	Sequence Tagging Reveals Unexpected Modifications in Toxicoproteomics. Chemical Research in Toxicology, 2011, 24, 204-216.	1.7	25
6115	PIDO: the primary immunodeficiency disease ontology. Bioinformatics, 2011, 27, 3193-3199.	1.8	7
6116	Sequence Analysis of the Genome of an Oil-Bearing Tree, <i>Jatropha curcas</i> L.. DNA Research, 2011, 18, 65-76.	1.5	294
6117	Sparse Latent Semantic Analysis. , 2011, , .		23
6119	Finding Correlated Biclusters from Gene Expression Data. IEEE Transactions on Knowledge and Data Engineering, 2011, 23, 568-584.	4.0	75
6120	starBase: a database for exploring microRNAâ€™mRNA interaction maps from Argonaute CLIP-Seq and Degradome-Seq data. Nucleic Acids Research, 2011, 39, D202-D209.	6.5	738
6121	Quantitative Proteomic Analysis of the Adipocyte Plasma Membrane. Journal of Proteome Research, 2011, 10, 4970-4982.	1.8	29
6122	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
6123	Differential Histone Modification and Protein Expression Associated with Cell Wall Removal and Regeneration in Rice (<i>Oryza sativa</i>). Journal of Proteome Research, 2011, 10, 551-563.	1.8	33
6124	Variability in training-induced skeletal muscle adaptation. Journal of Applied Physiology, 2011, 110, 846-853.	1.2	161
6125	Detecting and analyzing differentially activated pathways in brain regions of Alzheimer's disease patients. Molecular BioSystems, 2011, 7, 1441.	2.9	30
6126	Pulsed Stable Isotope Labeling of Amino Acids in Cell Culture Uncovers the Dynamic Interactions between HIV-1 and the Monocyte-Derived Macrophage. Journal of Proteome Research, 2011, 10, 2852-2862.	1.8	20
6127	Identifying temporal trace of biological process during phase transition. , 2011, , .		1
6128	A Shrinkage Approach to Gene-Set Analysis. Statistics in Biopharmaceutical Research, 2011, 3, 506-514.	0.6	1
6129	Insight into the Salivary Transcriptome and Proteome of <i>Dipetalogaster maxima</i>. Journal of Proteome Research, 2011, 10, 669-679.	1.8	42

#	ARTICLE	IF	CITATIONS
6130	Identifying Relevant Data for a Biological Database: Handcrafted Rules versus Machine Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 851-857.	1.9	10
6131	3did: identification and classification of domain-based interactions of known three-dimensional structure. Nucleic Acids Research, 2011, 39, D718-D723.	6.5	134
6132	A Regularized Hotellingâ€™s T^2 Test for Pathway Analysis in Proteomic Studies. Journal of the American Statistical Association, 2011, 106, 1345-1360.	1.8	68
6133	The what, where, how and why of gene ontology—a primer for bioinformaticians. Briefings in Bioinformatics, 2011, 12, 723-735.	3.2	122
6134	A novel Wavelet-Based Clustering Algorithm for Analysis of Gene Expression Patterns. Biophysical Journal, 2011, 100, 322a.	0.2	1
6135	Three Periods of Regulatory Innovation During Vertebrate Evolution. Science, 2011, 333, 1019-1024.	6.0	127
6136	Missing value imputation for gene expression data: computational techniques to recover missing data from available information. Briefings in Bioinformatics, 2011, 12, 498-513.	3.2	175
6137	Construction and characterization of Japanese medaka (<i>Oryzias latipes</i>) hepatic cDNA library and its implementation to biomarker screening in aquatic toxicology. Aquatic Toxicology, 2011, 105, 569-575.	1.9	8
6138	Genome-Wide Analysis of MuDR-Related Transposable Elements Insertion Population in Maize. Acta Agronomica Sinica, 2011, 37, 772-777.	0.3	2
6139	Mouse 3T3 fibroblasts under the influence of fibroblasts isolated from stroma of human basal cell carcinoma acquire properties of multipotent stem cells. Biology of the Cell, 2011, 103, 233-248.	0.7	23
6140	Do proteinâ€™protein interaction databases identify moonlighting proteins?. Molecular BioSystems, 2011, 7, 2379.	2.9	28
6141	Genome sequence and analysis of the tuber crop potato. Nature, 2011, 475, 189-195.	13.7	1,912
6142	Systematic computational prediction of protein interaction networks. Physical Biology, 2011, 8, 035008.	0.8	35
6146	Web Tools for the Prioritization of Candidate Disease Genes. Methods in Molecular Biology, 2011, 760, 189-206.	0.4	18
6147	Systems Biology of Interferon Responses. Journal of Interferon and Cytokine Research, 2011, 31, 5-11.	0.5	101
6148	Proteome Analysis of Erythrocytes Lacking AMP-Activated Protein Kinase Reveals a Role of PAK2 Kinase in Eryptosis. Journal of Proteome Research, 2011, 10, 1690-1697.	1.8	83
6149	High-level organization of isochores into gigantic superstructures in the human genome. Physical Review E, 2011, 83, 031908.	0.8	20
6150	Integration of Evolutionary Biology Concepts for Functional Annotation and Automation of Complex Research in Evolution: The Multi-Agent Software System DAGOBAH. , 2011, , 71-87.		26

#	ARTICLE	IF	CITATIONS
6151	Creating Fuzzy Concepts: the One-Sided Threshold, Fuzzy Closure and Factor Analysis Methods. Lecture Notes in Computer Science, 2011, , 127-134.	1.0	3
6153	Application of Gene Ontology to Gene Identification. Methods in Molecular Biology, 2011, 760, 141-157.	0.4	12
6156	Evolution of domain promiscuity in eukaryotic genomesâ€™a perspective from the inferred ancestral domain architectures. Molecular BioSystems, 2011, 7, 784-792.	2.9	17
6157	Using CisGenome to Analyze ChIPâ€™chip and ChIPâ€™seq Data. Current Protocols in Bioinformatics, 2011, 33, Unit2.13.	25.8	34
6158	Functional annotation of an expressed sequence tag library from Haliotis diversicolor and analysis of its plant-like sequences. Marine Genomics, 2011, 4, 189-196.	0.4	10
6159	Transcriptome analysis in Concholepas concholepas (Gastropoda, Muricidae): Mining and characterization of new genomic and molecular markers. Marine Genomics, 2011, 4, 197-205.	0.4	22
6160	System-Wide Temporal Characterization of the Proteome and Phosphoproteome of Human Embryonic Stem Cell Differentiation. Science Signaling, 2011, 4, rs3.	1.6	389
6161	Strategies for Pathway Analysis from GWAS Data. Current Protocols in Human Genetics, 2011, 71, Unit1.20.	3.5	13
6162	Two-Dimensional Differential in Gel Electrophoresis (2D-DIGE) Analysis of Grape Berry Proteome during Postharvest Withering. Journal of Proteome Research, 2011, 10, 429-446.	1.8	61
6163	Data Standards for Omics Data: The Basis of Data Sharing and Reuse. Methods in Molecular Biology, 2011, 719, 31-69.	0.4	73
6164	Omics Data Management and Annotation. Methods in Molecular Biology, 2011, 719, 71-96.	0.4	12
6165	Insights into Global Mechanisms and Disease by Gene Expression Profiling. Methods in Molecular Biology, 2011, 719, 269-298.	0.4	2
6166	Integration, Warehousing, and Analysis Strategies of Omics Data. Methods in Molecular Biology, 2011, 719, 399-414.	0.4	6
6167	Omics and Literature Mining. Methods in Molecular Biology, 2011, 719, 457-477.	0.4	4
6168	Statistical Design and Analysis of Label-free LC-MS Proteomic Experiments: A Case Study of Coronary Artery Disease. Methods in Molecular Biology, 2011, 728, 293-319.	0.4	6
6169	Deep proteome and transcriptome mapping of a human cancer cell line. Molecular Systems Biology, 2011, 7, 548.	3.2	878
6170	PRIN: a predicted rice interactome network. BMC Bioinformatics, 2011, 12, 161.	1.2	157
6171	A comparison of the functional modules identified from time course and static PPI network data. BMC Bioinformatics, 2011, 12, 339.	1.2	103

#	ARTICLE	IF	CITATIONS
6172	Simple Shared Motifs (SSM) in conserved region of promoters: a new approach to identify co-regulation patterns. BMC Bioinformatics, 2011, 12, 365.	1.2	2
6173	An iterative approach of protein function prediction. BMC Bioinformatics, 2011, 12, 437.	1.2	31
6174	Snat: a SNP annotation tool for bovine by integrating various sources of genomic information. BMC Genetics, 2011, 12, 85.	2.7	8
6175	GO Trimming: Systematically reducing redundancy in large Gene Ontology datasets. BMC Research Notes, 2011, 4, 267.	0.6	86
6176	The RICORDO approach to semantic interoperability for biomedical data and models: strategy, standards and solutions. BMC Research Notes, 2011, 4, 313.	0.6	33
6177	CastorDB: a comprehensive knowledge base for Ricinus communis. BMC Research Notes, 2011, 4, 356.	0.6	6
6178	gViz, a novel tool for the visualization of co-expression networks. BMC Research Notes, 2011, 4, 452.	0.6	9
6179	The Use of Proteomics in the Study of Molecular Responses and Toxicity Pathways in Biological Systems. Advances in Molecular Toxicology, 2011, 5, 45-109.	0.4	4
6180	Mining Protein Sequence Databases for Remote Homologues That Can Display Considerable Domain Length Variations. , 2011, , .		0
6183	Influence of Prior Knowledge in Constraint-Based Learning of Gene Regulatory Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 130-142.	1.9	25
6184	Gene clusters reflecting macrodomain structure respond to nucleoid perturbations. Molecular BioSystems, 2011, 7, 878-888.	2.9	24
6185	Comparing two approaches to creating fuzzy concept lattices. , 2011, , .		5
6186	Yeast Systems Biology. Methods in Molecular Biology, 2011, , .	0.4	7
6187	Aberrant epigenetic grooming of miRNAs in pancreatic cancer: a systems biology perspective. Epigenomics, 2011, 3, 747-759.	1.0	19
6188	<i>Pectobacterium carotovorum</i> Elicits Plant Cell Death with DspE/F but the <i>P. carotovorum</i> DspE Does Not Suppress Callose or Induce Expression of Plant Genes Early in Plant-Microbe Interactions. Molecular Plant-Microbe Interactions, 2011, 24, 773-786.	1.4	60
6190	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. Genome Research, 2011, 21, 885-897.	2.4	329
6192	Adaptive and Natural Computing Algorithms. Lecture Notes in Computer Science, 2011, , .	1.0	2
6193	Kernel-based Data Fusion for Machine Learning. Studies in Computational Intelligence, 2011, , .	0.7	14

#	ARTICLE	IF	CITATIONS
6194	Toward microRNA-mediated gene regulatory networks in plants. <i>Briefings in Bioinformatics</i> , 2011, 12, 645-659.	3.2	53
6195	PREDICT: a method for inferring novel drug indications with application to personalized medicine. <i>Molecular Systems Biology</i> , 2011, 7, 496.	3.2	655
6196	Taxonomic classification of metagenomic shotgun sequences with CARMA3. <i>Nucleic Acids Research</i> , 2011, 39, e91-e91.	6.5	99
6197	Literature mining, ontologies and information visualization for drug repurposing. <i>Briefings in Bioinformatics</i> , 2011, 12, 357-368.	3.2	200
6199	MiRNA miRNA synergistic network: construction via co-regulating functional modules and disease miRNA topological features. <i>Nucleic Acids Research</i> , 2011, 39, 825-836.	6.5	245
6200	The Semantic Web: Research and Applications. <i>Lecture Notes in Computer Science</i> , 2011, , .	1.0	7
6201	Gene Expression Profiling. <i>Methods in Molecular Biology</i> , 2011, , .	0.4	3
6203	Evolutionary plasticity of segmentation clock networks. <i>Development (Cambridge)</i> , 2011, 138, 2783-2792.	1.2	166
6204	Microarray Analysis of mRNAs: Experimental Design and Data Analysis Fundamentals. <i>Methods in Molecular Biology</i> , 2011, 784, 27-40.	0.4	3
6205	Microarray Time Course Experiments: Finding Profiles. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 464-475.	1.9	6
6206	Metagenomic Analyses: Past and Future Trends. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1153-1161.	1.4	597
6207	Predicting non-classical secretory proteins by using Gene Ontology terms and physicochemical properties. , 2011, , .		0
6208	Quantitative Analysis of the Intra- and Inter-Individual Variability of the Normal Urinary Proteome. <i>Journal of Proteome Research</i> , 2011, 10, 637-645.	1.8	215
6209	Network Biology. <i>Methods in Molecular Biology</i> , 2011, , .	0.4	3
6210	Proteome of Skeletal Muscle Lipid Droplet Reveals Association with Mitochondria and Apolipoprotein A-I. <i>Journal of Proteome Research</i> , 2011, 10, 4757-4768.	1.8	170
6211	Proteomic Analysis of an Immortalized Mouse Pancreatic Stellate Cell Line Identifies Differentially-Expressed Proteins in Activated vs Nonproliferating Cell States. <i>Journal of Proteome Research</i> , 2011, 10, 4835-4844.	1.8	36
6212	Visualization and Analysis of the Complexome Network of <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2011, 10, 4744-4756.	1.8	25
6213	Multiobjective Genetic Algorithms for Clustering. , 2011, , .		85

#	ARTICLE	IF	CITATIONS
6214	Chemogenomics and Chemical Genetics. , 2011, , .		5
6216	Functional Enrichment Analysis with Structural Variants: Pitfalls and Strategies. Cytogenetic and Genome Research, 2011, 135, 277-285.	0.6	24
6217	The draft genome of the carcinogenic human liver fluke <i>Clonorchis sinensis</i> . Genome Biology, 2011, 12, R107.	13.9	183
6218	BioGraph: unsupervised biomedical knowledge discovery via automated hypothesis generation. Genome Biology, 2011, 12, R57.	13.9	109
6219	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of <i>Trichoderma</i> . Genome Biology, 2011, 12, R40.	3.8	594
6220	The CRIT framework for identifying cross patterns in systems biology and application to chemogenomics. Genome Biology, 2011, 12, R32.	13.9	2
6221	Strong functional patterns in the evolution of eukaryotic genomes revealed by the reconstruction of ancestral protein domain repertoires. Genome Biology, 2011, 12, R4.	13.9	84
6222	Transcriptome instability in colorectal cancer identified by exon microarray analyses: Associations with splicing factor expression levels and patient survival. Genome Medicine, 2011, 3, 32.	3.6	73
6223	The gene expression profile of preclinical autoimmune arthritis and its modulation by a tolerogenic disease-protective antigenic challenge. Arthritis Research and Therapy, 2011, 13, R143.	1.6	6
6224	Characterization of the Human Gastric Fluid Proteome Reveals Distinct pH-Dependent Protein Profiles: Implications for Biomarker Studies. Journal of Proteome Research, 2011, 10, 4535-4546.	1.8	22
6226	Pathway-based analysis of genetic susceptibility to cervical cancer in situ: HLA-DPB1 affects risk in Swedish women. Genes and Immunity, 2011, 12, 605-614.	2.2	24
6227	Essential Protein Discovery Based on Network Motif and Gene Ontology. , 2011, , .		24
6228	Using OrthoMCL to Assign Proteins to OrthoMCLâ€DB Groups or to Cluster Proteomes Into New Ortholog Groups. Current Protocols in Bioinformatics, 2011, 35, Unit 6.12.1-19.	25.8	397
6229	Multi-level prioritization of autism susceptibility genes based on different models. , 2011, , .		0
6230	Mechanisms of stable lipid loss in a social insect. Journal of Experimental Biology, 2011, 214, 3808-3821.	0.8	88
6232	Progranulin Is a Chemoattractant for Microglia and Stimulates Their Endocytic Activity. American Journal of Pathology, 2011, 178, 284-295.	1.9	103
6233	Development and assessment of oligonucleotide microarrays for Atlantic salmon (<i>Salmo salar</i> L.). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2011, 6, 31-38.	0.4	86
6234	Control of Embryonic Stem Cell Lineage Commitment by Core Promoter Factor, TAF3. Cell, 2011, 146, 720-731.	13.5	155

#	ARTICLE	IF	CITATIONS
6235	A Protein Complex Network of <i>Drosophila melanogaster</i> . <i>Cell</i> , 2011, 147, 690-703.	13.5	593
6236	A Long Noncoding RNA Controls Muscle Differentiation by Functioning as a Competing Endogenous RNA. <i>Cell</i> , 2011, 147, 358-369.	13.5	2,390
6237	Structural Basis and Sequence Rules for Substrate Recognition by Tankyrase Explain the Basis for Cherubism Disease. <i>Cell</i> , 2011, 147, 1340-1354.	13.5	214
6238	SIRT1 Activates MAO-A in the Brain to Mediate Anxiety and Exploratory Drive. <i>Cell</i> , 2011, 147, 1459-1472.	13.5	202
6239	The GÃ©nolevures database. <i>Comptes Rendus - Biologies</i> , 2011, 334, 585-589.	0.1	9
6240	Tandem gene arrays, plastic chromosomal organizations. <i>Comptes Rendus - Biologies</i> , 2011, 334, 639-646.	0.1	7
6241	Early response of bovine alveolar macrophages to infection with live and heat-killed <i>Mycobacterium bovis</i> . <i>Developmental and Comparative Immunology</i> , 2011, 35, 580-591.	1.0	16
6242	Genome-Wide RNAi Screens Identify Genes Required for Ricin and PE Intoxications. <i>Developmental Cell</i> , 2011, 21, 231-244.	3.1	61
6243	FungiFun: A web-based application for functional categorization of fungal genes and proteins. <i>Fungal Genetics and Biology</i> , 2011, 48, 353-358.	0.9	103
6244	Cataloging and profiling genes expressed in <i>Lentinula edodes</i> fruiting body by massive cDNA pyrosequencing and LongSAGE. <i>Fungal Genetics and Biology</i> , 2011, 48, 359-369.	0.9	17
6245	Connecting genotype to phenotype in the era of high-throughput sequencing. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2011, 1810, 967-977.	1.1	28
6246	RANK signaling induces interferon-stimulated genes in the fetal thymic stroma. <i>Biochemical and Biophysical Research Communications</i> , 2011, 408, 530-536.	1.0	13
6247	Dissecting Out the Crosstalk Between Salinity and Hormones in Roots of <i>Arabidopsis</i> . <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 913-924.	1.0	9
6248	Assembling global maps of cellular function through integrative analysis of physical and genetic networks. <i>Nature Protocols</i> , 2011, 6, 1308-1323.	5.5	23
6249	The <i>Selaginella</i> Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	6.0	794
6250	Distance-based differential analysis of gene curves. <i>Bioinformatics</i> , 2011, 27, 3135-3141.	1.8	24
6251	iLoc-Plant: a multi-label classifier for predicting the subcellular localization of plant proteins with both single and multiple sites. <i>Molecular BioSystems</i> , 2011, 7, 3287.	2.9	198
6252	Microarray analyses of laser-captured hippocampus reveal distinct gray and white matter signatures associated with incipient Alzheimer's disease. <i>Journal of Chemical Neuroanatomy</i> , 2011, 42, 118-126.	1.0	201

#	ARTICLE	IF	CITATIONS
6253	Preparation and application of a partially degradable gel in mass spectrometry-based proteomic analysis. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2011, 879, 2957-2962.	1.2	8
6254	On the way toward systems biology of <i>Aspergillus fumigatus</i> infection. <i>International Journal of Medical Microbiology</i> , 2011, 301, 453-459.	1.5	10
6255	Macrophages.com: An on-line community resource for innate immunity research. <i>Immunobiology</i> , 2011, 216, 1203-1211.	0.8	17
6256	Systems biology of infectious diseases: a focus on fungal infections. <i>Immunobiology</i> , 2011, 216, 1212-1227.	0.8	30
6257	Low dose radiation response curves, networks and pathways in human lymphoblastoid cells exposed from 1 to 10cGy of acute gamma radiation. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2011, 722, 119-130.	0.9	37
6258	Representational Difference Analysis (RDA) reveals differential expression of conserved as well as novel genes during caste-specific development of the honey bee (<i>Apis mellifera</i> L.) ovary. <i>Insect Biochemistry and Molecular Biology</i> , 2011, 41, 602-612.	1.2	30
6259	Transcriptome and gene expression profile of ovarian follicle tissue of the triatomine bug <i>Rhodnius prolixus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2011, 41, 823-831.	1.2	49
6260	Prediction of protein-protein interactions between human host and a pathogen and its application to three pathogenic bacteria. <i>International Journal of Biological Macromolecules</i> , 2011, 48, 613-619.	3.6	49
6261	Biased three-dimensional cell migration and collagen matrix modification. <i>Mathematical Biosciences</i> , 2011, 231, 105-119.	0.9	6
6262	Transcriptional profiling of intrinsic PNS factors in the postnatal mouse. <i>Molecular and Cellular Neurosciences</i> , 2011, 46, 32-44.	1.0	53
6263	From in silico target prediction to multi-target drug design: Current databases, methods and applications. <i>Journal of Proteomics</i> , 2011, 74, 2554-2574.	1.2	243
6264	A comparative proteome analysis links tyrosine kinase 2 (Tyk2) to the regulation of cellular glucose and lipid metabolism in response to poly(I:C). <i>Journal of Proteomics</i> , 2011, 74, 2866-2880.	1.2	17
6265	An insight into the sialotranscriptome and proteome of the coarse bontlegged tick, <i>Hyalomma marginatum rufipes</i> . <i>Journal of Proteomics</i> , 2011, 74, 2892-2908.	1.2	62
6266	Proteomic analysis of a rat pancreatic stellate cell line using liquid chromatography tandem mass spectrometry (LC-MS/MS). <i>Journal of Proteomics</i> , 2011, 75, 708-717.	1.2	31
6267	The utility of geometrical and chemical restraint information extracted from predicted ligand-binding sites in protein structure refinement. <i>Journal of Structural Biology</i> , 2011, 173, 558-569.	1.3	5
6268	iWRAP: An Interface Threading Approach with Application to Prediction of Cancer-Related Protein-Protein Interactions. <i>Journal of Molecular Biology</i> , 2011, 405, 1295-1310.	2.0	56
6269	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	2.0	131
6270	Arabidopsis Plasmodesmal Proteome. <i>PLoS ONE</i> , 2011, 6, e18880.	1.1	238

#	ARTICLE	IF	CITATIONS
6271	The representation of heart development in the gene ontology. <i>Developmental Biology</i> , 2011, 354, 9-17.	0.9	35
6272	A search for factors specifying tonotopy implicates DNER in hair-cell development in the chick's cochlea. <i>Developmental Biology</i> , 2011, 354, 221-231.	0.9	35
6273	Cross-species Functionome analysis identifies proteins associated with DNA repair, translation and aerobic respiration as conserved modulators of UV-toxicity. <i>Genomics</i> , 2011, 97, 133-147.	1.3	6
6274	Gene set analysis of genome-wide association studies: Methodological issues and perspectives. <i>Genomics</i> , 2011, 98, 1-8.	1.3	180
6275	A new disease-specific machine learning approach for the prediction of cancer-causing missense variants. <i>Genomics</i> , 2011, 98, 310-317.	1.3	68
6276	Capturing changes in gene expression dynamics by gene set differential coordination analysis. <i>Genomics</i> , 2011, 98, 469-477.	1.3	11
6277	Single-cell proteomic analysis of glucosinolate-rich S-cells in <i>Arabidopsis thaliana</i> . <i>Methods</i> , 2011, 54, 413-423.	1.9	52
6278	Computational approaches to selecting and optimising targets for structural biology. <i>Methods</i> , 2011, 55, 3-11.	1.9	7
6279	Mitochondrial gene expression in the human annulus: in vivo data from annulus cells and selectively harvested senescent annulus cells. <i>Spine Journal</i> , 2011, 11, 782-791.	0.6	41
6280	Virus-host interactomes and global models of virus-infected cells. <i>Trends in Microbiology</i> , 2011, 19, 501-508.	3.5	61
6281	Differential regulation of polysome mRNA levels in mouse Hepa-1C1C7 cells exposed to dioxin. <i>Toxicology in Vitro</i> , 2011, 25, 1457-1467.	1.1	10
6282	Statistical and Biological Evaluation of Different Gene Set Analysis Methods. <i>Procedia Environmental Sciences</i> , 2011, 8, 693-699.	1.3	5
6283	Identification of nigral dopaminergic neuron-enriched genes in adult rats. <i>Neurobiology of Aging</i> , 2011, 32, 313-326.	1.5	42
6284	Rare De Novo Variants Associated with Autism Implicate a Large Functional Network of Genes Involved in Formation and Function of Synapses. <i>Neuron</i> , 2011, 70, 898-907.	3.8	641
6285	A Transcriptomic Atlas of Mouse Neocortical Layers. <i>Neuron</i> , 2011, 71, 605-616.	3.8	266
6286	Microarray analysis of gene expression changes in the brains of NR2B-induced memory-enhanced mice. <i>Neuroscience</i> , 2011, 197, 121-131.	1.1	24
6287	Nitric oxide metabolism controlled by formaldehyde dehydrogenase (fdh, homolog of mammalian) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 <i>Chemistry</i> , 2011, 24, 17-24.	1.2	23
6288	Transcriptome analysis and SNP/SSR marker information of red pepper variety YCM334 and Taeon. <i>Scientia Horticulturae</i> , 2011, 129, 38-45.	1.7	42

#	ARTICLE	IF	CITATIONS
6289	Differential Gene Expression Profile of Porcine Livers Subjected to Warm Ischemia Alone. Transplantation Proceedings, 2011, 43, 3460-3464.	0.3	2
6290	Cloning One CIPK Gene from a Thermo-Sensitive Genic Self-Incompatible Line in Maize Expressing Under Different Temperatures. Agricultural Sciences in China, 2011, 10, 813-819.	0.6	4
6291	Construction of a Full-Length cDNA Library of Gossypium hirsutum L. and Identification of Two MADS-Box Genes. Agricultural Sciences in China, 2011, 10, 28-40.	0.6	1
6292	EST-Based Identification of Genes Expressed in Skeletal Muscle of the Mandarin Fish (Siniperca chuatsi) Tj ETQq1 1,0,784314 rgBT /Ove 3.0	3.0	4
6293	Complete genome sequence of the filamentous gliding predatory bacterium Herpetosiphon aurantiacus type strain (114-95T). Standards in Genomic Sciences, 2011, 5, 356-370.	1.5	47
6294	High responders to resistance exercise training demonstrate differential regulation of skeletal muscle microRNA expression. Journal of Applied Physiology, 2011, 110, 309-317.	1.2	292
6295	A Systematic Comparison of Genome Scale Clustering Algorithms. Lecture Notes in Computer Science, 2011, , 416-427.	1.0	2
6296	Quantitative knowledge-based analysis in compound safety assessment. Expert Opinion on Drug Metabolism and Toxicology, 2011, 7, 287-298.	1.5	9
6297	UniProt Knowledgebase: a hub of integrated protein data. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar009-bar009.	1.4	1,271
6298	Correlation between Protein Function and Ligand Binding Profiles. Journal of Proteome Research, 2011, 10, 2538-2545.	1.8	12
6299	Proteomic and phosphoproteomic comparison of human ES and iPS cells. Nature Methods, 2011, 8, 821-827.	9.0	254
6300	Computational methods for Gene Orthology inference. Briefings in Bioinformatics, 2011, 12, 379-391.	3.2	217
6301	Comprehensive Proteomic Analysis of Membrane Proteins in Toxoplasma gondii. Molecular and Cellular Proteomics, 2011, 10, M110.000745.	2.5	32
6302	The Dynamic Proteome of the Nucleolus. , 2011, , 29-42.		0
6303	Spermidine and resveratrol induce autophagy by distinct pathways converging on the acetylproteome. Journal of Cell Biology, 2011, 192, 615-629.	2.3	439
6304	Breast tumors from CHEK2 1100delC- mutation carriers: genomic landscape and clinical implications. Breast Cancer Research, 2011, 13, R90.	2.2	55
6305	A Guide to UniProt for Protein Scientists. Methods in Molecular Biology, 2011, 694, 25-35.	0.4	15
6306	Protein Bioinformatics Databases and Resources. Methods in Molecular Biology, 2011, 694, 3-24.	0.4	27

#	ARTICLE	IF	CITATIONS
6307	Developmental Transcriptomic Features of the Carcinogenic Liver Fluke, <i>Clonorchis sinensis</i> . PLoS Neglected Tropical Diseases, 2011, 5, e1208.	1.3	72
6308	Modeling Contaminants in AP-MS/MS Experiments. Journal of Proteome Research, 2011, 10, 886-895.	1.8	45
6309	Differential expression of genes in adipose tissue of first-lactation dairy cattle. Journal of Dairy Science, 2011, 94, 361-369.	1.4	51
6310	A Strategy for the Identification of New Abiotic Stress Determinants in <i>Arabidopsis</i> Using Web-Based Data Mining and Reverse Genetics. OMICS A Journal of Integrative Biology, 2011, 15, 935-947.	1.0	6
6311	BBX32, an <i>Arabidopsis</i> B-Box Protein, Functions in Light Signaling by Suppressing HY5-Regulated Gene Expression and Interacting with STH2/BBX21. Plant Physiology, 2011, 156, 2109-2123.	2.3	140
6312	Differential transcriptomic profile in spermatozoa achieving pregnancy or not via ICSI. Reproductive BioMedicine Online, 2011, 22, 25-36.	1.1	76
6313	Genetic Variants of NPAT-ATM and AURKA are Associated With an Early Adverse Reaction in the Gastrointestinal Tract of Patients With Cervical Cancer Treated With Pelvic Radiation Therapy. International Journal of Radiation Oncology Biology Physics, 2011, 81, 1144-1152.	0.4	17
6314	The function of histamine receptor H4R in the brain revealed by interaction partners. Frontiers in Bioscience - Scholar, 2011, S3, 1058-1066.	0.8	4
6315	A case study for integrating public safety data using semantic technologies. Information Polity, 2011, 16, 261-275.	0.5	9
6316	FDR-FET: an optimizing gene set enrichment analysis method. Advances and Applications in Bioinformatics and Chemistry, 2011, Volume 4, 37-42.	1.6	2
6317	Tbx20 regulates a genetic program essential to adult mouse cardiomyocyte function. Journal of Clinical Investigation, 2011, 121, 4640-4654.	3.9	136
6318	Prediction of Human Disease-Related Gene Clusters by Clustering Analysis. International Journal of Biological Sciences, 2011, 7, 61-73.	2.6	50
6319	Weighted Graph Compression for Parameter-free Clustering With PaCCo. , 2011, , .		5
6320	A novel high-throughput analysis approach: immune response-related genes are upregulated in age-related hearing loss. Open Access Bioinformatics, 2011, , 107.	0.9	1
6321	Basidiomycetes Telomeres – A Bioinformatics Approach. , 0, , .		4
6322	Functional Interpretation of Omics Data by Profiling Genes and Diseases Using MeSH – Controlled Vocabulary. , 0, , .		2
6323	Targeted Metabolomics for Clinical Biomarker Discovery in Multifactorial Diseases. , 0, , .		1
6324	Analyses of Expressed Sequence Tags from <i>Chironomus riparius</i> Using Pyrosequencing : Molecular Ecotoxicology Perspective. Environmental Health and Toxicology, 2011, 26, e2011010.	1.8	13

#	ARTICLE	IF	CITATIONS
6325	Databases and Bioinformatics Tools for the Study of DNA Repair. <i>Molecular Biology International</i> , 2011, 2011, 1-9.	1.7	6
6326	Discussion of "Biomedical Ontologies: Toward Scientific Debate". <i>Methods of Information in Medicine</i> , 2011, 50, 217-236.	0.7	8
6327	Translational Oncogenomics and Human Cancer Interactome Networks. <i>Nature Precedings</i> , 2011, , .	0.1	1
6328	Early Diagnosis of Alzheimer's disease by NIRF Spectroscopy and Nuclear Medicine. <i>Nature Precedings</i> , 2011, , .	0.1	0
6329	Single Cancer Cell Detection by Near Infrared Microspectroscopy, Infrared Chemical Imaging and Fluorescence Microspectroscopy. <i>Nature Precedings</i> , 2011, , .	0.1	0
6330	Survey of the genetic information carried in the genome of <i>Eucalyptus camaldulensis</i> . <i>Plant Biotechnology</i> , 2011, 28, 471-480.	0.5	33
6331	Genome Profiling and Potential Biomarkers in Neurodegenerative Disorders. , 2011, , .		0
6332	Data Integration in Bioinformatics: Current Efforts and Challenges. , 0, , .		18
6335	Bioinformatics Identification of Modules of Transcription Factor Binding Sites in Alzheimer's Disease-Related Genes by In Silico Promoter Analysis and Microarrays. <i>International Journal of Alzheimer's Disease</i> , 2011, 2011, 1-13.	1.1	18
6336	Functional Genomics of Rice Pollen and Seed Development by Genome-wide Transcript Profiling and <i>DS</i> Insertion Mutagenesis. <i>International Journal of Biological Sciences</i> , 2011, 7, 28-40.	2.6	8
6337	Using biomedical networks to prioritize gene–disease associations. <i>Open Access Bioinformatics</i> , 2011, , 123.	0.9	3
6338	Data Retrieval and Visualization for Setting Research Priorities in Biomedical Research. , 2011, , .		0
6339	Design and Evaluation of a Complex Phytoceutical Formulation for Circulatory Diseases. , 2011, , .		0
6340	Crosstalk between viruses and PML nuclear bodies: a network-based approach. <i>Frontiers in Bioscience - Landmark</i> , 2011, 16, 2910.	3.0	12
6341	Protein Structural Modularity and Robustness Are Associated with Evolvability. <i>Genome Biology and Evolution</i> , 2011, 3, 456-475.	1.1	34
6342	The Human Genome Retains Relics of Its Prokaryotic Ancestry: Human Genes of Archaeobacterial and Eubacterial Origin Exhibit Remarkable Differences. <i>Genome Biology and Evolution</i> , 2011, 3, 782-790.	1.1	18
6343	Analysis of Potential Biomarkers and Modifier Genes Affecting the Clinical Course of CLN3 Disease. <i>Molecular Medicine</i> , 2011, 17, 1253-1261.	1.9	50
6344	Genome-wide gene expression analysis in mouse embryonic stem cells. <i>International Journal of Developmental Biology</i> , 2011, 55, 995-1006.	0.3	12

#	ARTICLE	IF	CITATIONS
6345	Comparative Transcriptome and Network Biology Analyses Demonstrate Antiproliferative and Hyperapoptotic Phenotypes in Human Keratoconus Corneas. , 2011, 52, 6181.		40
6346	MicroArray Technology - Expression Profiling of mRNA and MicroRNA in Breast Cancer. , 0, , .		2
6347	Analysis of Complement Expression in Light-Induced Retinal Degeneration: Synthesis and Deposition of C3 by Microglia/Macrophages Is Associated with Focal Photoreceptor Degeneration. , 2011, 52, 5347.		84
6348	Plant-Bacteria Association and Symbiosis: Are There Common Genomic Traits in Alphaproteobacteria?. Genes, 2011, 2, 1017-1032.	1.0	78
6349	Functional characterization of three cDNA libraries from the diploid wheatTriticum monoccocum(AmAm) with different growth habits. Cereal Research Communications, 2011, 39, 475-486.	0.8	0
6350	Pathway-based gene selection for disease classification. , 2011, , .		2
6351	GenSensor Suite: A Web-Based Tool for the Analysis of Gene and Protein Interactions, Pathways, and Regulation. Advances in Bioinformatics, 2011, 2011, 1-7.	5.7	6
6352	Urine Glycoprotein Profile Reveals Novel Markers for Chronic Kidney Disease. International Journal of Proteomics, 2011, 2011, 1-18.	2.0	35
6353	Changes in Gene Expression in Human Meibomian Gland Dysfunction. , 2011, 52, 2727.		66
6354	Ontologies and Standards in Bioscience Research: For Machine or for Human. Frontiers in Physiology, 2011, 2, 5.	1.3	7
6356	Systems Biology Reveals MicroRNA-Mediated Gene Regulation. Frontiers in Genetics, 2011, 2, 29.	1.1	28
6357	Pathway-Wide Association Study Implicates Multiple Sterol Transport and Metabolism Genes in HDL Cholesterol Regulation. Frontiers in Genetics, 2011, 2, 41.	1.1	13
6358	Large-Scale Analysis of Gene Expression and Connectivity in the Rodent Brain: Insights through Data Integration. Frontiers in Neuroinformatics, 2011, 5, 12.	1.3	36
6359	The Cognitive Atlas: Toward a Knowledge Foundation for Cognitive Neuroscience. Frontiers in Neuroinformatics, 2011, 5, 17.	1.3	269
6360	Data Ontology and an Information System Realization for Web-Based Management of Image Measurements. Frontiers in Neuroinformatics, 2011, 5, 25.	1.3	4
6361	Channelpedia: An Integrative and Interactive Database for Ion Channels. Frontiers in Neuroinformatics, 2011, 5, 36.	1.3	65
6362	Exploiting statistical methodologies and controlled vocabularies for prioritized functional analysis of genomic experiments: the StRAnGER web application. Frontiers in Neuroscience, 2011, 5, 8.	1.4	30
6363	Cortical gene expression in spinal cord injury and repair: insight into the functional complexity of the neural regeneration program. Frontiers in Molecular Neuroscience, 2011, 4, 26.	1.4	17

#	ARTICLE	IF	CITATIONS
6364	Information Management of Genome Enabled Data Streams for <i>Pseudomonas syringae</i> on the <i>Pseudomonas-Plant Interaction (PPI) Website</i> . <i>Genes</i> , 2011, 2, 841-852.	1.0	1
6365	Advanced Computational Biology Methods Identify Molecular Switches for Malignancy in an EGF Mouse Model of Liver Cancer. <i>PLoS ONE</i> , 2011, 6, e17738.	1.1	17
6366	Comparison of Four ChIP-Seq Analytical Algorithms Using Rice Endosperm H3K27 Trimethylation Profiling Data. <i>PLoS ONE</i> , 2011, 6, e25260.	1.1	54
6367	Sequencing and Bioinformatics-Based Analyses of the microRNA Transcriptome in Hepatitis B-Related Hepatocellular Carcinoma. <i>PLoS ONE</i> , 2011, 6, e15304.	1.1	69
6368	Genetic Variation among Major Human Geographic Groups Supports a Peculiar Evolutionary Trend in PAX9. <i>PLoS ONE</i> , 2011, 6, e15656.	1.1	13
6369	Genome-Wide Polymorphism and Comparative Analyses in the White-Tailed Deer (<i>Odocoileus</i>) Tj ETQq1 1 0.784314_rgBT /Overlock 10	1.1	41
6370	Genome-Wide Analysis of PDZ Domain Binding Reveals Inherent Functional Overlap within the PDZ Interaction Network. <i>PLoS ONE</i> , 2011, 6, e16047.	1.1	42
6371	Directed Partial Correlation: Inferring Large-Scale Gene Regulatory Network through Induced Topology Disruptions. <i>PLoS ONE</i> , 2011, 6, e16835.	1.1	29
6372	SOD2 Deficient Erythroid Cells Up-Regulate Transferrin Receptor and Down-Regulate Mitochondrial Biogenesis and Metabolism. <i>PLoS ONE</i> , 2011, 6, e16894.	1.1	16
6373	MEK2 Is Sufficient but Not Necessary for Proliferation and Anchorage-Independent Growth of SK-MEL-28 Melanoma Cells. <i>PLoS ONE</i> , 2011, 6, e17165.	1.1	16
6374	Two Phosphodiesterase Genes, PDEL and PDEH, Regulate Development and Pathogenicity by Modulating Intracellular Cyclic AMP Levels in <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , 2011, 6, e17241.	1.1	83
6375	Transcriptome Analysis of the Desert Locust Central Nervous System: Production and Annotation of a <i>Schistocerca gregaria</i> EST Database. <i>PLoS ONE</i> , 2011, 6, e17274.	1.1	90
6376	AGeS: A Software System for Microbial Genome Sequence Annotation. <i>PLoS ONE</i> , 2011, 6, e17469.	1.1	19
6377	HMMerThread: Detecting Remote, Functional Conserved Domains in Entire Genomes by Combining Relaxed Sequence-Database Searches with Fold Recognition. <i>PLoS ONE</i> , 2011, 6, e17568.	1.1	2
6378	Unveiling Protein Functions through the Dynamics of the Interaction Network. <i>PLoS ONE</i> , 2011, 6, e17679.	1.1	14
6379	A Protein Domain Co-Occurrence Network Approach for Predicting Protein Function and Inferring Species Phylogeny. <i>PLoS ONE</i> , 2011, 6, e17906.	1.1	30
6380	A Comprehensive Analysis of the Dynamic Biological Networks in HCV Induced Hepatocarcinogenesis. <i>PLoS ONE</i> , 2011, 6, e18516.	1.1	24
6381	Computational Integration of Homolog and Pathway Gene Module Expression Reveals General Stemness Signatures. <i>PLoS ONE</i> , 2011, 6, e18968.	1.1	9

#	ARTICLE	IF	CITATIONS
6382	A Customized Pigmentation SNP Array Identifies a Novel SNP Associated with Melanoma Predisposition in the SLC45A2 Gene. PLoS ONE, 2011, 6, e19271.	1.1	18
6383	Citools: Analysis and Visualisation of Genomic Data Using Interactive Heat-Maps. PLoS ONE, 2011, 6, e19541.	1.1	252
6384	Knowledge-Driven Multi-Locus Analysis Reveals Gene-Gene Interactions Influencing HDL Cholesterol Level in Two Independent EMR-Linked Biobanks. PLoS ONE, 2011, 6, e19586.	1.1	60
6385	A Gene-Phenotype Network for the Laboratory Mouse and Its Implications for Systematic Phenotyping. PLoS ONE, 2011, 6, e19693.	1.1	12
6386	HIVToolbox, an Integrated Web Application for Investigating HIV. PLoS ONE, 2011, 6, e20122.	1.1	8
6387	Gene Network Landscape of the Ciliate <i>Tetrahymena thermophila</i> . PLoS ONE, 2011, 6, e20124.	1.1	28
6388	From SNPs to Genes: Disease Association at the Gene Level. PLoS ONE, 2011, 6, e20133.	1.1	61
6389	Regional Regulation of Transcription in the Bovine Genome. PLoS ONE, 2011, 6, e20413.	1.1	1
6390	Unraveling Molecular Signatures of Immunostimulatory Adjuvants in the Female Genital Tract through Systems Biology. PLoS ONE, 2011, 6, e20448.	1.1	17
6391	Markov Models of Amino Acid Substitution to Study Proteins with Intrinsically Disordered Regions. PLoS ONE, 2011, 6, e20488.	1.1	36
6392	A Multi-Label Classifier for Predicting the Subcellular Localization of Gram-Negative Bacterial Proteins with Both Single and Multiple Sites. PLoS ONE, 2011, 6, e20592.	1.1	235
6393	Predicting Housekeeping Genes Based on Fourier Analysis. PLoS ONE, 2011, 6, e21012.	1.1	26
6394	Integrated Bio-Entity Network: A System for Biological Knowledge Discovery. PLoS ONE, 2011, 6, e21474.	1.1	29
6395	Transcriptome Sequencing and De Novo Analysis for Yesso Scallop (<i>Patinopecten yessoensis</i>) Using 454 GS FLX. PLoS ONE, 2011, 6, e21560.	1.1	204
6396	Enzymes Are Enriched in Bacterial Essential Genes. PLoS ONE, 2011, 6, e21683.	1.1	16
6397	Interoperability between Biomedical Ontologies through Relation Expansion, Upper-Level Ontologies and Automatic Reasoning. PLoS ONE, 2011, 6, e22006.	1.1	38
6398	Functional Integrative Levels in the Human Interactome Recapitulate Organ Organization. PLoS ONE, 2011, 6, e22051.	1.1	20
6399	Evidence That Gene Activation and Silencing during Stem Cell Differentiation Requires a Transcriptionally Paused Intermediate State. PLoS ONE, 2011, 6, e22416.	1.1	12

#	ARTICLE	IF	CITATIONS
6400	Calcium Prevents Tumorigenesis in a Mouse Model of Colorectal Cancer. PLoS ONE, 2011, 6, e22566.	1.1	28
6401	The Fat Body Transcriptomes of the Yellow Fever Mosquito <i>Aedes aegypti</i> , Pre- and Post- Blood Meal. PLoS ONE, 2011, 6, e22573.	1.1	77
6402	Identification of Human Housekeeping Genes and Tissue-Selective Genes by Microarray Meta-Analysis. PLoS ONE, 2011, 6, e22859.	1.1	124
6403	Dominating Biological Networks. PLoS ONE, 2011, 6, e23016.	1.1	85
6404	Evaluating Experimental Bias and Completeness in Comparative Phosphoproteomics Analysis. PLoS ONE, 2011, 6, e23276.	1.1	12
6405	The Transcriptome of <i>Trichuris suis</i> – First Molecular Insights into a Parasite with Curative Properties for Key Immune Diseases of Humans. PLoS ONE, 2011, 6, e23590.	1.1	43
6406	DELLA-Induced Early Transcriptional Changes during Etiolated Development in <i>Arabidopsis thaliana</i> . PLoS ONE, 2011, 6, e23918.	1.1	63
6407	Genome-Wide Functional Profiling Reveals Genes Required for Tolerance to Benzene Metabolites in Yeast. PLoS ONE, 2011, 6, e24205.	1.1	49
6408	Identification of Hub Genes Related to the Recovery Phase of Irradiation Injury by Microarray and Integrated Gene Network Analysis. PLoS ONE, 2011, 6, e24680.	1.1	19
6409	pubmed2ensembl: A Resource for Mining the Biological Literature on Genes. PLoS ONE, 2011, 6, e24716.	1.1	33
6410	Analysis of VEGF-A Regulated Gene Expression in Endothelial Cells to Identify Genes Linked to Angiogenesis. PLoS ONE, 2011, 6, e24887.	1.1	23
6411	Determining Signalling Nodes for Apoptosis by a Genetic High-Throughput Screen. PLoS ONE, 2011, 6, e25023.	1.1	5
6412	High-Throughput Analysis of Promoter Occupancy Reveals New Targets for Arx, a Gene Mutated in Mental Retardation and Interneuronopathies. PLoS ONE, 2011, 6, e25181.	1.1	36
6413	Gene Expression Analysis Reveals the Cell Cycle and Kinetochore Genes Participating in Ischemia Reperfusion Injury and Early Development in Kidney. PLoS ONE, 2011, 6, e25679.	1.1	11
6414	Quantitative Proteomics Reveals Cellular Targets of Celastrol. PLoS ONE, 2011, 6, e26634.	1.1	48
6415	Genome-Wide Functional Analysis of the Cotton Transcriptome by Creating an Integrated EST Database. PLoS ONE, 2011, 6, e26980.	1.1	102
6416	Gene Expression Profile Change and Associated Physiological and Pathological Effects in Mouse Liver Induced by Fasting and Refeeding. PLoS ONE, 2011, 6, e27553.	1.1	49
6417	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

#	ARTICLE	IF	CITATIONS
6418	A Simple Yeast-Based Strategy to Identify Host Cellular Processes Targeted by Bacterial Effector Proteins. PLoS ONE, 2011, 6, e27698.	1.1	12
6419	Transcriptomics of a Giant Freshwater Prawn (<i>Macrobrachium rosenbergii</i>): De Novo Assembly, Annotation and Marker Discovery. PLoS ONE, 2011, 6, e27938.	1.1	94
6420	Gene Expression Profiling of Embryonic Human Neural Stem Cells and Dopaminergic Neurons from Adult Human Substantia Nigra. PLoS ONE, 2011, 6, e28420.	1.1	30
6421	A Brain Region-Specific Predictive Gene Map for Autism Derived by Profiling a Reference Gene Set. PLoS ONE, 2011, 6, e28431.	1.1	20
6422	Generation of ESTs for Flowering Gene Discovery and SSR Marker Development in Upland Cotton. PLoS ONE, 2011, 6, e28676.	1.1	17
6423	Physical Properties of Biological Entities: An Introduction to the Ontology of Physics for Biology. PLoS ONE, 2011, 6, e28708.	1.1	30
6424	ProKinO: An Ontology for Integrative Analysis of Protein Kinases in Cancer. PLoS ONE, 2011, 6, e28782.	1.1	34
6425	CrossQuery: A Web Tool for Easy Associative Querying of Transcriptome Data. PLoS ONE, 2011, 6, e28990.	1.1	2
6426	CASSys: an integrated software-system for the interactive analysis of ChIP-seq data. Journal of Integrative Bioinformatics, 2011, 8, 1-13.	1.0	4
6427	The SuBliMinaL Toolbox: automating steps in the reconstruction of metabolic networks. Journal of Integrative Bioinformatics, 2011, 8, 187-203.	1.0	67
6430	MicroRNA Expression Profiles for Classification and Analysis of Tumor Samples. IEICE Transactions on Information and Systems, 2011, E94-D, 416-422.	0.4	5
6431	Extraction of Informative Genes from Multiple Microarray Data Integrated by Rank-Based Approach. IEICE Transactions on Information and Systems, 2011, E94-D, 841-854.	0.4	0
6432	Adapting non-hierarchical multilabel classification methods for hierarchical multilabel classification. Intelligent Data Analysis, 2011, 15, 861-887.	0.4	14
6433	Comparative Genomic Analysis of the <i>Streptococcus dysgalactiae</i> Species Group: Gene Content, Molecular Adaptation, and Promoter Evolution. Genome Biology and Evolution, 2011, 3, 168-185.	1.1	52
6434	Modeling pulmonary fibrosis with bleomycin. Current Opinion in Pulmonary Medicine, 2011, 17, 355-361.	1.2	259
6435	Enriching regulatory networks by bootstrap learning using optimised GO-based gene similarity and gene links mined from PubMed abstracts. International Journal of Computational Biology and Drug Design, 2011, 4, 56.	0.3	4
6436	Identification of conserved protein complexes by module alignment. International Journal of Data Mining and Bioinformatics, 2011, 5, 593.	0.1	4
6437	The modENCODE Data Coordination Center: lessons in harvesting comprehensive experimental details. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar023.	1.4	32

#	ARTICLE	IF	CITATIONS
6438	Hypergraph visualization and enrichment statistics: how the EGAN paradigm facilitates organic discovery from big data. Proceedings of SPIE, 2011, , .	0.8	5
6439	The curation paradigm and application tool used for manual curation of the scientific literature at the Comparative Toxicogenomics Database. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar034-bar034.	1.4	35
6440	Selection for Translation Efficiency on Synonymous Polymorphisms in Recent Human Evolution. Genome Biology and Evolution, 2011, 3, 749-761.	1.1	41
6441	Biosynthetic Regulation of Floral Scent in Phalaenopsis. , 2011, , 145-180.		1
6442	Genome-Wide Computational Function Prediction of Arabidopsis Proteins by Integration of Multiple Data Sources. Plant Physiology, 2011, 155, 271-281.	2.3	29
6443	The InterPro BioMart: federated query and web service access to the InterPro Resource. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar033-bar033.	1.4	12
6444	The Accumulation of Gene Regulation Through Time. Genome Biology and Evolution, 2011, 3, 667-673.	1.1	31
6445	Computational Polypharmacology with Text Mining and Ontologies. Current Pharmaceutical Biotechnology, 2011, 12, 449-457.	0.9	19
6446	In-silico human genomics with GeneCards. Human Genomics, 2011, 5, 709.	1.4	186
6447	The IGS Standard Operating Procedure for Automated Prokaryotic Annotation. Standards in Genomic Sciences, 2011, 4, 244-251.	1.5	127
6448	Genome Sequence of Campylobacter jejuni strain 327, a strain isolated from a turkey slaughterhouse. Standards in Genomic Sciences, 2011, 4, 113-122.	1.5	12
6449	Complete genome sequence of Leadbetterella byssophila type strain (4M15T). Standards in Genomic Sciences, 2011, 4, 2-12.	1.5	22
6450	Complete genome sequence of Hydrogenobacter thermophilus type strain (TK-6T). Standards in Genomic Sciences, 2011, 4, 131-143.	1.5	12
6451	Complete genome sequence of Paludibacter propionigenes type strain (WB4T). Standards in Genomic Sciences, 2011, 4, 36-44.	1.5	30
6452	Complete genome sequence of Bacteroides helcogenes type strain (P 36-108T). Standards in Genomic Sciences, 2011, 4, 45-53.	1.5	14
6453	Complete genome sequence of Weeksella virosa type strain (9751T). Standards in Genomic Sciences, 2011, 4, 81-90.	1.5	15
6454	Complete genome sequence of Desulfobulbus propionicus type strain (1pr3T). Standards in Genomic Sciences, 2011, 4, 100-110.	1.5	51
6455	Complete genome sequence of Marivirga tractuosa type strain (H-43T). Standards in Genomic Sciences, 2011, 4, 154-162.	1.5	18

#	ARTICLE	IF	CITATIONS
6456	Complete genome sequence of <i>Desulfurococcus mucosus</i> type strain (O7/1T). Standards in Genomic Sciences, 2011, 4, 173-182.	1.5	10
6457	Permanent draft genome sequence of <i>Vibrio tubiashii</i> strain NCIMB 1337 (ATCC19106). Standards in Genomic Sciences, 2011, 4, 183-190.	1.5	19
6458	Complete genome sequence of <i>Cellulophaga lytica</i> type strain (LIM-21T). Standards in Genomic Sciences, 2011, 4, 221-232.	1.5	33
6459	Non-contiguous finished genome sequence of <i>Bacteroides coprosuis</i> type strain (PC139T). Standards in Genomic Sciences, 2011, 4, 233-243.	1.5	9
6460	Complete genome sequence of <i>Rhodospirillum rubrum</i> type strain (S1T). Standards in Genomic Sciences, 2011, 4, 293-302.	1.5	44
6461	Complete genome sequence of the extremely halophilic <i>Halanaerobium praevalens</i> type strain (GSLT). Standards in Genomic Sciences, 2011, 4, 312-321.	1.5	36
6462	Complete genome sequence of <i>Nitratifractor salsuginis</i> type strain (E9I37-1T). Standards in Genomic Sciences, 2011, 4, 322-330.	1.5	13
6463	Draft genome sequence of strain HIMB100, a cultured representative of the SAR116 clade of marine Alphaproteobacteria. Standards in Genomic Sciences, 2011, 5, 269-278.	1.5	27
6464	Complete genome sequence of <i>Mahella australiensis</i> type strain (50-1 BONT). Standards in Genomic Sciences, 2011, 4, 331-341.	1.5	7
6465	Complete genome sequence of <i>Treponema succinifaciens</i> type strain (6091T). Standards in Genomic Sciences, 2011, 4, 361-370.	1.5	41
6466	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FIGlyRT). Standards in Genomic Sciences, 2011, 4, 371-380.	1.5	11
6467	Complete genome sequence of the hyperthermophilic chemolithoautotroph <i>Pyrolobus fumarii</i> type strain (1AT). Standards in Genomic Sciences, 2011, 4, 381-392.	1.5	13
6468	Complete genome sequence of <i>Staphylothermus hellenicus</i> P8T. Standards in Genomic Sciences, 2011, 5, 12-20.	1.5	7
6469	Complete genome sequence of the acetate-degrading sulfate reducer <i>Desulfobacca acetoxidans</i> type strain (ASRB2T). Standards in Genomic Sciences, 2011, 4, 393-401.	1.5	25
6470	Complete genome sequence of <i>Enterobacter lignolyticus</i> SCF1. Standards in Genomic Sciences, 2011, 5, 69-85.	1.5	76
6471	Complete genome sequence of the thermophilic, hydrogen-oxidizing <i>Bacillus tusciae</i> type strain (T2T) and reclassification in the new genus, <i>Kyrpidia</i> gen. nov. as <i>Kyrpidia tusciae</i> comb. nov. and emendation of the family Alicyclobacillaceae da Costa and Rainey, 2010.. Standards in Genomic Sciences, 2011, 5, 121-134.	1.5	51
6472	Complete genome sequence of the gliding, heparinolytic <i>Pedobacter saltans</i> type strain (113T). Standards in Genomic Sciences, 2011, 5, 30-40.	1.5	16
6473	Non-contiguous finished genome sequence of the opportunistic oral pathogen <i>Prevotella multisaccharivorax</i> type strain (PPPA20T). Standards in Genomic Sciences, 2011, 5, 41-49.	1.5	7

#	ARTICLE	IF	CITATIONS
6474	Complete genome sequence of <i>Tolomonas auensis</i> type strain (TA 4T). Standards in Genomic Sciences, 2011, 5, 112-120.	1.5	6
6475	Complete genome sequence of <i>Hirschia baltica</i> type strain (IFAM 1418T). Standards in Genomic Sciences, 2011, 5, 287-297.	1.5	12
6476	Complete genome sequence of <i>Parvibaculum lavamentivorans</i> type strain (DS-1T). Standards in Genomic Sciences, 2011, 5, 298-310.	1.5	37
6477	Complete genome sequence of <i>Ferroglobus placidus</i> AEDII12DO. Standards in Genomic Sciences, 2011, 5, 50-60.	1.5	32
6478	Genome sequence of <i>Haemophilus parasuis</i> strain 29755. Standards in Genomic Sciences, 2011, 5, 61-68.	1.5	17
6479	High quality draft genome sequence of <i>Segniliparus rugosus</i> CDC 945T= (ATCC BAA-974T). Standards in Genomic Sciences, 2011, 5, 389-397.	1.5	6
6480	Complete genome sequence of the halophilic and highly halotolerant <i>Chromohalobacter salexigens</i> type strain (1H11T). Standards in Genomic Sciences, 2011, 5, 379-388.	1.5	35
6481	Complete genome sequence of <i>Allochromatium vinosum</i> DSM 180T. Standards in Genomic Sciences, 2011, 5, 311-330.	1.5	65
6482	Genome sequence of the filamentous, gliding <i>Thiothrix nivea</i> neotype strain (JP2T). Standards in Genomic Sciences, 2011, 5, 398-406.	1.5	22
6483	Complete Genome Sequence of a thermotolerant sporogenic lactic acid bacterium, <i>Bacillus coagulans</i> strain 36D1. Standards in Genomic Sciences, 2011, 5, 331-340.	1.5	28
6484	Complete genome sequence of <i>Desulfurispirillum indicum</i> strain S5T. Standards in Genomic Sciences, 2011, 5, 371-378.	1.5	11
6485	Complete genome sequence of the thermophilic sulfur-reducer <i>Desulfurobacterium thermolithotrophum</i> type strain (BSAT) from a deep-sea hydrothermal vent. Standards in Genomic Sciences, 2011, 5, 407-415.	1.5	11
6486	Analyzing Protein-Protein Interaction Networks with Web Tools. Current Bioinformatics, 2011, 6, 389-397.	0.7	3
6487	Computational Approaches for the Prediction of Protein-Protein Interactions: A Survey. Current Bioinformatics, 2011, 6, 398-414.	0.7	27
6488	Complete genome sequence of <i>Calditerrivibrio nitroreducens</i> type strain (Yu37-1T). Standards in Genomic Sciences, 2011, 4, 54-62.	1.5	10
6489	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24T). Standards in Genomic Sciences, 2011, 4, 91-99.	1.5	46
6490	Complete genome sequence of <i>Bacteroides salanitronis</i> type strain (BL78T). Standards in Genomic Sciences, 2011, 4, 191-199.	1.5	11
6491	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6T). Standards in Genomic Sciences, 2011, 4, 200-209.	1.5	96

#	ARTICLE	IF	CITATIONS
6492	Complete genome sequence of <i>Oceanithermus profundus</i> type strain (506T). <i>Standards in Genomic Sciences</i> , 2011, 4, 210-220.	1.5	4
6493	Draft genome sequence of the coccolithovirus EhV-84. <i>Standards in Genomic Sciences</i> , 2011, 5, 1-11.	1.5	20
6494	Complete genome sequence of <i>Tsukamurella paurometabola</i> type strain (no. 33T). <i>Standards in Genomic Sciences</i> , 2011, 4, 342-351.	1.5	10
6495	Complete genome sequence of <i>Mycobacterium</i> sp. strain (Spyr1) and reclassification to <i>Mycobacterium gilvum</i> Spyr1. <i>Standards in Genomic Sciences</i> , 2011, 5, 144-153.	1.5	22
6496	Draft genome sequence of <i>Caminibacter mediatlanticus</i> strain TB-2T, an epsilonproteobacterium isolated from a deep-sea hydrothermal vent. <i>Standards in Genomic Sciences</i> , 2011, 5, 135-143.	1.5	17
6497	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium <i>Ktedonobacter racemifer</i> type strain (SOSP1-21T). <i>Standards in Genomic Sciences</i> , 2011, 5, 97-111.	1.5	115
6498	PlantPls – An Interactive Web Resource on Plant Protease Inhibitors. <i>Current Protein and Peptide Science</i> , 2011, 12, 448-454.	0.7	10
6499	Data shopping in an open marketplace: Introducing the Ontogrator web application for marking up data using ontologies and browsing using facets. <i>Standards in Genomic Sciences</i> , 2011, 4, 286-292.	1.5	4
6500	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1BT). <i>Standards in Genomic Sciences</i> , 2011, 4, 63-71.	1.5	46
6501	Complete genome sequence of <i>Cellulophaga algicola</i> type strain (IC166T). <i>Standards in Genomic Sciences</i> , 2011, 4, 72-80.	1.5	28
6502	Complete genome sequence of <i>Riemerella anatipestifer</i> type strain (ATCC 11845T). <i>Standards in Genomic Sciences</i> , 2011, 4, 144-153.	1.5	33
6503	Complete genome sequence of the thermophilic sulfur-reducer <i>Hippea maritima</i> type strain (MH2T). <i>Standards in Genomic Sciences</i> , 2011, 4, 303-311.	1.5	8
6504	Complete genome sequence of <i>Haliscomenobacter hydrossis</i> type strain (OT). <i>Standards in Genomic Sciences</i> , 2011, 4, 352-360.	1.5	26
6505	Complete genome sequence of the gliding freshwater bacterium <i>Fluviicola taffensis</i> type strain (RW262T). <i>Standards in Genomic Sciences</i> , 2011, 5, 21-29.	1.5	23
6506	Complete genome of the onion pathogen <i>Enterobacter cloacae</i> EcWSU1. <i>Standards in Genomic Sciences</i> , 2011, 5, 279-286.	1.5	27
6507	Genome sequence of the moderately thermophilic halophile <i>Flexistipes sinusarabici</i> strain (MAS10T). <i>Standards in Genomic Sciences</i> , 2011, 5, 86-96.	1.5	12
6508	Ceci n'est pas un hamburger: modelling and representing the scholarly article. <i>Learned Publishing</i> , 2011, 24, 207-220.	0.8	15
6509	Differential Hematopoietic Supportive Potential and Gene Expression of Stroma Cell Lines from Midgestation Mouse Placenta and Adult Bone Marrow. <i>Cell Transplantation</i> , 2011, 20, 707-726.	1.2	5

#	ARTICLE	IF	CITATIONS
6510	RNA-seq analysis of 2 closely related leukemia clones that differ in their self-renewal capacity. <i>Blood</i> , 2011, 117, e27-e38.	0.6	57
6511	Gene expression analysis uncovers similarity and differences among Burkitt lymphoma subtypes. <i>Blood</i> , 2011, 117, 3596-3608.	0.6	128
6512	Disease and Phenotype Data at Ensembl. <i>Current Protocols in Human Genetics</i> , 2011, 69, Unit 6.11.	3.5	3
6513	Restructuring the Gene Ontology to emphasise regulative pathways and to improve gene similarity queries. <i>International Journal of Computational Biology and Drug Design</i> , 2011, 4, 220.	0.3	1
6514	Combining multiple perspective as intelligent agents into robust approach for biomarker detection in gene expression data. <i>International Journal of Data Mining and Bioinformatics</i> , 2011, 5, 332.	0.1	3
6515	Incorporating biological information into linear models: A Bayesian approach to the selection of pathways and genes. <i>Annals of Applied Statistics</i> , 2011, 5, 1978-2002.	0.5	119
6516	Flexibility and utility of the cell cycle ontology. <i>Applied Ontology</i> , 2011, 6, 247-261.	1.0	2
6517	Designing core ontologies. <i>Applied Ontology</i> , 2011, 6, 177-221.	1.0	53
6518	RGD: A comparative genomics platform. <i>Human Genomics</i> , 2011, 5, 124-9.	1.4	23
6519	Complete genome sequence of <i>Deinococcus maricopensis</i> type strain (LB-34T). <i>Standards in Genomic Sciences</i> , 2011, 4, 163-172.	1.5	14
6520	Exploring and challenging the network of angiogenesis. <i>Scientific Reports</i> , 2011, 1, 61.	1.6	10
6521	A Protocol for Computer-Based Protein Structure and Function Prediction. <i>Journal of Visualized Experiments</i> , 2011, , e3259.	0.2	54
6522	EXTRACTING BIO-MOLECULAR EVENTS FROM LITERATURE-THE BIONLP'09 SHARED TASK. <i>Computational Intelligence</i> , 2011, 27, 513-540.	2.1	40
6523	HIGH-PRECISION BIOLOGICAL EVENT EXTRACTION: EFFECTS OF SYSTEM AND OF DATA. <i>Computational Intelligence</i> , 2011, 27, 681-701.	2.1	21
6524	Genomic expression profiles of blood and placenta reveal significant immune-related pathways and categories in Chinese women with gestational diabetes mellitus. <i>Diabetic Medicine</i> , 2011, 28, 237-246.	1.2	45
6525	Candidate gene expression and intramuscular fat content in pigs. <i>Journal of Animal Breeding and Genetics</i> , 2011, 128, 28-34.	0.8	62
6526	Muscle transcriptome profiling in divergent phenotype swine breeds during growth using microarray and RT-PCR tools. <i>Animal Genetics</i> , 2011, 42, 501-509.	0.6	10
6527	Interpopulation patterns of divergence and selection across the transcriptome of the copepod <i>Tigriopus californicus</i> . <i>Molecular Ecology</i> , 2011, 20, 560-572.	2.0	61

#	ARTICLE	IF	CITATIONS
6528	Transcriptomic responses to salinity stress in invasive and native blue mussels (genus <i>Mytilus</i>). <i>Molecular Ecology</i> , 2011, 20, 517-529.	2.0	155
6529	Differential sensitivity of coral larvae to natural levels of ultraviolet radiation during the onset of larval competence. <i>Molecular Ecology</i> , 2011, 20, 2955-2972.	2.0	47
6530	Somatic cell nuclear reprogramming of mouse oocytes endures beyond reproductive decline. <i>Aging Cell</i> , 2011, 10, 80-95.	3.0	21
6531	Mitochondrially encoded methionine is inversely related to longevity in mammals. <i>Aging Cell</i> , 2011, 10, 198-207.	3.0	48
6532	ANALYSIS OF EXPRESSED SEQUENCE TAGS FROM THE GREEN ALGA <i>DUNALIELLA SALINA</i> (CHLOROPHYTA). <i>Journal of Phycology</i> , 2011, 47, 1454-1460.	1.0	13
6533	Sequence Information on Simple Sequence Repeats and Single Nucleotide Polymorphisms through Transcriptome Analysis of Mungbean. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 63-73.	4.1	58
6534	Expression Profiling of Cassava Storage Roots Reveals an Active Process of Glycolysis/Gluconeogenesis. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 193-211.	4.1	89
6535	Global expression profile of silkworm genes from larval to pupal stages: Toward a comprehensive understanding of sexual differences. <i>Insect Science</i> , 2011, 18, 607-618.	1.5	19
6536	The proteome analysis of oleaginous yeast <i>Lipomyces starkeyi</i> . <i>FEMS Yeast Research</i> , 2011, 11, 42-51.	1.1	43
6537	SIR2 and other genes are abundantly expressed in long-lived natural segregants for replicative aging of the budding yeast <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2011, 11, 345-355.	1.1	10
6538	High conservation of transcription factor binding and evidence for combinatorial regulation across six <i>Drosophila</i> species. <i>Nature Genetics</i> , 2011, 43, 414-420.	9.4	122
6539	Channeling the data deluge. <i>Nature Methods</i> , 2011, 8, 463-465.	9.0	13
6540	Needles in stacks of needles: finding disease-causal variants in a wealth of genomic data. <i>Nature Reviews Genetics</i> , 2011, 12, 628-640.	7.7	531
6541	Variable set enrichment analysis in genome-wide association studies. <i>European Journal of Human Genetics</i> , 2011, 19, 893-900.	1.4	14
6542	Gene set analysis of SNP data: benefits, challenges, and future directions. <i>European Journal of Human Genetics</i> , 2011, 19, 837-843.	1.4	128
6543	Gene-ontology enrichment analysis in two independent family-based samples highlights biologically plausible processes for autism spectrum disorders. <i>European Journal of Human Genetics</i> , 2011, 19, 1082-1089.	1.4	39
6544	Peripheral blood gene expression profiles in metabolic syndrome, coronary artery disease and type 2 diabetes. <i>Genes and Immunity</i> , 2011, 12, 341-351.	2.2	55
6545	Preadipocytes of type 2 diabetes subjects display an intrinsic gene expression profile of decreased differentiation capacity. <i>International Journal of Obesity</i> , 2011, 35, 1154-1164.	1.6	66

#	ARTICLE	IF	CITATIONS
6546	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	13.7	541
6547	Mapping and analysis of chromatin state dynamics in nine human cell types. <i>Nature</i> , 2011, 473, 43-49.	13.7	2,630
6548	Ancestral polyploidy in seed plants and angiosperms. <i>Nature</i> , 2011, 473, 97-100.	13.7	1,862
6549	Mutant p53R175H upregulates Twist1 expression and promotes epithelialâ€mesenchymal transition in immortalized prostate cells. <i>Cell Death and Differentiation</i> , 2011, 18, 271-281.	5.0	136
6550	Functional genomics of a living fossil tree, <i>Ginkgo</i> , based on nextâ€generation sequencing technology. <i>Physiologia Plantarum</i> , 2011, 143, 207-218.	2.6	41
6551	Comparison of the mesophilic cellulosomeâ€producing <i>Clostridium cellulovorans</i> genome with other cellulosomeâ€related clostridial genomes. <i>Microbial Biotechnology</i> , 2011, 4, 64-73.	2.0	56
6552	A Critical Comparative Assessment of Predictions of Protein-Binding Sites for Biologically Relevant Organic Compounds. <i>Structure</i> , 2011, 19, 613-621.	1.6	59
6553	Phosphorylation in Protein-Protein Binding: Effect on Stability and Function. <i>Structure</i> , 2011, 19, 1807-1815.	1.6	246
6554	The MycoBrowser portal: A comprehensive and manually annotated resource for mycobacterial genomes. <i>Tuberculosis</i> , 2011, 91, 8-13.	0.8	355
6555	Transcriptional profiling of stage specific gene expression in the parasitic ciliate <i>Ichthyophthirius multifiliis</i> . <i>Molecular and Biochemical Parasitology</i> , 2011, 178, 29-39.	0.5	17
6556	High-abundance mRNAs in <i>Apis mellifera</i> : Comparison between nurses and foragers. <i>Journal of Insect Physiology</i> , 2011, 57, 274-279.	0.9	38
6557	Inhibition of Gsk3 β in cartilage induces osteoarthritic features through activation of the canonical Wnt signaling pathway. <i>Osteoarthritis and Cartilage</i> , 2011, 19, 1363-1372.	0.6	58
6558	Disease embryo development network reveals the relationship between disease genes and embryo development genes. <i>Journal of Theoretical Biology</i> , 2011, 287, 100-108.	0.8	9
6559	A genotype and phenotype database of genetically modified malaria-parasites. <i>Trends in Parasitology</i> , 2011, 27, 31-39.	1.5	51
6560	Exposure of human fetal penile cells to different PCB mixtures: transcriptome analysis points to diverse modes of interference on external genitalia programming. <i>Reproductive Toxicology</i> , 2011, 32, 1-14.	1.3	13
6561	Protein function prediction: towards integration of similarity metrics. <i>Current Opinion in Structural Biology</i> , 2011, 21, 180-188.	2.6	42
6562	GRISSOM Platform: Enabling Distributed Processing and Management of Biological Data Through Fusion of Grid and Web Technologies. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2011, 15, 83-92.	3.6	3
6563	Variations in aggrecan localization and gene expression patterns characterize increasing stages of human intervertebral disk degeneration. <i>Experimental and Molecular Pathology</i> , 2011, 91, 534-539.	0.9	37

#	ARTICLE	IF	CITATIONS
6564	Engineering topology and kinetics of sucrose metabolism in <i>Saccharomyces cerevisiae</i> for improved ethanol yield. <i>Metabolic Engineering</i> , 2011, 13, 694-703.	3.6	98
6565	Current and future use of genomics data in toxicology: Opportunities and challenges for regulatory applications. <i>Regulatory Toxicology and Pharmacology</i> , 2011, 61, 141-153.	1.3	33
6566	The study of the solvability of the genome annotation problem on sets of elementary motifs. <i>Pattern Recognition and Image Analysis</i> , 2011, 21, 652-662.	0.6	30
6567	Network-based group variable selection for detecting expression quantitative trait loci (eQTL). <i>BMC Bioinformatics</i> , 2011, 12, 269.	1.2	5
6568	Unintended consequences of existential quantifications in biomedical ontologies. <i>BMC Bioinformatics</i> , 2011, 12, 456.	1.2	6
6569	A unified framework for managing provenance information in translational research. <i>BMC Bioinformatics</i> , 2011, 12, 461.	1.2	18
6570	New concepts for building vocabulary for cell image ontologies. <i>BMC Bioinformatics</i> , 2011, 12, 487.	1.2	7
6571	MotifMap: integrative genome-wide maps of regulatory motif sites for model species. <i>BMC Bioinformatics</i> , 2011, 12, 495.	1.2	154
6572	Meta-analysis of gene expression microarrays with missing replicates. <i>BMC Bioinformatics</i> , 2011, 12, 84.	1.2	2
6573	A proteomics approach to decipher the molecular nature of planarian stem cells. <i>BMC Genomics</i> , 2011, 12, 133.	1.2	33
6574	Improving gene expression data interpretation by finding latent factors that co-regulate gene modules with clinical factors. <i>BMC Genomics</i> , 2011, 12, 563.	1.2	3
6575	De novo assembly and characterization of a maternal and developmental transcriptome for the emerging model crustacean <i>Parhyale hawaiiensis</i> . <i>BMC Genomics</i> , 2011, 12, 581.	1.2	85
6576	An insight into the sialome of <i>Simulium guianense</i> (DIPTERA:SIMULIIDAE), the main vector of River Blindness Disease in Brazil. <i>BMC Genomics</i> , 2011, 12, 612.	1.2	19
6577	An expression map for <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2011, 12, 620.	1.2	22
6578	Generation of a reference transcriptome for evaluating rainbow trout responses to various stressors. <i>BMC Genomics</i> , 2011, 12, 626.	1.2	54
6579	Haploinsufficiency and the sex chromosomes from yeasts to humans. <i>BMC Biology</i> , 2011, 9, 15.	1.7	26
6580	Medusa: A tool for exploring and clustering biological networks. <i>BMC Research Notes</i> , 2011, 4, 384.	0.6	49
6581	Comparisons of seven algorithms for pathway analysis using the WTCCC Crohn's Disease dataset. <i>BMC Research Notes</i> , 2011, 4, 386.	0.6	49

#	ARTICLE	IF	CITATIONS
6582	Functional Genomics Assistant (FUGA): a toolbox for the analysis of complex biological networks. BMC Research Notes, 2011, 4, 462.	0.6	17
6583	A shortest-path graph kernel for estimating gene product semantic similarity. Journal of Biomedical Semantics, 2011, 2, 3.	0.9	31
6584	Brucellosis Ontology (IDOBRLU) as an extension of the Infectious Disease Ontology. Journal of Biomedical Semantics, 2011, 2, 9.	0.9	22
6585	An open annotation ontology for science on web 3.0. Journal of Biomedical Semantics, 2011, 2, S4.	0.9	93
6586	Developing a kidney and urinary pathway knowledge base. Journal of Biomedical Semantics, 2011, 2, S7.	0.9	29
6587	Ontology design patterns to disambiguate relations between genes and gene products in GENIA. Journal of Biomedical Semantics, 2011, 2, S1.	0.9	7
6588	Event extraction for DNA methylation. Journal of Biomedical Semantics, 2011, 2, S2.	0.9	11
6589	An analysis of gene/protein associations at PubMed scale. Journal of Biomedical Semantics, 2011, 2, S5.	0.9	2
6590	Stringent response of Escherichia coli: revisiting the bibliome using literature mining. Microbial Informatics and Experimentation, 2011, 1, 14.	7.6	9
6591	Microenvironmental genomic alterations reveal signaling networks for head and neck squamous cell carcinoma. Journal of Clinical Bioinformatics, 2011, 1, 21.	1.2	5
6592	Elucidating the identity of resistance mechanisms to prednisolone exposure in acute lymphoblastic leukemia cells through transcriptomic analysis: A computational approach. Journal of Clinical Bioinformatics, 2011, 1, 36.	1.2	8
6593	Temporal characterisation of the organ-specific Rhipicephalus microplus transcriptional response to Anaplasma marginale infection. International Journal for Parasitology, 2011, 41, 851-860.	1.3	51
6594	NanoParticle Ontology for cancer nanotechnology research. Journal of Biomedical Informatics, 2011, 44, 59-74.	2.5	96
6595	Evolution of the Sequence Ontology terms and relationships. Journal of Biomedical Informatics, 2011, 44, 87-93.	2.5	68
6596	Multiple ontologies in action: Composite annotations for biosimulation models. Journal of Biomedical Informatics, 2011, 44, 146-154.	2.5	55
6597	Desiderata for ontologies to be used in semantic annotation of biomedical documents. Journal of Biomedical Informatics, 2011, 44, 94-101.	2.5	26
6598	The Biomedical Resource Ontology (BRO) to enable resource discovery in clinical and translational research. Journal of Biomedical Informatics, 2011, 44, 137-145.	2.5	50
6599	Protein annotation from protein interaction networks and Gene Ontology. Journal of Biomedical Informatics, 2011, 44, 824-829.	2.5	24

#	ARTICLE	IF	CITATIONS
6600	DW4TR: A Data Warehouse for Translational Research. <i>Journal of Biomedical Informatics</i> , 2011, 44, 1004-1019.	2.5	48
6601	Global gene expression profile induced by the UV-filter 2-ethyl-hexyl-4-trimethoxycinnamate (EHMC) in zebrafish (<i>Danio rerio</i>). <i>Environmental Pollution</i> , 2011, 159, 3086-3096.	3.7	55
6602	Changed gene expression for candidate ageing genes in long-lived <i>Bicyclus anynana</i> butterflies. <i>Experimental Gerontology</i> , 2011, 46, 426-434.	1.2	18
6603	Construction of a cDNA library from female adult of <i>Toxocara canis</i> , and analysis of EST and immune-related genes expressions. <i>Experimental Parasitology</i> , 2011, 129, 120-126.	0.5	9
6604	Valproic acid perturbs hematopoietic homeostasis by inhibition of erythroid differentiation and activation of the myelo-monocytic pathway. <i>Biochemical Pharmacology</i> , 2011, 81, 498-509.	2.0	34
6605	Assessment of nanomaterial cytotoxicity with SOLiD sequencing-based microRNA expression profiling. <i>Biomaterials</i> , 2011, 32, 9021-9030.	5.7	64
6606	The determination of stem cell fate by 3D scaffold structures through the control of cell shape. <i>Biomaterials</i> , 2011, 32, 9188-9196.	5.7	264
6607	The influence of scaffold elasticity on germ layer specification of human embryonic stem cells. <i>Biomaterials</i> , 2011, 32, 9612-9621.	5.7	130
6608	Deep insights into <i>Dictyocaulus viviparus</i> transcriptomes provides unique prospects for new drug targets and disease intervention. <i>Biotechnology Advances</i> , 2011, 29, 261-271.	6.0	31
6609	Atypical (RIO) protein kinases from <i>Haemonchus contortus</i> " Promise as new targets for nematocidal drugs. <i>Biotechnology Advances</i> , 2011, 29, 338-350.	6.0	28
6612	A Approach to Clinical Proteomics Data Quality Control and Import. <i>Lecture Notes in Computer Science</i> , 2011, , 168-182.	1.0	2
6613	Systematic prediction of gene function in <i>Arabidopsis thaliana</i> using a probabilistic functional gene network. <i>Nature Protocols</i> , 2011, 6, 1429-1442.	5.5	41
6614	An ontology of fungal subcellular traits. <i>American Journal of Botany</i> , 2011, 98, 1504-1510.	0.8	13
6615	In Silico Knowledge and Content Tracking. <i>Methods in Molecular Biology</i> , 2011, 760, 129-140.	0.4	3
6616	Automating Knowledge Discovery Workflow Composition Through Ontology-Based Planning. <i>IEEE Transactions on Automation Science and Engineering</i> , 2011, 8, 253-264.	3.4	55
6617	Proteomic comparison of colorectal tumours and non-neoplastic mucosa from paired patient samples using iTRAQ mass spectrometry. <i>Molecular BioSystems</i> , 2011, 7, 2997.	2.9	31
6618	Analytical Strategies in Mass Spectrometry-Based Phosphoproteomics. <i>Methods in Molecular Biology</i> , 2011, 753, 183-213.	0.4	18
6619	Large-Scale Protein Profiling in Human Cell Lines Using Antibody-Based Proteomics. <i>Journal of Proteome Research</i> , 2011, 10, 4066-4075.	1.8	19

#	ARTICLE	IF	CITATIONS
6620	Yeast: An Experimental Organism for 21st Century Biology. <i>Genetics</i> , 2011, 189, 695-704.	1.2	450
6621	An Iron Regulatory Gene Signature Predicts Outcome in Breast Cancer. <i>Cancer Research</i> , 2011, 71, 6728-6737.	0.4	181
6622	Embryonic stem cells: protein interaction networks. <i>Biomolecular Concepts</i> , 2011, 2, 13-25.	1.0	12
6623	Abundant Pleiotropy in Human Complex Diseases and Traits. <i>American Journal of Human Genetics</i> , 2011, 89, 607-618.	2.6	478
6624	Shared and Unique Components of Human Population Structure and Genome-Wide Signals of Positive Selection in South Asia. <i>American Journal of Human Genetics</i> , 2011, 89, 731-744.	2.6	149
6625	The evolution of the RCSB Protein Data Bank website. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2011, 1, 782-789.	6.2	7
6626	A survey of hierarchical classification across different application domains. <i>Data Mining and Knowledge Discovery</i> , 2011, 22, 31-72.	2.4	693
6627	Identification of defence-related genes expressed in coffee and citrus during infection by <i>Xylella fastidiosa</i> . <i>European Journal of Plant Pathology</i> , 2011, 130, 529-540.	0.8	5
6628	Population transcriptomics: insights from <i>Drosophila simulans</i> , <i>Drosophila sechellia</i> and their hybrids. <i>Genetica</i> , 2011, 139, 465-477.	0.5	13
6629	Tractable Extensions of the Description Logic \mathcal{EL} with Numerical Datatypes. <i>Journal of Automated Reasoning</i> , 2011, 47, 427-450.	1.1	9
6630	Carboxylator: incorporating solvent-accessible surface area for identifying protein carboxylation sites. <i>Journal of Computer-Aided Molecular Design</i> , 2011, 25, 987-995.	1.3	26
6631	Using ontology databases for scalable query answering, inconsistency detection, and data integration. <i>Journal of Intelligent Information Systems</i> , 2011, 37, 217-244.	2.8	17
6632	A Unified Architecture for Biomedical Search Engines Based on Semantic Web Technologies. <i>Journal of Medical Systems</i> , 2011, 35, 237-249.	2.2	9
6633	Genome-wide comparison of two poplar genotypes with different growth rates. <i>Plant Molecular Biology</i> , 2011, 76, 575-591.	2.0	19
6634	Discovery of Genes Expressed in Basal Endosperm Transfer Cells in Maize Using 454 Transcriptome Sequencing. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 835-847.	1.0	23
6635	Gene Expression is Highly Regulated in Early Developing Fruit of Apple. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 885-897.	1.0	40
6636	A new approach to assess and predict the functional roles of proteins across all known structures. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 9-20.	1.2	4
6637	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 45-54.	1.2	65

#	ARTICLE	IF	CITATIONS
6638	Multi-way set enumeration in weight tensors. <i>Machine Learning</i> , 2011, 82, 123-155.	3.4	15
6639	Candidate genes involved in tanshinone biosynthesis in hairy roots of <i>Salvia miltiorrhiza</i> revealed by cDNA microarray. <i>Molecular Biology Reports</i> , 2011, 38, 2471-2478.	1.0	46
6640	In silico gene expression analysis in <i>Codonopsis lanceolata</i> root. <i>Molecular Biology Reports</i> , 2011, 38, 3541-3549.	1.0	5
6641	Down-regulated energy metabolism genes associated with mitochondria oxidative phosphorylation and fatty acid metabolism in viral cardiomyopathy mouse heart. <i>Molecular Biology Reports</i> , 2011, 38, 4007-4013.	1.0	21
6642	Structural characterization and mapping of functional EST-SSR markers in <i>Theobroma cacao</i> . <i>Tree Genetics and Genomes</i> , 2011, 7, 799-817.	0.6	21
6643	Genome-wide BAC-end sequencing of <i>Musa acuminata</i> DH Pahang reveals further insights into the genome organization of banana. <i>Tree Genetics and Genomes</i> , 2011, 7, 933-940.	0.6	3
6644	Generation of a large-scale genomic resource for functional and comparative genomics in <i>Liriodendron tulipifera</i> L. <i>Tree Genetics and Genomes</i> , 2011, 7, 941-954.	0.6	13
6645	Analysis of a botryllid enriched-full-length cDNA library: insight into the evolution of spliced leader trans-splicing in tunicates. <i>Development Genes and Evolution</i> , 2011, 220, 329-336.	0.4	9
6646	Isolation, annotation and applications of expressed sequence tags from the olive fly, <i>Bactrocera oleae</i> . <i>Molecular Genetics and Genomics</i> , 2011, 285, 33-45.	1.0	21
6647	Genome-wide screen for inositol auxotrophy in <i>Saccharomyces cerevisiae</i> implicates lipid metabolism in stress response signaling. <i>Molecular Genetics and Genomics</i> , 2011, 285, 125-149.	1.0	53
6648	A genome-wide screen identifies yeast genes required for protection against or enhanced cytotoxicity of the antimalarial drug quinine. <i>Molecular Genetics and Genomics</i> , 2011, 286, 333-346.	1.0	15
6649	Transcriptomic analysis of cell-free fetal RNA suggests a specific molecular phenotype in trisomy 18. <i>Human Genetics</i> , 2011, 129, 295-305.	1.8	44
6650	Integrative computational biology for cancer research. <i>Human Genetics</i> , 2011, 130, 465-481.	1.8	28
6651	Identification of vimentin- and elastin-like transcripts specifically expressed in developing notochord of Atlantic salmon (<i>Salmo salar</i> L.). <i>Cell and Tissue Research</i> , 2011, 346, 191-202.	1.5	9
6652	Integrative computational protocol for the discovery of inhibitors of the <i>Helicobacter pylori</i> nickel response regulator (NikR). <i>Journal of Molecular Modeling</i> , 2011, 17, 3075-3084.	0.8	5
6653	Development of Expressed Sequence Tags from the Pearl Oyster, <i>Pinctada martensii</i> Dunker. <i>Marine Biotechnology</i> , 2011, 13, 275-283.	1.1	35
6654	Differential Growth-Related Gene Expression in Abalone (<i>Haliotis midae</i>). <i>Marine Biotechnology</i> , 2011, 13, 1125-1139.	1.1	36
6655	Transferase activity function and system development process are critical in cattle embryo development. <i>Functional and Integrative Genomics</i> , 2011, 11, 139-150.	1.4	9

#	ARTICLE	IF	CITATIONS
6656	PR-10, defensin and cold dehydrin genes are among those over expressed in <i>Oxytropis</i> (Fabaceae) species adapted to the arctic. <i>Functional and Integrative Genomics</i> , 2011, 11, 497-505.	1.4	40
6657	Angiogenesis-Associated Crosstalk Between Collagens, CXC Chemokines, and Thrombospondin Domain-Containing Proteins. <i>Annals of Biomedical Engineering</i> , 2011, 39, 2213-2222.	1.3	41
6658	Generation and analysis of expressed sequence tags from a normalized cDNA library of young leaf from Ma bamboo (<i>Dendrocalamus latiflorus</i> Munro). <i>Plant Cell Reports</i> , 2011, 30, 2045-2057.	2.8	24
6659	Human and chicken TLR pathways: manual curation and computer-based orthology analysis. <i>Mammalian Genome</i> , 2011, 22, 130-138.	1.0	18
6660	Transcriptional responses of Italian ryegrass during interaction with <i>Xanthomonas translucens</i> pv. <i>graminis</i> reveal novel candidate genes for bacterial wilt resistance. <i>Theoretical and Applied Genetics</i> , 2011, 122, 567-579.	1.8	13
6661	Sensitivity and gene expression profile of fresh human acute myeloid leukemia cells exposed ex vivo to AS602868. <i>Cancer Chemotherapy and Pharmacology</i> , 2011, 68, 97-105.	1.1	4
6662	Short Regions of Sequence Identity Between the Genomes of Bacteria and Human. <i>Current Microbiology</i> , 2011, 62, 770-776.	1.0	3
6663	Viperin mRNA is a novel target for the human RNase MRP/RNase P endoribonuclease. <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 2469-2480.	2.4	32
6664	Overexpression of SUMO perturbs the growth and development of <i>Caenorhabditis elegans</i> . <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 3219-3232.	2.4	15
6665	Proteome Evolution and the Metabolic Origins of Translation and Cellular Life. <i>Journal of Molecular Evolution</i> , 2011, 72, 14-33.	0.8	57
6666	Selection-Driven Divergence After Gene Duplication in <i>Arabidopsis thaliana</i> . <i>Journal of Molecular Evolution</i> , 2011, 73, 153-165.	0.8	16
6667	Molecular evolution of immunoglobulin superfamily genes in primates. <i>Immunogenetics</i> , 2011, 63, 417-428.	1.2	10
6668	Helix-helix interfaces and ligand binding. <i>Journal of Theoretical Biology</i> , 2011, 283, 92-102.	0.8	19
6669	Correlation between the flexibility and periodic dinucleotide patterns in yeast nucleosomal DNA sequences. <i>Journal of Theoretical Biology</i> , 2011, 284, 92-98.	0.8	6
6670	Learning-based concept-hierarchy refinement through exploiting topology, content and social information. <i>Information Sciences</i> , 2011, 181, 2512-2528.	4.0	5
6671	A proteomic analysis of engineered tendon formation under dynamic mechanical loading in vitro. <i>Biomaterials</i> , 2011, 32, 4085-4095.	5.7	40
6672	Identification of candidate molecular markers of nasopharyngeal Carcinoma by tissue microarray and in situ hybridization. <i>Medical Oncology</i> , 2011, 28, 341-348.	1.2	31
6673	Human Protein Reference Database and Human Proteinpedia as Discovery Resources for Molecular Biotechnology. <i>Molecular Biotechnology</i> , 2011, 48, 87-95.	1.3	87

#	ARTICLE	IF	CITATIONS
6674	A model-based strategy to investigate the role of microRNA regulation in cancer signalling networks. <i>Theory in Biosciences</i> , 2011, 130, 55-69.	0.6	18
6675	Answering biological questions: querying a systems biology database for nutrigenomics. <i>Genes and Nutrition</i> , 2011, 6, 81-87.	1.2	4
6676	An Expressed Sequence Tag Analysis for the Fast-Growing Shoots of <i>Bambusa edulis</i> Murno. <i>Journal of Plant Biology</i> , 2011, 54, 402-408.	0.9	7
6677	Dual Blockade of PKA and NF- κ B Inhibits H2 Relaxin-Mediated Castrate-Resistant Growth of Prostate Cancer Sublines and Induces Apoptosis. <i>Hormones and Cancer</i> , 2011, 2, 224-238.	4.9	32
6678	Bioinformatic analysis of fruit-specific expressed sequence tag libraries of <i>Diospyros kaki</i> Thunb.: view at the transcriptome at different developmental stages. <i>3 Biotech</i> , 2011, 1, 35-45.	1.1	8
6680	Identification of the unfolded protein response (UPR)-related genes from <i>Bombyx mori</i> cell lines by a subtractive hybridization approach. <i>Genes and Genomics</i> , 2011, 33, 119-126.	0.5	1
6681	Dose-response functional gene analysis by exposure to 3 different polycyclic aromatic hydrocarbons in human hepatocytes. <i>Molecular and Cellular Toxicology</i> , 2011, 7, 221-232.	0.8	9
6682	Cross experimental analysis of microarray gene expression data from volatile organic compounds treated targets. <i>Molecular and Cellular Toxicology</i> , 2011, 7, 233-241.	0.8	11
6683	Identification and characterization of seed-specific transcription factors regulating anthocyanin biosynthesis in black rice. <i>Journal of Applied Genetics</i> , 2011, 52, 161-169.	1.0	36
6684	Functional modules with disease discrimination abilities for various cancers. <i>Science China Life Sciences</i> , 2011, 54, 189-193.	2.3	3
6685	Pathway-based analysis for genome-wide association studies of schizophrenia to provide new insight in schizophrenia study. <i>Science Bulletin</i> , 2011, 56, 3398-3402.	1.7	2
6686	Learning from imbalanced data sets with a Min-Max modular support vector machine. <i>Frontiers of Electrical and Electronic Engineering in China: Selected Publications From Chinese Universities</i> , 2011, 6, 56-71.	0.6	13
6687	Web Service management system for bioinformatics research: a case study. <i>Service Oriented Computing and Applications</i> , 2011, 5, 1-15.	1.3	6
6688	A cDNA microarray, UniShrimpChip, for identification of genes relevant to testicular development in the black tiger shrimp (<i>Penaeus monodon</i>). <i>BMC Molecular Biology</i> , 2011, 12, 15.	3.0	23
6689	A systems biology model of the regulatory network in <i>Populus</i> leaves reveals interacting regulators and conserved regulation. <i>BMC Plant Biology</i> , 2011, 11, 13.	1.6	26
6690	Analysis of positional candidate genes in the AAA1 susceptibility locus for abdominal aortic aneurysms on chromosome 19. <i>BMC Medical Genetics</i> , 2011, 12, 14.	2.1	18
6691	A Cross-Species Analysis of a Mouse Model of Breast Cancer-Specific Osteolysis and Human Bone Metastases Using Gene Expression Profiling. <i>BMC Cancer</i> , 2011, 11, 304.	1.1	13
6692	1,000 structures and more from the MCSG. <i>BMC Structural Biology</i> , 2011, 11, 2.	2.3	14

#	ARTICLE	IF	CITATIONS
6693	Benchmarks for flexible and rigid transcription factor-DNA docking. <i>BMC Structural Biology</i> , 2011, 11, 45.	2.3	12
6694	SciReader enables reading of medical content with instantaneous definitions. <i>BMC Medical Informatics and Decision Making</i> , 2011, 11, 4.	1.5	2
6695	Long noncoding intronic RNAs are differentially expressed in primary and metastatic pancreatic cancer. <i>Molecular Cancer</i> , 2011, 10, 141.	7.9	153
6696	Comparative Proteomic Analysis of <i>saccharopolyspora spinosa</i> SP06081 and PR2 strains reveals the differentially expressed proteins correlated with the increase of spinosad yield. <i>Proteome Science</i> , 2011, 9, 40.	0.7	21
6697	Comparison of human glomerulus proteomic profiles obtained from low quantities of samples by different mass spectrometry with the comprehensive database. <i>Proteome Science</i> , 2011, 9, 47.	0.7	14
6698	Decomposing PPI networks for complex discovery. <i>Proteome Science</i> , 2011, 9, S15.	0.7	26
6699	Ontology integration to identify protein complex in protein interaction networks. <i>Proteome Science</i> , 2011, 9, S7.	0.7	18
6700	Bioinformatic detection of E47, E2F1 and SREBP1 transcription factors as potential regulators of genes associated to acquisition of endometrial receptivity. <i>Reproductive Biology and Endocrinology</i> , 2011, 9, 14.	1.4	51
6701	Modularity analysis based on predicted protein-protein interactions provides new insights into pathogenicity and cellular process of <i>Escherichia coli</i> O157:H7. <i>Theoretical Biology and Medical Modelling</i> , 2011, 8, 47.	2.1	8
6702	Module-based multiscale simulation of angiogenesis in skeletal muscle. <i>Theoretical Biology and Medical Modelling</i> , 2011, 8, 6.	2.1	60
6703	WordCluster: detecting clusters of DNA words and genomic elements. <i>Algorithms for Molecular Biology</i> , 2011, 6, 2.	0.3	21
6704	WordCloud: a Cytoscape plugin to create a visual semantic summary of networks. <i>Source Code for Biology and Medicine</i> , 2011, 6, 7.	1.7	120
6705	An integrative approach to inferring biologically meaningful gene modules. <i>BMC Systems Biology</i> , 2011, 5, 117.	3.0	12
6706	Integrating systems biology models and biomedical ontologies. <i>BMC Systems Biology</i> , 2011, 5, 124.	3.0	44
6707	Exploring pathway interactions in insulin resistant mouse liver. <i>BMC Systems Biology</i> , 2011, 5, 127.	3.0	17
6708	Environmental versatility promotes modularity in genome-scale metabolic networks. <i>BMC Systems Biology</i> , 2011, 5, 135.	3.0	16
6709	MicroRNAs coordinately regulate protein complexes. <i>BMC Systems Biology</i> , 2011, 5, 136.	3.0	49
6710	In Silico discovery of transcription factors as potential diagnostic biomarkers of ovarian cancer. <i>BMC Systems Biology</i> , 2011, 5, 144.	3.0	12

#	ARTICLE	IF	CITATIONS
6711	Initial characterization of the human central proteome. <i>BMC Systems Biology</i> , 2011, 5, 17.	3.0	66
6712	Inferring pleiotropy by network analysis: linked diseases in the human PPI network. <i>BMC Systems Biology</i> , 2011, 5, 179.	3.0	53
6713	Regulatory coordination of clustered microRNAs based on microRNA-transcription factor regulatory network. <i>BMC Systems Biology</i> , 2011, 5, 199.	3.0	57
6714	Global network analysis of drug tolerance, mode of action and virulence in methicillin-resistant <i>S. aureus</i> . <i>BMC Systems Biology</i> , 2011, 5, 68.	3.0	36
6715	Using next generation transcriptome sequencing to predict an ectomycorrhizal metabolome. <i>BMC Systems Biology</i> , 2011, 5, 70.	3.0	60
6716	Improved functional overview of protein complexes using inferred epistatic relationships. <i>BMC Systems Biology</i> , 2011, 5, 80.	3.0	3
6717	Proteomic patterns of cervical cancer cell lines, a network perspective. <i>BMC Systems Biology</i> , 2011, 5, 96.	3.0	52
6718	Network target for screening synergistic drug combinations with application to traditional Chinese medicine. <i>BMC Systems Biology</i> , 2011, 5, S10.	3.0	309
6719	A comprehensive network and pathway analysis of candidate genes in major depressive disorder. <i>BMC Systems Biology</i> , 2011, 5, S12.	3.0	89
6720	Biological network motif detection and evaluation. <i>BMC Systems Biology</i> , 2011, 5, S5.	3.0	38
6721	Nonlinear gene cluster analysis with labeling for microarray gene expression data in organ development. <i>BMC Proceedings</i> , 2011, 5, S3.	1.8	7
6722	Rare variant collapsing in conjunction with mean log p-value and gradient boosting approaches applied to Genetic Analysis Workshop 17 data. <i>BMC Proceedings</i> , 2011, 5, S94.	1.8	2
6723	Integrative analysis of next generation sequencing for small non-coding RNAs and transcriptional regulation in Myelodysplastic Syndromes. <i>BMC Medical Genomics</i> , 2011, 4, 19.	0.7	41
6724	Immunological network signatures of cancer progression and survival. <i>BMC Medical Genomics</i> , 2011, 4, 28.	0.7	17
6725	Functional microarray analysis suggests repressed cell-cell signaling and cell survival-related modules inhibit progression of head and neck squamous cell carcinoma. <i>BMC Medical Genomics</i> , 2011, 4, 33.	0.7	6
6726	A large scale survey reveals that chromosomal copy-number alterations significantly affect gene modules involved in cancer initiation and progression. <i>BMC Medical Genomics</i> , 2011, 4, 37.	0.7	5
6727	Comprehensive expressional analyses of antisense transcripts in colon cancer tissues using artificial antisense probes. <i>BMC Medical Genomics</i> , 2011, 4, 42.	0.7	1
6728	Cell cycle and aging, morphogenesis, and response to stimuli genes are individualized biomarkers of glioblastoma progression and survival. <i>BMC Medical Genomics</i> , 2011, 4, 49.	0.7	86

#	ARTICLE	IF	CITATIONS
6729	Co-regulatory expression quantitative trait loci mapping: method and application to endometrial cancer. <i>BMC Medical Genomics</i> , 2011, 4, 6.	0.7	16
6730	Integrative network analysis identifies key genes and pathways in the progression of hepatitis C virus induced hepatocellular carcinoma. <i>BMC Medical Genomics</i> , 2011, 4, 62.	0.7	38
6731	Gene network analyses point to the importance of human tissue kallikreins in melanoma progression. <i>BMC Medical Genomics</i> , 2011, 4, 76.	0.7	22
6732	Detection of changes in gene regulatory patterns, elicited by perturbations of the Hsp90 molecular chaperone complex, by visualizing multiple experiments with an animation. <i>BioData Mining</i> , 2011, 4, 15.	2.2	14
6733	pGQL: A probabilistic graphical query language for gene expression time courses. <i>BioData Mining</i> , 2011, 4, 9.	2.2	2
6734	FARO server: Meta-analysis of gene expression by matching gene expression signatures to a compendium of public gene expression data. <i>BMC Research Notes</i> , 2011, 4, 181.	0.6	2
6735	Comparison of RNA expression profiles on generations of <i>Porphyra yezoensis</i> (Rhodophyta), based on suppression subtractive hybridization (SSH). <i>BMC Research Notes</i> , 2011, 4, 428.	0.6	9
6736	A DIGE study on the effects of salbutamol on the rat muscle proteome - an exemplar of best practice for data sharing in proteomics. <i>BMC Research Notes</i> , 2011, 4, 86.	0.6	6
6737	A 44K microarray dataset of the changing transcriptome in developing Atlantic salmon (<i>Salmo salar</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.6	48
6738	Gene discovery in <i>Triatoma infestans</i> . <i>Parasites and Vectors</i> , 2011, 4, 39.	1.0	7
6739	Major prospects for exploring canine vector borne diseases and novel intervention methods using 'omic technologies. <i>Parasites and Vectors</i> , 2011, 4, 53.	1.0	2
6740	A noise-reduction GWAS analysis implicates altered regulation of neurite outgrowth and guidance in autism. <i>Molecular Autism</i> , 2011, 2, 1.	2.6	191
6741	TAFEL: Independent Enrichment Analysis of gene sets. <i>BMC Bioinformatics</i> , 2011, 12, 171.	1.2	1
6742	MINE: Module Identification in Networks. <i>BMC Bioinformatics</i> , 2011, 12, 192.	1.2	87
6743	Assessing the functional coherence of modules found in multiple-evidence networks from <i>Arabidopsis</i> . <i>BMC Bioinformatics</i> , 2011, 12, 203.	1.2	14
6744	Multiple testing for gene sets from microarray experiments. <i>BMC Bioinformatics</i> , 2011, 12, 209.	1.2	5
6745	Noise reduction in protein-protein interaction graphs by the implementation of a novel weighting scheme. <i>BMC Bioinformatics</i> , 2011, 12, 239.	1.2	14
6746	GraphCrunch 2: Software tool for network modeling, alignment and clustering. <i>BMC Bioinformatics</i> , 2011, 12, 24.	1.2	63

#	ARTICLE	IF	CITATIONS
6747	Dissecting protein loops with a statistical scalpel suggests a functional implication of some structural motifs. BMC Bioinformatics, 2011, 12, 247.	1.2	7
6748	Deregulation upon DNA damage revealed by joint analysis of context-specific perturbation data. BMC Bioinformatics, 2011, 12, 249.	1.2	1
6749	Sparse PLS discriminant analysis: biologically relevant feature selection and graphical displays for multiclass problems. BMC Bioinformatics, 2011, 12, 253.	1.2	699
6750	BioAssay Ontology (BAO): a semantic description of bioassays and high-throughput screening results. BMC Bioinformatics, 2011, 12, 257.	1.2	102
6751	Computable visually observed phenotype ontological framework for plants. BMC Bioinformatics, 2011, 12, 260.	1.2	7
6752	Detection of lineage-specific evolutionary changes among primate species. BMC Bioinformatics, 2011, 12, 274.	1.2	19
6753	A novel method to identify cooperative functional modules: study of module coordination in the Saccharomyces cerevisiae cell cycle. BMC Bioinformatics, 2011, 12, 281.	1.2	17
6754	Algal Functional Annotation Tool: a web-based analysis suite to functionally interpret large gene lists using integrated annotation and expression data. BMC Bioinformatics, 2011, 12, 282.	1.2	84
6755	S3QL: A distributed domain specific language for controlled semantic integration of life sciences data. BMC Bioinformatics, 2011, 12, 285.	1.2	13
6756	Bio::Homology::InterologWalk - A Perl module to build putative protein-protein interaction networks through interolog mapping. BMC Bioinformatics, 2011, 12, 289.	1.2	16
6757	Investigating the effect of paralogs on microarray gene-set analysis. BMC Bioinformatics, 2011, 12, 29.	1.2	1
6758	Prototype semantic infrastructure for automated small molecule classification and annotation in lipidomics. BMC Bioinformatics, 2011, 12, 303.	1.2	19
6759	Worm Phenotype Ontology: Integrating phenotype data within and beyond the C. elegans community. BMC Bioinformatics, 2011, 12, 32.	1.2	62
6760	How the gene ontology evolves. BMC Bioinformatics, 2011, 12, 325.	1.2	32
6761	Development and application of a modified dynamic time warping algorithm (DTW-S) to analyses of primate brain expression time series. BMC Bioinformatics, 2011, 12, 347.	1.2	22
6762	GO-based Functional Dissimilarity of Gene Sets. BMC Bioinformatics, 2011, 12, 360.	1.2	17
6763	The representation of protein complexes in the Protein Ontology (PRO). BMC Bioinformatics, 2011, 12, 371.	1.2	14
6764	Quantification of protein group coherence and pathway assignment using functional association. BMC Bioinformatics, 2011, 12, 373.	1.2	11

#	ARTICLE	IF	CITATIONS
6765	GOmotif: A web server for investigating the biological role of protein sequence motifs. BMC Bioinformatics, 2011, 12, 379.	1.2	0
6766	Enriching a biomedical event corpus with meta-knowledge annotation. BMC Bioinformatics, 2011, 12, 393.	1.2	57
6767	The BioLexicon: a large-scale terminological resource for biomedical text mining. BMC Bioinformatics, 2011, 12, 397.	1.2	41
6768	SegMine workflows for semantic microarray data analysis in Orange4WS. BMC Bioinformatics, 2011, 12, 416.	1.2	20
6769	Improving ontologies by automatic reasoning and evaluation of logical definitions. BMC Bioinformatics, 2011, 12, 418.	1.2	29
6770	Gene ontology based transfer learning for protein subcellular localization. BMC Bioinformatics, 2011, 12, 44.	1.2	59
6771	RedundancyMiner: De-replication of redundant GO categories in microarray and proteomics analysis. BMC Bioinformatics, 2011, 12, 52.	1.2	18
6772	Using Stochastic Causal Trees to Augment Bayesian Networks for Modeling eQTL Datasets. BMC Bioinformatics, 2011, 12, 7.	1.2	15
6773	Statistical Test of Expression Pattern (STEPath): a new strategy to integrate gene expression data with genomic information in individual and meta-analysis studies. BMC Bioinformatics, 2011, 12, 92.	1.2	4
6774	Comparative analysis of protein interaction networks reveals that conserved pathways are susceptible to HIV-1 interception. BMC Bioinformatics, 2011, 12, S19.	1.2	6
6775	GARNET – gene set analysis with exploration of annotation relations. BMC Bioinformatics, 2011, 12, S25.	1.2	11
6776	GOChase-II: correcting semantic inconsistencies from Gene Ontology-based annotations for gene products. BMC Bioinformatics, 2011, 12, S40.	1.2	11
6777	Coregulation of transcription factors and microRNAs in human transcriptional regulatory network. BMC Bioinformatics, 2011, 12, S41.	1.2	84
6778	Scenario driven data modelling: a method for integrating diverse sources of data and data streams. BMC Bioinformatics, 2011, 12, S17.	1.2	4
6779	Enhancing the accuracy of HMM-based conserved pathway prediction using global correspondence scores. BMC Bioinformatics, 2011, 12, S6.	1.2	4
6780	Discovery of error-tolerant biclusters from noisy gene expression data. BMC Bioinformatics, 2011, 12, S1.	1.2	13
6781	Investigation and identification of protein $\hat{\text{I}}^3$ -glutamyl carboxylation sites. BMC Bioinformatics, 2011, 12, S10.	1.2	8
6782	Network-based functional enrichment. BMC Bioinformatics, 2011, 12, S14.	1.2	12

#	ARTICLE	IF	CITATIONS
6783	A quantitative analysis of monochromaticity in genetic interaction networks. BMC Bioinformatics, 2011, 12, S16.	1.2	7
6784	Building the process-drug side effect network to discover the relationship between biological Processes and side effects. BMC Bioinformatics, 2011, 12, S2.	1.2	54
6785	SNP and gene networks construction and analysis from classification of copy number variations data. BMC Bioinformatics, 2011, 12, S4.	1.2	13
6786	The gene normalization task in BioCreative III. BMC Bioinformatics, 2011, 12, S2.	1.2	101
6787	BioCreative III interactive task: an overview. BMC Bioinformatics, 2011, 12, S4.	1.2	65
6788	Genetic basis of wing morphogenesis in <i>Drosophila</i> : sexual dimorphism and non-allometric effects of shape variation. BMC Developmental Biology, 2011, 11, 32.	2.1	50
6789	Genome-wide analysis of gene expression during <i>Xenopus tropicalis</i> tadpole tail regeneration. BMC Developmental Biology, 2011, 11, 70.	2.1	74
6790	Genetic mechanisms involved in the evolution of the cephalopod camera eye revealed by transcriptomic and developmental studies. BMC Evolutionary Biology, 2011, 11, 180.	3.2	17
6791	Visualization and Exploration of Conserved Regulatory Modules Using ReXSpecies 2. BMC Evolutionary Biology, 2011, 11, 267.	3.2	3
6792	Back to the sea twice: identifying candidate plant genes for molecular evolution to marine life. BMC Evolutionary Biology, 2011, 11, 8.	3.2	88
6793	An annotated genetic map of loblolly pine based on microsatellite and cDNA markers. BMC Genetics, 2011, 12, 17.	2.7	60
6794	Gene- or region-based association study via kernel principal component analysis. BMC Genetics, 2011, 12, 75.	2.7	14
6795	Analysis of genome-wide association study data using the protein knowledge base. BMC Genetics, 2011, 12, 98.	2.7	10
6796	Transcriptome characterization and high throughput SSRs and SNPs discovery in <i>Cucurbita pepo</i> (Cucurbitaceae). BMC Genomics, 2011, 12, 104.	1.2	177
6797	Meta-analysis of muscle transcriptome data using the MADMuscle database reveals biologically relevant gene patterns. BMC Genomics, 2011, 12, 113.	1.2	19
6798	Distinct colonization patterns and cDNA-AFLP transcriptome profiles in compatible and incompatible interactions between melon and different races of <i>Fusarium oxysporum</i> f. sp. <i>melonis</i> . BMC Genomics, 2011, 12, 122.	1.2	33
6799	Comparative tissue transcriptomics reveal prompt inter-organ communication in response to local bacterial kidney infection. BMC Genomics, 2011, 12, 123.	1.2	16
6800	Deep sequencing of the <i>Camellia sinensis</i> transcriptome revealed candidate genes for major metabolic pathways of tea-specific compounds. BMC Genomics, 2011, 12, 131.	1.2	374

#	ARTICLE	IF	CITATIONS
6801	A further insight into the sialome of the tropical bont tick, <i>Amblyomma variegatum</i> . BMC Genomics, 2011, 12, 136.	1.2	81
6802	Transcriptome sequencing and annotation of the microalgae <i>Dunaliella tertiolecta</i> : Pathway description and gene discovery for production of next-generation biofuels. BMC Genomics, 2011, 12, 148.	1.2	258
6803	Sequential analysis of global gene expression profiles in immature and in vitro matured bovine oocytes: potential molecular markers of oocyte maturation. BMC Genomics, 2011, 12, 151.	1.2	70
6804	Composite transcriptome assembly of RNA-seq data in a sheep model for delayed bone healing. BMC Genomics, 2011, 12, 158.	1.2	63
6805	RS-SNP: a random-set method for genome-wide association studies. BMC Genomics, 2011, 12, 166.	1.2	1
6806	Stochastic variation of transcript abundance in C57BL/6J mice. BMC Genomics, 2011, 12, 167.	1.2	25
6807	Expansion and functional diversification of a leucyl aminopeptidase family that encodes the major protein constituents of <i>Drosophila</i> sperm. BMC Genomics, 2011, 12, 177.	1.2	35
6808	Gene expression patterns in four brain areas associate with quantitative measure of estrous behavior in dairy cows. BMC Genomics, 2011, 12, 200.	1.2	16
6809	Physical mapping and BAC-end sequence analysis provide initial insights into the flax (<i>Linum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422	1.2	64
6810	The midgut transcriptome of <i>Phlebotomus (Larroussius) perniciosus</i> , a vector of <i>Leishmania infantum</i> : comparison of sugar fed and blood fed sand flies. BMC Genomics, 2011, 12, 223.	1.2	30
6811	Comprehensive transcriptome analysis of the highly complex <i>Pisum sativum</i> genome using next generation sequencing. BMC Genomics, 2011, 12, 227.	1.2	140
6812	Profiling the venom gland transcriptomes of Costa Rican snakes by 454 pyrosequencing. BMC Genomics, 2011, 12, 259.	1.2	96
6813	Novel transposable elements from <i>Anopheles gambiae</i> . BMC Genomics, 2011, 12, 260.	1.2	19
6814	GiSAO.db: a database for ageing research. BMC Genomics, 2011, 12, 262.	1.2	3
6815	Polyomic profiling reveals significant hepatic metabolic alterations in glucagon-receptor (GCGR) knockout mice: implications on anti-glucagon therapies for diabetes. BMC Genomics, 2011, 12, 281.	1.2	72
6816	Characterisation of the transcriptome of a wild great tit <i>Parus major</i> population by next generation sequencing. BMC Genomics, 2011, 12, 283.	1.2	67
6817	A honey bee (<i>Apis mellifera</i> L.) PeptideAtlas crossing castes and tissues. BMC Genomics, 2011, 12, 290.	1.2	15
6818	Analysis of BAC end sequences in oak, a keystone forest tree species, providing insight into the composition of its genome. BMC Genomics, 2011, 12, 292.	1.2	33

#	ARTICLE	IF	CITATIONS
6819	De novo sequencing and characterization of floral transcriptome in two species of buckwheat (<i>Fagopyrum</i>). <i>BMC Genomics</i> , 2011, 12, 30.	1.2	132
6820	Evolutionarily conserved bias of amino-acid usage refines the definition of PDZ-binding motif. <i>BMC Genomics</i> , 2011, 12, 300.	1.2	14
6821	Single nucleotide polymorphism discovery in elite north american potato germplasm. <i>BMC Genomics</i> , 2011, 12, 302.	1.2	196
6822	Identification of ejaculated proteins in the house mouse (<i>Mus domesticus</i>) via isotopic labeling. <i>BMC Genomics</i> , 2011, 12, 306.	1.2	58
6823	InterMitoBase: An annotated database and analysis platform of protein-protein interactions for human mitochondria. <i>BMC Genomics</i> , 2011, 12, 335.	1.2	9
6824	Divergent responses to peptidoglycans derived from different <i>E. coli</i> serotypes influence inflammatory outcome in trout, <i>Oncorhynchus mykiss</i> , macrophages. <i>BMC Genomics</i> , 2011, 12, 34.	1.2	18
6825	Immunogenicity of autoantigens. <i>BMC Genomics</i> , 2011, 12, 340.	1.2	52
6826	Transcriptomic analysis of grain amaranth (<i>Amaranthus hypochondriacus</i>) using 454 pyrosequencing: comparison with <i>A. tuberculatus</i> , expression profiling in stems and in response to biotic and abiotic stress. <i>BMC Genomics</i> , 2011, 12, 363.	1.2	95
6827	Sequencing of a QTL-rich region of the <i>Theobroma cacao</i> genome using pooled BACs and the identification of trait specific candidate genes. <i>BMC Genomics</i> , 2011, 12, 379.	1.2	20
6828	Artemisinin resistance in <i>Plasmodium falciparum</i> is associated with an altered temporal pattern of transcription. <i>BMC Genomics</i> , 2011, 12, 391.	1.2	135
6829	Differential gene expression in male and female rainbow trout embryos prior to the onset of gross morphological differentiation of the gonads. <i>BMC Genomics</i> , 2011, 12, 404.	1.2	48
6830	<i>Drosophila</i> selenophosphate synthetase 1 regulates vitamin B6 metabolism: prediction and confirmation. <i>BMC Genomics</i> , 2011, 12, 426.	1.2	18
6831	Tissue-specific gene expression templates for accurate molecular characterization of the normal physiological states of multiple human tissues with implication in development and cancer studies. <i>BMC Genomics</i> , 2011, 12, 439.	1.2	14
6832	New resources for functional analysis of omics data for the genus <i>Aspergillus</i> . <i>BMC Genomics</i> , 2011, 12, 486.	1.2	28
6833	Physical properties of naked DNA influence nucleosome positioning and correlate with transcription start and termination sites in yeast. <i>BMC Genomics</i> , 2011, 12, 489.	1.2	31
6834	Skin healing and scale regeneration in fed and unfed sea bream, <i>Sparus auratus</i> . <i>BMC Genomics</i> , 2011, 12, 490.	1.2	58
6835	Effect of the down-regulation of the high Grain Protein Content (GPC) genes on the wheat transcriptome during monocarpic senescence. <i>BMC Genomics</i> , 2011, 12, 492.	1.2	75
6836	Chipster: user-friendly analysis software for microarray and other high-throughput data. <i>BMC Genomics</i> , 2011, 12, 507.	1.2	295

#	ARTICLE	IF	CITATIONS
6837	Meta-analysis and genome-wide interpretation of genetic susceptibility to drug addiction. BMC Genomics, 2011, 12, 508.	1.2	34
6838	Functional annotation of the transcriptome of <i>Sorghum bicolor</i> in response to osmotic stress and abscisic acid. BMC Genomics, 2011, 12, 514.	1.2	197
6839	The classification of mRNA expression levels by the phosphorylation state of RNAPII CTD based on a combined genome-wide approach. BMC Genomics, 2011, 12, 516.	1.2	36
6840	Development of a novel multiplex DNA microarray for <i>Fusarium graminearum</i> and analysis of azole fungicide responses. BMC Genomics, 2011, 12, 52.	1.2	108
6841	Conjugating effects of symbionts and environmental factors on gene expression in deep-sea hydrothermal vent mussels. BMC Genomics, 2011, 12, 530.	1.2	24
6842	Whole genome resequencing of black Angus and Holstein cattle for SNP and CNV discovery. BMC Genomics, 2011, 12, 559.	1.2	153
6843	Transcriptome dynamics and molecular cross-talk between bovine oocyte and its companion cumulus cells. BMC Genomics, 2011, 12, 57.	1.2	74
6844	Transcriptional responses underlying the hormetic and detrimental effects of the plant secondary metabolite gossypol on the generalist herbivore <i>Helicoverpa armigera</i> . BMC Genomics, 2011, 12, 575.	1.2	95
6845	Characterization of the <i>Conus bullatus</i> genome and its venom-duct transcriptome. BMC Genomics, 2011, 12, 60.	1.2	112
6846	Mining the Gene Wiki for functional genomic knowledge. BMC Genomics, 2011, 12, 603.	1.2	8
6847	The maternal and early embryonic transcriptome of the milkweed bug <i>Oncopeltus fasciatus</i> . BMC Genomics, 2011, 12, 61.	1.2	110
6848	A tandem sequence motif acts as a distance-dependent enhancer in a set of genes involved in translation by binding the proteins NonO and SFPQ. BMC Genomics, 2011, 12, 624.	1.2	10
6849	Proteomic analysis of endothelial cold-adaptation. BMC Genomics, 2011, 12, 630.	1.2	19
6850	Gene set enrichment analysis of microarray data from <i>Pimephales promelas</i> (Rafinesque), a non-mammalian model organism. BMC Genomics, 2011, 12, 66.	1.2	34
6851	Model SNP development for complex genomes based on hexaploid oat using high-throughput 454 sequencing technology. BMC Genomics, 2011, 12, 77.	1.2	84
6852	Eukaryote-wide sequence analysis of mitochondrial β -barrel outer membrane proteins. BMC Genomics, 2011, 12, 79.	1.2	36
6853	Assessing the utility of gene co-expression stability in combination with correlation in the analysis of protein-protein interaction networks. BMC Genomics, 2011, 12, S19.	1.2	9
6854	A robust tool for discriminative analysis and feature selection in paired samples impacts the identification of the genes essential for reprogramming lung tissue to adenocarcinoma. BMC Genomics, 2011, 12, S24.	1.2	18

#	ARTICLE	IF	CITATIONS
6855	Cutoff Scanning Matrix (CSM): structural classification and function prediction by protein inter-residue distance patterns. <i>BMC Genomics</i> , 2011, 12, S12.	1.2	58
6856	Predicting adverse side effects of drugs. <i>BMC Genomics</i> , 2011, 12, S11.	1.2	105
6857	Transcriptomic profiles of peripheral white blood cells in type II diabetes and racial differences in expression profiles. <i>BMC Genomics</i> , 2011, 12, S12.	1.2	12
6858	Immunome database for marsupials and monotremes. <i>BMC Immunology</i> , 2011, 12, 48.	0.9	27
6859	Flavivirus NS3 and NS5 proteins interaction network: a high-throughput yeast two-hybrid screen. <i>BMC Microbiology</i> , 2011, 11, 234.	1.3	91
6860	Proteome driven re-evaluation and functional annotation of the <i>Streptococcus pyogenes</i> SF370 genome. <i>BMC Microbiology</i> , 2011, 11, 249.	1.3	8
6861	Integrative data mining to identify novel candidate serum biomarkers for pre-eclampsia screening. <i>Prenatal Diagnosis</i> , 2011, 31, 1153-1159.	1.1	20
6862	Analysis of protein function and its prediction from amino acid sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2086-2096.	1.5	124
6863	Charged residues at protein interaction interfaces: Unexpected conservation and orchestrated divergence. <i>Protein Science</i> , 2011, 20, 1275-1284.	3.1	21
6864	The calcium sensor STIM1 is regulated by androgens in prostate stromal cells. <i>Prostate</i> , 2011, 71, 1646-1655.	1.2	27
6865	Two-dimensional gel proteome reference map of INS-1E cells. <i>Proteomics</i> , 2011, 11, 1365-1369.	1.3	10
6866	Membrane proteomic signatures of karyotypically normal and abnormal human embryonic stem cell lines and derivatives. <i>Proteomics</i> , 2011, 11, 2515-2527.	1.3	17
6867	Proteomic analysis of the maize rachis: Potential roles of constitutive and induced proteins in resistance to <i>Aspergillus flavus</i> infection and aflatoxin accumulation. <i>Proteomics</i> , 2011, 11, 114-127.	1.3	50
6868	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
6869	Less label, more free: Approaches in label-free quantitative mass spectrometry. <i>Proteomics</i> , 2011, 11, 535-553.	1.3	613
6870	<i>Visualize</i> : A free and open source multifunction tool for proteomics data analysis. <i>Proteomics</i> , 2011, 11, 1058-1063.	1.3	30
6871	Time to articulate a vision for the future of plant proteomics – A global perspective: An initiative for establishing the International Plant Proteomics Organization (INPPO). <i>Proteomics</i> , 2011, 11, 1559-1568.	1.3	31
6872	Proteomics analyses of microvesicles released by <i>Drosophila</i> Kc167 and S2 cells. <i>Proteomics</i> , 2011, 11, 4397-4410.	1.3	36

#	ARTICLE	IF	CITATIONS
6873	ProteoConnections: A bioinformatics platform to facilitate proteome and phosphoproteome analyses. <i>Proteomics</i> , 2011, 11, 2654-2671.	1.3	23
6874	Quantitative phosphoproteomics reveals link between <i>Helicobacter pylori</i> infection and RNA splicing modulation in host cells. <i>Proteomics</i> , 2011, 11, 2798-2811.	1.3	35
6875	Proteome profile of the pipping muscle in broiler embryos. <i>Proteomics</i> , 2011, 11, 4262-4265.	1.3	11
6876	Site-specific analysis of bacterial phosphoproteomes. <i>Proteomics</i> , 2011, 11, 3002-3011.	1.3	54
6877	Comprehensive proteomic analysis of human bile. <i>Proteomics</i> , 2011, 11, 4443-4453.	1.3	44
6878	A SATS algorithm for jointly identifying multiple differentially expressed gene sets. <i>Statistics in Medicine</i> , 2011, 30, 2028-2039.	0.8	3
6879	Agent-based modeling and biomedical ontologies: a roadmap. <i>Wiley Interdisciplinary Reviews: Computational Statistics</i> , 2011, 3, 343-356.	2.1	29
6880	Informatics and standards for nanomedicine technology. <i>Wiley Interdisciplinary Reviews: Nanomedicine and Nanobiotechnology</i> , 2011, 3, 511-532.	3.3	36
6881	Signaling pathways in early cardiac development. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 191-205.	6.6	15
6882	Network biology: a direct approach to study biological function. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 379-391.	6.6	53
6883	SVM based prediction of RNA-binding proteins using binding residues and evolutionary information. <i>Journal of Molecular Recognition</i> , 2011, 24, 303-313.	1.1	130
6884	Benefits of random-priming: Exhaustive survey of a cDNA library from lung tissue of a SARS patient. <i>Journal of Medical Virology</i> , 2011, 83, 574-586.	2.5	0
6885	Altered expression of miRNA-21 and its targets in the hippocampus after traumatic brain injury. <i>Journal of Neuroscience Research</i> , 2011, 89, 212-221.	1.3	110
6886	Dietary L-carnitine alters gene expression in skeletal muscle of piglets. <i>Molecular Nutrition and Food Research</i> , 2011, 55, 419-429.	1.5	32
6887	Mass spectrometry of peptides and proteins from human blood. <i>Mass Spectrometry Reviews</i> , 2011, 30, 685-732.	2.8	57
6888	Global identification of transcription start sites in the genome of <i>Apis mellifera</i> using 5'-LongSAGE. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2011, 316B, 500-514.	0.6	4
6889	Similarities and differences in peripheral blood gene expression signatures of individuals with schizophrenia and their first-degree biological relatives. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2011, 156, 869-887.	1.1	53
6891	Preinvasive colorectal lesion transcriptomes correlate with endoscopic morphology (polypoid) Tj ETQq1 1 0.784314 ggBT /Overlock 10 T	3.3	39

#	ARTICLE	IF	CITATIONS
6892	The dynamics of T cells during persistent <i>Staphylococcus aureus</i> infection: from antigen reactivity to <i>in vivo</i> anergy. <i>EMBO Molecular Medicine</i> , 2011, 3, 652-666.	3.3	56
6893	Integrative genomic characterization and a genomic staging system for gastrointestinal stromal tumors. <i>Cancer</i> , 2011, 117, 380-389.	2.0	35
6894	Biomashups: the new world of exploratory bioinformatics?. <i>Concurrency Computation Practice and Experience</i> , 2011, 23, 1169-1178.	1.4	6
6895	Integrating computational protein function prediction into drug discovery initiatives. <i>Drug Development Research</i> , 2011, 72, 4-16.	1.4	7
6896	Amino acid-induced gene expression profiling in clonal β cell line INS-1E cells. <i>Diabetes/Metabolism Research and Reviews</i> , 2011, 27, 120-176.	1.7	8
6897	Performance of mutation pathogenicity prediction methods on missense variants. <i>Human Mutation</i> , 2011, 32, 358-368.	1.1	468
6898	Bioinformatics for Human Genetics: Promises and Challenges. <i>Human Mutation</i> , 2011, 32, 495-500.	1.1	21
6899	Characterization of copy number stable regions in the human genome. <i>Human Mutation</i> , 2011, 32, 947-955.	1.1	19
6900	Self-directed student research through analysis of microarray datasets: A computer-based functional genomics practical class for masters-level students. <i>Biochemistry and Molecular Biology Education</i> , 2011, 39, 440-447.	0.5	0
6901	Microarray expression profiling of <i>Spodoptera litura</i> in response to oxidative stress. <i>Archives of Insect Biochemistry and Physiology</i> , 2011, 77, 145-162.	0.6	1
6902	In vitro study of the effects of ELF electric fields on gene expression in human epidermal cells. <i>Bioelectromagnetics</i> , 2011, 32, 28-36.	0.9	19
6903	An overview of techniques for linking high-dimensional molecular data to time-to-event endpoints by risk prediction models. <i>Biometrical Journal</i> , 2011, 53, 170-189.	0.6	15
6904	Leveraging external knowledge on molecular interactions in classification methods for risk prediction of patients. <i>Biometrical Journal</i> , 2011, 53, 190-201.	0.6	18
6905	Towards a comprehensive human cell-surface immunome database. <i>Immunology Letters</i> , 2011, 134, 183-187.	1.1	52
6906	Noise-robust algorithm for identifying functionally associated biclusters from gene expression data. <i>Information Sciences</i> , 2011, 181, 435-449.	4.0	10
6907	E-photosynthesis: Web-based platform for modeling of complex photosynthetic processes. <i>BioSystems</i> , 2011, 103, 115-124.	0.9	12
6908	Complexity of automated gene annotation. <i>BioSystems</i> , 2011, 104, 1-8.	0.9	2
6909	Bacterial protein structures reveal phylum dependent divergence. <i>Computational Biology and Chemistry</i> , 2011, 35, 24-33.	1.1	10

#	ARTICLE	IF	CITATIONS
6910	Large-scale mining co-expressed genes in Arabidopsis anther: From pair to group. Computational Biology and Chemistry, 2011, 35, 62-68.	1.1	3
6911	Enabling the development of base domain ontology through extraction of knowledge from engineering domain handbooks. Advanced Engineering Informatics, 2011, 25, 288-296.	4.0	39
6912	Supporting concurrent ontology development: Framework, algorithms and tool. Data and Knowledge Engineering, 2011, 70, 146-164.	2.1	36
6913	Estrogen-responsive genes in macrophages of the bony fish gilthead seabream: A transcriptomic approach. Developmental and Comparative Immunology, 2011, 35, 840-849.	1.0	26
6914	Propositionalized attribute taxonomies from data for data-driven construction of concise classifiers. Expert Systems With Applications, 2011, 38, 12739-12746.	4.4	7
6915	Induction and selection of the most interesting Gene Ontology based multiattribute rules for descriptions of gene groups. Pattern Recognition Letters, 2011, 32, 258-269.	2.6	16
6916	Proteomic analysis of human cataract aqueous humour: Comparison of one-dimensional gel LCMS with two-dimensional LCMS of unlabelled and iTRAQ®-labelled specimens. Journal of Proteomics, 2011, 74, 151-166.	1.2	79
6917	Unraveling tobacco BY-2 protein complexes with BN PAGE/LC-MS/MS and clustering methods. Journal of Proteomics, 2011, 74, 1201-1217.	1.2	15
6918	Comprehensive proteomic profiling of adult Angiostrongylus costaricensis, a human parasitic nematode. Journal of Proteomics, 2011, 74, 1545-1559.	1.2	30
6919	Some remarks on protein attribute prediction and pseudo amino acid composition. Journal of Theoretical Biology, 2011, 273, 236-247.	0.8	1,236
6920	iLoc-Virus: A multi-label learning classifier for identifying the subcellular localization of virus proteins with both single and multiple sites. Journal of Theoretical Biology, 2011, 284, 42-51.	0.8	252
6921	Computational identification of signalling pathways in Plasmodium falciparum. Infection, Genetics and Evolution, 2011, 11, 755-764.	1.0	15
6922	Proteomics – The key to understanding systems biology of Arabidopsis trichomes. Phytochemistry, 2011, 72, 1061-1070.	1.4	10
6923	Next generation functional proteomics in non-model plants: A survey on techniques and applications for the analysis of protein complexes and post-translational modifications. Phytochemistry, 2011, 72, 1192-1218.	1.4	28
6924	Autophosphorylation profiling of Arabidopsis protein kinases using the cell-free system. Phytochemistry, 2011, 72, 1136-1144.	1.4	51
6925	Network-based function prediction and interactomics: The case for metabolic enzymes. Metabolic Engineering, 2011, 13, 1-10.	3.6	43
6926	Changes in DNA Methylation and Gene Expression during 2,3,7,8-Tetrachlorodibenzo-p-dioxin-Induced Suppression of the Lipopolysaccharide-Stimulated IgM Response in Splenocytes. Toxicological Sciences, 2011, 120, 339-348.	1.4	24
6927	Genes and biochemical pathways in human skeletal muscle affecting resting energy expenditure and fuel partitioning. Journal of Applied Physiology, 2011, 110, 746-755.	1.2	14

#	ARTICLE	IF	CITATIONS
6928	Functional analysis of human whole brain regions based on gene expression. , 2011, , .		2
6929	Genome-wide identification of conserved regulatory function in diverged sequences. <i>Genome Research</i> , 2011, 21, 1139-1149.	2.4	72
6930	Genome-Wide Analysis of a Wnt1-Regulated Transcriptional Network Implicates Neurodegenerative Pathways. <i>Science Signaling</i> , 2011, 4, ra65.	1.6	50
6931	Identification of Multiple Subcellular Locations for Proteins in Budding Yeast. <i>Current Bioinformatics</i> , 2011, 6, 71-80.	0.7	18
6932	Inferring Functional Relationships and Causal Network Structure from Gene Expression Profiles. <i>Methods in Enzymology</i> , 2011, 487, 133-146.	0.4	1
6933	Decreased Secretion and Unfolded Protein Response Upregulation. <i>Methods in Enzymology</i> , 2011, 491, 235-260.	0.4	15
6934	Standardizing radiation oncology data for future modelling of side effects after radiation therapy. , 2011, , .		0
6935	YEASTRACT: providing a programmatic access to curated transcriptional regulatory associations in <i>Saccharomyces cerevisiae</i> through a web services interface. <i>Nucleic Acids Research</i> , 2011, 39, D136-D140.	6.5	171
6936	SVA: software for annotating and visualizing sequenced human genomes. <i>Bioinformatics</i> , 2011, 27, 1998-2000.	1.8	62
6937	BioTRON. , 2011, , .		0
6938	MU2Aâ€”reconciling the genome and transcriptome to determine the effects of base substitutions. <i>Bioinformatics</i> , 2011, 27, 416-418.	1.8	7
6939	The role of indirect connections in gene networks in predicting function. <i>Bioinformatics</i> , 2011, 27, 1860-1866.	1.8	71
6940	Generalized random set framework for functional enrichment analysis using primary genomics datasets. <i>Bioinformatics</i> , 2011, 27, 70-77.	1.8	18
6941	Complex Network and Gene Ontology in Pharmacology Approaches: Mapping Natural Compounds on Potential Drug Target Colon Cancer Network. <i>Current Bioinformatics</i> , 2011, 6, 44-52.	0.7	14
6942	The polymath project. , 2011, , .		61
6943	Using semantic technologies to describe robotic embodiments. , 2011, , .		15
6944	Algorithm for low-variance biclusters to identify coregulation modules in sequencing datasets. , 2011, , .		0
6945	Clustering with relative constraints. , 2011, , .		12

#	ARTICLE	IF	CITATIONS
6946	Fuse. , 2011, , .		5
6947	Scalable multiple global network alignment for biological data. , 2011, , .		1
6948	Multi-view prediction of protein function. , 2011, , .		5
6949	A Bayesian integration model for improved gene functional inference from heterogeneous data sources. , 2011, , .		2
6950	Using ontologies for supporting genomic sequence annotation projects. , 2011, , .		0
6951	The Proteome Folding Project: Proteome-scale prediction of structure and function. <i>Genome Research</i> , 2011, 21, 1981-1994.	2.4	40
6952	Generation and Comprehensive Analysis of an Influenza Virus Polymerase Cellular Interaction Network. <i>Journal of Virology</i> , 2011, 85, 13010-13018.	1.5	69
6953	Soybean Homologs of MPK4 Negatively Regulate Defense Responses and Positively Regulate Growth and Development. <i>Plant Physiology</i> , 2011, 157, 1363-1378.	2.3	130
6954	Bioinformatics Analysis of Functional Relations Between CNPs Regions. <i>Current Bioinformatics</i> , 2011, 6, 122-128.	0.7	11
6956	Combining Drug and Gene Similarity Measures for Drug-Target Elucidation. <i>Journal of Computational Biology</i> , 2011, 18, 133-145.	0.8	174
6957	Measuring the evolutionary rate of protein-protein interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 8725-8730.	3.3	50
6958	Multi-Label Learning for Prediction of Subcellular Localization of Human Proteins. , 2011, , .		0
6959	Extracting Between-Pathway Models from E-MAP Interactions Using Expected Graph Compression. <i>Journal of Computational Biology</i> , 2011, 18, 379-390.	0.8	4
6960	Dynamics of Time-Lagged Gene-to-Metabolite Networks of <i>Escherichia coli</i> Elucidated by Integrative Omics Approach. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 15-23.	1.0	28
6961	The effect of narrow bandwidth infrared radiation on the growth of <i>Escherichia coli</i> . <i>Applied Physics Letters</i> , 2011, 99, 163704.	1.5	8
6962	High-Dimensional ODEs Coupled With Mixed-Effects Modeling Techniques for Dynamic Gene Regulatory Network Identification. <i>Journal of the American Statistical Association</i> , 2011, 106, 1242-1258.	1.8	64
6963	A GRAPH-BASED SEMANTIC SIMILARITY MEASURE FOR THE GENE ONTOLOGY. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 681-695.	0.3	17
6964	â€™ome on the Range: Altitude Adaptation, Positive Selection, and Himalayan Genomics. <i>High Altitude Medicine and Biology</i> , 2011, 12, 133-139.	0.5	24

#	ARTICLE	IF	CITATIONS
6966	Gene expression analysis with integrated fuzzy C-means and pathway analysis. , 2011, 2011, 936-9.		5
6967	Hierarchical Generative Biclustering for MicroRNA Expression Analysis. <i>Journal of Computational Biology</i> , 2011, 18, 251-261.	0.8	21
6968	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
6969	Discovery of Versatile Temporal Subspace Patterns in 3-D Datasets. , 2011, , .		1
6970	A development of knowledge representation for thalassemia prevention and control program. , 2011, , .		0
6971	Inferring transcriptional regulators for sets of co-expressed genes by multi-objective evolutionary optimization. , 2011, , .		0
6972	Expression of microRNAs and their target mRNAs in human stem cell-derived cardiomyocyte clusters and in heart tissue. <i>Physiological Genomics</i> , 2011, 43, 581-594.	1.0	24
6973	BioProfiling.de: analytical web portal for high-throughput cell biology. <i>Nucleic Acids Research</i> , 2011, 39, W323-W327.	6.5	108
6974	HitPredict: a database of quality assessed protein-protein interactions in nine species. <i>Nucleic Acids Research</i> , 2011, 39, D744-D749.	6.5	111
6975	PhenOMIM: An OMIM-based secondary database purported for phenotypic comparison. , 2011, 2011, 3589-92.		5
6976	Extending CATH: increasing coverage of the protein structure universe and linking structure with function. <i>Nucleic Acids Research</i> , 2011, 39, D420-D426.	6.5	126
6977	SVS: Data and knowledge integration in computational biology. , 2011, 2011, 6474-8.		5
6978	Using semantic web technologies to manage complexity and change in biomedical data. , 2011, 2011, 3708-11.		2
6979	Phenotype-difference oriented identification of molecular functions for diabetes progression in Goto-Kakizaki rat. , 2011, , .		0
6980	ICGA-PSO-ELM Approach for Accurate Multiclass Cancer Classification Resulting in Reduced Gene Sets in Which Genes Encoding Secreted Proteins Are Highly Represented. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 452-463.	1.9	93
6981	ER α -Dependent E2F Transcription Can Mediate Resistance to Estrogen Deprivation in Human Breast Cancer. <i>Cancer Discovery</i> , 2011, 1, 338-351.	7.7	284
6982	Toward an understanding of the protein interaction network of the human liver. <i>Molecular Systems Biology</i> , 2011, 7, 536.	3.2	194
6983	An algorithm for computing the semantic similarity among terminologies in gene ontology. , 2011, , .		1

#	ARTICLE	IF	CITATIONS
6984	Notice of Retraction: Finding Significant Gene Sets with Weighted Distribution of Gene Expression. , 2011, , .		0
6985	Bioinformatics for Comparative Proteomics. Methods in Molecular Biology, 2011, , .	0.4	3
6986	Semantic-JSON: a lightweight web service interface for Semantic Web contents integrating multiple life science databases. Nucleic Acids Research, 2011, 39, W533-W540.	6.5	21
6987	Toward a Cooperative Natural Language Query Interface for Biological Databases. , 2011, , .		0
6988	ROAR: A Reference Ontology for Anatomical Relations. , 2011, , .		1
6989	PredUs: a web server for predicting protein interfaces using structural neighbors. Nucleic Acids Research, 2011, 39, W283-W287.	6.5	101
6990	Topology aware functional similarity of protein interaction networks based on gene ontology. , 2011, 2011, 6857-60.		0
6991	Genomic Differentiation Between Temperate and Tropical Australian Populations of <i>Drosophila melanogaster</i> . Genetics, 2011, 187, 245-260.	1.2	217
6992	Small sets of interacting proteins suggest functional linkage mechanisms via Bayesian analogical reasoning. Bioinformatics, 2011, 27, i374-i382.	1.8	0
6993	Prognostic gene-expression signature of carcinoma-associated fibroblasts in non-small cell lung cancer. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7160-7165.	3.3	317
6994	INOH: ontology-based highly structured database of signal transduction pathways. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar052-bar052.	1.4	57
6995	The Rat Genome Database Pathway Portal. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar010-bar010.	1.4	18
6996	The annotation of the asparagine N-linked glycosylation pathway in the Reactome database. Glycobiology, 2011, 21, 1395-1400.	1.3	7
6997	IsoBase: a database of functionally related proteins across PPI networks. Nucleic Acids Research, 2011, 39, D295-D300.	6.5	90
6998	Genomic signatures of diet-related shifts during human origins. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 961-969.	1.2	48
6999	A tool for multi-scale modelling of the renal nephron. Interface Focus, 2011, 1, 417-425.	1.5	9
7000	Prediction of human protein-protein interaction by a mixed Bayesian model and its application to exploring underlying cancer-related pathway crosstalk. Journal of the Royal Society Interface, 2011, 8, 555-567.	1.5	16
7001	Using human demographic history to infer natural selection reveals contrasting patterns on different families of immune genes. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 1587-1594.	1.2	9

#	ARTICLE	IF	CITATIONS
7002	ARISTO: ontological classification of small molecules by electron ionization-mass spectrometry. <i>Nucleic Acids Research</i> , 2011, 39, W505-W510.	6.5	8
7003	Calling Cards enable multiplexed identification of the genomic targets of DNA-binding proteins. <i>Genome Research</i> , 2011, 21, 748-755.	2.4	45
7004	In Vivo Liver Regeneration Potential of Human Induced Pluripotent Stem Cells from Diverse Origins. <i>Science Translational Medicine</i> , 2011, 3, 82ra39.	5.8	211
7005	mESAdb: microRNA Expression and Sequence Analysis Database. <i>Nucleic Acids Research</i> , 2011, 39, D170-D180.	6.5	34
7006	Generative probabilistic models for protein-protein interaction networks—the biclique perspective. <i>Bioinformatics</i> , 2011, 27, i142-i148.	1.8	25
7007	Gene expression profile in the liver tissue of geese after overfeeding. <i>Poultry Science</i> , 2011, 90, 107-117.	1.5	46
7008	PhenomeNET: a whole-phenome approach to disease gene discovery. <i>Nucleic Acids Research</i> , 2011, 39, e119-e119.	6.5	195
7009	Epigenetics: DNA demethylation promotes skeletal myotube maturation. <i>FASEB Journal</i> , 2011, 25, 3861-3872.	0.2	59
7010	A novel method for assigning functional linkages to proteins using enhanced phylogenetic trees. <i>Bioinformatics</i> , 2011, 27, 700-706.	1.8	16
7011	Using computational predictions to improve literature-based Gene Ontology annotations: a feasibility study. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar004-bar004.	1.4	16
7012	Analysis of Escherichia coli RNase E and RNase III activity in vivo using tiling microarrays. <i>Nucleic Acids Research</i> , 2011, 39, 3188-3203.	6.5	112
7013	The RCSB Protein Data Bank: redesigned web site and web services. <i>Nucleic Acids Research</i> , 2011, 39, D392-D401.	6.5	549
7014	Analysis of Muscle and Ovary Transcriptome of Sus scrofa: Assembly, Annotation and Marker Discovery. <i>DNA Research</i> , 2011, 18, 343-351.	1.5	20
7015	Specific inhibition of NF-Y subunits triggers different cell proliferation defects. <i>Nucleic Acids Research</i> , 2011, 39, 5356-5368.	6.5	73
7016	MIPS: curated databases and comprehensive secondary data resources in 2010. <i>Nucleic Acids Research</i> , 2011, 39, D220-D224.	6.5	77
7017	DLK1-DIO3 Genomic Imprinted MicroRNA Cluster at 14q32.2 Defines a Stemlike Subtype of Hepatocellular Carcinoma Associated with Poor Survival. <i>Journal of Biological Chemistry</i> , 2011, 286, 30706-30713.	1.6	147
7018	ViralZone: a knowledge resource to understand virus diversity. <i>Nucleic Acids Research</i> , 2011, 39, D576-D582.	6.5	312
7019	A novel network-based method for measuring the functional relationship between gene sets. <i>Bioinformatics</i> , 2011, 27, 1521-1528.	1.8	19

#	ARTICLE	IF	CITATIONS
7020	GreenPhylDB v2.0: comparative and functional genomics in plants. <i>Nucleic Acids Research</i> , 2011, 39, D1095-D1102.	6.5	106
7021	PiNGO: a Cytoscape plugin to find candidate genes in biological networks. <i>Bioinformatics</i> , 2011, 27, 1030-1031.	1.8	41
7022	Combined Gene Expression Profiling and RNAi Screening in Clear Cell Renal Cell Carcinoma Identify PLK1 and Other Therapeutic Kinase Targets. <i>Cancer Research</i> , 2011, 71, 5225-5234.	0.4	31
7023	Quantitative Phospho-proteomics to Investigate the Polo-like Kinase 1-Dependent Phospho-proteome. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.008540.	2.5	61
7024	Transcriptional regulation via TF-modifying enzymes: an integrative model-based analysis. <i>Nucleic Acids Research</i> , 2011, 39, e78-e78.	6.5	7
7025	B2G-FAR, a species-centered GO annotation repository. <i>Bioinformatics</i> , 2011, 27, 919-924.	1.8	137
7026	ARTADE2DB: Improved Statistical Inferences for Arabidopsis Gene Functions and Structure Predictions by Dynamic Structure-Based Dynamic Expression (DSDE) Analyses. <i>Plant and Cell Physiology</i> , 2011, 52, 254-264.	1.5	15
7027	Curation of characterized glycoside hydrolases of Fungal origin. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar020-bar020.	1.4	97
7028	Human Embryonic Stem Cell Derived Hepatocyte-Like Cells as a Tool for In Vitro Hazard Assessment of Chemical Carcinogenicity. <i>Toxicological Sciences</i> , 2011, 124, 278-290.	1.4	66
7029	Ongoing and future developments at the Universal Protein Resource. <i>Nucleic Acids Research</i> , 2011, 39, D214-D219.	6.5	649
7030	Lineage-Specific Variation in Intensity of Natural Selection in Mammals. <i>Molecular Biology and Evolution</i> , 2011, 28, 383-398.	3.5	38
7031	PCDB: a database of protein conformational diversity. <i>Nucleic Acids Research</i> , 2011, 39, D475-D479.	6.5	25
7032	Integrated genome-wide chromatin occupancy and expression analyses identify key myeloid pro-differentiation transcription factors repressed by Myb. <i>Nucleic Acids Research</i> , 2011, 39, 4664-4679.	6.5	89
7033	MaizeGDB: curation and outreach go hand-in-hand. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar022-bar022.	1.4	66
7034	A systems biology approach sheds new light on Escherichia coli acid resistance. <i>Nucleic Acids Research</i> , 2011, 39, 7512-7528.	6.5	86
7035	Drug-target network in myocardial infarction reveals multiple side effects of unrelated drugs. <i>Scientific Reports</i> , 2011, 1, 52.	1.6	71
7036	Gene Expression Differences Among Primates Are Associated With Changes in a Histone Epigenetic Modification. <i>Genetics</i> , 2011, 187, 1225-1234.	1.2	89
7037	ADGO 2.0: interpreting microarray data and list of genes using composite annotations. <i>Nucleic Acids Research</i> , 2011, 39, W302-W306.	6.5	6

#	ARTICLE	IF	CITATIONS
7038	Community characterization of heterogeneous complex systems. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2011, 2011, P01019.	0.9	44
7039	Diversification at Transcription Factor Binding Sites within a Species and the Implications for Environmental Adaptation. <i>Molecular Biology and Evolution</i> , 2011, 28, 3331-3344.	3.5	5
7040	GeBP/GPL Transcription Factors Regulate a Subset of <i>CPR5</i> -Dependent Processes. <i>Plant Physiology</i> , 2011, 157, 1232-1242.	2.3	23
7041	Rfam: Wikipedia, clans and the "decimal" release. <i>Nucleic Acids Research</i> , 2011, 39, D141-D145.	6.5	355
7042	Stromal-epithelial interactions in early neoplasia. <i>Cancer Biomarkers</i> , 2011, 9, 141-155.	0.8	9
7043	HTSanalyzeR: an R/Bioconductor package for integrated network analysis of high-throughput screens. <i>Bioinformatics</i> , 2011, 27, 879-880.	1.8	131
7044	Silencing of p130Cas in Ovarian Carcinoma: A Novel Mechanism for Tumor Cell Death. <i>Journal of the National Cancer Institute</i> , 2011, 103, 1596-1612.	3.0	44
7045	Coordinated regulation of sulfur and phospholipid metabolism reflects the importance of methylation in the growth of yeast. <i>Molecular Biology of the Cell</i> , 2011, 22, 4192-4204.	0.9	43
7046	Literature-aided interpretation of gene expression data with the weighted global test. <i>Briefings in Bioinformatics</i> , 2011, 12, 518-529.	3.2	19
7047	LocDB: experimental annotations of localization for <i>Homo sapiens</i> and <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2011, 39, D230-D234.	6.5	47
7048	RiceFOX: A Database of <i>Arabidopsis</i> Mutant Lines Overexpressing Rice Full-Length cDNA that Contains a Wide Range of Trait Information to Facilitate Analysis of Gene Function. <i>Plant and Cell Physiology</i> , 2011, 52, 265-273.	1.5	72
7049	Interactome mapping suggests new mechanistic details underlying Alzheimer's disease. <i>Genome Research</i> , 2011, 21, 364-376.	2.4	121
7050	Ontology patterns for tabular representations of biomedical knowledge on neglected tropical diseases. <i>Bioinformatics</i> , 2011, 27, i349-i356.	1.8	4
7051	Molecular signatures database (MSigDB) 3.0. <i>Bioinformatics</i> , 2011, 27, 1739-1740.	1.8	4,752
7052	Reasoning with bio-ontologies: using relational closure rules to enable practical querying. <i>Bioinformatics</i> , 2011, 27, 1562-1568.	1.8	24
7053	GProX, a User-Friendly Platform for Bioinformatics Analysis and Visualization of Quantitative Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2011, 10, O110.007450.	2.5	150
7054	Ortholog identification in the presence of domain architecture rearrangement. <i>Briefings in Bioinformatics</i> , 2011, 12, 413-422.	3.2	28
7055	New approaches to the representation and analysis of phenotype knowledge in human diseases and their animal models. <i>Briefings in Functional Genomics</i> , 2011, 10, 258-265.	1.3	18

#	ARTICLE	IF	CITATIONS
7056	CoMetâ€”a web server for comparative functional profiling of metagenomes. <i>Nucleic Acids Research</i> , 2011, 39, W518-W523.	6.5	50
7057	The pharmacological screening process: the small molecule, the biological Screen, the robot, the signal and the information. , 2011, , 7-21.		1
7058	From sets to graphs: towards a realistic enrichment analysis of transcriptomic systems. <i>Bioinformatics</i> , 2011, 27, i366-i373.	1.8	64
7059	Mapping the sequences of potential guanine quadruplex motifs. <i>Nucleic Acids Research</i> , 2011, 39, 4917-4927.	6.5	29
7060	Unraveling networks of co-regulated genes on the sole basis of genome sequences. <i>Nucleic Acids Research</i> , 2011, 39, 6340-6358.	6.5	39
7061	Analysis of the proteome of human airway epithelial secretions. <i>Proteome Science</i> , 2011, 9, 4.	0.7	49
7062	Prospective Multicenter Phase II Trial of Systemic ADH-1 in Combination With Melphalan via Isolated Limb Infusion in Patients With Advanced Extremity Melanoma. <i>Journal of Clinical Oncology</i> , 2011, 29, 1210-1215.	0.8	73
7063	The RIKEN integrated database of mammals. <i>Nucleic Acids Research</i> , 2011, 39, D861-D870.	6.5	23
7064	TMPad: an integrated structural database for helix-packing folds in transmembrane proteins. <i>Nucleic Acids Research</i> , 2011, 39, D347-D355.	6.5	21
7065	CancerResource: a comprehensive database of cancer-relevant proteins and compound interactions supported by experimental knowledge. <i>Nucleic Acids Research</i> , 2011, 39, D960-D967.	6.5	70
7066	ICSNPPathway: identify candidate causal SNPs and pathways from genome-wide association study by one analytical framework. <i>Nucleic Acids Research</i> , 2011, 39, W437-W443.	6.5	69
7067	The genome of the leaf-cutting ant<i>Acromyrmex echinator</i> suggests key adaptations to advanced social life and fungus farming. <i>Genome Research</i> , 2011, 21, 1339-1348.	2.4	210
7068	mRNA/microRNA Profile at the Metamorphic Stage of Olive Flounder (<i>Paralichthys olivaceus</i>). <i>Comparative and Functional Genomics</i> , 2011, 2011, 1-12.	2.0	16
7069	Proteomic and Metabolomic Profiling of a Trait Anxiety Mouse Model Implicate Affected Pathways. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.008110.	2.5	68
7070	Cross-Genome Comparisons of Newly Identified Domains in <i>Mycoplasma gallisepticum</i> and Domain Architectures with Other <i>Mycoplasma</i> species. <i>Comparative and Functional Genomics</i> , 2011, 2011, 1-13.	2.0	0
7071	Evolution of Patchily Distributed Proteins Shared between Eukaryotes and Prokaryotes: <i>Dictyostelium</i> as a Case Study. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011, 20, 83-95.	1.0	18
7072	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. <i>Applied Ontology</i> , 2011, 6, 53-89.	1.0	23
7073	Patterns of Gene Expression in <i>Drosophila</i> InsP3 Receptor Mutant Larvae Reveal a Role for InsP3 Signaling in Carbohydrate and Energy Metabolism. <i>PLoS ONE</i> , 2011, 6, e24105.	1.1	5

#	ARTICLE	IF	CITATIONS
7074	A METHOD FOR THE DETECTION OF MEANINGFUL AND REPRODUCIBLE GROUP SIGNATURES FROM GENE EXPRESSION PROFILES. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 431-451.	0.3	4
7075	Efficient solution of an inverse problem in cell population dynamics. <i>Inverse Problems</i> , 2011, 27, 065009.	1.0	10
7076	Processes of fungal proteome evolution and gain of function: gene duplication and domain rearrangement. <i>Physical Biology</i> , 2011, 8, 035009.	0.8	10
7077	Histone H2B ubiquitylation and H3 lysine 4 methylation prevent ectopic silencing of euchromatic loci important for the cellular response to heat. <i>Molecular Biology of the Cell</i> , 2011, 22, 2741-2753.	0.9	13
7078	MAISTAS: a tool for automatic structural evaluation of alternative splicing products. <i>Bioinformatics</i> , 2011, 27, 1625-1629.	1.8	12
7079	PLIO: an ontology for formal description of protein-ligand interactions. <i>Bioinformatics</i> , 2011, 27, 1684-1690.	1.8	6
7080	Transcriptome Analysis of <i>Sarracenia</i> , an Insectivorous Plant. <i>DNA Research</i> , 2011, 18, 253-261.	1.5	28
7081	Genome Sequence of <i>Weissella thailandensis</i> fsh4-2. <i>Journal of Bacteriology</i> , 2011, 193, 5868-5868.	1.0	6
7082	Novel hub protein classification and interaction rules in protein-protein interaction network in <i>Saccharomyces cerevisiae</i> . , 2011, , .		0
7083	g:Profiler—a web server for functional interpretation of gene lists (2011 update). <i>Nucleic Acids Research</i> , 2011, 39, W307-W315.	6.5	454
7084	SLiMSearch 2.0: biological context for short linear motifs in proteins. <i>Nucleic Acids Research</i> , 2011, 39, W56-W60.	6.5	68
7085	Independent Analysis of the Flagellum Surface and Matrix Proteomes Provides Insight into Flagellum Signaling in Mammalian-infectious <i>Trypanosoma brucei</i> . <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010538.	2.5	147
7086	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
7087	Effects of an enteral glucose supply on protein synthesis, proteolytic pathways, and proteome in human duodenal mucosa. <i>American Journal of Clinical Nutrition</i> , 2011, 94, 784-794.	2.2	9
7088	BSDB: the biomolecule stretching database. <i>Nucleic Acids Research</i> , 2011, 39, D443-D450.	6.5	35
7089	A common layer of interoperability for biomedical ontologies based on OWL EL. <i>Bioinformatics</i> , 2011, 27, 1001-1008.	1.8	35
7090	RAC2, AEP, and ICAM1 expression are associated with CNS disease in a mouse model of pre-B childhood acute lymphoblastic leukemia. <i>Blood</i> , 2011, 118, 638-649.	0.6	49
7091	Gene Expression Profiling Reveals Renin mRNA Overexpression in Human Hypertensive Kidneys and a Role for MicroRNAs. <i>Hypertension</i> , 2011, 58, 1093-1098.	1.3	208

#	ARTICLE	IF	CITATIONS
7092	Development and Independent Validation of a Prognostic Assay for Stage II Colon Cancer Using Formalin-Fixed Paraffin-Embedded Tissue. <i>Journal of Clinical Oncology</i> , 2011, 29, 4620-4626.	0.8	178
7093	MicroRNA-423 promotes cell growth and regulates G 1 /S transition by targeting p21Cip1/Waf1 in hepatocellular carcinoma. <i>Carcinogenesis</i> , 2011, 32, 1641-1647.	1.3	107
7094	REVIGO Summarizes and Visualizes Long Lists of Gene Ontology Terms. <i>PLoS ONE</i> , 2011, 6, e21800.	1.1	5,347
7095	Dynamic Changes in the MicroRNA Expression Profile Reveal Multiple Regulatory Mechanisms in the Spinal Nerve Ligation Model of Neuropathic Pain. <i>PLoS ONE</i> , 2011, 6, e17670.	1.1	123
7096	Phylogenetic-based propagation of functional annotations within the Gene Ontology consortium. <i>Briefings in Bioinformatics</i> , 2011, 12, 449-462.	3.2	723
7097	Construction of co-complex score matrix for protein complex prediction from AP-MS data. <i>Bioinformatics</i> , 2011, 27, i159-i166.	1.8	34
7098	VIZ-GRAIL: visualizing functional connections across disease loci. <i>Bioinformatics</i> , 2011, 27, 1589-1590.	1.8	13
7099	Effects of HMGN variants on the cellular transcription profile. <i>Nucleic Acids Research</i> , 2011, 39, 4076-4087.	6.5	38
7100	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
7101	myMIR: a genome-wide microRNA targets identification and annotation tool. <i>Briefings in Bioinformatics</i> , 2011, 12, 588-600.	3.2	23
7102	Adaptive Elastic-Net Sparse Principal Component Analysis for Pathway Association Testing. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.2	10
7103	Computational network analysis of the anatomical and genetic organizations in the mouse brain. <i>Bioinformatics</i> , 2011, 27, 3293-3299.	1.8	15
7104	Analysis of the workers head transcriptome of the Asian subterranean termite, <i>Coptotermes gestroi</i> . <i>Bulletin of Entomological Research</i> , 2011, 101, 383-391.	0.5	15
7105	Tests for High-Dimensional Regression Coefficients With Factorial Designs. <i>Journal of the American Statistical Association</i> , 2011, 106, 260-274.	1.8	91
7106	Guest Editorial: Special Focus on Bioinformatics and Systems Biology. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 292-293.	1.9	0
7107	Controlled vocabularies and semantics in systems biology. <i>Molecular Systems Biology</i> , 2011, 7, 543.	3.2	246
7108	Antisense expression increases gene expression variability and locus interdependency. <i>Molecular Systems Biology</i> , 2011, 7, 468.	3.2	173
7109	Programmed fluctuations in sense/antisense transcript ratios drive sexual differentiation in <i>S. pombe</i> . <i>Molecular Systems Biology</i> , 2011, 7, 559.	3.2	41

#	ARTICLE	IF	CITATIONS
7110	Massive Changes in Genome Architecture Accompany the Transition to Self-Fertility in the Filamentous Fungus <i>Neurospora tetrasperma</i> . <i>Genetics</i> , 2011, 189, 55-69.	1.2	69
7111	Network Topological Indices from Chem-Bioinformatics to Legal Sciences and back. <i>Current Bioinformatics</i> , 2011, 6, 53-70.	0.7	14
7112	Evolution and applications of plant pathway resources and databases. <i>Briefings in Bioinformatics</i> , 2011, 12, 530-544.	3.2	12
7113	Customizable views on semantically integrated networks for systems biology. <i>Bioinformatics</i> , 2011, 27, 1299-1306.	1.8	9
7114	Positional integratomic approach in identification of genomic candidate regions for Parkinson's disease. <i>Bioinformatics</i> , 2011, 27, 1971-1978.	1.8	15
7115	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
7116	Biphasic Gene Expression Changes Elicited by <i>Phakopsora pachyrhizi</i> in Soybean Correlate with Fungal Penetration and Haustoria Formation. <i>Plant Physiology</i> , 2011, 157, 355-371.	2.3	59
7117	Information Systems Evolution. <i>Lecture Notes in Business Information Processing</i> , 2011, , .	0.8	2
7118	Molecular Evolution, Mutation Size and Gene Pleiotropy: A Geometric Reexamination. <i>Genetics</i> , 2011, 187, 877-885.	1.2	22
7119	Endothelin-1 Increases Collagen Accumulation in Renal Mesangial Cells by Stimulating a Chemokine and Cytokine Autocrine Signaling Loop. <i>Journal of Biological Chemistry</i> , 2011, 286, 11003-11008.	1.6	59
7120	Interorgan Coordination of the Murine Adaptive Response to Fasting. <i>Journal of Biological Chemistry</i> , 2011, 286, 16332-16343.	1.6	50
7121	Global Identification of SMAD2 Target Genes Reveals a Role for Multiple Co-regulatory Factors in Zebrafish Early Gastrulas. <i>Journal of Biological Chemistry</i> , 2011, 286, 28520-28532.	1.6	50
7122	A yeast-based assay identifies drugs active against human mitochondrial disorders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11989-11994.	3.3	73
7123	Effect of Estradiol on Gene Expression Profile in <i>Cynomolgus</i> Macaque Liver: Implications for Drug-Metabolizing Enzymes. <i>Drug Metabolism and Disposition</i> , 2011, 39, 2003-2007.	1.7	7
7124	Suppression of autophagy by FIP200 deletion inhibits mammary tumorigenesis. <i>Genes and Development</i> , 2011, 25, 1510-1527.	2.7	335
7125	Aberrant Epigenetic and Genetic Marks Are Seen in Myelodysplastic Leukocytes and Reveal Dock4 as a Candidate Pathogenic Gene on Chromosome 7q. <i>Journal of Biological Chemistry</i> , 2011, 286, 25211-25223.	1.6	41
7126	Network-based prediction for sources of transcriptional dysregulation using latent pathway identification analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13347-13352.	3.3	36
7127	Secretoglobin 3A2 Suppresses Bleomycin-induced Pulmonary Fibrosis by Transforming Growth Factor β Signaling Down-regulation. <i>Journal of Biological Chemistry</i> , 2011, 286, 19682-19692.	1.6	31

#	ARTICLE	IF	CITATIONS
7128	Defective photoreceptor phagocytosis in a mouse model of enhanced Sâ€šone syndrome causes progressive retinal degeneration. <i>FASEB Journal</i> , 2011, 25, 3157-3176.	0.2	76
7129	Integrated Quantitative Analysis of the Phosphoproteome and Transcriptome in Tamoxifen-resistant Breast Cancer. <i>Journal of Biological Chemistry</i> , 2011, 286, 818-829.	1.6	42
7130	Towards a genome-wide transcriptogram: the <i>Saccharomyces cerevisiae</i> case. <i>Nucleic Acids Research</i> , 2011, 39, 3005-3016.	6.5	25
7131	A Gene Expression Signature from Human Breast Cancer Cells with Acquired Hormone Independence Identifies MYC as a Mediator of Antiestrogen Resistance. <i>Clinical Cancer Research</i> , 2011, 17, 2024-2034.	3.2	88
7133	High-throughput mapping of the promoters of the mouse olfactory receptor genes reveals a new type of mammalian promoter and provides insight into olfactory receptor gene regulation. <i>Genome Research</i> , 2011, 21, 1249-1259.	2.4	61
7134	Retrieval, alignment, and clustering of computational models based on semantic annotations. <i>Molecular Systems Biology</i> , 2011, 7, 512.	3.2	32
7136	Systems biology of the autophagy-lysosomal pathway. <i>Autophagy</i> , 2011, 7, 477-489.	4.3	116
7137	NOA: a novel Network Ontology Analysis method. <i>Nucleic Acids Research</i> , 2011, 39, e87-e87.	6.5	101
7138	Unexpected functional similarities between gatekeeper tumour suppressor genes and proto-oncogenes revealed by systems biology. <i>Journal of Human Genetics</i> , 2011, 56, 369-376.	1.1	4
7139	Medusa structure of the gene regulatory network: dominance of transcription factors in cancer subtype classification. <i>Experimental Biology and Medicine</i> , 2011, 236, 628-636.	1.1	20
7140	Transcriptome Analysis of High-Temperature Stress in Developing Barley Caryopses: Early Stress Responses and Effects on Storage Compound Biosynthesis. <i>Molecular Plant</i> , 2011, 4, 97-115.	3.9	141
7141	ncFANs: a web server for functional annotation of long non-coding RNAs. <i>Nucleic Acids Research</i> , 2011, 39, W118-W124.	6.5	123
7142	Analysis of Expressed Sequence Tags from the Placenta of the Live-Bearing Fish <i>Poeciliopsis</i> (<i>Poeciliidae</i>). <i>Journal of Heredity</i> , 2011, 102, 352-361.	1.0	16
7143	mirConnX: condition-specific mRNA-microRNA network integrator. <i>Nucleic Acids Research</i> , 2011, 39, W416-W423.	6.5	109
7144	Functional Homogeneity in microRNA Target Heterogeneityâ€”a New Sight into Human microRNomics. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 25-35.	1.0	10
7145	Antennal transcriptome of <i>Manduca sexta</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7449-7454.	3.3	269
7146	Kino: A Generic Document Management System for Biologists Using SA-REST and Faceted Search. , 2011, , .		13
7147	Multisource biological pathway consolidation. , 2011, , .		2

#	ARTICLE	IF	CITATIONS
7148	Ontology module extraction based on semantic query. , 2011, , .		0
7149	Protein Biological Function Clustering with GO and KO. , 2011, , .		0
7150	Transgenic, an operator for evolutionary algorithms. , 2011, , .		5
7151	Exploratory Factor Analysis of Pathway Copy Number Data with an Application Towards the Integration with Gene Expression Data. <i>Journal of Computational Biology</i> , 2011, 18, 729-741.	0.8	3
7152	Identification of maternally regulated fetal gene networks in the placenta with a novel embryo transfer system in mice. <i>Physiological Genomics</i> , 2011, 43, 317-324.	1.0	3
7154	Bioinformatics approaches in the discovery and understanding of reproduction-related biomarkers. <i>Expert Review of Proteomics</i> , 2011, 8, 187-195.	1.3	4
7155	CNCing Is Believing. <i>Science</i> , 2011, 333, 946-947.	6.0	0
7156	Integrative network alignment reveals large regions of global network similarity in yeast and human. <i>Bioinformatics</i> , 2011, 27, 1390-1396.	1.8	217
7157	Knowledge sharing and collaboration in translational research, and the DC-THERA Directory. <i>Briefings in Bioinformatics</i> , 2011, 12, 562-575.	3.2	8
7158	Effects of thermal acclimation on transcriptional responses to acute heat stress in the eurythermal fish <i>Gillichthys mirabilis</i> (Cooper). <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2011, 300, R1373-R1383.	0.9	107
7159	Regulation of alternative splicing by the core spliceosomal machinery. <i>Genes and Development</i> , 2011, 25, 373-384.	2.7	181
7160	An efficient hierarchical generalized linear mixed model for pathway analysis of genome-wide association studies. <i>Bioinformatics</i> , 2011, 27, 686-692.	1.8	50
7161	Modular analysis of the probabilistic genetic interaction network. <i>Bioinformatics</i> , 2011, 27, 853-859.	1.8	10
7162	ppiTrim: constructing non-redundant and up-to-date interactomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar036.	1.4	12
7163	Genes and biological processes commonly disrupted in rare and heterogeneous developmental delay syndromes. <i>Human Molecular Genetics</i> , 2011, 20, 880-893.	1.4	23
7164	<i>Trans</i> genomic capture and sequencing of primate exomes reveals new targets of positive selection. <i>Genome Research</i> , 2011, 21, 1686-1694.	2.4	111
7165	Pathway Commons, a web resource for biological pathway data. <i>Nucleic Acids Research</i> , 2011, 39, D685-D690.	6.5	980
7166	Finished Genome of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> Reveals Dispensome Structure, Chromosome Plasticity, and Stealth Pathogenesis. <i>PLoS Genetics</i> , 2011, 7, e1002070.	1.5	532

#	ARTICLE	IF	CITATIONS
7167	QlicRice: a web interface for abiotic stress responsive QTL and loci interaction channels in rice. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar037.	1.4	29
7168	Identification of New SRF Binding Sites in Genes Modulated by SRF Over-Expression in Mouse Hearts. Gene Regulation and Systems Biology, 2011, 5, GRSB.S7457.	2.3	10
7169	Mapping Protein Interactions between Dengue Virus and Its Human and Insect Hosts. PLoS Neglected Tropical Diseases, 2011, 5, e954.	1.3	93
7170	Handbook of Conceptual Modeling. , 2011, , .		38
7171	Comprehensive Analysis of Yeast Surface Displayed cDNA Library Selection Outputs by Exon Microarray to Identify Novel Protein-Ligand Interactions. Molecular and Cellular Proteomics, 2011, 10, M110.005116.	2.5	16
7172	Impact of exercise training on endothelial transcriptional profiles in healthy swine: a genome-wide microarray analysis. American Journal of Physiology - Heart and Circulatory Physiology, 2011, 301, H555-H564.	1.5	15
7173	HKC: An Algorithm to Predict Protein Complexes in Protein-Protein Interaction Networks. Journal of Biomedicine and Biotechnology, 2011, 2011, 1-14.	3.0	10
7174	MicroRNA-Driven Developmental Remodeling in the Brain Distinguishes Humans from Other Primates. PLoS Biology, 2011, 9, e1001214.	2.6	198
7175	Integrative Analysis of Many Weighted Co-Expression Networks Using Tensor Computation. PLoS Computational Biology, 2011, 7, e1001106.	1.5	101
7176	Protein Networks as Logic Functions in Development and Cancer. PLoS Computational Biology, 2011, 7, e1002180.	1.5	86
7177	Prediction of Drug Combinations by Integrating Molecular and Pharmacological Data. PLoS Computational Biology, 2011, 7, e1002323.	1.5	173
7178	The Genome Sequence of the Leaf-Cutter Ant <i>Atta cephalotes</i> Reveals Insights into Its Obligate Symbiotic Lifestyle. PLoS Genetics, 2011, 7, e1002007.	1.5	231
7179	Variance of Gene Expression Identifies Altered Network Constraints in Neurological Disease. PLoS Genetics, 2011, 7, e1002207.	1.5	132
7180	Gender-Associated Genes in Filarial Nematodes Are Important for Reproduction and Potential Intervention Targets. PLoS Neglected Tropical Diseases, 2011, 5, e947.	1.3	26
7181	The bZIP Transcription Factor MoAP1 Mediates the Oxidative Stress Response and Is Critical for Pathogenicity of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . PLoS Pathogens, 2011, 7, e1001302.	2.1	266
7182	Metabolic Regulation in Progression to Autoimmune Diabetes. PLoS Computational Biology, 2011, 7, e1002257.	1.5	74
7183	Global Gene Expression Profiling of a Population Exposed to a Range of Benzene Levels. Environmental Health Perspectives, 2011, 119, 628-640.	2.8	94
7184	VISTA Region Viewer (RViewer)â€”a computational system for prioritizing genomic intervals for biomedical studies. Bioinformatics, 2011, 27, 2595-2597.	1.8	11

#	ARTICLE	IF	CITATIONS
7185	Network Approaches to the Functional Analysis of Microbial Proteins. <i>Advances in Microbial Physiology</i> , 2011, 59, 101-133.	1.0	6
7186	RIP: the regulatory interaction predictor—a machine learning-based approach for predicting target genes of transcription factors. <i>Bioinformatics</i> , 2011, 27, 2239-2247.	1.8	16
7187	SNPsyn: detection and exploration of SNP–SNP interactions. <i>Nucleic Acids Research</i> , 2011, 39, W444-W449.	6.5	35
7188	Identification of a Novel Class of Farnesylation Targets by Structure-Based Modeling of Binding Specificity. <i>PLoS Computational Biology</i> , 2011, 7, e1002170.	1.5	58
7189	Consensus-Phenotype Integration of Transcriptomic and Metabolomic Data Implies a Role for Metabolism in the Chemosensitivity of Tumour Cells. <i>PLoS Computational Biology</i> , 2011, 7, e1001113.	1.5	83
7190	Genome-based analysis of the nonhuman primate <i>Macaca fascicularis</i> as a model for drug safety assessment. <i>Genome Research</i> , 2011, 21, 1746-1756.	2.4	119
7191	Reliability-Oriented bioinformatic networks visualization. <i>Bioinformatics</i> , 2011, 27, 1583-1584.	1.8	1
7192	Signaling gateway molecule pages—a data model perspective. <i>Bioinformatics</i> , 2011, 27, 1736-1738.	1.8	33
7193	TparvaDB: a database to support <i>Theileria parva</i> vaccine development. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar015-bar015.	1.4	1
7194	Latent topic feedback for information retrieval. , 2011, , .		59
7195	Hymenoptera Genome Database: integrated community resources for insect species of the order Hymenoptera. <i>Nucleic Acids Research</i> , 2011, 39, D658-D662.	6.5	142
7196	GO-Module: functional synthesis and improved interpretation of Gene Ontology patterns. <i>Bioinformatics</i> , 2011, 27, 1444-1446.	1.8	97
7197	DNA Free Energy-Based Promoter Prediction and Comparative Analysis of Arabidopsis and Rice Genomes. <i>Plant Physiology</i> , 2011, 156, 1300-1315.	2.3	43
7198	Multi-source and ontology-based retrieval engine for maize mutant phenotypes. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar012-bar012.	1.4	6
7199	Fenfluramine-Induced Gene Dysregulation in Human Pulmonary Artery Smooth Muscle and Endothelial Cells. <i>Pulmonary Circulation</i> , 2011, 1, 405-418.	0.8	7
7200	Proinflammatory Caspase-2-Mediated Macrophage Cell Death Induced by a Rough Attenuated <i>Brucella suis</i> Strain. <i>Infection and Immunity</i> , 2011, 79, 2460-2469.	1.0	46
7201	Defining a relationship between dietary fatty acids and the cytochrome P450 system in a mouse model of fatty liver disease. <i>Physiological Genomics</i> , 2011, 43, 121-135.	1.0	15
7202	Global identification of the genes and pathways differentially expressed in hypothalamus in early and established neurogenic hypertension. <i>Physiological Genomics</i> , 2011, 43, 766-771.	1.0	28

#	ARTICLE	IF	CITATIONS
7203	Tripal: a construction toolkit for online genome databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar044-bar044.	1.4	60
7204	Gene Expression Profiling in Human High-Grade Astrocytomas. Comparative and Functional Genomics, 2011, 2011, 1-10.	2.0	25
7205	Gramene database in 2010: updates and extensions. Nucleic Acids Research, 2011, 39, D1085-D1094.	6.5	182
7206	Characterization of STAT6 Target Genes in Human B Cells and Lung Epithelial Cells. DNA Research, 2011, 18, 379-392.	1.5	20
7207	Testing SNPs and sets of SNPs for importance in association studies. Biostatistics, 2011, 12, 18-32.	0.9	36
7208	The Biomolecular Interaction Network Database in PSI-MI 2.5. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq037.	1.4	95
7209	miRGator v2.0 : an integrated system for functional investigation of microRNAs. Nucleic Acids Research, 2011, 39, D158-D162.	6.5	50
7210	PHOSIDA 2011: the posttranslational modification database. Nucleic Acids Research, 2011, 39, D253-D260.	6.5	366
7211	An efficient network querying method based on conditional random fields. Bioinformatics, 2011, 27, 3173-3178.	1.8	14
7212	PILGRM: an interactive data-driven discovery platform for expert biologists. Nucleic Acids Research, 2011, 39, W368-W374.	6.5	27
7213	Protein Complexes are Central in the Yeast Genetic Landscape. PLoS Computational Biology, 2011, 7, e1001092.	1.5	57
7214	Exploring Off-Targets and Off-Systems for Adverse Drug Reactions via Chemical-Protein Interactome " Clozapine-Induced Agranulocytosis as a Case Study. PLoS Computational Biology, 2011, 7, e1002016.	1.5	93
7215	Modification of Gene Duplicability during the Evolution of Protein Interaction Network. PLoS Computational Biology, 2011, 7, e1002029.	1.5	44
7216	Gene Coexpression Network Alignment and Conservation of Gene Modules between Two Grass Species: Maize and Rice. Plant Physiology, 2011, 156, 1244-1256.	2.3	141
7217	The Cardiac Transcription Network Modulated by Gata4, Mef2a, Nkx2.5, Srf, Histone Modifications, and MicroRNAs. PLoS Genetics, 2011, 7, e1001313.	1.5	180
7218	A Functional Phylogenomic View of the Seed Plants. PLoS Genetics, 2011, 7, e1002411.	1.5	134
7219	The strategies WDK: a graphical search interface and web development kit for functional genomics databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar027-bar027.	1.4	15
7220	High expression of BMP pathway genes distinguishes a subset of atypical teratoid/rhabdoid tumors associated with shorter survival. Neuro-Oncology, 2011, 13, 1296-1307.	0.6	52

#	ARTICLE	IF	CITATIONS
7221	Benchmarking Ontologies: Bigger or Better?. <i>PLoS Computational Biology</i> , 2011, 7, e1001055.	1.5	18
7222	Pathway Analysis of Expression Data: Deciphering Functional Building Blocks of Complex Diseases. <i>PLoS Computational Biology</i> , 2011, 7, e1002053.	1.5	101
7223	Automatic Annotation of Spatial Expression Patterns via Sparse Bayesian Factor Models. <i>PLoS Computational Biology</i> , 2011, 7, e1002098.	1.5	7
7224	Role of the estrogen/estrogen-receptor-beta axis in the genomic response to pressure overload-induced hypertrophy. <i>Physiological Genomics</i> , 2011, 43, 438-446.	1.0	59
7225	Impact of aging vs. estrogen loss on cardiac gene expression: estrogen replacement and inflammation. <i>Physiological Genomics</i> , 2011, 43, 1065-1073.	1.0	36
7226	Natural Selection on Functional Modules, a Genome-Wide Analysis. <i>PLoS Computational Biology</i> , 2011, 7, e1001093.	1.5	12
7227	Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9T). <i>Standards in Genomic Sciences</i> , 2011, 4, 13-22.	1.5	35
7228	The quantitative proteome of a human cell line. <i>Molecular Systems Biology</i> , 2011, 7, 549.	3.2	691
7229	Biological assessment of robust noise models in microarray data analysis. <i>Bioinformatics</i> , 2011, 27, 807-814.	1.8	27
7230	The Evolution of Aerobic Fermentation in <i>Schizosaccharomyces pombe</i> Was Associated with Regulatory Reprogramming but not Nucleosome Reorganization. <i>Molecular Biology and Evolution</i> , 2011, 28, 1407-1413.	3.5	11
7231	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
7232	Structural Requirements for the Activity of the MirB Ferrisiderophore Transporter of <i>Aspergillus fumigatus</i> . <i>Eukaryotic Cell</i> , 2012, 11, 1333-1344.	3.4	57
7233	Cytoskeletal defects in Bmpr2-associated pulmonary arterial hypertension. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2012, 302, L474-L484.	1.3	90
7234	Chapter 8: Biological Knowledge Assembly and Interpretation. <i>PLoS Computational Biology</i> , 2012, 8, e1002858.	1.5	3
7235	Cofilin-1: A Modulator of Anxiety in Mice. <i>PLoS Genetics</i> , 2012, 8, e1002970.	1.5	28
7236	Uncovering Arabidopsis Membrane Protein Interactome Enriched in Transporters Using Mating-Based Split Ubiquitin Assays and Classification Models. <i>Frontiers in Plant Science</i> , 2012, 3, 124.	1.7	42
7237	Patterns of Evolutionary Conservation of Essential Genes Correlate with Their Compensability. <i>PLoS Genetics</i> , 2012, 8, e1002803.	1.5	74
7238	Prediction of Breast Cancer Metastasis by Gene Expression Profiles: A Comparison of Metagenes and Single Genes. <i>Cancer Informatics</i> , 2012, 11, CIN.S10375.	0.9	5

#	ARTICLE	IF	CITATIONS
7239	Combined transcriptomic and metabolomic approach uncovers molecular mechanisms of cold tolerance in a temperate flesh fly. <i>Physiological Genomics</i> , 2012, 44, 764-777.	1.0	128
7240	SWI/SNF-Like Chromatin Remodeling Factor Fun30 Supports Point Centromere Function in <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2012, 8, e1002974.	1.5	38
7241	PINA v2.0: mining interactome modules. <i>Nucleic Acids Research</i> , 2012, 40, D862-D865.	6.5	321
7242	Modelling Translation Initiation under the Influence of sRNA. <i>International Journal of Molecular Sciences</i> , 2012, 13, 16223-16240.	1.8	9
7243	Feature Screening via Distance Correlation Learning. <i>Journal of the American Statistical Association</i> , 2012, 107, 1129-1139.	1.8	510
7244	CombFunc: predicting protein function using heterogeneous data sources. <i>Nucleic Acids Research</i> , 2012, 40, W466-W470.	6.5	63
7245	The renal transcriptome of <i>db/db</i> mice identifies putative urinary biomarker proteins in patients with type 2 diabetes: a pilot study. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 302, F820-F829.	1.3	33
7246	Network-Assisted Investigation of Combined Causal Signals from Genome-Wide Association Studies in Schizophrenia. <i>PLoS Computational Biology</i> , 2012, 8, e1002587.	1.5	98
7247	Drug Target Prediction Based on the Herbs Components: The Study on the Multitargets Pharmacological Mechanism of Qishenkeli Acting on the Coronary Heart Disease. <i>Evidence-based Complementary and Alternative Medicine</i> , 2012, 2012, 1-10.	0.5	73
7248	Inherent and Benzo[a]pyrene-Induced Differential Aryl Hydrocarbon Receptor Signaling Greatly Affects Life Span, Atherosclerosis, Cardiac Gene Expression, and Body and Heart Growth in Mice. <i>Toxicological Sciences</i> , 2012, 126, 391-404.	1.4	58
7249	Bayesian ontology querying for accurate and noise-tolerant semantic searches. <i>Bioinformatics</i> , 2012, 28, 2502-2508.	1.8	55
7250	Development of expressed sequence tag and expressed sequence tag-simple sequence repeat marker resources for <i>Musa acuminata</i> . <i>AoB PLANTS</i> , 2012, 2012, pls030.	1.2	21
7251	RESQUE: Network reduction using semi-Markov random walk scores for efficient querying of biological networks. <i>Bioinformatics</i> , 2012, 28, 2129-2136.	1.8	20
7252	How to link ontologies and protein-protein interactions to literature: text-mining approaches and the BioCreative experience. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas017-bas017.	1.4	27
7253	SynaptomeDB: an ontology-based knowledgebase for synaptic genes. <i>Bioinformatics</i> , 2012, 28, 897-899.	1.8	120
7254	A Limited Role for Gene Duplications in the Evolution of Platypus Venom. <i>Molecular Biology and Evolution</i> , 2012, 29, 167-177.	3.5	33
7255	Quantifying the white blood cell transcriptome as an accessible window to the multiorgan transcriptome. <i>Bioinformatics</i> , 2012, 28, 538-545.	1.8	52
7256	Characterization of Outer Membrane Vesicles from <i>Brucella melitensis</i> and Protection Induced in Mice. <i>Clinical and Developmental Immunology</i> , 2012, 2012, 1-13.	3.3	79

#	ARTICLE	IF	CITATIONS
7257	Molecular Networks Involved in the Immune Control of BK Polyomavirus. <i>Clinical and Developmental Immunology</i> , 2012, 2012, 1-9.	3.3	7
7258	Mining and visualization of microarray and metabolomic data reveal extensive cell wall remodeling during winter hardening in Sitka spruce (<i>Picea sitchensis</i>). <i>Frontiers in Plant Science</i> , 2012, 3, 241.	1.7	11
7259	Predicting the Fission Yeast Protein Interaction Network. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 453-467.	0.8	29
7260	Ontologies and tag-statistics. <i>New Journal of Physics</i> , 2012, 14, 053009.	1.2	5
7261	MiR-138 induces cell cycle arrest by targeting cyclin D3 in hepatocellular carcinoma. <i>Carcinogenesis</i> , 2012, 33, 1113-1120.	1.3	196
7262	The Biofuel Feedstock Genomics Resource: a web-based portal and database to enable functional genomics of plant biofuel feedstock species. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bar061.	1.4	22
7263	Gowinda: unbiased analysis of gene set enrichment for genome-wide association studies. <i>Bioinformatics</i> , 2012, 28, 2084-2085.	1.8	116
7265	Biogeography and phylogenetic diversity of a cluster of exclusively marine myxobacteria. <i>ISME Journal</i> , 2012, 6, 1260-1272.	4.4	67
7266	Recombination is associated with the evolution of genome structure and worker behavior in honey bees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18012-18017.	3.3	82
7267	NeXML: Rich, Extensible, and Verifiable Representation of Comparative Data and Metadata. <i>Systematic Biology</i> , 2012, 61, 675-689.	2.7	90
7268	Use of Pleiotropy to Model Genetic Interactions in a Population. <i>PLoS Genetics</i> , 2012, 8, e1003010.	1.5	22
7269	Voronto: mapper for expression data to ontologies. <i>Bioinformatics</i> , 2012, 28, 2281-2282.	1.8	10
7270	Expressed sequence tags from organ-specific cDNA libraries of tea (<i>Camellia sinensis</i>) and polymorphisms and transferability of EST-SSRs across <i>Camellia</i> species. <i>Breeding Science</i> , 2012, 62, 186-195.	0.9	23
7271	On the Use of Gene Ontology Annotations to Assess Functional Similarity among Orthologs and Paralogs: A Short Report. <i>PLoS Computational Biology</i> , 2012, 8, e1002386.	1.5	91
7272	Robust Detection of Hierarchical Communities from <i>Escherichia coli</i> Gene Expression Data. <i>PLoS Computational Biology</i> , 2012, 8, e1002391.	1.5	35
7273	The CanOE Strategy: Integrating Genomic and Metabolic Contexts across Multiple Prokaryote Genomes to Find Candidate Genes for Orphan Enzymes. <i>PLoS Computational Biology</i> , 2012, 8, e1002540.	1.5	32
7274	Suppressed Expression of T-Box Transcription Factors Is Involved in Senescence in Chronic Obstructive Pulmonary Disease. <i>PLoS Computational Biology</i> , 2012, 8, e1002597.	1.5	18
7275	The Ortholog Conjecture Is Untestable by the Current Gene Ontology but Is Supported by RNA Sequencing Data. <i>PLoS Computational Biology</i> , 2012, 8, e1002784.	1.5	72

#	ARTICLE	IF	CITATIONS
7276	Chapter 5: Network Biology Approach to Complex Diseases. PLoS Computational Biology, 2012, 8, e1002820.	1.5	239
7277	Genome-Wide Functional Profiling Identifies Genes and Processes Important for Zinc-Limited Growth of <i>Saccharomyces cerevisiae</i> . PLoS Genetics, 2012, 8, e1002699.	1.5	57
7278	Salivary Gland Transcriptomes and Proteomes of <i>Phlebotomus tobbi</i> and <i>Phlebotomus sergenti</i> , Vectors of Leishmaniasis. PLoS Neglected Tropical Diseases, 2012, 6, e1660.	1.3	66
7279	Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. PLoS Pathogens, 2012, 8, e1003037.	2.1	595
7280	ProteinHistorian: Tools for the Comparative Analysis of Eukaryote Protein Origin. PLoS Computational Biology, 2012, 8, e1002567.	1.5	89
7281	Regulatory Network Structure as a Dominant Determinant of Transcription Factor Evolutionary Rate. PLoS Computational Biology, 2012, 8, e1002734.	1.5	6
7282	A Quantitative, High-Throughput Reverse Genetic Screen Reveals Novel Connections between Pre-mRNA Splicing and 5' and 3' End Transcript Determinants. PLoS Genetics, 2012, 8, e1002530.	1.5	29
7283	Tcf7 Is an Important Regulator of the Switch of Self-Renewal and Differentiation in a Multipotential Hematopoietic Cell Line. PLoS Genetics, 2012, 8, e1002565.	1.5	88
7284	A Semantic Problem Solving Environment for Integrative Parasite Research: Identification of Intervention Targets for <i>Trypanosoma cruzi</i> . PLoS Neglected Tropical Diseases, 2012, 6, e1458.	1.3	5
7285	Teaching the Fundamentals of Biological Data Integration Using Classroom Games. PLoS Computational Biology, 2012, 8, e1002789.	1.5	21
7286	Systematic Identification of Rhythmic Genes Reveals <i>camk1gb</i> as a New Element in the Circadian Clockwork. PLoS Genetics, 2012, 8, e1003116.	1.5	37
7287	Chapter 12: Human Microbiome Analysis. PLoS Computational Biology, 2012, 8, e1002808.	1.5	408
7288	On the Deep Order-Preserving Submatrix Problem: A Best Effort Approach. IEEE Transactions on Knowledge and Data Engineering, 2012, 24, 309-325.	4.0	19
7289	Linkers of Cell Polarity and Cell Cycle Regulation in the Fission Yeast Protein Interaction Network. PLoS Computational Biology, 2012, 8, e1002732.	1.5	14
7290	AraPath: a knowledgebase for pathway analysis in <i>Arabidopsis</i> . Bioinformatics, 2012, 28, 2291-2292.	1.8	27
7291	Discriminative local subspaces in gene expression data for effective gene function prediction. Bioinformatics, 2012, 28, 2256-2264.	1.8	8
7292	Proteomic Analysis of the Organ of Corti Using Nanoscale Liquid Chromatography Coupled with Tandem Mass Spectrometry. International Journal of Molecular Sciences, 2012, 13, 8171-8188.	1.8	12
7293	Genomic DNA Methylation Changes in NYGGF4-Overexpression 3T3-L1 Adipocytes. International Journal of Molecular Sciences, 2012, 13, 15575-15587.	1.8	6

#	ARTICLE	IF	CITATIONS
7294	Proteomic Analysis of Lamellar Bodies Isolated from Amniotic Fluid: Implications for Function. <i>American Journal of Perinatology</i> , 2012, 29, 419-428.	0.6	2
7295	CvManGO, a method for leveraging computational predictions to improve literature-based Gene Ontology annotations. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas001.	1.4	9
7296	Whole Genome Analysis of <i>Leptospira icterohaemolyticum</i> Provides Insight into Leptospiral Evolution and Pathogenicity. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1853.	1.3	60
7297	Correlation networks visualization. <i>Frontiers in Plant Science</i> , 2012, 3, 240.	1.7	24
7298	Functional and biochemical characterization of soleus muscle in Down syndrome mice: insight into the muscle dysfunction seen in the human condition. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2012, 303, R1251-R1260.	0.9	26
7299	“Guilt by Association” Is the Exception Rather Than the Rule in Gene Networks. <i>PLoS Computational Biology</i> , 2012, 8, e1002444.	1.5	183
7300	Obesity Is Mediated by Differential Aryl Hydrocarbon Receptor Signaling in Mice Fed a Western Diet. <i>Environmental Health Perspectives</i> , 2012, 120, 1252-1259.	2.8	74
7301	Chapter 2: Data-Driven View of Disease Biology. <i>PLoS Computational Biology</i> , 2012, 8, e1002816.	1.5	15
7302	Fitness Landscape Transformation through a Single Amino Acid Change in the Rho Terminator. <i>PLoS Genetics</i> , 2012, 8, e1002744.	1.5	37
7303	Comparison of human cardiac gene expression profiles in paired samples of right atrium and left ventricle collected in vivo. <i>Physiological Genomics</i> , 2012, 44, 89-98.	1.0	43
7304	Fast Inference for the Latent Space Network Model Using a Case-Control Approximate Likelihood. <i>Journal of Computational and Graphical Statistics</i> , 2012, 21, 901-919.	0.9	93
7305	GabiPD “The GABI Primary Database integrates plant proteomic data with gene-centric information. <i>Frontiers in Plant Science</i> , 2012, 3, 154.	1.7	23
7306	Predictive networks: a flexible, open source, web application for integration and analysis of human gene networks. <i>Nucleic Acids Research</i> , 2012, 40, D866-D875.	6.5	28
7307	Transcriptome Analysis of the Oriental River Prawn, <i>Macrobrachium nipponense</i> Using 454 Pyrosequencing for Discovery of Genes and Markers. <i>PLoS ONE</i> , 2012, 7, e39727.	1.1	95
7308	LegumelP: an integrative database for comparative genomics and transcriptomics of model legumes. <i>Nucleic Acids Research</i> , 2012, 40, D1221-D1229.	6.5	91
7309	Evidence for a Contribution of ALA Synthesis to Plastid-To-Nucleus Signaling. <i>Frontiers in Plant Science</i> , 2012, 3, 236.	1.7	41
7310	Functional Analysis of ABP57 Gene by Microarray in Transgenic Rice Plants. <i>Han'guk Yukchong Hakhoe Chi</i> , 2012, 44, 538-546.	0.2	0
7311	Transcriptome Analysis and SSR/SNP Markers Information of the Blunt Snout Bream (<i>Megalobrama</i>) Tj ETQq1 1 0.784314 rgBT/Overl	1.1	175

#	ARTICLE	IF	CITATIONS
7312	Karyotype and DNA-Methylation Responses in Myelodysplastic Syndromes following Treatment with Traditional Chinese Formula Containing Arsenic. Evidence-based Complementary and Alternative Medicine, 2012, 2012, 1-8.	0.5	10
7313	Understanding Dupuytren's Disease Using Systems Biology: A Move Away from Reductionism. Frontiers in Physiology, 2012, 3, 316.	1.3	2
7314	Genome-Wide Characterization of ISR Induced in Arabidopsis thaliana by Trichoderma hamatum T382 Against Botrytis cinerea Infection. Frontiers in Plant Science, 2012, 3, 108.	1.7	209
7315	Systematic Detection of Epistatic Interactions Based on Allele Pair Frequencies. PLoS Genetics, 2012, 8, e1002463.	1.5	15
7316	A defeasible reasoning approach for description logic ontologies. , 2012, , .		2
7317	Protein function prediction using weak-label learning. , 2012, , .		8
7318	Data mining methodologies for pharmacovigilance. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2012, 14, 35-42.	3.2	21
7319	Dysregulation of miR-31 and miR-21 induced by zinc deficiency promotes esophageal cancer. Carcinogenesis, 2012, 33, 1736-1744.	1.3	108
7320	Gene Set Analysis of Survival Following Ovarian Cancer Implicates Macrolide Binding and Intracellular Signaling Genes. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 529-536.	1.1	7
7321	E3Net: A System for Exploring E3-mediated Regulatory Networks of Cellular Functions. Molecular and Cellular Proteomics, 2012, 11, O111.014076.	2.5	29
7322	MetaCrop 2.0: managing and exploring information about crop plant metabolism. Nucleic Acids Research, 2012, 40, D1173-D1177.	6.5	56
7323	PhenoM: a database of morphological phenotypes caused by mutation of essential genes in Saccharomyces cerevisiae. Nucleic Acids Research, 2012, 40, D687-D694.	6.5	13
7324	Coiled-coil networking shapes cell molecular machinery. Molecular Biology of the Cell, 2012, 23, 3911-3922.	0.9	69
7325	Mapping of Chikungunya Virus Interactions with Host Proteins Identified nsP2 as a Highly Connected Viral Component. Journal of Virology, 2012, 86, 3121-3134.	1.5	98
7326	MACIE: exploring the diversity of biochemical reactions. Nucleic Acids Research, 2012, 40, D783-D789.	6.5	73
7327	Draft Genome Sequence of the Novel Agarolytic Bacterium Aquimarina agarilytica ZC1. Journal of Bacteriology, 2012, 194, 2769-2769.	1.0	13
7328	INRICH: interval-based enrichment analysis for genome-wide association studies. Bioinformatics, 2012, 28, 1797-1799.	1.8	218
7329	LocTree2 predicts localization for all domains of life. Bioinformatics, 2012, 28, i458-i465.	1.8	91

#	ARTICLE	IF	CITATIONS
7330	Interactomeâ€“transcriptome integration for predicting distant metastasis in breast cancer. <i>Bioinformatics</i> , 2012, 28, 672-678.	1.8	22
7331	Planteome annotation wiki. , 2012, , .		0
7332	Savant Genome Browser 2: visualization and analysis for population-scale genomics. <i>Nucleic Acids Research</i> , 2012, 40, W615-W621.	6.5	52
7333	The Gene Ontology: enhancements for 2011. <i>Nucleic Acids Research</i> , 2012, 40, D559-D564.	6.5	191
7334	Borrowing strength: a likelihood ratio test for related sparse signals. <i>Bioinformatics</i> , 2012, 28, 1980-1989.	1.8	2
7335	Chitinase-like Proteins are Candidate Biomarkers for Sepsis-induced Acute Kidney Injury. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013094.	2.5	42
7336	Data-driven information retrieval in heterogeneous collections of transcriptomics data links SIM2s to malignant pleural mesothelioma. <i>Bioinformatics</i> , 2012, 28, 246-253.	1.8	13
7337	Discovering the hidden sub-network component in a ranked list of genes or proteins derived from genomic experiments. <i>Nucleic Acids Research</i> , 2012, 40, e158-e158.	6.5	22
7338	CORECLUST: identification of the conserved CRM grammar together with prediction of gene regulation. <i>Nucleic Acids Research</i> , 2012, 40, e93-e93.	6.5	9
7339	OGEE: an online gene essentiality database. <i>Nucleic Acids Research</i> , 2012, 40, D901-D906.	6.5	187
7340	A Mass Spectrometry Proteomics Data Management Platform. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 824-831.	2.5	31
7341	Identification of Novel Type 1 Diabetes Candidate Genes by Integrating Genome-Wide Association Data, Protein-Protein Interactions, and Human Pancreatic Islet Gene Expression. <i>Diabetes</i> , 2012, 61, 954-962.	0.3	105
7342	Deregulation of a Hox Protein Regulatory Network Spanning Prostate Cancer Initiation and Progression. <i>Clinical Cancer Research</i> , 2012, 18, 4291-4302.	3.2	61
7343	Bcl-2â€“Modifying Factor Induces Renal Proximal Tubular Cell Apoptosis in Diabetic Mice. <i>Diabetes</i> , 2012, 61, 474-484.	0.3	48
7344	Tetrahymena genome database Wiki: a community-maintained model organism database. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas007-bas007.	1.4	38
7345	Mining and evaluation of molecular relationships in literature. <i>Bioinformatics</i> , 2012, 28, 709-714.	1.8	7
7346	IntScore: a web tool for confidence scoring of biological interactions. <i>Nucleic Acids Research</i> , 2012, 40, W140-W146.	6.5	51
7347	neXtProt: a knowledge platform for human proteins. <i>Nucleic Acids Research</i> , 2012, 40, D76-D83.	6.5	167

#	ARTICLE	IF	CITATIONS
7348	ViPR: an open bioinformatics database and analysis resource for virology research. <i>Nucleic Acids Research</i> , 2012, 40, D593-D598.	6.5	610
7349	Evolution of 5' Untranslated Region Length and Gene Expression Reprogramming in Yeasts. <i>Molecular Biology and Evolution</i> , 2012, 29, 81-89.	3.5	48
7350	Genome-wide polymorphisms show unexpected targets of natural selection. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 1412-1420.	1.2	47
7351	Implications of functional similarity for gene regulatory interactions. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1625-1636.	1.5	7
7352	A novel method to quantify gene set functional association based on gene ontology. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1063-1072.	1.5	43
7353	An infrastructure for ontology-based information systems in biomedicine: RICORDO case study. <i>Bioinformatics</i> , 2012, 28, 448-450.	1.8	10
7354	Significance analysis and statistical dissection of variably methylated regions. <i>Biostatistics</i> , 2012, 13, 166-178.	0.9	92
7355	Network of Cancer Genes (NCG 3.0): integration and analysis of genetic and network properties of cancer genes. <i>Nucleic Acids Research</i> , 2012, 40, D978-D983.	6.5	38
7356	Comparative Proteomics Reveals a Significant Bias Toward Alternative Protein Isoforms with Conserved Structure and Function. <i>Molecular Biology and Evolution</i> , 2012, 29, 2265-2283.	3.5	71
7357	Effects of β 24 integrin expression on microRNA patterns in breast cancer. <i>Biology Open</i> , 2012, 1, 658-666.	0.6	22
7358	The ChEBI reference database and ontology for biologically relevant chemistry: enhancements for 2013. <i>Nucleic Acids Research</i> , 2012, 41, D456-D463.	6.5	508
7359	Ovarian Kaleidoscope Database: Ten Years and Beyond ¹ . <i>Biology of Reproduction</i> , 2012, 86, 192.	1.2	24
7360	Incomplete Sex Chromosome Dosage Compensation in the Indian Meal Moth, <i>Plodia interpunctella</i> , Based on De Novo Transcriptome Assembly. <i>Genome Biology and Evolution</i> , 2012, 4, 1118-1126.	1.1	64
7361	Inference of modules associated to eQTLs. <i>Nucleic Acids Research</i> , 2012, 40, e98-e98.	6.5	12
7362	One Hand Clapping: detection of condition-specific transcription factor interactions from genome-wide gene activity data. <i>Nucleic Acids Research</i> , 2012, 40, 8883-8892.	6.5	2
7363	GeneDB--an annotation database for pathogens. <i>Nucleic Acids Research</i> , 2012, 40, D98-D108.	6.5	217
7364	Breaking free from the chains of pathway annotation: <i>de novo</i> pathway discovery for the analysis of disease processes. <i>Pharmacogenomics</i> , 2012, 13, 1967-1978.	0.6	6
7365	Manual GO annotation of predictive protein signatures: the InterPro approach to GO curation. Database: the Journal of Biological Databases and Curation, 2012, 2012, bar068-bar068.	1.4	108

#	ARTICLE	IF	CITATIONS
7366	Protein Databases on the Internet. <i>Current Protocols in Molecular Biology</i> , 2012, 97, Unit 19.4..	2.9	6
7367	Relating drug-protein interaction network with drug side effects. <i>Bioinformatics</i> , 2012, 28, i522-i528.	1.8	176
7368	Cell type-specific genomics of <i>Drosophila</i> neurons. <i>Nucleic Acids Research</i> , 2012, 40, 9691-9704.	6.5	138
7369	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2012, 41, D8-D20.	6.5	459
7370	Structural bioinformatics of the human spliceosomal proteome. <i>Nucleic Acids Research</i> , 2012, 40, 7046-7065.	6.5	40
7371	Prioritizing cancer-related key miRNA-target interactions by integrative genomics. <i>Nucleic Acids Research</i> , 2012, 40, 7653-7665.	6.5	30
7372	Manual Gene Ontology annotation workflow at the Mouse Genome Informatics Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas045-bas045.	1.4	19
7373	Event extraction across multiple levels of biological organization. <i>Bioinformatics</i> , 2012, 28, i575-i581.	1.8	107
7374	MoNetFamily: a web server to infer homologous modules and module-module interaction networks in vertebrates. <i>Nucleic Acids Research</i> , 2012, 40, W263-W270.	6.5	15
7375	Graphlet-based edge clustering reveals pathogen-interacting proteins. <i>Bioinformatics</i> , 2012, 28, i480-i486.	1.8	57
7376	On the Role of PDZ Domain-Encoding Genes in <i>Drosophila</i> Border Cell Migration. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1379-1391.	0.8	24
7377	The percentage of bacterial genes on leading versus lagging strands is influenced by multiple balancing forces. <i>Nucleic Acids Research</i> , 2012, 40, 8210-8218.	6.5	41
7378	Xanthusbase after five years expands to become Openmods. <i>Nucleic Acids Research</i> , 2012, 40, D1288-D1294.	6.5	1
7379	Combinatorial control of diverse metabolic and physiological functions by transcriptional regulators of the yeast sulfur assimilation pathway. <i>Molecular Biology of the Cell</i> , 2012, 23, 3008-3024.	0.9	36
7380	Sequences and transcriptional analysis of <i>Coffea arabica</i> var. Caturra and <i>Coffea liberica</i> plant responses to coffee berry borer <i>Hypothenemus hampei</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf50 177 T		
7381	Analysis of Tissue Proteomes of the Gulf Killifish, <i>Fundulus grandis</i> , by 2D Electrophoresis and MALDI-TOF/TOF Mass Spectrometry. <i>Integrative and Comparative Biology</i> , 2012, 52, 626-635.	0.9	7
7382	Transcriptome Analysis Using a High-Density Oligomicroarray under Drought Stress in Various Genotypes of Cassava: An Important Tropical Crop. <i>DNA Research</i> , 2012, 19, 335-345.	1.5	101
7383	NetwoRx: connecting drugs to networks and phenotypes in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2012, 41, D720-D727.	6.5	8

#	ARTICLE	IF	CITATIONS
7384	Biocuration workflows and text mining: overview of the BioCreative 2012 Workshop Track II. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas043-bas043.	1.4	67
7385	EcoGene 3.0. Nucleic Acids Research, 2012, 41, D613-D624.	6.5	180
7386	Role of ARABIDOPSIS A-FIFTEEN in regulating leaf senescence involves response to reactive oxygen species and is dependent on ETHYLENE INSENSITIVE2. Journal of Experimental Botany, 2012, 63, 275-292.	2.4	32
7387	Quantitative Image Analysis of Cellular Heterogeneity in Breast Tumors Complements Genomic Profiling. Science Translational Medicine, 2012, 4, 157ra143.	5.8	356
7388	Establishment of single-cell screening system for the rapid identification of transcriptional modulators involved in direct cell reprogramming. Nucleic Acids Research, 2012, 40, e165-e165.	6.5	10
7389	GONUTS: the Gene Ontology Normal Usage Tracking System. Nucleic Acids Research, 2012, 40, D1262-D1269.	6.5	22
7390	Loss of giant obscurins promotes breast epithelial cell survival through apoptotic resistance. FASEB Journal, 2012, 26, 2764-2775.	0.2	30
7391	Plastids Are Major Regulators of Light Signaling in Arabidopsis. Plant Physiology, 2012, 159, 366-390.	2.3	85
7392	Hyperglycemia and Renin-Dependent Hypertension Synergize to Model Diabetic Nephropathy. Journal of the American Society of Nephrology: JASN, 2012, 23, 405-411.	3.0	40
7393	Poplar Wood Rays Are Involved in Seasonal Remodeling of Tree Physiology. Plant Physiology, 2012, 160, 1515-1529.	2.3	34
7394	When humans are the exception: Cross-species databases at the interface of biological and clinical research. Social Studies of Science, 2012, 42, 214-236.	1.5	41
7395	DNA methylation analyses of urothelial carcinoma reveal distinct epigenetic subtypes and an association between gene copy number and methylation status. Epigenetics, 2012, 7, 858-867.	1.3	44
7396	In Silico Prediction of Adverse Drug Reactions and Toxicities Based on Structural, Biological and Clinical Data. Current Drug Safety, 2012, 7, 225-237.	0.3	1
7397	A Systems Biology Perspective on Rational Design of Peptide Vaccine Against Virus Infections. Current Topics in Medicinal Chemistry, 2012, 12, 1310-1319.	1.0	14
7398	Identification of Common and Distinctive Mechanisms of Resistance to Different Anti-IGF-IR Agents in Ewing's Sarcoma. Molecular Endocrinology, 2012, 26, 1603-1616.	3.7	53
7399	A highly integrated and complex PPARGC1A transcription factor binding network in HepG2 cells. Genome Research, 2012, 22, 1668-1679.	2.4	75
7400	Towards an automatic construction of Contextual Attribute-Value Taxonomies. , 2012, , .		2
7401	A Distinct Smoothed Mutation Causes Severe Cerebellar Developmental Defects and Medulloblastoma in a Novel Transgenic Mouse Model. Molecular and Cellular Biology, 2012, 32, 4104-4115.	1.1	39

#	ARTICLE	IF	CITATIONS
7402	Increased Genome Sampling Reveals a Dynamic Relationship between Gene Duplicability and the Structure of the Primate Protein-Protein Interaction Network. <i>Molecular Biology and Evolution</i> , 2012, 29, 3563-3573.	3.5	7
7403	Discriminating response groups in metabolic and regulatory pathway networks. <i>Bioinformatics</i> , 2012, 28, 947-954.	1.8	1
7404	MAGNET: MicroArray Gene expression and Network Evaluation Toolkit. <i>Nucleic Acids Research</i> , 2012, 40, W152-W156.	6.5	11
7405	Gene Expression Analysis of the Embryonic Subplate. <i>Cerebral Cortex</i> , 2012, 22, 1343-1359.	1.6	83
7406	Gemma: a resource for the reuse, sharing and meta-analysis of expression profiling data. <i>Bioinformatics</i> , 2012, 28, 2272-2273.	1.8	114
7407	Data determination, disambiguation, and referencing in molecular biology. , 2012, , .		0
7408	LINEAR COHERENT BI-CLUSTERING VIA BEAM SEARCHING AND SAMPLE SET CLUSTERING. <i>Discrete Mathematics, Algorithms and Applications</i> , 2012, 04, 1250023.	0.4	2
7409	Identifying multi-layer gene regulatory modules from multi-dimensional genomic data. <i>Bioinformatics</i> , 2012, 28, 2458-2466.	1.8	123
7410	Independent transcriptional reprogramming and apoptosis induction by cisplatin. <i>Cell Cycle</i> , 2012, 11, 3472-3480.	1.3	32
7411	Dissecting Plant Genomes with the PLAZA Comparative Genomics Platform. <i>Plant Physiology</i> , 2012, 158, 590-600.	2.3	238
7412	Targeting the PyMT Oncogene to Diverse Mammary Cell Populations Enhances Tumor Heterogeneity and Generates Rare Breast Cancer Subtypes. <i>Genes and Cancer</i> , 2012, 3, 550-563.	0.6	20
7413	CellOrganizer: Image-Derived Models of Subcellular Organization and Protein Distribution. <i>Methods in Cell Biology</i> , 2012, 110, 179-193.	0.5	37
7414	Article Withdrawn: GNARE: A Grid-based Server for the Analysis of User Submitted Genomes. <i>Nucleic Acids Research</i> , 2012, 40, e177-e177.	6.5	4
7415	The Transcriptome Analysis and Comparison Explorer-T-ACE: a platform-independent, graphical tool to process large RNAseq datasets of non-model organisms. <i>Bioinformatics</i> , 2012, 28, 777-783.	1.8	10
7416	An Insight Into the Sialotranscriptome of <i>Triatoma rubida</i> (Hemiptera: Heteroptera). <i>Journal of Medical Entomology</i> , 2012, 49, 563-572.	0.9	29
7417	Semantic integration of physiology phenotypes with an application to the Cellular Phenotype Ontology. <i>Bioinformatics</i> , 2012, 28, 1783-1789.	1.8	22
7418	Efficient regression testing of ontology-driven systems. , 2012, , .		6
7419	Transductive multi-label ensemble classification for protein function prediction. , 2012, , .		34

#	ARTICLE	IF	CITATIONS
7420	Nesting the context for pervasive robotics. , 2012, , .		0
7421	Supervised logistic principal component analysis for pathway based genome-wide association studies. , 2012, , .		3
7422	Inferring novel associations between SNP sets and gene sets in eQTL study using sparse graphical model. , 2012, , .		6
7423	Extraction and analysis of the structure of labels in biomedical ontologies. , 2012, , .		4
7424	Investigating the Contribution of Common Genetic Variants to the Risk and Pathogenesis of ADHD. American Journal of Psychiatry, 2012, 169, 186-194.	4.0	174
7425	CHROMATRA: a Galaxy tool for visualizing genome-wide chromatin signatures. Bioinformatics, 2012, 28, 717-718.	1.8	14
7426	IMP: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. Nucleic Acids Research, 2012, 40, W484-W490.	6.5	105
7427	Gene3D: a domain-based resource for comparative genomics, functional annotation and protein network analysis. Nucleic Acids Research, 2012, 40, D465-D471.	6.5	98
7428	Autotaxin and Its Product Lysophosphatidic Acid Suppress Brown Adipose Differentiation and Promote Diet-Induced Obesity in Mice. Molecular Endocrinology, 2012, 26, 786-797.	3.7	59
7429	Analysis of microRNA expression in organ of Corti in neonatal and adult rats. Journal of Otology, 2012, 7, 4-8.	0.4	0
7430	Comparative study of Trichoderma gene expression in interactions with tomato plants using high-density oligonucleotide microarrays. Microbiology (United Kingdom), 2012, 158, 119-128.	0.7	57
7431	Drastic expression change of transposon-derived piRNA-like RNAs and microRNAs in early stages of chicken embryos implies a role in gastrulation. RNA Biology, 2012, 9, 212-227.	1.5	39
7432	CTGR-Span: Efficient mining of cross-timepoint gene regulation sequential patterns from microarray datasets. , 2012, , .		0
7433	Gene Ontology Annotations and Resources. Nucleic Acids Research, 2012, 41, D530-D535.	6.5	456
7434	Algorithm to Identify Frequent Coupled Modules from Two-Layered Network Series: Application to Study Transcription and Splicing Coupling. Journal of Computational Biology, 2012, 19, 710-730.	0.8	15
7435	Three-dimensional reconstruction of protein networks provides insight into human genetic disease. Nature Biotechnology, 2012, 30, 159-164.	9.4	378
7436	DBGSA: a novel method of distance-based gene set analysis. Journal of Human Genetics, 2012, 57, 642-653.	1.1	4
7437	Incorporating semantic similarity into clustering process for identifying protein complexes from Affinity Purification/Mass Spectrometry data. , 2012, , .		0

#	ARTICLE	IF	CITATIONS
7438	Deciphering a global network of functionally associated post-translational modifications. <i>Molecular Systems Biology</i> , 2012, 8, 599.	3.2	216
7439	nEASE: a method for gene ontology subclassification of high-throughput gene expression data. <i>Bioinformatics</i> , 2012, 28, 726-728.	1.8	6
7440	Improved Feature Selection by Incorporating Gene Similarity Into the LASSO. , 2012, , .		1
7441	Exploration of Cellular Relationships from Characteristically Expressed Genes by Partial Canonical Correlation Analysis. , 2012, , .		0
7442	A Genome Sequence Resource for the Aye-Aye (<i>Daubentonia madagascariensis</i>), a Nocturnal Lemur from Madagascar. <i>Genome Biology and Evolution</i> , 2012, 4, 126-135.	1.1	59
7443	Ontologies as integrative tools for plant science. <i>American Journal of Botany</i> , 2012, 99, 1263-1275.	0.8	79
7444	Using expression data to help pathway curation. , 2012, , .		2
7445	Functional genomic analysis unravels a metabolic-inflammatory interplay in adrenoleukodystrophy. <i>Human Molecular Genetics</i> , 2012, 21, 1062-1077.	1.4	62
7446	GO-function: deriving biologically relevant functions from statistically significant functions. <i>Briefings in Bioinformatics</i> , 2012, 13, 216-227.	3.2	71
7447	Identification and analysis of gene clusters in biological data. , 2012, , .		0
7448	MaTSE: The microarray time-series explorer. , 2012, , .		9
7449	Hierarchical modular structure in gene coexpression networks. , 2012, , .		2
7450	Reverse Engineering and Analysis of Genome-Wide Gene Regulatory Networks from Gene Expression Profiles Using High-Performance Computing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 668-678.	1.9	13
7451	A Framework for Incorporating Functional Interrelationships into Protein Function Prediction Algorithms. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 740-753.	1.9	37
7452	A comparative transcriptomic study of an allotetraploid and its diploid progenitors illustrates the unique advantages and challenges of RNA-seq in plant species. <i>American Journal of Botany</i> , 2012, 99, 383-396.	0.8	80
7453	Global transcriptional profiling reveals similarities and differences between human stem cell-derived cardiomyocyte clusters and heart tissue. <i>Physiological Genomics</i> , 2012, 44, 245-258.	1.0	65
7454	GeneCodis3: a non-redundant and modular enrichment analysis tool for functional genomics. <i>Nucleic Acids Research</i> , 2012, 40, W478-W483.	6.5	515
7455	Incorporating Gene Significance in the Impact Analysis of Signaling Pathways. , 2012, , .		16

#	ARTICLE	IF	CITATIONS
7456	A VERSION MANAGEMENT FRAMEWORK FOR RDF TRIPLE STORES. <i>International Journal of Software Engineering and Knowledge Engineering</i> , 2012, 22, 85-106.	0.6	30
7457	Epigenetic remodelling of gene expression profiles of neoplastic and normal tissues: immunotherapeutic implications. <i>British Journal of Cancer</i> , 2012, 107, 1116-1124.	2.9	20
7458	Multi-locus genome-wide association analysis supports the role of glutamatergic synaptic transmission in the etiology of major depressive disorder. <i>Translational Psychiatry</i> , 2012, 2, e184-e184.	2.4	77
7459	Gene Expression Profile Changes After Short-activating RNA-mediated Induction of Endogenous Pluripotency Factors in Human Mesenchymal Stem Cells. <i>Molecular Therapy - Nucleic Acids</i> , 2012, 1, e35.	2.3	28
7460	INTERFEROME v2.0: an updated database of annotated interferon-regulated genes. <i>Nucleic Acids Research</i> , 2012, 41, D1040-D1046.	6.5	732
7461	Robustness and accuracy of functional modules in integrated network analysis. <i>Bioinformatics</i> , 2012, 28, 1887-1894.	1.8	29
7462	Cell-type-specific nuclei purification from whole animals for genome-wide expression and chromatin profiling. <i>Genome Research</i> , 2012, 22, 766-777.	2.4	112
7463	Phytozome: a comparative platform for green plant genomics. <i>Nucleic Acids Research</i> , 2012, 40, D1178-D1186.	6.5	4,204
7464	Bioinformatics advances in saliva diagnostics. <i>International Journal of Oral Science</i> , 2012, 4, 85-87.	3.6	34
7465	Improving GO semantic similarity measures by exploring the ontology beneath the terms and modelling uncertainty. <i>Bioinformatics</i> , 2012, 28, 1383-1389.	1.8	73
7466	Identification and Characterization of Novel Immunomodulatory Bursal-derived Pentapeptide-II (BPP-II). <i>Journal of Biological Chemistry</i> , 2012, 287, 3798-3807.	1.6	11
7467	Identification and Characterization of Lineage-Specific Highly Conserved Noncoding Sequences in Mammalian Genomes. <i>Genome Biology and Evolution</i> , 2012, 4, 641-657.	1.1	27
7468	Genomic characterization of the <i>Bacillus cereus</i> sensu lato species: Backdrop to the evolution of <i>Bacillus anthracis</i> . <i>Genome Research</i> , 2012, 22, 1512-1524.	2.4	148
7469	Differentially expressed plasma microRNAs in premature ovarian failure patients and the potential regulatory function of mir-23a in granulosa cell apoptosis. <i>Reproduction</i> , 2012, 144, 235-244.	1.1	148
7470	An Insight into the Sialotranscriptome of <i>Triatoma matogrossensis</i> , a Kissing Bug Associated with Fogo Selvagem in South America. <i>American Journal of Tropical Medicine and Hygiene</i> , 2012, 86, 1005-1014.	0.6	38
7471	BIPS: BIANA Interolog Prediction Server. A tool for protein-protein interaction inference. <i>Nucleic Acids Research</i> , 2012, 40, W147-W151.	6.5	57
7472	Vitrification at the pre-antral stage transiently alters inner mitochondrial membrane potential but proteome of in vitro grown and matured mouse oocytes appears unaffected. <i>Human Reproduction</i> , 2012, 27, 1096-1111.	0.4	37
7473	TOPAC: ALIGNMENT OF GENE REGULATORY NETWORKS USING TOPOLOGY-AWARE COLORING. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1240001.	0.3	11

#	ARTICLE	IF	CITATIONS
7474	Sequence and structural analyses of nuclear export signals in the NESdb database. <i>Molecular Biology of the Cell</i> , 2012, 23, 3677-3693.	0.9	123
7475	High Expression Hampers Horizontal Gene Transfer. <i>Genome Biology and Evolution</i> , 2012, 4, 523-532.	1.1	95
7476	Changes in Gene Expression Associated with Reproductive Maturation in Wild Female Baboons. <i>Genome Biology and Evolution</i> , 2012, 4, 102-109.	1.1	9
7477	Identification and Properties of 1,119 Candidate LincRNA Loci in the <i>Drosophila melanogaster</i> Genome. <i>Genome Biology and Evolution</i> , 2012, 4, 427-442.	1.1	217
7478	Genes Involved in the Evolution of Herbivory by a Leaf-Mining, <i>Drosophilid</i> Fly. <i>Genome Biology and Evolution</i> , 2012, 4, 900-916.	1.1	57
7479	Dual transcriptional activator and repressor roles of TBX20 regulate adult cardiac structure and function. <i>Human Molecular Genetics</i> , 2012, 21, 2194-2204.	1.4	75
7480	SP Transcription Factor Paralogs and DNA-Binding Sites Coevolve and Adaptively Converge in Mammals and Birds. <i>Genome Biology and Evolution</i> , 2012, 4, 1102-1117.	1.1	8
7481	Increased Immune Gene Expression and Immune Cell Infiltration in High-Grade Astrocytoma Distinguish Long-Term from Short-Term Survivors. <i>Journal of Immunology</i> , 2012, 189, 1920-1927.	0.4	62
7482	<i>Caenorhabditis elegans</i> RNA-processing Protein TDP-1 Regulates Protein Homeostasis and Life Span. <i>Journal of Biological Chemistry</i> , 2012, 287, 8371-8382.	1.6	58
7483	Building an HIV data mashup using Bio2RDF. <i>Briefings in Bioinformatics</i> , 2012, 13, 98-106.	3.2	15
7484	Transcription Factors Are Targeted by Differentially Expressed miRNAs in Primates. <i>Genome Biology and Evolution</i> , 2012, 4, 552-564.	1.1	30
7485	Discovery of multi-dimensional modules by integrative analysis of cancer genomic data. <i>Nucleic Acids Research</i> , 2012, 40, 9379-9391.	6.5	305
7486	PlantNATsDB: a comprehensive database of plant natural antisense transcripts. <i>Nucleic Acids Research</i> , 2012, 40, D1187-D1193.	6.5	76
7487	iTRAQ Quantitative Proteomics in the Analysis of Tears in Dry Eye Patients. , 2012, 53, 5052.		112
7488	Congenital diaphragmatic hernia candidate genes derived from embryonic transcriptomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2978-2983.	3.3	78
7489	NOT THAT RIGID MIDGETS AND NOT SO FLEXIBLE GIANTS: ON THE ABUNDANCE AND ROLES OF INTRINSIC DISORDER IN SHORT AND LONG PROTEINS. <i>Journal of Biological Systems</i> , 2012, 20, 471-511.	0.5	19
7490	Molecular Pathways and Crosstalk Characterizing the Cardiorenal Syndrome. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 105-112.	1.0	18
7491	Techniques to cope with missing data in hostâ€‘pathogen protein interaction prediction. <i>Bioinformatics</i> , 2012, 28, i466-i472.	1.8	36

#	ARTICLE	IF	CITATIONS
7492	Never-ending learning principles in gene ontology classification using genetic algorithms. , 2012, , .		3
7493	Extending ontologies by finding siblings using set expansion techniques. <i>Bioinformatics</i> , 2012, 28, i292-i300.	1.8	10
7494	A non-parametric Bayesian clustering for gene expression data. , 2012, , .		0
7495	A modified QT-clustering algorithm over Gene Expression data. , 2012, , .		1
7496	DBETH: A Database of Bacterial Exotoxins for Human. <i>Nucleic Acids Research</i> , 2012, 40, D615-D620.	6.5	53
7497	De Novo Sequencing and Characterization of the Floral Transcriptome of <i>Dendrocalamus latiflorus</i> (Poaceae: Bambusoideae). <i>PLoS ONE</i> , 2012, 7, e42082.	1.1	111
7498	PathVar: analysis of gene and protein expression variance in cellular pathways using microarray data. <i>Bioinformatics</i> , 2012, 28, 446-447.	1.8	11
7499	Activation of the Carbon Concentrating Mechanism by CO ₂ Deprivation Coincides with Massive Transcriptional Restructuring in <i>Chlamydomonas reinhardtii</i> . <i>Plant Cell</i> , 2012, 24, 1860-1875.	3.1	121
7500	Genetic variation in radiation-induced cell death. <i>Genome Research</i> , 2012, 22, 332-339.	2.4	33
7501	Efficient Computational Prediction and Scoring of Human Protein-Protein Interactions Using a Novel Gene Expression Programming Methodology. <i>Communications in Computer and Information Science</i> , 2012, , 472-481.	0.4	1
7502	DOG4DAG. , 2011, , .		9
7503	Identification of Genomic Targets of Transcription Factor Aebp1 and its role in Survival of Glioma Cells. <i>Molecular Cancer Research</i> , 2012, 10, 1039-1051.	1.5	37
7504	BEYOND COMPARING MEANS: THE USEFULNESS OF ANALYZING INTERINDIVIDUAL VARIATION IN GENE EXPRESSION FOR IDENTIFYING GENES ASSOCIATED WITH CANCER DEVELOPMENT. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1241013.	0.3	11
7505	The Signature of Maternal Rearing in the Methylome in Rhesus Macaque Prefrontal Cortex and T Cells. <i>Journal of Neuroscience</i> , 2012, 32, 15626-15642.	1.7	340
7506	EcoliWiki: a wiki-based community resource for <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2012, 40, D1270-D1277.	6.5	27
7507	The combination of a genome-wide association study of lymphocyte count and analysis of gene expression data reveals novel asthma candidate genes. <i>Human Molecular Genetics</i> , 2012, 21, 2111-2123.	1.4	46
7508	Proteome-wide Detection of Abl1 SH3-binding Peptides by Integrating Computational Prediction and Peptide Microarray. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.010389.	2.5	24
7509	Optimal timepoint sampling in high-throughput gene expression experiments. <i>Bioinformatics</i> , 2012, 28, 2773-2781.	1.8	11

#	ARTICLE	IF	CITATIONS
7510	PomBase: a comprehensive online resource for fission yeast. <i>Nucleic Acids Research</i> , 2012, 40, D695-D699.	6.5	288
7511	Resistance exercise training influences skeletal muscle immune activation: a microarray analysis. <i>Journal of Applied Physiology</i> , 2012, 112, 443-453.	1.2	79
7512	Complete genome sequence of <i>Liberibacter crescens</i> BT-1. <i>Standards in Genomic Sciences</i> , 2012, 7, 271-283.	1.5	96
7513	Mining Gene Ontology Data with AGENDA. <i>Bioinformatics and Biology Insights</i> , 2012, 6, BBI.S9101.	1.0	0
7514	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
7515	LCGbase: A Comprehensive Database for Lineage-Based Co-regulated Genes. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S8540.	0.6	7
7516	EvoluCode: Evolutionary Barcodes as a Unifying Framework for Multilevel Evolutionary Data. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S8814.	0.6	4
7517	Doxorubicin and NRG-1/erbB4-Deficiency Affect Gene Expression Profile: Involving Protein Homeostasis in Mouse. <i>ISRN Cardiology</i> , 2012, 2012, 1-11.	1.6	8
7518	Cis-regulatory properties of medaka synexpression groups. <i>Development (Cambridge)</i> , 2012, 139, 917-928.	1.2	9
7519	Analysis of <i>Cryptococcus neoformans</i> Sexual Development Reveals Rewiring of the Pheromone-Response Network by a Change in Transcription Factor Identity. <i>Genetics</i> , 2012, 191, 435-449.	1.2	27
7520	An Insight into the Sialomes of Bloodsucking Heteroptera. <i>Psyche: Journal of Entomology</i> , 2012, 2012, 1-16.	0.4	16
7521	PASSIOMA: Exploring Expressed Sequence Tags during Flower Development in <i>Passiflora</i> spp.. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-11.	2.0	18
7522	Identification and Functional Annotation of Genome-Wide ER-Regulated Genes in Breast Cancer Based on ChIP-Seq Data. <i>Computational and Mathematical Methods in Medicine</i> , 2012, 2012, 1-10.	0.7	8
7523	DNA in 3R: Repair, Replication, and Recombination. <i>Molecular Biology International</i> , 2012, 2012, 1-1.	1.7	2
7524	YB-1, the E2F Pathway, and Regulation of Tumor Cell Growth. <i>Journal of the National Cancer Institute</i> , 2012, 104, 133-146.	3.0	102
7525	ADHDgene: a genetic database for attention deficit hyperactivity disorder. <i>Nucleic Acids Research</i> , 2012, 40, D1003-D1009.	6.5	62
7526	Predicting and Scoring Links in Anatomical Ontology Mapping. <i>Biomath</i> , 2012, 1, .	0.3	1
7527	Mining the Unknown: A Systems Approach to Metabolite Identification Combining Genetic and Metabolic Information. <i>PLoS Genetics</i> , 2012, 8, e1003005.	1.5	170

#	ARTICLE	IF	CITATIONS
7528	Genome sequence of the moderately thermophilic, amino-acid-degrading and sulfur-reducing bacterium <i>Thermovirga lienii</i> type strain (Cas60314T). <i>Standards in Genomic Sciences</i> , 2012, 6, 230-239.	1.5	26
7529	Genomic Analysis of the Hydrocarbon-Producing, Cellulolytic, Endophytic Fungus <i>Ascocoryne sarcoides</i> . <i>PLoS Genetics</i> , 2012, 8, e1002558.	1.5	76
7530	A dictionary-based approach to normalizing gene names in one domain of knowledge from the biomedical literature. <i>Journal of Documentation</i> , 2012, 68, 5-30.	0.9	13
7531	Phosphoproteome of <i>Pristionchus pacificus</i> Provides Insights into Architecture of Signaling Networks in Nematode Models. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1631-1639.	2.5	30
7532	Identification and Comparative Analysis of ncRNAs in Human, Mouse and Zebrafish Indicate a Conserved Role in Regulation of Genes Expressed in Brain. <i>PLoS ONE</i> , 2012, 7, e52275.	1.1	29
7533	MEDIC: a practical disease vocabulary used at the Comparative Toxicogenomics Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bar065-bar065.	1.4	136
7534	Identifying functional modules in interaction networks through overlapping Markov clustering. <i>Bioinformatics</i> , 2012, 28, i473-i479.	1.8	93
7535	Roundup 2.0: enabling comparative genomics for over 1800 genomes. <i>Bioinformatics</i> , 2012, 28, 715-716.	1.8	38
7536	ASGARD: an open-access database of annotated transcriptomes for emerging model arthropod species. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas048-bas048.	1.4	21
7537	Abundant Gene-by-Environment Interactions in Gene Expression Reaction Norms to Copper within <i>Saccharomyces cerevisiae</i> . <i>Genome Biology and Evolution</i> , 2012, 4, 1061-1079.	1.1	37
7538	Combination of Chemical Genetics and Phosphoproteomics for Kinase Signaling Analysis Enables Confident Identification of Cellular Downstream Targets. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.012351.	2.5	50
7539	Unravelling the complex trait of seed quality: using natural variation through a combination of physiology, genetics and -omics technologies. <i>Seed Science Research</i> , 2012, 22, S45-S52.	0.8	9
7540	Hsp110 is required for spindle length control. <i>Journal of Cell Biology</i> , 2012, 198, 623-636.	2.3	19
7541	Prediction and analysis of nucleotide-binding residues using sequence and sequence-derived structural descriptors. <i>Bioinformatics</i> , 2012, 28, 331-341.	1.8	106
7542	Quantifying the white blood cell transcriptome as an accessible window to the multiorgan transcriptome. <i>Bioinformatics</i> , 2012, 28, 905-905.	1.8	22
7543	Bayesian assignment of gene ontology terms to gene expression experiments. <i>Bioinformatics</i> , 2012, 28, i603-i610.	1.8	5
7544	Transcriptome Analysis of a North American Songbird, <i>Melospiza melodia</i> . <i>DNA Research</i> , 2012, 19, 325-333.	1.5	16
7545	A Machine Learning Approach To Identify Hydrogenosomal Proteins in <i>Trichomonas vaginalis</i> . <i>Eukaryotic Cell</i> , 2012, 11, 217-228.	3.4	24

#	ARTICLE	IF	CITATIONS
7546	Evolutionary rate covariation reveals shared functionality and coexpression of genes. <i>Genome Research</i> , 2012, 22, 714-720.	2.4	89
7547	FlyBase 101 - the basics of navigating FlyBase. <i>Nucleic Acids Research</i> , 2012, 40, D706-D714.	6.5	337
7548	Comparative interactomics with Funcoup 2.0. <i>Nucleic Acids Research</i> , 2012, 40, D821-D828.	6.5	49
7549	PhosphoSitePlus: a comprehensive resource for investigating the structure and function of experimentally determined post-translational modifications in man and mouse. <i>Nucleic Acids Research</i> , 2012, 40, D261-D270.	6.5	1,388
7550	Identification of high-confidence somatic mutations in whole genome sequence of formalin-fixed breast cancer specimens. <i>Nucleic Acids Research</i> , 2012, 40, e107-e107.	6.5	78
7551	Genome-Wide Mapping of Cystitis Due to <i>Streptococcus agalactiae</i> and <i>Escherichia coli</i> in Mice Identifies a Unique Bladder Transcriptome That Signifies Pathogen-Specific Antimicrobial Defense against Urinary Tract Infection. <i>Infection and Immunity</i> , 2012, 80, 3145-3160.	1.0	46
7552	Regulation of conditional gene expression by coupled transcription repression and RNA degradation. <i>Nucleic Acids Research</i> , 2012, 40, 871-883.	6.5	11
7553	Identifying aberrant pathways through integrated analysis of knowledge in pharmacogenomics. <i>Bioinformatics</i> , 2012, 28, 2169-2175.	1.8	39
7554	Upgraded genomic information of <i>Jatropha curcas</i> L.. <i>Plant Biotechnology</i> , 2012, 29, 123-130.	0.5	74
7555	Considerations for creating and annotating the budding yeast Genome Map at SGD: a progress report. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bar057-bar057.	1.4	10
7556	Candidate Pathway Based Analysis for Cleft Lip with or without Cleft Palate. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, .	0.2	7
7557	The Genome Portal of the Department of Energy Joint Genome Institute. <i>Nucleic Acids Research</i> , 2012, 40, D26-D32.	6.5	439
7558	A Model-Based Analysis to Infer the Functional Content of a Gene List. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, .	0.2	13
7559	IMID: integrated molecular interaction database. <i>Bioinformatics</i> , 2012, 28, 747-749.	1.8	15
7560	Prediction of essential proteins using topological properties in GO-pruned PPI network based on machine learning methods. <i>Tsinghua Science and Technology</i> , 2012, 17, 645-658.	4.1	42
7561	An extension of the Plant Ontology project supporting wood anatomy and development research. <i>IAWA Journal</i> , 2012, 33, 113-117.	2.7	8
7562	VIROME: a standard operating procedure for analysis of viral metagenome sequences. <i>Standards in Genomic Sciences</i> , 2012, 6, 427-439.	1.5	169
7563	Genome sequence of the orange-pigmented seawater bacterium <i>Owenweeksia hongkongensis</i> type strain (UST20020801T). <i>Standards in Genomic Sciences</i> , 2012, 7, 120-130.	1.5	11

#	ARTICLE	IF	CITATIONS
7564	Identification of Autophagosome-associated Proteins and Regulators by Quantitative Proteomic Analysis and Genetic Screens. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014035.	2.5	118
7565	A single source <i>k</i> -shortest paths algorithm to infer regulatory pathways in a gene network. <i>Bioinformatics</i> , 2012, 28, i49-i58.	1.8	31
7566	Chaperones Divide Yeast Proteins into Classes of Expression Level and Evolutionary Rate. <i>Genome Biology and Evolution</i> , 2012, 4, 618-625.	1.1	22
7567	Proteomic analysis of grapevine resistance induced by <i>Trichoderma harzianum</i> T39 reveals specific defence pathways activated against downy mildew. <i>Journal of Experimental Botany</i> , 2012, 63, 6237-6251.	2.4	101
7568	Transcriptome-wide mining of the differentially expressed transcripts for natural variation of floral organ size in <i>Physalis philadelphica</i> . <i>Journal of Experimental Botany</i> , 2012, 63, 6457-6465.	2.4	9
7569	DNA polymerase β variant Ile260Met generates global gene expression changes related to cellular transformation. <i>Mutagenesis</i> , 2012, 27, 683-691.	1.0	5
7570	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	6.5	921
7571	Comparative Analysis of Clustering and Biclustering Algorithms for Grouping of Genes: Co-Function and Co-Regulation. <i>Current Bioinformatics</i> , 2012, 7, 63-76.	0.7	4
7572	Visualization and analysis of 3D gene expression patterns in zebrafish using web services. <i>Proceedings of SPIE</i> , 2012, , .	0.8	0
7573	Complete genome sequence of the moderately thermophilic mineral-sulfide-oxidizing firmicute <i>Sulfobacillus acidophilus</i> type strain (NALT). <i>Standards in Genomic Sciences</i> , 2012, 6, 293-303.	1.5	23
7574	Visualization of mappings between the gene ontology and cluster trees. , 2012, , .		2
7575	Complete genome sequence of the termite hindgut bacterium <i>Spirochaeta coccoides</i> type strain (SPN1T), reclassification in the genus <i>Sphaerochaeta</i> as <i>Sphaerochaeta coccoides</i> comb. nov. and emendations of the family Spirochaetaceae and the genus <i>Sphaerochaeta</i> . <i>Standards in Genomic Sciences</i> , 2012, 6, 194-209.	1.5	58
7576	Let-7a inhibits proliferation and induces apoptosis by targeting EZH2 in nasopharyngeal carcinoma cells. <i>Oncology Reports</i> , 2012, 28, 2101-2106.	1.2	30
7577	454-Pyrosequencing of the Transcriptome in Leaf and Flower Buds of Japanese Apricot (<i>Prunus mume</i>) Tj ETQq1 1 0.784314 rgBT /Over 239-250.	0.8	29
7579	Mitochondrial Dysfunction and Immune Activation are Detectable in Early Alzheimer's Disease Blood. <i>Journal of Alzheimer's Disease</i> , 2012, 30, 685-710.	1.2	141
7580	Permanent draft genome sequence of the gliding predator <i>Saprospira grandis</i> strain Sa g1 (= HR1). <i>Standards in Genomic Sciences</i> , 2012, 6, 210-219.	1.5	3
7581	Expression Profile of Early Estradiol-responsive Genes in Cynomolgus Macaque Liver: Implications for Drug-metabolizing Enzymes. <i>Drug Metabolism and Pharmacokinetics</i> , 2012, 27, 451-455.	1.1	1
7582	Expression Profile of Hepatic Genes in Cynomolgus Macaques Bred in Cambodia, China, and Indonesia: Implications for Cytochrome P450 Genes. <i>Drug Metabolism and Pharmacokinetics</i> , 2012, 27, 307-316.	1.1	12

#	ARTICLE	IF	CITATIONS
7583	A Bayesian analysis of the chromosome architecture of human disorders by integrating reductionist data. <i>Scientific Reports</i> , 2012, 2, 513.	1.6	0
7584	GenomicTools: an open source platform for developing high-throughput analytics in genomics. , 2012, , 189-220.		0
7585	Complex-disease networks of trait-associated single-nucleotide polymorphisms (SNPs) unveiled by information theory. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2012, 19, 295-305.	2.2	42
7586	Complete genome sequence of <i>Paenibacillus</i> sp. strain JDR-2. <i>Standards in Genomic Sciences</i> , 2012, 6, 1-10.	1.5	15
7587	Complete genome sequence of the melanogenic marine bacterium <i>Marinomonas mediterranea</i> type strain (MMB-1T).. <i>Standards in Genomic Sciences</i> , 2012, 6, 63-73.	1.5	21
7588	Complete genome sequence of <i>Treponema pallidum</i> strain DAL-1. <i>Standards in Genomic Sciences</i> , 2012, 7, 12-21.	1.5	37
7589	Genome sequence of the soil bacterium <i>Saccharomonospora azurea</i> type strain (NA-128T). <i>Standards in Genomic Sciences</i> , 2012, 6, 220-229.	1.5	13
7590	Complete genome sequence of the facultatively anaerobic, appendaged bacterium <i>Muricauda ruestringensis</i> type strain (B1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 185-193.	1.5	10
7591	Generation and analysis of expressed sequence tags in the extreme large genomes <i>Lilium</i> and <i>Tulipa</i> . <i>BMC Genomics</i> , 2012, 13, 640.	1.2	62
7592	Ethnic variability in the allelic distribution of pharmacogenes between Korean and other populations. <i>Pharmacogenetics and Genomics</i> , 2012, 22, 829-836.	0.7	9
7593	Complete genome sequence of <i>Dehalogenimonas lykanthroporepellens</i> type strain (BL-DC-9T) and comparison to "Dehalococcoides" strains. <i>Standards in Genomic Sciences</i> , 2012, 6, 251-264.	1.5	51
7594	Complete genome sequence of <i>Oscillibacter valericigenes</i> Sjm18-20T (=NBRC 101213T). <i>Standards in Genomic Sciences</i> , 2012, 6, 406-414.	1.5	36
7595	Non-contiguous finished genome sequence and description of <i>Paenibacillus senegalensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2012, 7, 70-81.	1.5	66
7596	Genome sequence of strain HIMB624, a cultured representative from the OM43 clade of marine Betaproteobacteria. <i>Standards in Genomic Sciences</i> , 2012, 6, 11-20.	1.5	55
7597	Complete genome sequence of <i>Polynucleobacter necessarius</i> subsp. <i>asymbioticus</i> type strain (QLW-P1DMWA-1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 74-83.	1.5	33
7598	Non-contiguous finished genome sequence and description of <i>Anaerococcus senegalensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2012, 6, 116-125.	1.5	106
7599	Complete genome sequence of the aerobic, heterotroph <i>Marinithermus hydrothermalis</i> type strain (T1T) from a deep-sea hydrothermal vent chimney. <i>Standards in Genomic Sciences</i> , 2012, 6, 21-30.	1.5	8
7600	Complete genome sequence of the aquatic bacterium <i>Runella slithyformis</i> type strain (LSU 4T). <i>Standards in Genomic Sciences</i> , 2012, 6, 145-154.	1.5	24

#	ARTICLE	IF	CITATIONS
7601	Complete Genome Sequence of <i>Paenibacillus</i> strain Y4.12MC10, a Novel <i>Paenibacillus lautus</i> strain Isolated from Obsidian Hot Spring in Yellowstone National Park. <i>Standards in Genomic Sciences</i> , 2012, 6, 381-400.	1.5	32
7602	Genome sequence and description of <i>Alistipes senegalensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2012, 6, 304-314.	1.5	61
7603	Complete genome sequence of <i>Pyrobaculum ognuniense</i> . <i>Standards in Genomic Sciences</i> , 2012, 6, 336-345.	1.5	10
7604	Genome sequence of the ocean sediment bacterium <i>Saccharomonospora marina</i> type strain (XMU15T). <i>Standards in Genomic Sciences</i> , 2012, 6, 265-275.	1.5	5
7605	Complete genome sequence of the thermophilic sulfate-reducing ocean bacterium <i>Thermodesulfator indicus</i> type strain (CIR29812T). <i>Standards in Genomic Sciences</i> , 2012, 6, 155-164.	1.5	14
7606	Non-contiguous finished genome sequence and description of <i>Alistipes timonensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2012, 6, 315-324.	1.5	89
7607	Complete genome sequence of <i>Thauera aminoaromatica</i> strain MZ1T. <i>Standards in Genomic Sciences</i> , 2012, 6, 325-335.	1.5	53
7608	Complete genome sequence of <i>Serratia plymuthica</i> strain AS12. <i>Standards in Genomic Sciences</i> , 2012, 6, 165-173.	1.5	19
7609	Non-contiguous finished genome sequence and description of <i>Anaerococcus vaginalis</i> . <i>Standards in Genomic Sciences</i> , 2012, 6, 356-365.	1.5	11
7610	Genome sequence of the homoacetogenic bacterium <i>Holophaga foetida</i> type strain (TMBS4T). <i>Standards in Genomic Sciences</i> , 2012, 6, 174-184.	1.5	26
7611	Complete genome sequence of the orange-red pigmented, radioresistant <i>Deinococcus proteolyticus</i> type strain (MRPT). <i>Standards in Genomic Sciences</i> , 2012, 6, 240-250.	1.5	14
7612	Non-contiguous finished genome sequence and description of <i>Clostridium senegalense</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2012, 6, 401-410.	1.5	70
7613	Non contiguous-finished genome sequence and description of <i>Bacillus timonensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2012, 6, 346-355.	1.5	70
7614	Complete genome sequence of <i>Thermovibrio ammonificans</i> HB-1T, a thermophilic, chemolithoautotrophic bacterium isolated from a deep-sea hydrothermal vent. <i>Standards in Genomic Sciences</i> , 2012, 7, 82-90.	1.5	11
7615	Non contiguous-finished genome sequence and description of <i>Peptoniphilus timonensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2012, 7, 1-11.	1.5	93
7616	Complete genome sequence of the plant-associated <i>Serratia plymuthica</i> strain AS13. <i>Standards in Genomic Sciences</i> , 2012, 7, 22-30.	1.5	22
7617	Complete genome sequence of <i>Marinomonas posidonica</i> type strain (IVIA-Po-181T). <i>Standards in Genomic Sciences</i> , 2012, 7, 31-43.	1.5	10
7618	Complete genome sequence of <i>Syntrophobacter fumaroxidans</i> strain (MPOBT). <i>Standards in Genomic Sciences</i> , 2012, 7, 91-106.	1.5	55

#	ARTICLE	IF	CITATIONS
7619	Complete genome sequence of <i>Corynebacterium pseudotuberculosis</i> biovar ovis strain P54B96 isolated from antelope in South Africa obtained by rapid next generation sequencing technology. Standards in Genomic Sciences, 2012, 7, 189-199.	1.5	8
7620	Non-contiguous finished genome sequence and description of <i>Herbaspirillum massiliense</i> sp. nov.. Standards in Genomic Sciences, 2012, 7, 1-14.	1.5	70
7621	Genome sequence of the flexirubin-pigmented soil bacterium <i>Niabella soli</i> type strain (JS13-8T). Standards in Genomic Sciences, 2012, 7, 210-220.	1.5	2
7622	Non-contiguous finished genome sequence and description of <i>Kurthia massiliensis</i> sp. nov.. Standards in Genomic Sciences, 2012, 7, 221-232.	1.5	55
7623	Genome sequence of the Antarctic rhodopsins-containing flavobacterium <i>Gillisia limnaea</i> type strain (R-8282T). Standards in Genomic Sciences, 2012, 7, 107-119.	1.5	16
7624	Complete genome sequence of the sulfate-reducing firmicute <i>Desulfotomaculum ruminis</i> type strain (DLT). Standards in Genomic Sciences, 2012, 7, 304-319.	1.5	22
7625	Genome sequence of the halotolerant bacterium <i>Corynebacterium halotolerans</i> type strain YIM 70093T (= DSM 44683T). Standards in Genomic Sciences, 2012, 7, 284-293.	1.5	9
7626	Non-contiguous finished genome sequence and description of <i>Brevibacterium senegalense</i> sp. nov.. Standards in Genomic Sciences, 2012, 7, 233-245.	1.5	64
7627	Genome sequence and description of <i>Aeromicrobium massiliense</i> sp. nov.. Standards in Genomic Sciences, 2012, 7, 246-257.	1.5	76
7628	Non contiguous-finished genome sequence and description of <i>Cellulomonas massiliensis</i> sp. nov.. Standards in Genomic Sciences, 2012, 7, 258-270.	1.5	66
7629	An Intelligent System Approach for Integrating Anatomical Ontologies. Biotechnology and Biotechnological Equipment, 2012, 26, 3173-3181.	0.5	5
7630	Complete genome sequence of <i>Polynucleobacter necessarius</i> subsp. <i>asymbioticus</i> type strain (QLW-P1DMWA-1T). Standards in Genomic Sciences, 2012, 6, 1-14.	1.5	30
7631	Complete genome sequence of <i>Halopiger xanaduensis</i> type strain (SH-6T). Standards in Genomic Sciences, 2012, 6, 31-42.	1.5	9
7632	Complete Genome Sequence of <i>Clostridium clariflavum</i> DSM 19732. Standards in Genomic Sciences, 2012, 6, 104-115.	1.5	48
7633	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093T). Standards in Genomic Sciences, 2012, 7, 44-58.	1.5	16
7634	Complete genome sequence of <i>Terriglobus saanensis</i> type strain SP1PR4T, an Acidobacteria from tundra soil. Standards in Genomic Sciences, 2012, 7, 59-69.	1.5	20
7635	Complete genome sequence of the motile actinomycete <i>Actinoplanes missouriensis</i> 431T (= NBRC) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.5	28
7636	Genome-Wide DNA Methylation Differences Between Late-Onset Alzheimer's Disease and Cognitively Normal Controls in Human Frontal Cortex. Journal of Alzheimer's Disease, 2012, 29, 571-588.	1.2	231

#	ARTICLE	IF	CITATIONS
7637	The Units Ontology: a tool for integrating units of measurement in science. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas033-bas033.	1.4	78
7638	Chemotherapy-induced toxicity is highly heritable in <i>Drosophila melanogaster</i> . Pharmacogenetics and Genomics, 2012, 22, 285-289.	0.7	11
7639	Proteomic Analysis of Formalin-Fixed Paraffin-Embedded Pancreatic Tissue Using Liquid Chromatography Tandem Mass Spectrometry. Pancreas, 2012, 41, 175-185.	0.5	30
7640	Genome-wide association study indicates variants associated with insulin signaling and inflammation mediate lipoprotein responses to fenofibrate. Pharmacogenetics and Genomics, 2012, 22, 750-757.	0.7	15
7641	Clinical utility and implementation of gene-expression profiling in myeloma: current status and challenges. International Journal of Hematologic Oncology, 2012, 1, 133-146.	0.7	0
7642	Genome-Wide Gene Expression Profiling of Human Narcolepsy. Gene Expression, 2012, 15, 171-181.	0.5	11
7643	PathCase-SB. ACM SIGBioinformatics Record, 2012, 2, 19-25.	0.3	0
7644	Genomics of estradiol-3-sulfate action in the ovine fetal hypothalamus. Physiological Genomics, 2012, 44, 669-677.	1.0	23
7645	Detection of significant pathways in osteoporosis based on graph clustering. Molecular Medicine Reports, 2012, 6, 1325-1332.	1.1	14
7646	An ontology derived from heterogeneous sustainability indicator set documents. , 2012, , .		6
7647	NEXT-GENERATION ANALYSIS OF CATARACTS: DETERMINING KNOWLEDGE DRIVEN GENE-GENE INTERACTIONS USING BIOFILTER, AND GENE-ENVIRONMENT INTERACTIONS USING THE PHENX TOOLKIT. , 2012, , .		9
7648	INDI: a computational framework for inferring drug interactions and their associated recommendations. Molecular Systems Biology, 2012, 8, 592.	3.2	208
7649	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricurvum kujijense</i> type strain (YK-1T). Standards in Genomic Sciences, 2012, 6, 94-103.	1.5	37
7650	Identifying cancer highly-expressed membrane receptors for targeted drug delivery. International Journal of Bioinformatics Research and Applications, 2012, 8, 192.	0.1	5
7651	Draft genome sequence of <i>Arthrospira platensis</i> C1 (PCC9438). Standards in Genomic Sciences, 2012, 6, 43-53.	1.5	47
7652	Taking the Next Step: Building an Arabidopsis Information Portal. Plant Cell, 2012, 24, 2248-2256.	3.1	38
7653	Impact of salt on cardiac differential gene expression and coronary lesion in normotensive mineralocorticoid-treated mice. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2012, 302, R1025-R1033.	0.9	9
7654	Proteomic analysis of <i>Plasmodium</i> in the mosquito: progress and pitfalls. Parasitology, 2012, 139, 1131-1145.	0.7	35

#	ARTICLE	IF	CITATIONS
7655	Transcriptional changes in <i>Teladorsagia circumcincta</i> upon encountering host tissue of differing immune status. <i>Parasitology</i> , 2012, 139, 387-405.	0.7	9
7656	Employing functional interactions for characterisation and detection of sparse complexes from yeast PPI networks. <i>International Journal of Bioinformatics Research and Applications</i> , 2012, 8, 286.	0.1	29
7657	Functional identification in correlation networks using gene ontology edge annotation. <i>International Journal of Computational Biology and Drug Design</i> , 2012, 5, 222.	0.3	5
7658	Associating functional groups to multiple clinical types using combined t-test scores and contingency-based measures: a study on breast cancer genes. <i>International Journal of Computational Biology and Drug Design</i> , 2012, 5, 261.	0.3	1
7659	Select Your SNPs (SYSNPs): a web tool for automatic and massive selection of SNPs. <i>International Journal of Data Mining and Bioinformatics</i> , 2012, 6, 324.	0.1	20
7661	Needs for an Expanded Ontology-Based Classification of Adverse Drug Reactions and Related Mechanisms. <i>Clinical Pharmacology and Therapeutics</i> , 2012, 91, 963-965.	2.3	20
7662	Roles and Applications of Biomedical Ontologies in Experimental Animal Science. <i>Experimental Animals</i> , 2012, 61, 365-373.	0.7	0
7663	Microarray and gene ontology analyses reveal downregulation of DNA repair and apoptotic pathways in diethylstilbestrol-exposed testicular Leydig cells. <i>Journal of Toxicological Sciences</i> , 2012, 37, 287-295.	0.7	9
7664	Microarray Analysis Shows That Recessive Resistance to <i>Watermelon mosaic virus</i> in Melon Is Associated with the Induction of Defense Response Genes. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 107-118.	1.4	25
7665	Bayesian joint modeling of multiple gene networks and diverse genomic data to identify target genes of a transcription factor. <i>Annals of Applied Statistics</i> , 2012, 6, 334-355.	0.5	15
7666	Detecting Phenotype-Specific Interactions between Biological Processes from Microarray Data and Annotations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1399-1409.	1.9	5
7667	<i>Insect Genomics.</i> , 2012, , 1-29.		0
7668	Evolutionary Rate and Duplicability in the <i>Arabidopsis thaliana</i> Protein-Protein Interaction Network. <i>Genome Biology and Evolution</i> , 2012, 4, 1263-1274.	1.1	52
7669	Proteomic profiling of the effect of metabolic acidosis on the apical membrane of the proximal convoluted tubule. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 302, F1465-F1477.	1.3	14
7670	Graphs and networks in chemical and biological informatics: past, present and future. <i>Future Medicinal Chemistry</i> , 2012, 4, 2039-2047.	1.1	4
7671	Data platforms in integrative biodiversity research. <i>Ecological Informatics</i> , 2012, 11, 1-4.	2.3	8
7672	A Deep Exploration of the Transcriptome and Excretory/Secretory Proteome of Adult <i>Fascioloides magna</i> . <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1340-1353.	2.5	35
7673	Regional Features of the Expression of Genes Involved in Neurogenesis and Apoptosis in the Brain of Adult Rats. <i>Bulletin of Experimental Biology and Medicine</i> , 2012, 153, 746-749.	0.3	5

#	ARTICLE	IF	CITATIONS
7674	Next-generation sequencing-based transcriptomic and proteomic analysis of the common reed, <i>Phragmites australis</i> (Poaceae), reveals genes involved in invasiveness and rhizome specificity. <i>American Journal of Botany</i> , 2012, 99, 232-247.	0.8	49
7675	A Hierarchical Semiparametric Model for Incorporating Intergene Information for Analysis of Genomic Data. <i>Biometrics</i> , 2012, 68, 1168-1177.	0.8	2
7676	Reprogramming cell fates: insights from combinatorial approaches. <i>Annals of the New York Academy of Sciences</i> , 2012, 1266, 7-17.	1.8	19
7677	Bioinformatic identification of genes suppressing genome instability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3251-9.	3.3	25
7678	Survivin Is a Therapeutic Target in Merkel Cell Carcinoma. <i>Science Translational Medicine</i> , 2012, 4, 133ra56.	5.8	117
7679	A travel guide to Cytoscape plugins. <i>Nature Methods</i> , 2012, 9, 1069-1076.	9.0	1,289
7680	Text-mining solutions for biomedical research: enabling integrative biology. <i>Nature Reviews Genetics</i> , 2012, 13, 829-839.	7.7	194
7681	Gene expression associated with apogamy commitment in <i>Ceratopteris richardii</i> . <i>Sexual Plant Reproduction</i> , 2012, 25, 293-304.	2.2	17
7682	The simple fool's guide to population genomics via <i>RNA-Seq</i> : an introduction to high-throughput sequencing data analysis. <i>Molecular Ecology Resources</i> , 2012, 12, 1058-1067.	2.2	229
7683	Gene expression profiles of pheochromocytomas with <i>ERBB2</i> overexpression reveal a new molecular mechanism tumourigenicity. <i>Clinical Endocrinology</i> , 2012, 77, 399-406.	1.2	5
7684	Exploration and characterization of genes involved in the synthesis of diterpene defence secretion in nasute termite soldiers. <i>Insect Molecular Biology</i> , 2012, 21, 545-557.	1.0	16
7685	Genome-wide patterns of latitudinal differentiation among populations of <i>Drosophila melanogaster</i> from North America. <i>Molecular Ecology</i> , 2012, 21, 4748-4769.	2.0	256
7686	Identification of a complex genetic network underlying <i>Saccharomyces cerevisiae</i> colony morphology. <i>Molecular Microbiology</i> , 2012, 86, 225-239.	1.2	71
7687	Systematic identification of edited microRNAs in the human brain. <i>Genome Research</i> , 2012, 22, 1533-1540.	2.4	163
7688	B Cells With High Side Scatter Parameter by Flow Cytometry Correlate With Inferior Survival in Diffuse Large B-Cell Lymphoma. <i>American Journal of Clinical Pathology</i> , 2012, 137, 805-814.	0.4	12
7689	Spermatogenesis in mammals: proteomic insights. <i>Systems Biology in Reproductive Medicine</i> , 2012, 58, 179-190.	1.0	73
7690	Integrating Biomolecular and Clinical Data for Cancer Research: Concepts and Challenges. , 2012, , 159-172.		0
7691	EnrichNet: network-based gene set enrichment analysis. <i>Bioinformatics</i> , 2012, 28, i451-i457.	1.8	269

#	ARTICLE	IF	CITATIONS
7692	The genetics of alcohol dependence: Advancing towards systems-based approaches. <i>Drug and Alcohol Dependence</i> , 2012, 125, 179-191.	1.6	26
7693	Associations with early-life socio-economic position in adult DNA methylation. <i>International Journal of Epidemiology</i> , 2012, 41, 62-74.	0.9	380
7694	Simvastatin Modulates the Alzheimer's Disease-Related Gene <i>seladin-1</i> . <i>Journal of Alzheimer's Disease</i> , 2012, 28, 297-301.	1.2	13
7695	Shotgun analysis of membrane proteomes by an improved SDS-assisted sample preparation method coupled with liquid chromatography-tandem mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2012, 911, 6-14.	1.2	9
7696	Understanding the Relationship Between Brain Gene Expression and Social Behavior: Lessons from the Honey Bee. <i>Annual Review of Genetics</i> , 2012, 46, 591-615.	3.2	166
7697	Using the NeAT Toolbox to Compare Networks to Networks, Clusters to Clusters, and Network to Clusters. <i>Methods in Molecular Biology</i> , 2012, 804, 327-342.	0.4	6
7698	Biomarker Identification and Cancer Classification Based on Microarray Data Using Laplace Naive Bayes Model with Mean Shrinkage. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1649-1662.	1.9	44
7699	The Evolutionary Landscape of Alternative Splicing in Vertebrate Species. <i>Science</i> , 2012, 338, 1587-1593.	6.0	905
7700	Human-protein-derived peptides for intracellular delivery of biomolecules. <i>Biochemical Journal</i> , 2012, 442, 583-593.	1.7	13
7701	Genome-wide identification of differentially expressed genes under water deficit stress in upland cotton (<i>Gossypium hirsutum</i> L.). <i>BMC Plant Biology</i> , 2012, 12, 90.	1.6	62
7702	Constitutive activation of STAT3 is predictive of poor prognosis in human gastric cancer. <i>Journal of Molecular Medicine</i> , 2012, 90, 1037-1046.	1.7	59
7703	Data mining for microbiologists. <i>Methods in Microbiology</i> , 2012, 39, 27-79.	0.4	8
7704	Global network alignment using multiscale spectral signatures. <i>Bioinformatics</i> , 2012, 28, 3105-3114.	1.8	175
7705	Gene expression analysis of whole blood, peripheral blood mononuclear cells, and lymphoblastoid cell lines from the Framingham Heart Study. <i>Physiological Genomics</i> , 2012, 44, 59-75.	1.0	61
7706	Protein misinteraction avoidance causes highly expressed proteins to evolve slowly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E831-40.	3.3	160
7707	Sex peptide of <i>Drosophila melanogaster</i> males is a global regulator of reproductive processes in females. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 4423-4432.	1.2	73
7708	Cross Species Integration of Functional Genomics Experiments. <i>International Review of Neurobiology</i> , 2012, 104, 1-24.	0.9	5
7709	Genome-wide gene-environment interaction analysis for asbestos exposure in lung cancer susceptibility. <i>Carcinogenesis</i> , 2012, 33, 1531-1537.	1.3	44

#	ARTICLE	IF	CITATIONS
7710	Systems Analysis of Plant Functional, Transcriptional, Physical Interaction, and Metabolic Networks. <i>Plant Cell</i> , 2012, 24, 3859-3875.	3.1	96
7711	CPSS: a computational platform for the analysis of small RNA deep sequencing data. <i>Bioinformatics</i> , 2012, 28, 1925-1927.	1.8	55
7712	Induced Pluripotent Stem Cell Consensus Genes: Implication for the Risk of Tumorigenesis and Cancers in Induced Pluripotent Stem Cell Therapy. <i>Stem Cells and Development</i> , 2012, 21, 955-964.	1.1	47
7713	Improving the description of metabolic networks: the TCA cycle as example. <i>FASEB Journal</i> , 2012, 26, 3625-3636.	0.2	22
7714	Ezh2 augments leukemogenicity by reinforcing differentiation blockage in acute myeloid leukemia. <i>Blood</i> , 2012, 120, 1107-1117.	0.6	161
7715	Prioritization of pathogenic mutations in the protein kinase superfamily. <i>BMC Genomics</i> , 2012, 13, S3.	1.2	21
7716	A molecular analysis of desiccation tolerance mechanisms in the anhydrobiotic nematode <i>Panagrolaimus superbus</i> using expressed sequenced tags. <i>BMC Research Notes</i> , 2012, 5, 68.	0.6	41
7717	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
7718	EpiExplorer: live exploration and global analysis of large epigenomic datasets. <i>Genome Biology</i> , 2012, 13, R96.	13.9	72
7719	Predicting the effects of frameshifting indels. <i>Genome Biology</i> , 2012, 13, R9.	13.9	99
7720	Defining the molecular profile of planarian pluripotent stem cells using a combinatorial RNA-seq, RNA interference and irradiation approach. <i>Genome Biology</i> , 2012, 13, R19.	13.9	135
7721	The Transcription Factor Encyclopedia. <i>Genome Biology</i> , 2012, 13, R24.	13.9	103
7722	High levels of RNA-editing site conservation amongst 15 laboratory mouse strains. <i>Genome Biology</i> , 2012, 13, R26.	13.9	149
7723	A metagenomic study of diet-dependent interaction between gut microbiota and host in infants reveals differences in immune response. <i>Genome Biology</i> , 2012, 13, R32.	13.9	218
7724	The genome of the polar eukaryotic microalga <i>Coccomyxa subellipsoidea</i> reveals traits of cold adaptation. <i>Genome Biology</i> , 2012, 13, R39.	13.9	289
7725	The genomic landscape shaped by selection on transposable elements across 18 mouse strains. <i>Genome Biology</i> , 2012, 13, R45.	13.9	170
7726	Regulation of alternative splicing by the circadian clock and food related cues. <i>Genome Biology</i> , 2012, 13, R54.	13.9	89
7727	Conserved rules govern genetic interaction degree across species. <i>Genome Biology</i> , 2012, 13, R57.	13.9	48

#	ARTICLE	IF	CITATIONS
7728	CIDeR: multifactorial interaction networks in human diseases. <i>Genome Biology</i> , 2012, 13, R62.	13.9	28
7729	A gene expression profile of stem cell pluripotentiality and differentiation is conserved across diverse solid and hematopoietic cancers. <i>Genome Biology</i> , 2012, 13, R71.	13.9	69
7730	Association Study of Nonsynonymous Single Nucleotide Polymorphisms in Schizophrenia. <i>Biological Psychiatry</i> , 2012, 71, 169-177.	0.7	78
7731	Identification of Differentially Expressed Gene Profiles in Young Roots of Tea [<i>Camellia sinensis</i> (L.) O. Kuntze] Subjected to Drought Stress Using Suppression Subtractive Hybridization. <i>Plant Molecular Biology Reporter</i> , 2012, 30, 1088-1101.	1.0	55
7732	1,3-bis(sn)-sn-glycerol-3-phosphate regulation of gene expression in preadipocytes and adipocytes. <i>BioFactors</i> , 2012, 38, 450-457.	2.6	22
7733	Omics-Based Systems Vaccinology for Vaccine Target Identification. <i>Drug Development Research</i> , 2012, 73, 559-568.	1.4	12
7734	Knockdown of nucleosome assembly protein 1 promotes dimethyl sulfoxide-induced differentiation of P19CL6 cells into cardiomyocytes. <i>Journal of Cellular Biochemistry</i> , 2012, 113, 3788-3796.	1.2	12
7735	Systems-level analysis of clinically different phenotypes of juvenile nasopharyngeal angiofibromas. <i>Laryngoscope</i> , 2012, 122, 2728-2735.	1.1	7
7736	Gene copy number and differential gene expression in haploid and diploid males of the stingless bee, <i>Melipona quadrifasciata</i> . <i>Insectes Sociaux</i> , 2012, 59, 587-598.	0.7	5
7737	From genome-wide association studies to disease mechanisms: celiac disease as a model for autoimmune diseases. <i>Seminars in Immunopathology</i> , 2012, 34, 567-580.	2.8	127
7738	Transcriptome profiling and in silico analysis of somatic embryos in Japanese larch (<i>Larix leptolepis</i>). <i>Plant Cell Reports</i> , 2012, 31, 1637-1657.	2.8	44
7739	Computational tools for comparative phenomics: the role and promise of ontologies. <i>Mammalian Genome</i> , 2012, 23, 669-679.	1.0	19
7740	Web-based digital gene expression atlases for the mouse. <i>Mammalian Genome</i> , 2012, 23, 525-538.	1.0	24
7741	U-statistics in genetic association studies. <i>Human Genetics</i> , 2012, 131, 1395-1401.	1.8	12
7742	Labellum transcriptome reveals alkene biosynthetic genes involved in orchid sexual deception and pollination-induced senescence. <i>Functional and Integrative Genomics</i> , 2012, 12, 693-703.	1.4	11
7743	Interchanging lexical resources on the Semantic Web. <i>Language Resources and Evaluation</i> , 2012, 46, 701-719.	1.8	106
7744	Evolutionary rate of human tissue-specific genes are related with transposable element insertions. <i>Genetica</i> , 2012, 140, 513-523.	0.5	7
7745	miRDeepFinder: a miRNA analysis tool for deep sequencing of plant small RNAs. <i>Plant Molecular Biology</i> , 2012, 80, 75-84.	2.0	1,159

#	ARTICLE	IF	CITATIONS
7746	Transcriptome profiling of female alates and egg-laying queens of the Formosan subterranean termite. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2012, 7, 14-27.	0.4	15
7747	Genome-wide transcript profiling indicates induction of energy-generating pathways and an adaptive immune response in the liver of sows during lactation. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2012, 7, 370-381.	0.4	16
7748	<i>Drosophila</i> Auditory Organ Genes and Genetic Hearing Defects. <i>Cell</i> , 2012, 150, 1042-1054.	13.5	197
7749	A Census of Human Soluble Protein Complexes. <i>Cell</i> , 2012, 150, 1068-1081.	13.5	781
7750	Microcephaly Gene Links Trithorax and REST/NRSF to Control Neural Stem Cell Proliferation and Differentiation. <i>Cell</i> , 2012, 151, 1097-1112.	13.5	153
7751	Proteomic Analysis of Lysine Acetylation Sites in Rat Tissues Reveals Organ Specificity and Subcellular Patterns. <i>Cell Reports</i> , 2012, 2, 419-431.	2.9	493
7752	The Genomic Landscape and Evolutionary Resolution of Antagonistic Pleiotropy in Yeast. <i>Cell Reports</i> , 2012, 2, 1399-1410.	2.9	177
7753	A defect in iron uptake enhances the susceptibility of <i>Cryptococcus neoformans</i> to azole antifungal drugs. <i>Fungal Genetics and Biology</i> , 2012, 49, 955-966.	0.9	48
7754	GeneSetDB: A comprehensive meta-database, statistical and visualisation framework for gene set analysis. <i>FEBS Open Bio</i> , 2012, 2, 76-82.	1.0	69
7755	Advances in the methods for studying gut microbiota and their relevance to the research of dietary fiber functions. <i>Food Research International</i> , 2012, 48, 916-929.	2.9	49
7756	Finding disease similarity based on implicit semantic similarity. <i>Journal of Biomedical Informatics</i> , 2012, 45, 363-371.	2.5	122
7757	Transforming semi-structured life science diagrams into meaningful domain ontologies with DiDON. <i>Journal of Biomedical Informatics</i> , 2012, 45, 482-494.	2.5	11
7758	Ontological labels for automated location of anatomical shape differences. <i>Journal of Biomedical Informatics</i> , 2012, 45, 522-527.	2.5	8
7759	A transcriptional study of acidogenic chemostat cells of <i>Clostridium acetobutylicum</i> – Cellular behavior in adaptation to n-butanol. <i>Journal of Biotechnology</i> , 2012, 161, 366-377.	1.9	45
7760	The temporal analysis of yeast exponential phase using shotgun proteomics as a fermentation monitoring technique. <i>Journal of Proteomics</i> , 2012, 75, 5206-5214.	1.2	7
7761	Proteomic analysis of liver development of lean Pekin duck (<i>Anas platyrhynchos domestica</i>). <i>Journal of Proteomics</i> , 2012, 75, 5396-5413.	1.2	19
7762	Proteome signatures of inflammatory activated primary human peripheral blood mononuclear cells. <i>Journal of Proteomics</i> , 2012, 76, 150-162.	1.2	43
7763	The different proteomes of <i>Chlamydomonas reinhardtii</i> . <i>Journal of Proteomics</i> , 2012, 75, 5883-5887.	1.2	16

#	ARTICLE	IF	CITATIONS
7764	In-depth analysis of the secretome identifies three major independent secretory pathways in differentiating human myoblasts. <i>Journal of Proteomics</i> , 2012, 77, 344-356.	1.2	125
7765	Cannabidiol affects the expression of genes involved in zinc homeostasis in BV-2 microglial cells. <i>Neurochemistry International</i> , 2012, 61, 923-930.	1.9	28
7766	Determination of protein subcellular localization in apicomplexan parasites. <i>Trends in Parasitology</i> , 2012, 28, 546-554.	1.5	15
7767	Microbial virus genome annotationâ€”Mustering the troops to fight the sequence onslaught. <i>Virology</i> , 2012, 434, 175-180.	1.1	12
7768	VIP DB â€” A viral protein domain usage and distribution database. <i>Genomics</i> , 2012, 100, 149-156.	1.3	0
7769	Identification and characterization of transposable element-mediated chimeric transcripts from porcine Refseq and EST databases. <i>Genes and Genomics</i> , 2012, 34, 409-414.	0.5	3
7770	Cross-experimental analysis of microarray gene expression datasets for in silico risk assessment of TiO2 nano-particles. <i>Molecular and Cellular Toxicology</i> , 2012, 8, 229-239.	0.8	8
7771	Ontology Learning from Online Chinese Encyclopedias. <i>AASRI Procedia</i> , 2012, 1, 287-292.	0.6	0
7772	Quantitative Proteome Profiling of Normal Human Circulating Microparticles. <i>Journal of Proteome Research</i> , 2012, 11, 2154-2163.	1.8	56
7773	Semantic patient information aggregation and medicinal decision support. <i>Computer Methods and Programs in Biomedicine</i> , 2012, 108, 724-735.	2.6	28
7774	Predicting protein functions from PPI networks using functional aggregation. <i>Mathematical Biosciences</i> , 2012, 240, 63-69.	0.9	14
7775	Pancreatic Damage in Fetal and Newborn Cystic Fibrosis Pigs Involves the Activation of Inflammatory and Remodeling Pathways. <i>American Journal of Pathology</i> , 2012, 181, 499-507.	1.9	56
7776	Systematic Identification of Functional Plant Modules through the Integration of Complementary Data Sources Â Â. <i>Plant Physiology</i> , 2012, 159, 884-901.	2.3	108
7777	A semantic integration system for heterogeneous bioinformatics data. , 2012, , .		1
7778	PPIExtractor: A protein-protein interaction Extractor for biomédical literature. , 2012, , .		1
7779	Significance analysis by minimizing false discovery rate. , 2012, , .		1
7780	Information Flow in Interaction Networks II: Channels, Path Lengths, and Potentials. <i>Journal of Computational Biology</i> , 2012, 19, 379-403.	0.8	15
7781	Comprehensive human membrane protein database. , 2012, , .		0

#	ARTICLE	IF	CITATIONS
7782	RGRank: Ranking Semantically Related Genes. , 2012, , .		3
7783	Clarifying Omics Concepts, Challenges, and Opportunities for <i>Prunus</i> Breeding in the Postgenomic Era. OMICS A Journal of Integrative Biology, 2012, 16, 268-283.	1.0	32
7784	Fault Model Libraries for Safety Analysis and their Ontology-based Reuse. , 2012, , .		2
7785	Gene selection using biological knowledge and fuzzy clustering. , 2012, , .		2
7786	Exploiting the Functional and Taxonomic Structure of Genomic Data by Probabilistic Topic Modeling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 980-991.	1.9	17
7787	A Systems Biology Approach to Solving the Puzzle of Unknown Genomic Gene-Function Association Using Grid-Ready SVM Committee Machines. IEEE Computational Intelligence Magazine, 2012, 7, 46-54.	3.4	1
7788	RNA-seq coverage effects on biological pathways and GO tag clouds. , 2012, , .		0
7789	O(6)-Methylguanine-DNA Methyltransferase Is a Novel Negative Effector of Invasion in Glioblastoma Multiforme. Molecular Cancer Therapeutics, 2012, 11, 2440-2450.	1.9	21
7790	A systems biology approach to identify the signalling network regulated by Rho-GDI β during neural stem cell differentiation. Molecular BioSystems, 2012, 8, 2916.	2.9	5
7791	DEFOG: discrete enrichment of functionally organized genes. Integrative Biology (United Kingdom), 2012, 4, 795.	0.6	3
7792	Identifying core features of adaptive metabolic mechanisms for chronic heat stress attenuation contributing to systems robustness. Integrative Biology (United Kingdom), 2012, 4, 480.	0.6	65
7793	Extension of cortical synaptic development distinguishes humans from chimpanzees and macaques. Genome Research, 2012, 22, 611-622.	2.4	224
7794	Is newer better?â€”evaluating the effects of data curation on integrated analyses in <i>Saccharomyces cerevisiae</i> . Integrative Biology (United Kingdom), 2012, 4, 715-727.	0.6	2
7795	ppiPre - an R package for predicting protein-protein interactions. , 2012, , .		1
7796	Aligning protein-protein interaction networks using random neural networks. , 2012, , .		14
7797	Unipept: Tryptic Peptide-Based Biodiversity Analysis of Metaproteome Samples. Journal of Proteome Research, 2012, 11, 5773-5780.	1.8	116
7798	Inferring gene functions from metabolic reactions. , 2012, , .		0
7799	Automatic Prediction of Enzyme Functions from Domain Compositions Using Enzyme Reaction Prediction Scheme. , 2012, , .		0

#	ARTICLE	IF	CITATIONS
7800	Biologically relevant association rules for classification of microarray data. ACM SIGAPP Applied Computing Review: A Publication of the Special Interest Group on Applied Computing, 2012, 12, 12-23.	0.5	1
7801	Wiki-Genome: A model-driven genome data management environment. , 2012, , .		0
7802	A data-driven urban research environment for Australia. , 2012, , .		9
7803	PlateletWeb: a systems biologic analysis of signaling networks in human platelets. Blood, 2012, 119, e22-e34.	0.6	84
7804	SNPEffect 4.0: on-line prediction of molecular and structural effects of protein-coding variants. Nucleic Acids Research, 2012, 40, D935-D939.	6.5	235
7805	Function Prediction and Analysis of Mycobacterium tuberculosis Hypothetical Proteins. International Journal of Molecular Sciences, 2012, 13, 7283-7302.	1.8	88
7806	Controlled reoxygenation cardiopulmonary bypass is associated with reduced transcriptomic changes in cyanotic tetralogy of Fallot patients undergoing surgery. Physiological Genomics, 2012, 44, 1098-1106.	1.0	18
7807	Application of an algorithm for the computation of functional similarity in the research of protein interaction. , 2012, , .		0
7808	Caenorhabditis elegans screen reveals role of PAR-5 in RAB-11-recycling endosome positioning and apicobasal cell polarity. Nature Cell Biology, 2012, 14, 666-676.	4.6	96
7809	Inferring gene functions through dissection of relevance networks: interleaving the intra- and inter-species views. Molecular BioSystems, 2012, 8, 2233.	2.9	9
7810	An integrative framework for identifying consistent microRNA expression signatures associated with clear cell renal cell carcinoma. , 2012, , .		0
7811	TrAnsFuSE refines the search for protein function: oxidoreductases. Integrative Biology (United Tj ETQq1 1 0.784314 rgBT /Qverlock 10	0.6	9
7812	Alterations of protein complexes and pathways in genetic information flow and response to stimulus contribute to Escherichia coli resistance to balofloxacin. Molecular BioSystems, 2012, 8, 2303.	2.9	7
7813	Predicting Gene Functions Using Semi-supervised Clustering Algorithms with Objective Function Optimization. , 2012, , .		0
7814	Signaling network prediction by the Ontology Fingerprint enhanced Bayesian network. BMC Systems Biology, 2012, 6, S3.	3.0	18
7815	Understanding the lethality of low degree essential proteins. , 2012, , .		0
7816	Interleukin 1-beta upregulates brain-derived neurotrophic factor, neurotrophin 3 and neuropilin 2 gene expression and NGF production in annulus cells. Biotechnic and Histochemistry, 2012, 87, 506-511.	0.7	52
7817	An Ontology for ActionCenter-Oriented Collaboration Platforms. , 2012, , .		3

#	ARTICLE	IF	CITATIONS
7818	Authority Control for Scientific Data: The Case of Molecular Biology. <i>Journal of Library Metadata</i> , 2012, 12, 61-82.	0.6	6
7819	Large-scale discovery of enhancers from human heart tissue. <i>Nature Genetics</i> , 2012, 44, 89-93.	9.4	257
7820	COFACTOR: an accurate comparative algorithm for structure-based protein function annotation. <i>Nucleic Acids Research</i> , 2012, 40, W471-W477.	6.5	582
7821	Identification of Prostate-Enriched Proteins by In-depth Proteomic Analyses of Expressed Prostatic Secretions in Urine. <i>Journal of Proteome Research</i> , 2012, 11, 2386-2396.	1.8	56
7822	Molecular Analysis of Differentially Expressed Genes in Birch (<i>Betula Platyphylla</i>) Inflorescence. <i>Biotechnology and Biotechnological Equipment</i> , 2012, 26, 2844-2854.	0.5	1
7824	Combining literature text mining with microarray data: advances for system biology modeling. <i>Briefings in Bioinformatics</i> , 2012, 13, 61-82.	3.2	59
7825	Label-Free Quantitative LC-MS Proteomics of Alzheimer's Disease and Normally Aged Human Brains. <i>Journal of Proteome Research</i> , 2012, 11, 3053-3067.	1.8	131
7826	Clinical and molecular characteristics of congenital glioblastoma. <i>Neuro-Oncology</i> , 2012, 14, 931-941.	0.6	45
7827	Ontology-Driven Construction of Domain Corpus with Frame Semantics Annotations. <i>Lecture Notes in Computer Science</i> , 2012, , 54-65.	1.0	2
7828	Computational Linguistics and Intelligent Text Processing. <i>Lecture Notes in Computer Science</i> , 2012, , .	1.0	0
7829	Transcriptomic Response of Skeletal Muscle to Lipopolysaccharide in the Gilthead Seabream (<i>Sparus</i>) Tj ETQq0 0 0 igBT /Overlock 10 Tf	1.1	19
7830	Multidimensional Identification of Tissue Biomarkers of Gastric Cancer. <i>Journal of Proteome Research</i> , 2012, 11, 3405-3413.	1.8	14
7831	Identification of oncogenic genes for colon adenocarcinoma from genomics data. , 2012, , .		1
7832	Hierarchical Modeling for Synthetic Biology. <i>ACS Synthetic Biology</i> , 2012, 1, 353-364.	1.9	16
7833	C-GRAAL: Common-neighbors-based global GRaph ALignment of biological networks. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 734.	0.6	79
7834	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	13.7	2,249
7835	Implicit Biology in Peptide Spectral Libraries. <i>Analytical Chemistry</i> , 2012, 84, 7919-7925.	3.2	3
7836	Proteomic Analysis of Hepatitis C Virus (HCV) Core Protein Transfection and Host Regulator PA28 ³ Knockout in HCV Pathogenesis: A Network-Based Study. <i>Journal of Proteome Research</i> , 2012, 11, 3664-3679.	1.8	13

#	ARTICLE	IF	CITATIONS
7837	Salivaomics. Journal of the American Dental Association, 2012, 143, 19S-24S.	0.7	118
7838	Providing the Missing Link: the Exposure Science Ontology ExO. Environmental Science & Technology, 2012, 46, 3046-3053.	4.6	57
7839	Proteomic Profiling of the Planarian Schmidtea mediterranea and Its Mucous Reveals Similarities with Human Secretions and Those Predicted for Parasitic Flatworms. Molecular and Cellular Proteomics, 2012, 11, 681-691.	2.5	27
7840	Responses of Mouse Liver to Dechlorane Plus Exposure by Integrative Transcriptomic and Metabonomic Studies. Environmental Science & Technology, 2012, 46, 10758-10764.	4.6	66
7841	Direct data transfer between SOAP web services in orchestration. , 2012, , .		6
7842	Construction and analysis of genome-wide SNP networks. , 2012, , .		0
7843	Sex hormone activity in alcohol addiction: Integrating organizational and activational effects. Progress in Neurobiology, 2012, 96, 136-163.	2.8	119
7844	A prioritization analysis of disease association by data-mining of functional annotation of human genes. Genomics, 2012, 99, 1-9.	1.3	11
7845	Gene transcripts associated with BMI in the motor cortex and caudate nucleus of calorie restricted rhesus monkeys. Genomics, 2012, 99, 144-151.	1.3	8
7846	Evolutionary informatics: unifying knowledge about the diversity of life. Trends in Ecology and Evolution, 2012, 27, 94-103.	4.2	99
7847	Time to change how we describe biodiversity. Trends in Ecology and Evolution, 2012, 27, 78-84.	4.2	120
7848	Analysis of the proteomic profile of chronic pressure ulcers. Wound Repair and Regeneration, 2012, 20, 378-401.	1.5	49
7849	Systematic Localization of Common Disease-Associated Variation in Regulatory DNA. Science, 2012, 337, 1190-1195.	6.0	3,129
7850	Detecting protein complexes in a PPI network: a gene ontology based multi-objective evolutionary approach. Molecular BioSystems, 2012, 8, 3036.	2.9	44
7851	Computational design of genomic transcriptional networks with adaptation to varying environments. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15277-15282.	3.3	14
7852	Network-Induced Classification Kernels for Gene Expression Profile Analysis. Journal of Computational Biology, 2012, 19, 694-709.	0.8	29
7853	Genome-scale analysis of interaction dynamics reveals organization of biological networks. Bioinformatics, 2012, 28, 1873-1878.	1.8	50
7854	Charting the Landscape of Tandem BRCT Domain-Mediated Protein Interactions. Science Signaling, 2012, 5, rs6.	1.6	88

#	ARTICLE	IF	CITATIONS
7855	Global Secretome Characterization of Herpes Simplex Virus 1-Infected Human Primary Macrophages. <i>Journal of Virology</i> , 2012, 86, 12770-12778.	1.5	45
7856	Genetic Adaptation of the Hypoxia-Inducible Factor Pathway to Oxygen Pressure among Eurasian Human Populations. <i>Molecular Biology and Evolution</i> , 2012, 29, 3359-3370.	3.5	29
7857	Genome-Wide Patterns of Genetic Distances Reveal Candidate Loci Contributing to Human Population-Specific Traits. <i>Annals of Human Genetics</i> , 2012, 76, 142-158.	0.3	12
7858	CCAAT-enhancer-binding protein-beta expression <i>in vivo</i> is associated with muscle strength. <i>Aging Cell</i> , 2012, 11, 262-268.	3.0	23
7859	Structure-based prediction of protein-protein interactions on a genome-wide scale. <i>Nature</i> , 2012, 490, 556-560.	13.7	652
7860	<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
7861	Quality assessment of protein model-structures based on structural and functional similarities. <i>BMC Bioinformatics</i> , 2012, 13, 242.	1.2	11
7862	Systematic Prediction of cis-Regulatory Elements in the <i>Chlamydomonas reinhardtii</i> Genome Using Comparative Genomics. <i>Plant Physiology</i> , 2012, 160, 613-623.	2.3	25
7863	Dinoflagellate tandem array gene transcripts are highly conserved and not polycistronic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15793-15798.	3.3	73
7864	Identification of human protein complexes from local sub-graphs of protein-protein interaction network based on random forest with topological structure features. <i>Analytica Chimica Acta</i> , 2012, 718, 32-41.	2.6	14
7865	Modulating Protein-Protein Interactions with Small Molecules: The Importance of Binding Hotspots. <i>Journal of Molecular Biology</i> , 2012, 415, 443-453.	2.0	61
7866	Genomic Organization of Evolutionarily Correlated Genes in Bacteria: Limits and Strategies. <i>Journal of Molecular Biology</i> , 2012, 419, 369-386.	2.0	33
7867	Predicting plant protein subcellular multi-localization by Chou's PseAAC formulation based multi-label homolog knowledge transfer learning. <i>Journal of Theoretical Biology</i> , 2012, 310, 80-87.	0.8	106
7868	Comprehensive comparative analysis and identification of RNA-binding protein domains: Multi-class classification and feature selection. <i>Journal of Theoretical Biology</i> , 2012, 312, 65-75.	0.8	10
7869	Ranking Gene Ontology terms for predicting non-classical secretory proteins in eukaryotes and prokaryotes. <i>Journal of Theoretical Biology</i> , 2012, 312, 105-113.	0.8	12
7870	The mRNA-Bound Proteome and Its Global Occupancy Profile on Protein-Coding Transcripts. <i>Molecular Cell</i> , 2012, 46, 674-690.	4.5	1,077
7871	A comprehensive representation scheme for video semantic ontology and its applications in semantic concept detection. <i>Neurocomputing</i> , 2012, 95, 29-39.	3.5	5
7872	Pathway analysis of genome-wide association studies on uric acid concentrations. <i>Human Immunology</i> , 2012, 73, 805-810.	1.2	29

#	ARTICLE	IF	CITATIONS
7873	The sialotranscriptome of <i>Antricola delacruzi</i> female ticks is compatible with non-hematophagous behavior and an alternative source of food. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 332-342.	1.2	52
7874	De novo sequencing and analysis of the termite mushroom (<i>Termitomyces albuminosus</i>) transcriptome to discover putative genes involved in bioactive component biosynthesis. <i>Journal of Bioscience and Bioengineering</i> , 2012, 114, 228-231.	1.1	17
7875	Shotgun analysis of membrane proteomes using a novel combinative strategy of solution-based sample preparation coupled with liquid chromatography-tandem mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2012, 901, 18-24.	1.2	13
7876	The effect of selenium enrichment on baker's yeast proteome. <i>Journal of Proteomics</i> , 2012, 75, 1018-1030.	1.2	16
7877	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
7878	Proteomic atlas of the human olfactory bulb. <i>Journal of Proteomics</i> , 2012, 75, 4005-4016.	1.2	30
7879	A systems genetic analysis of high density lipoprotein metabolism and network preservation across mouse models. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2012, 1821, 435-447.	1.2	27
7880	Altered proteomic pattern in platelets of rats with sepsis. <i>Blood Cells, Molecules, and Diseases</i> , 2012, 48, 30-35.	0.6	15
7881	Domain-mediated protein interaction prediction: From genome to network. <i>FEBS Letters</i> , 2012, 586, 2751-2763.	1.3	48
7882	The age of the genome: Genome, transcriptome and proteome data set collection and analysis. <i>Brain Research Bulletin</i> , 2012, 88, 294-301.	1.4	13
7883	The multi-reference contrast method: Facilitating set enrichment analysis. <i>Computers in Biology and Medicine</i> , 2012, 42, 188-194.	3.9	5
7884	An effective measure for assessing the quality of biclusters. <i>Computers in Biology and Medicine</i> , 2012, 42, 245-256.	3.9	38
7885	Gene expression analysis of clams <i>Ruditapes philippinarum</i> and <i>Ruditapes decussatus</i> following bacterial infection yields molecular insights into pathogen resistance and immunity. <i>Developmental and Comparative Immunology</i> , 2012, 36, 140-149.	1.0	51
7886	Functional genomics resources for the North Atlantic copepod, <i>Calanus finmarchicus</i> : EST database and physiological microarray. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2012, 7, 110-123.	0.4	26
7887	Identification of differentially expressed genes and quantitative expression of complement genes in the liver of marine medaka <i>Oryzias melastigma</i> challenged with <i>Vibrio parahaemolyticus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2012, 7, 191-200.	0.4	20
7888	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. <i>Cell</i> , 2012, 148, 1293-1307.	13.5	1,134
7889	Single-Cell Exome Sequencing Reveals Single-Nucleotide Mutation Characteristics of a Kidney Tumor. <i>Cell</i> , 2012, 148, 886-895.	13.5	622
7890	Global Patterns of Tissue-Specific Alternative Polyadenylation in <i>Drosophila</i> . <i>Cell Reports</i> , 2012, 1, 277-289.	2.9	201

#	ARTICLE	IF	CITATIONS
7891	Identifying gnostic predictors of the vaccine response. <i>Current Opinion in Immunology</i> , 2012, 24, 332-336.	2.4	17
7892	Identifying and tracking proteins through the marine water column: Insights into the inputs and preservation mechanisms of protein in sediments. <i>Geochimica Et Cosmochimica Acta</i> , 2012, 83, 324-359.	1.6	44
7893	Comparative transcriptomics and gene expression in larval tiger salamander (<i>Ambystoma tigrinum</i>) gill and lung tissues as revealed by pyrosequencing. <i>Gene</i> , 2012, 492, 329-338.	1.0	23
7894	Study on the age-dependent tissue expression of FUT1 gene in porcine and its relationship to E. coli F18 receptor. <i>Gene</i> , 2012, 497, 336-339.	1.0	11
7895	Aberrant brain microRNA target and miRISC gene expression in the anx/anx anorexia mouse model. <i>Gene</i> , 2012, 497, 181-190.	1.0	12
7896	Identification of cis-regulatory elements specific for different types of reactive oxygen species in <i>Arabidopsis thaliana</i> . <i>Gene</i> , 2012, 499, 52-60.	1.0	36
7897	RNA-Seq Atlas—a reference database for gene expression profiling in normal tissue by next-generation sequencing. <i>Bioinformatics</i> , 2012, 28, 1184-1185.	1.8	178
7898	Reconstructing Models from Proteomics Data. , 2012, , 23-80.		0
7899	Systems Pharmacology: Network Analysis to Identify Multiscale Mechanisms of Drug Action. <i>Annual Review of Pharmacology and Toxicology</i> , 2012, 52, 505-521.	4.2	288
7900	Can simple codon pair usage predict proteinâ€“protein interaction?. <i>Molecular BioSystems</i> , 2012, 8, 1396.	2.9	28
7901	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1350-1360.	1.4	264
7902	Functional classification of skeletal muscle networks. I. Normal physiology. <i>Journal of Applied Physiology</i> , 2012, 113, 1884-1901.	1.2	14
7903	An RNAi Screen Reveals Intestinal Regulators of Branching Morphogenesis, Differentiation, and Stem Cell Proliferation in Planarians. <i>Developmental Cell</i> , 2012, 23, 691-704.	3.1	115
7904	New genes expressed in human brains: Implications for annotating evolving genomes. <i>BioEssays</i> , 2012, 34, 982-991.	1.2	54
7905	Assessment of gene-by-sex interaction effect on bone mineral density. <i>Journal of Bone and Mineral Research</i> , 2012, 27, 2051-2064.	3.1	47
7906	The Internet as Scientific Knowledge Base: Navigating the Chemâ€“Bio Space. <i>Molecular Informatics</i> , 2012, 31, 543-546.	1.4	6
7907	<scp>MS D</scp>ata <scp>M</scp>iner: A webâ€“based software tool to analyze, compare, and share mass spectrometry protein identifications. <i>Proteomics</i> , 2012, 12, 2792-2796.	1.3	45
7908	Inâ€“depth analysis of low abundant proteins in bovine colostrum using different fractionation techniques. <i>Proteomics</i> , 2012, 12, 2866-2878.	1.3	44

#	ARTICLE	IF	CITATIONS
7909	Vasculogenic and Osteogenesis-Enhancing Potential of Human Umbilical Cord Blood Endothelial Colony-Forming Cells. <i>Stem Cells</i> , 2012, 30, 1911-1924.	1.4	72
7910	Directing Differentiation of Human Embryonic Stem Cells Toward Anterior Neural Ectoderm Using Small Molecules. <i>Stem Cells</i> , 2012, 30, 1875-1884.	1.4	61
7911	Dual Lineage-Specific Expression of Sox17 During Mouse Embryogenesis. <i>Stem Cells</i> , 2012, 30, 2297-2308.	1.4	47
7912	A genome resource to address mechanisms of developmental programming: determination of the fetal sheep heart transcriptome. <i>Journal of Physiology</i> , 2012, 590, 2873-2884.	1.3	15
7913	OLSVis: an animated, interactive visual browser for bio-ontologies. <i>BMC Bioinformatics</i> , 2012, 13, 116.	1.2	20
7914	Biomine: predicting links between biological entities using network models of heterogeneous databases. <i>BMC Bioinformatics</i> , 2012, 13, 119.	1.2	50
7915	The language of gene ontology: a Zipf's law analysis. <i>BMC Bioinformatics</i> , 2012, 13, 127.	1.2	11
7916	Genes2FANs: connecting genes through functional association networks. <i>BMC Bioinformatics</i> , 2012, 13, 156.	1.2	28
7917	Concept annotation in the CRAFT corpus. <i>BMC Bioinformatics</i> , 2012, 13, 161.	1.2	188
7918	Detecting pore-lining regions in transmembrane protein sequences. <i>BMC Bioinformatics</i> , 2012, 13, 169.	1.2	63
7919	Evaluating the consistency of gene sets used in the analysis of bacterial gene expression data. <i>BMC Bioinformatics</i> , 2012, 13, 193.	1.2	8
7920	TFinDit: transcription factor-DNA interaction data depository. <i>BMC Bioinformatics</i> , 2012, 13, 220.	1.2	8
7921	Independent Principal Component Analysis for biologically meaningful dimension reduction of large biological data sets. <i>BMC Bioinformatics</i> , 2012, 13, 24.	1.2	111
7922	Cluster-based assessment of protein-protein interaction confidence. <i>BMC Bioinformatics</i> , 2012, 13, 262.	1.2	26
7923	Effects of protein interaction data integration, representation and reliability on the use of network properties for drug target prediction. <i>BMC Bioinformatics</i> , 2012, 13, 294.	1.2	24
7924	Bioinformatics resource manager v2.3: an integrated software environment for systems biology with microRNA and cross-species analysis tools. <i>BMC Bioinformatics</i> , 2012, 13, 311.	1.2	21
7925	BLANNOTATOR: enhanced homology-based function prediction of bacterial proteins. <i>BMC Bioinformatics</i> , 2012, 13, 33.	1.2	12
7926	The Bone Dysplasia Ontology: integrating genotype and phenotype information in the skeletal dysplasia domain. <i>BMC Bioinformatics</i> , 2012, 13, 50.	1.2	22

#	ARTICLE	IF	CITATIONS
7927	Fitting hidden Markov models of protein domains to a target species: application to <i>Plasmodium falciparum</i> . <i>BMC Bioinformatics</i> , 2012, 13, 67.	1.2	14
7928	A Bayesian variable selection procedure to rank overlapping gene sets. <i>BMC Bioinformatics</i> , 2012, 13, 73.	1.2	7
7929	THINK Back: KNowledge-based Interpretation of High Throughput data. <i>BMC Bioinformatics</i> , 2012, 13, S4.	1.2	12
7930	FUSE: a profit maximization approach for functional summarization of biological networks. <i>BMC Bioinformatics</i> , 2012, 13, S10.	1.2	29
7931	Scalable global alignment for multiple biological networks. <i>BMC Bioinformatics</i> , 2012, 13, S11.	1.2	27
7932	Argot2: a large scale function prediction tool relying on semantic similarity of weighted Gene Ontology terms. <i>BMC Bioinformatics</i> , 2012, 13, S14.	1.2	137
7933	BEAT: Bioinformatics Exon Array Tool to store, analyze and visualize Affymetrix GeneChip Human Exon Array data from disease experiments. <i>BMC Bioinformatics</i> , 2012, 13, S21.	1.2	5
7934	Improving biomarker list stability by integration of biological knowledge in the learning process. <i>BMC Bioinformatics</i> , 2012, 13, S22.	1.2	14
7935	Identification of novel mitosis regulators through data mining with human centromere/kinetochore proteins as group queries. <i>BMC Cell Biology</i> , 2012, 13, 15.	3.0	50
7936	Protein interactions of the transcription factor <i>Hoxa1</i> . <i>BMC Developmental Biology</i> , 2012, 12, 29.	2.1	43
7937	Dissecting the role of low-complexity regions in the evolution of vertebrate proteins. <i>BMC Evolutionary Biology</i> , 2012, 12, 155.	3.2	77
7938	Investigating the molecular basis of local adaptation to thermal stress: population differences in gene expression across the transcriptome of the copepod <i>Tigriopus californicus</i> . <i>BMC Evolutionary Biology</i> , 2012, 12, 170.	3.2	150
7939	The relationship between the hierarchical position of proteins in the human signal transduction network and their rate of evolution. <i>BMC Evolutionary Biology</i> , 2012, 12, 192.	3.2	21
7940	Expression variation in connected recombinant populations of <i>Arabidopsis thaliana</i> highlights distinct transcriptome architectures. <i>BMC Genomics</i> , 2012, 13, 117.	1.2	34
7941	A searchable cross-platform gene expression database reveals connections between drug treatments and disease. <i>BMC Genomics</i> , 2012, 13, 12.	1.2	40
7942	Comparative analysis of mycobacterium and related actinomycetes yields insight into the evolution of mycobacterium tuberculosis pathogenesis. <i>BMC Genomics</i> , 2012, 13, 120.	1.2	80
7943	De novo assembly and characterization of the root transcriptome of <i>Aegilops variabilis</i> during an interaction with the cereal cyst nematode. <i>BMC Genomics</i> , 2012, 13, 133.	1.2	63
7944	Comprehensive transcriptome analysis reveals novel genes involved in cardiac glycoside biosynthesis and mlncRNAs associated with secondary metabolism and stress response in <i>Digitalis purpurea</i> . <i>BMC Genomics</i> , 2012, 13, 15.	1.2	69

#	ARTICLE	IF	CITATIONS
7945	Functional organization and its implication in evolution of the human protein-protein interaction network. <i>BMC Genomics</i> , 2012, 13, 150.	1.2	9
7946	Transcriptome analysis of a long-lived natural <i>Drosophila</i> variant: a prominent role of stress- and reproduction-genes in lifespan extension. <i>BMC Genomics</i> , 2012, 13, 167.	1.2	43
7947	Genomic characterization of the conditionally dispensable chromosome in <i>Alternaria arborescens</i> provides evidence for horizontal gene transfer. <i>BMC Genomics</i> , 2012, 13, 171.	1.2	81
7948	Genome-wide expression profiling shows transcriptional reprogramming in <i>Fusarium graminearum</i> by <i>Fusarium graminearum</i> virus 1-DK21 infection. <i>BMC Genomics</i> , 2012, 13, 173.	1.2	40
7949	Genome wide response to dietary tetradecylthioacetic acid supplementation in the heart of Atlantic Salmon (<i>Salmo salar</i> L). <i>BMC Genomics</i> , 2012, 13, 180.	1.2	2
7950	Transcripts with in silico predicted RNA structure are enriched everywhere in the mouse brain. <i>BMC Genomics</i> , 2012, 13, 214.	1.2	12
7951	Widespread uncoupling between transcriptome and translatoe variations after a stimulus in mammalian cells. <i>BMC Genomics</i> , 2012, 13, 220.	1.2	113
7952	Yeast glucose pathways converge on the transcriptional regulation of trehalose biosynthesis. <i>BMC Genomics</i> , 2012, 13, 239.	1.2	30
7953	Transcriptomic analysis of the stress response to weaning at housing in bovine leukocytes using RNA-seq technology. <i>BMC Genomics</i> , 2012, 13, 250.	1.2	46
7954	Developing the anemone <i>Aiptasia</i> as a tractable model for cnidarian-dinoflagellate symbiosis: the transcriptome of aposymbiotic <i>A. pallida</i> . <i>BMC Genomics</i> , 2012, 13, 271.	1.2	99
7955	A genome-wide detection of copy number variations using SNP genotyping arrays in swine. <i>BMC Genomics</i> , 2012, 13, 273.	1.2	86
7956	NetWalker: a contextual network analysis tool for functional genomics. <i>BMC Genomics</i> , 2012, 13, 282.	1.2	99
7957	Elucidation of the molecular envenomation strategy of the cone snail <i>Conus geographus</i> through transcriptome sequencing of its venom duct. <i>BMC Genomics</i> , 2012, 13, 284.	1.2	83
7958	Transcriptome characterization via 454 pyrosequencing of the annelid <i>Pristina leidyi</i> , an emerging model for studying the evolution of regeneration. <i>BMC Genomics</i> , 2012, 13, 287.	1.2	22
7959	Comparative transcriptome analysis between planarian <i>Dugesia japonica</i> and other platyhelminth species. <i>BMC Genomics</i> , 2012, 13, 289.	1.2	34
7960	De novo transcriptome sequencing in a songbird, the dark-eyed junco (<i>Junco hyemalis</i>): genomic tools for an ecological model system. <i>BMC Genomics</i> , 2012, 13, 305.	1.2	35
7961	Brain transcriptome variation among behaviorally distinct strains of zebrafish (<i>Danio rerio</i>). <i>BMC Genomics</i> , 2012, 13, 323.	1.2	53
7962	atBioNetâ€” an integrated network analysis tool for genomics and biomarker discovery. <i>BMC Genomics</i> , 2012, 13, 325.	1.2	33

#	ARTICLE	IF	CITATIONS
7963	A microarray analysis of gnotobiotic mice indicating that microbial exposure during the neonatal period plays an essential role in immune system development. BMC Genomics, 2012, 13, 335.	1.2	43
7964	Patterns and architecture of genomic islands in marine bacteria. BMC Genomics, 2012, 13, 347.	1.2	84
7965	Profiling the resting venom gland of the scorpion <i>Tityus stigmurus</i> through a transcriptomic survey. BMC Genomics, 2012, 13, 362.	1.2	74
7966	The carbon starvation response of <i>Aspergillus niger</i> during submerged cultivation: Insights from the transcriptome and secretome. BMC Genomics, 2012, 13, 380.	1.2	108
7967	Maternal 3'UTRs: from egg to onset of zygotic transcription in Atlantic cod. BMC Genomics, 2012, 13, 443.	1.2	17
7968	CTen: a web-based platform for identifying enriched cell types from heterogeneous microarray data. BMC Genomics, 2012, 13, 460.	1.2	113
7969	Comparative genomic analysis of <i>Geobacter sulfurreducens</i> KN400, a strain with enhanced capacity for extracellular electron transfer and electricity production. BMC Genomics, 2012, 13, 471.	1.2	36
7970	Genome-wide landscape of liver X receptor chromatin binding and gene regulation in human macrophages. BMC Genomics, 2012, 13, 50.	1.2	69
7971	The diversity of cyanobacterial metabolism: genome analysis of multiple phototrophic microorganisms. BMC Genomics, 2012, 13, 56.	1.2	134
7972	De novo assembly of the pepper transcriptome (<i>Capsicum annuum</i>): a benchmark for in silico discovery of SNPs, SSRs and candidate genes. BMC Genomics, 2012, 13, 571.	1.2	109
7973	Large-scale sequencing based on full-length-enriched cDNA libraries in pigs: contribution to annotation of the pig genome draft sequence. BMC Genomics, 2012, 13, 581.	1.2	15
7974	Toward understanding the genetic basis of adaptation to high-elevation life in poikilothermic species: A comparative transcriptomic analysis of two ranid frogs, <i>Rana chensinensis</i> and <i>R. kukunoris</i> . BMC Genomics, 2012, 13, 588.	1.2	55
7975	Searching for resistance genes to <i>Bursaphelenchus xylophilus</i> using high throughput screening. BMC Genomics, 2012, 13, 599.	1.2	53
7976	The <i>Schistosoma mansoni</i> phylome: using evolutionary genomics to gain insight into a parasite's biology. BMC Genomics, 2012, 13, 617.	1.2	28
7977	RNA-seq and microarray complement each other in transcriptome profiling. BMC Genomics, 2012, 13, 629.	1.2	131
7978	Identification of maternally-loaded RNA transcripts in unfertilized eggs of <i>Tribolium castaneum</i> . BMC Genomics, 2012, 13, 671.	1.2	15
7979	Transcriptome analysis at four developmental stages of grape berry (<i>Vitis vinifera</i> cv. Shiraz) provides insights into regulated and coordinated gene expression. BMC Genomics, 2012, 13, 691.	1.2	125
7980	Genome-Wide Characterization of the Phosphate Starvation Response in <i>Schizosaccharomyces pombe</i> . BMC Genomics, 2012, 13, 697.	1.2	62

#	ARTICLE	IF	CITATIONS
7981	A genomic scale map of genetic diversity in <i>Trypanosoma cruzi</i> . BMC Genomics, 2012, 13, 736.	1.2	16
7982	Genomic variation in <i>Salmonella enterica</i> core genes for epidemiological typing. BMC Genomics, 2012, 13, 88.	1.2	76
7983	Comparative genome analysis of 19 <i>Ureaplasma urealyticum</i> and <i>Ureaplasma parvum</i> strains. BMC Microbiology, 2012, 12, 88.	1.3	91
7984	Transcript profiling reveals complex auxin signalling pathway and transcription regulation involved in dedifferentiation and redifferentiation during somatic embryogenesis in cotton. BMC Plant Biology, 2012, 12, 110.	1.6	135
7985	Genome-scale identification of cell-wall related genes in <i>Arabidopsis</i> based on co-expression network analysis. BMC Plant Biology, 2012, 12, 138.	1.6	56
7986	Comparative mapping in the Fagaceae and beyond with EST-SSRs. BMC Plant Biology, 2012, 12, 153.	1.6	54
7987	The tomato RLK superfamily: phylogeny and functional predictions about the role of the LRR-RLK subfamily in antiviral defense. BMC Plant Biology, 2012, 12, 229.	1.6	119
7988	Computational identification and experimental validation of microRNAs binding to the Alzheimer-related gene ADAM10. BMC Medical Genetics, 2012, 13, 35.	2.1	73
7989	Text-mining applied to autoimmune disease research: the Sjögren's syndrome knowledge base. BMC Musculoskeletal Disorders, 2012, 13, 119.	0.8	6
7990	Evolutionarily consistent families in SCOP: sequence, structure and function. BMC Structural Biology, 2012, 12, 27.	2.3	14
7991	De novo sequencing, assembly and analysis of the genome of the laboratory strain <i>Saccharomyces cerevisiae</i> CEN.PK113-7D, a model for modern industrial biotechnology. Microbial Cell Factories, 2012, 11, 36.	1.9	238
7992	A comparison of E15.5 fetus and newborn rat serum proteomes. Proteome Science, 2012, 10, 64.	0.7	3
7993	Dynamics of microRNAs in bull spermatozoa. Reproductive Biology and Endocrinology, 2012, 10, 82.	1.4	73
7994	MESSA: MEta-Server for protein Sequence Analysis. BMC Biology, 2012, 10, 82.	1.7	43
7995	A gene expression atlas of the domestic pig. BMC Biology, 2012, 10, 90.	1.7	199
7996	Transcriptome analysis of symptomatic and recovered leaves of geminivirus-infected pepper (<i>Capsicum</i>) Tj ETQq1 1,0,784314,rgBT / Ove 1.4	1.4	67
7997	Pathway-based classification of cancer subtypes. Biology Direct, 2012, 7, 21.	1.9	88
7998	Harnessing the complexity of gene expression data from cancer: from single gene to structural pathway methods. Biology Direct, 2012, 7, 44.	1.9	23

#	ARTICLE	IF	CITATIONS
7999	Integrating external biological knowledge in the construction of regulatory networks from time-series expression data. <i>BMC Systems Biology</i> , 2012, 6, 101.	3.0	49
8000	DREM 2.0: Improved reconstruction of dynamic regulatory networks from time-series expression data. <i>BMC Systems Biology</i> , 2012, 6, 104.	3.0	118
8001	Spatiotemporal network motif reveals the biological traits of developmental gene regulatory networks in <i>Drosophila melanogaster</i> . <i>BMC Systems Biology</i> , 2012, 6, 31.	3.0	20
8002	Organizational structure and the periphery of the gene regulatory network in B-cell lymphoma. <i>BMC Systems Biology</i> , 2012, 6, 38.	3.0	22
8003	From networks of protein interactions to networks of functional dependencies. <i>BMC Systems Biology</i> , 2012, 6, 44.	3.0	3
8004	Integrated pathway modules using time-course metabolic profiles and EST data from <i>Milnesium tardigradum</i> . <i>BMC Systems Biology</i> , 2012, 6, 72.	3.0	11
8005	Multiple independent analyses reveal only transcription factors as an enriched functional class associated with microRNAs. <i>BMC Systems Biology</i> , 2012, 6, 90.	3.0	21
8006	Transcriptomic analysis of the oleaginous microalga <i>Neochloris oleoabundans</i> reveals metabolic insights into triacylglyceride accumulation. <i>Biotechnology for Biofuels</i> , 2012, 5, 74.	6.2	178
8007	Bioenergy grass feedstock: current options and prospects for trait improvement using emerging genetic, genomic, and systems biology toolkits. <i>Biotechnology for Biofuels</i> , 2012, 5, 80.	6.2	53
8008	Systematically characterizing and prioritizing chemosensitivity related gene based on Gene Ontology and protein interaction network. <i>BMC Medical Genomics</i> , 2012, 5, 43.	0.7	9
8009	Subtypes of primary colorectal tumors correlate with response to targeted treatment in colorectal cell lines. <i>BMC Medical Genomics</i> , 2012, 5, 66.	0.7	202
8010	Murine colon proteome and characterization of the protein pathways. <i>BioData Mining</i> , 2012, 5, 11.	2.2	36
8011	Comparative analysis of grapevine whole-genome gene predictions, functional annotation, categorization and integration of the predicted gene sequences. <i>BMC Research Notes</i> , 2012, 5, 213.	0.6	176
8012	CytoITMprobe: a network information flow plugin for Cytoscape. <i>BMC Research Notes</i> , 2012, 5, 237.	0.6	3
8013	Human gene correlation analysis (HGCA): A tool for the identification of transcriptionally co-expressed genes. <i>BMC Research Notes</i> , 2012, 5, 265.	0.6	26
8014	LXtoo: an integrated live Linux distribution for the bioinformatics community. <i>BMC Research Notes</i> , 2012, 5, 360.	0.6	3
8015	Validation of MIMGO: a method to identify differentially expressed GO terms in a microarray dataset. <i>BMC Research Notes</i> , 2012, 5, 680.	0.6	0
8016	Analysis of <i>Babesia bovis</i> infection-induced gene expression changes in larvae from the cattle tick, <i>Rhipicephalus (Boophilus) microplus</i> . <i>Parasites and Vectors</i> , 2012, 5, 162.	1.0	29

#	ARTICLE	IF	CITATIONS
8017	Structure-based classification and ontology in chemistry. <i>Journal of Cheminformatics</i> , 2012, 4, 8.	2.8	40
8018	MicroRNAs from the same precursor have different targeting properties. <i>Silence: A Journal of RNA Regulation</i> , 2012, 3, 8.	8.0	57
8019	The Rice Oligonucleotide Array Database: an atlas of rice gene expression. <i>Rice</i> , 2012, 5, 17.	1.7	192
8020	Sequencing and analysis of the gastrula transcriptome of the brittle star <i>Ophiocoma wendtii</i> . <i>EvoDevo</i> , 2012, 3, 19.	1.3	19
8021	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
8022	Proteomics Wants cRacker: Automated Standardized Data Analysis of LC-MS Derived Proteomic Data. <i>Journal of Proteome Research</i> , 2012, 11, 5548-5555.	1.8	31
8023	A comprehensive cDNA library of light- and temperature-stressed <i>Saccharina latissima</i> (Phaeophyceae). <i>European Journal of Phycology</i> , 2012, 47, 83-94.	0.9	22
8024	Protein Databases on the Internet. <i>Current Protocols in Protein Science</i> , 2012, 70, Unit2.6.	2.8	11
8025	miR-16 inhibits the proliferation and angiogenesis-regulating potential of mesenchymal stem cells in severe pre-eclampsia. <i>FEBS Journal</i> , 2012, 279, 4510-4524.	2.2	102
8026	Protein arginine methylation in <i>Saccharomyces cerevisiae</i> . <i>FEBS Journal</i> , 2012, 279, 4423-4443.	2.2	45
8027	Next Generation Microarray Bioinformatics. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	8
8028	Fish Oil Alters Tamoxifen-Modulated Expression of mRNAs That Encode Genes Related to Differentiation, Proliferation, Metastasis, and Immune Response in Rat Mammary Tumors. <i>Nutrition and Cancer</i> , 2012, 64, 991-999.	0.9	7
8030	Mining Low-Support Discriminative Patterns from Dense and High-Dimensional Data. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2012, 24, 279-294.	4.0	33
8031	Highly Coordinated Proteome Dynamics during Reprogramming of Somatic Cells to Pluripotency. <i>Cell Reports</i> , 2012, 2, 1579-1592.	2.9	216
8032	A computational pipeline for comparative ChIP-seq analyses. <i>Nature Protocols</i> , 2012, 7, 45-61.	5.5	110
8033	A partitioning algorithm for large scale ontologies. , 2012, , .		5
8034	Commonly altered genomic regions in acute myeloid leukemia are enriched for somatic mutations involved in chromatin remodeling and splicing. <i>Blood</i> , 2012, 120, e83-e92.	0.6	131
8035	A functional selection model explains evolutionary robustness despite plasticity in regulatory networks. <i>Molecular Systems Biology</i> , 2012, 8, 619.	3.2	54

#	ARTICLE	IF	CITATIONS
8036	A Consistent Phylogenetic Backbone for the Fungi. <i>Molecular Biology and Evolution</i> , 2012, 29, 1319-1334.	3.5	129
8037	Predictive Cheminformatics in Drug Discovery: Statistical Modeling for Analysis of Micro-array and Gene Expression Data. <i>Methods in Molecular Biology</i> , 2012, 910, 165-194.	0.4	5
8038	Ectopic expression of the histone methyltransferase Ezh2 in haematopoietic stem cells causes myeloproliferative disease. <i>Nature Communications</i> , 2012, 3, 623.	5.8	103
8039	A Coclustering Approach for Mining Large Protein-Protein Interaction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 717-730.	1.9	29
8040	Adaptive Alternative Splicing Correlates with Less Environmental Risk of Parkinsonism. <i>Neurodegenerative Diseases</i> , 2012, 9, 87-98.	0.8	7
8041	CLASSIFYING PROCESSES: AN ESSAY IN APPLIED ONTOLOGY. <i>Ratio</i> , 2012, 25, 463-488.	0.3	23
8042	Deep brain stimulation induces rapidly reversible transcript changes in Parkinson's leucocytes. <i>Journal of Cellular and Molecular Medicine</i> , 2012, 16, 1496-1507.	1.6	15
8043	Transcriptome analysis of long non-coding RNA's of the nucleus accumbens in cocaine-conditioned mice. <i>Journal of Neurochemistry</i> , 2012, 123, 790-799.	2.1	46
8044	Pathway Analysis of a Genome-Wide Association Study of Ileal Crohn's Disease. <i>DNA and Cell Biology</i> , 2012, 31, 1549-1554.	0.9	18
8045	Ontologies for Human Behavior Analysis and Their Application to Clinical Data. <i>International Review of Neurobiology</i> , 2012, 103, 89-107.	0.9	10
8046	A Galaxy Workflow for the Functional Annotation of Metagenomic Samples. <i>Lecture Notes in Computer Science</i> , 2012, , 247-253.	1.0	3
8047	Biological Databases for Behavioral Neurobiology. <i>International Review of Neurobiology</i> , 2012, 103, 19-38.	0.9	2
8048	The Neurobehavior Ontology. <i>International Review of Neurobiology</i> , 2012, 103, 69-87.	0.9	31
8050	Bacterial Interactomes: From Interactions to Networks. <i>Methods in Molecular Biology</i> , 2012, 804, 15-33.	0.4	12
8051	VOLCANO PLOTS IN ANALYZING DIFFERENTIAL EXPRESSIONS WITH mRNA MICROARRAYS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1231003.	0.3	152
8052	Gel-Absorption-Based Sample Preparation Method for Shotgun Analysis of Membrane Proteome. <i>Methods in Molecular Biology</i> , 2012, 869, 385-392.	0.4	0
8053	Draft genome sequence of pigeonpea (<i>Cajanus cajan</i>), an orphan legume crop of resource-poor farmers. <i>Nature Biotechnology</i> , 2012, 30, 83-89.	9.4	788
8054	De novo Transcriptome Assembly and SNP Discovery in the Wing Polymorphic Salt Marsh Beetle <i>Pogonus chalceus</i> (Coleoptera, Carabidae). <i>PLoS ONE</i> , 2012, 7, e42605.	1.1	50

#	ARTICLE	IF	CITATIONS
8055	Genome-wide pathway analysis of genome-wide association studies on systemic lupus erythematosus and rheumatoid arthritis. <i>Molecular Biology Reports</i> , 2012, 39, 10627-10635.	1.0	114
8056	Decoding nonspecific interactions from nature. <i>Chemical Science</i> , 2012, 3, 3488.	3.7	96
8057	Using the Bioconductor GeneAnswers Package to Interpret Gene Lists. <i>Methods in Molecular Biology</i> , 2012, 802, 101-112.	0.4	22
8058	Integrated Inference and Analysis of Regulatory Networks from Multi-Level Measurements. <i>Methods in Cell Biology</i> , 2012, 110, 19-56.	0.5	17
8059	Augmented transitive relationships with high impact protein distillation in protein interaction prediction. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 1468-1475.	1.1	1
8060	Coordinating GWAS results with gene expression in a systems immunologic paradigm in autoimmunity. <i>Current Opinion in Immunology</i> , 2012, 24, 544-551.	2.4	14
8061	Revealing weak differential gene expressions and their reproducible functions associated with breast cancer metastasis. <i>Computational Biology and Chemistry</i> , 2012, 39, 1-5.	1.1	8
8062	Sparse regularized discriminant analysis with application to microarrays. <i>Computational Biology and Chemistry</i> , 2012, 39, 14-19.	1.1	1
8063	Hypothermia produces rat liver proteomic changes as in hibernating mammals but decreases endoplasmic reticulum chaperones. <i>Cryobiology</i> , 2012, 65, 104-112.	0.3	16
8064	Simplification and Desexualization of Gene Expression in Self-Fertile Nematodes. <i>Current Biology</i> , 2012, 22, 2167-2172.	1.8	68
8065	Transcriptomic analysis of <i>Ruditapes philippinarum</i> hemocytes reveals cytoskeleton disruption after in vitro <i>Vibrio tapetis</i> challenge. <i>Developmental and Comparative Immunology</i> , 2012, 38, 368-376.	1.0	26
8066	Sustained liver regeneration after portal vein embolization – A human molecular pilot study. <i>Digestive and Liver Disease</i> , 2012, 44, 681-688.	0.4	8
8067	Design and evaluation of Ubiquitous Information Systems and use in healthcare. <i>Decision Support Systems</i> , 2012, 54, 597-609.	3.5	41
8068	Proteomic analysis of podosome fractions from macrophages reveals similarities to spreading initiation centres. <i>European Journal of Cell Biology</i> , 2012, 91, 908-922.	1.6	62
8069	Systematic investigation of <i>Amphioxus</i> (<i>Branchiostoma floridae</i>) microRNAs. <i>Gene</i> , 2012, 508, 110-116.	1.0	5
8070	A sensitive method for computing GO-based functional similarities among genes with –shallow annotation–™. <i>Gene</i> , 2012, 509, 131-135.	1.0	7
8071	B-cell Ligand Processing Pathways Detected by Large-scale Comparative Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 142-152.	3.0	1
8072	Identification of genes differentially expressed in grapevine associated with resistance to <i>Elsinoe ampelina</i> through suppressive subtraction hybridization. <i>Plant Physiology and Biochemistry</i> , 2012, 58, 253-268.	2.8	30

#	ARTICLE	IF	CITATIONS
8073	Identification of dimorphism-involved genes of <i>Yarrowia lipolytica</i> by means of microarray analysis. <i>Research in Microbiology</i> , 2012, 163, 378-387.	1.0	42
8074	Current challenges in genome annotation through structural biology and bioinformatics. <i>Current Opinion in Structural Biology</i> , 2012, 22, 594-601.	2.6	14
8075	Identification of the pathogenic pathways in osteoarthritic hip cartilage: commonality and discord between hip and knee OA. <i>Osteoarthritis and Cartilage</i> , 2012, 20, 1029-1038.	0.6	81
8076	Expression of miRNAs Involved in Angiogenesis, Tumor Cell Proliferation, Tumor Suppressor Inhibition, Epithelial-Mesenchymal Transition and Activation of Metastasis in Bladder Cancer. <i>Journal of Urology</i> , 2012, 188, 615-623.	0.2	86
8077	Environmental microbiology through the lens of high-throughput DNA sequencing: Synopsis of current platforms and bioinformatics approaches. <i>Journal of Microbiological Methods</i> , 2012, 91, 106-113.	0.7	115
8078	Structural and genic characterization of stable genomic regions in breast cancer: Relevance to chemotherapy. <i>Molecular Oncology</i> , 2012, 6, 347-359.	2.1	15
8079	The pharmacogenetic background of hepatitis C treatment. <i>Mutation Research - Reviews in Mutation Research</i> , 2012, 751, 36-48.	2.4	8
8080	Prediction of Human Proteins Interacting with Human Papillomavirus Proteins. <i>Lecture Notes in Computer Science</i> , 2012, , 492-497.	1.0	0
8082	Urinary Proteome Analysis of Irritable Bowel Syndrome (IBS) Symptom Subgroups. <i>Journal of Proteome Research</i> , 2012, 11, 5650-5662.	1.8	31
8083	Gene Set Analysis as a Means of Facilitating the Interpretation of Microarray Results. , 2012, , 181-191.		0
8084	Exploring Genetic, Genomic, and Phenotypic Data at the Rat Genome Database. <i>Current Protocols in Bioinformatics</i> , 2012, 40, Unit1.14.	25.8	16
8085	PatternLab: From Mass Spectra to Label-Free Differential Shotgun Proteomics. <i>Current Protocols in Bioinformatics</i> , 2012, 40, Unit13.19.	25.8	39
8086	Simultaneously Learning DNA Motif along with Its Position and Sequence Rank Preferences through EM Algorithm. <i>Lecture Notes in Computer Science</i> , 2012, , 355-370.	1.0	3
8087	Data Mining Over Biological Datasets: An Integrated Approach Based on Computational Intelligence. <i>IEEE Computational Intelligence Magazine</i> , 2012, 7, 22-34.	3.4	17
8088	Functional Characterization of Human Genes from Exon Expression and RNA Interference Results. <i>Methods in Molecular Biology</i> , 2012, 910, 33-53.	0.4	0
8089	Using Functional Genomics to Identify Drug Targets: A Dupuytren's Disease Example. <i>Methods in Molecular Biology</i> , 2012, 910, 15-31.	0.4	1
8090	Linking Variants from Genome-Wide Association Analysis to Function via Transcriptional Network Analysis. <i>Methods in Molecular Biology</i> , 2012, 910, 297-308.	0.4	0
8091	Bacterial Genome Annotation. <i>Methods in Molecular Biology</i> , 2012, 881, 471-503.	0.4	7

#	ARTICLE	IF	CITATIONS
8092	Multiple apical plasma membrane constituents are associated with susceptibility to meconium ileus in individuals with cystic fibrosis. <i>Nature Genetics</i> , 2012, 44, 562-569.	9.4	177
8093	Discovering Patterns in Gene Order. <i>Methods in Molecular Biology</i> , 2012, 855, 431-455.	0.4	0
8094	Introduction to the Analysis of Environmental Sequences: Metagenomics with MEGAN. <i>Methods in Molecular Biology</i> , 2012, 856, 415-429.	0.4	74
8095	Complete genome sequence of the rapeseed plant-growth promoting <i>Serratia plymuthica</i> strain AS9. <i>Standards in Genomic Sciences</i> , 2012, 6, 54-62.	1.5	27
8096	Gene and protein responses of human lung tissue explants exposed to ambient particulate matter of different sizes. <i>Inhalation Toxicology</i> , 2012, 24, 966-975.	0.8	10
8097	Understanding Cancer Progression Using Protein Interaction Networks. , 2012, , 167-195.		1
8099	Is there a biological cost of protein disorder? Analysis of cancer-associated mutations. <i>Molecular BioSystems</i> , 2012, 8, 296-307.	2.9	43
8100	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
8101	Predicting the impact of deleterious single point mutations in SMAD gene family using structural bioinformatics approach. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2012, 4, 103-115.	2.2	6
8102	Application of a systems approach to study developmental gene regulation. <i>Biophysical Reviews</i> , 2012, 4, 245-253.	1.5	2
8103	Composite kernel based SVM for hierarchical multi-label gene function classification. , 2012, , .		4
8104	Modeling the relative relationship of transcription factor binding and histone modifications to gene expression levels in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , 2012, 40, 553-568.	6.5	145
8105	A Genome-Wide Regulatorâ€“DNA Interaction Network in the Human Pathogen <i>Mycobacterium tuberculosis</i> H37Rv. <i>Journal of Proteome Research</i> , 2012, 11, 4682-4692.	1.8	19
8106	â€œKeystone Speciesâ€“of Molecular Interaction Networks. <i>Developments in Environmental Modelling</i> , 2012, 25, 73-88.	0.3	0
8107	Growth of lung cancer cells in three-dimensional microenvironments reveals key features of tumor malignancy. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 440-448.	0.6	32
8108	Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	4
8109	Human Induced Pluripotent Stem Cells Derived Under Feeder-Free Conditions Display Unique Cell Cycle and DNA Replication Gene Profiles. <i>Stem Cells and Development</i> , 2012, 21, 206-216.	1.1	23
8110	Molecular target discovery for neural repair in the functional genomics era. <i>Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn</i> , 2012, 109, 595-616.	1.0	9

#	ARTICLE	IF	CITATIONS
8111	Gene expression profiling of hybridoma cells after bursal-derived bioactive factor BP5 treatment. <i>Amino Acids</i> , 2012, 43, 2443-2456.	1.2	10
8113	Codon Usage Methods for Horizontal Gene Transfer Detection Generate an Abundance of False Positive and False Negative Results. <i>Current Microbiology</i> , 2012, 65, 639-642.	1.0	19
8114	Gene expression patterns of the coral <i>Acropora millepora</i> in response to contact with macroalgae. <i>Coral Reefs</i> , 2012, 31, 1177-1192.	0.9	34
8115	Transcriptional network analysis of the tryptophan-accumulating rice mutant during grain filling. <i>Molecular Genetics and Genomics</i> , 2012, 287, 699-709.	1.0	1
8116	Detecting type 2 diabetes causal single nucleotide polymorphism combinations from a genome-wide association study dataset with optimal filtration. , 2012, , .		1
8117	The cell: an image library-CCDB: a curated repository of microscopy data. <i>Nucleic Acids Research</i> , 2012, 41, D1241-D1250.	6.5	51
8118	The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. <i>Nucleic Acids Research</i> , 2012, 40, D742-D753.	6.5	561
8119	Engineering Applications of Neural Networks. <i>Communications in Computer and Information Science</i> , 2012, , .	0.4	3
8120	Modular Analysis of Biological Networks. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 3-17.	0.8	27
8122	Proteomics Signature Profiling (PSP): A Novel Contextualization Approach for Cancer Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 1571-1581.	1.8	47
8123	Omics Era in Stem Cell Research: Data Integration of Multi-regulatory Layers. , 2012, , 119-137.		0
8124	Molecular Markers of Early-Stage Mycosis Fungoides. <i>Journal of Investigative Dermatology</i> , 2012, 132, 1698-1706.	0.3	88
8126	Vesicle and Vesicle-Free Extracellular Proteome of <i>Paracoccidioides brasiliensis</i> : Comparative Analysis with Other Pathogenic Fungi. <i>Journal of Proteome Research</i> , 2012, 11, 1676-1685.	1.8	160
8127	Comparative Analysis of Biological Networks: Hidden Markov model and Markov chain-based approach. <i>IEEE Signal Processing Magazine</i> , 2012, 29, 22-34.	4.6	23
8128	Convergent repression of <i>Foxp2</i> 3'UTR by miR-9 and miR-132 in embryonic mouse neocortex: implications for radial migration of neurons. <i>Development (Cambridge)</i> , 2012, 139, 3332-3342.	1.2	125
8129	Proteomic Analysis (GeLC-MS/MS) of ePFT-Collected Pancreatic Fluid in Chronic Pancreatitis. <i>Journal of Proteome Research</i> , 2012, 11, 1897-1912.	1.8	25
8130	Advances in Bioinformatics and Computational Biology. <i>Lecture Notes in Computer Science</i> , 2012, , .	1.0	1
8131	How Do You Find Transcription Factors? Computational Approaches to Compile and Annotate Repertoires of Regulators for Any Genome. <i>Methods in Molecular Biology</i> , 2012, 786, 3-19.	0.4	11

#	ARTICLE	IF	CITATIONS
8132	Identifying functional links between genes by evolutionary transcriptomics. <i>Molecular BioSystems</i> , 2012, 8, 2585.	2.9	3
8135	iLoc-Hum: using the accumulation-label scale to predict subcellular locations of human proteins with both single and multiple sites. <i>Molecular BioSystems</i> , 2012, 8, 629-641.	2.9	335
8136	Fish Lateral Line Innovation: Insights into the Evolutionary Genomic Dynamics of a Unique Mechanosensory Organ. <i>Molecular Biology and Evolution</i> , 2012, 29, 3887-3898.	3.5	11
8137	Access and Use of the GUDMAP Database of Genitourinary Development. <i>Methods in Molecular Biology</i> , 2012, 886, 185-201.	0.4	12
8138	Statistical Human Genetics. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	13
8140	Biomedical Text Mining: A Survey of Recent Progress. , 2012, , 465-517.		68
8141	Proteomic Profiling of the Influence of Iron Availability on <i>Cryptococcus gattii</i> . <i>Journal of Proteome Research</i> , 2012, 11, 189-205.	1.8	20
8142	Mining Text Data. , 2012, , .		639
8143	Information Computing and Applications. <i>Lecture Notes in Computer Science</i> , 2012, , .	1.0	6
8144	Transcriptional response of BALB/c mouse thyroids following in vivo astatine-211 exposure reveals distinct gene expression profiles. <i>EJNMMI Research</i> , 2012, 2, 32.	1.1	30
8145	Whole Genome Studies of Tetrahymena. <i>Methods in Cell Biology</i> , 2012, 109, 53-81.	0.5	30
8146	Bioinformatics and Drug Discovery. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	17
8147	1D and 2D annotation enrichment: a statistical method integrating quantitative proteomics with complementary high-throughput data. <i>BMC Bioinformatics</i> , 2012, 13, S12.	1.2	542
8148	Comparison of co-expression measures: mutual information, correlation, and model based indices. <i>BMC Bioinformatics</i> , 2012, 13, 328.	1.2	406
8149	Learning virulent proteins from integrated query networks. <i>BMC Bioinformatics</i> , 2012, 13, 321.	1.2	2
8150	HIDEN: Hierarchical decomposition of regulatory networks. <i>BMC Bioinformatics</i> , 2012, 13, 250.	1.2	9
8151	Process attributes in bio-ontologies. <i>BMC Bioinformatics</i> , 2012, 13, 217.	1.2	1
8152	Network-enabled gene expression analysis. <i>BMC Bioinformatics</i> , 2012, 13, 167.	1.2	14

#	ARTICLE	IF	CITATIONS
8153	An automated approach for the identification of horizontal gene transfers from complete genomes reveals the rhizome of Rickettsiales. <i>BMC Evolutionary Biology</i> , 2012, 12, 243.	3.2	13
8154	GLAD4U: deriving and prioritizing gene lists from PubMed literature. <i>BMC Genomics</i> , 2012, 13, S20.	1.2	108
8155	FastAnnotator- an efficient transcript annotation web tool. <i>BMC Genomics</i> , 2012, 13, S9.	1.2	51
8156	Preferential regulation of stably expressed genes in the human genome suggests a widespread expression buffering role of microRNAs. <i>BMC Genomics</i> , 2012, 13, S14.	1.2	14
8157	Space-related pharma-motifs for fast search of protein binding motifs and polypharmacological targets. <i>BMC Genomics</i> , 2012, 13, S21.	1.2	4
8158	The parasite specific substitution matrices improve the annotation of apicomplexan proteins. <i>BMC Genomics</i> , 2012, 13, S19.	1.2	4
8159	Assessing the gain of biological data integration in gene networks inference. <i>BMC Genomics</i> , 2012, 13, S7.	1.2	7
8160	Pathway Distiller - multisource biological pathway consolidation. <i>BMC Genomics</i> , 2012, 13, S18.	1.2	20
8161	Searching joint association signals in CATIE schizophrenia genome-wide association studies through a refined integrative network approach. <i>BMC Genomics</i> , 2012, 13, S15.	1.2	8
8162	A UML profile for the OBO relation ontology. <i>BMC Genomics</i> , 2012, 13, S3.	1.2	9
8163	A catalogue of putative unique transcripts from Douglas-fir (<i>Pseudotsuga menziesii</i>) based on 454 transcriptome sequencing of genetically diverse, drought stressed seedlings. <i>BMC Genomics</i> , 2012, 13, 673.	1.2	34
8164	Characterization of the transcriptome of an ecologically important avian species, the Vinous-throated Parrotbill <i>Paradoxornis webbianus bulomachus</i> (Paradoxornithidae; Aves). <i>BMC Genomics</i> , 2012, 13, 149.	1.2	12
8165	PMRD: a curated database for genes and mutants involved in plant male reproduction. <i>BMC Plant Biology</i> , 2012, 12, 215.	1.6	21
8166	A semantic proteomics dashboard (SemPoD) for data management in translational research. <i>BMC Systems Biology</i> , 2012, 6, S20.	3.0	8
8167	Detection of protein complexes from affinity purification/mass spectrometry data. <i>BMC Systems Biology</i> , 2012, 6, S4.	3.0	10
8168	Supervised maximum-likelihood weighting of composite protein networks for complex prediction. <i>BMC Systems Biology</i> , 2012, 6, S13.	3.0	36
8169	PCDq: human protein complex database with quality index which summarizes different levels of evidences of protein complexes predicted from H-Invitational protein-protein interactions integrative dataset. <i>BMC Systems Biology</i> , 2012, 6, S7.	3.0	61
8170	Systems Metabolic Engineering. , 2012, , .		11

#	ARTICLE	IF	CITATIONS
8171	Bacterial Molecular Networks. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	13
8172	Genome-Wide Analysis of Pain-, Nerve- and Neurotrophin -Related Gene Expression in the Degenerating Human Annulus. <i>Molecular Pain</i> , 2012, 8, 1744-8069-8-63.	1.0	52
8173	Four new loci associations discovered by pathway-based and network analyses of the genome-wide variability profile of Hirschsprungâ€™s disease. <i>Orphanet Journal of Rare Diseases</i> , 2012, 7, 103.	1.2	7
8174	Visualising associations between paired â€™omicsâ€™ data sets. <i>BioData Mining</i> , 2012, 5, 19.	2.2	261
8175	Differential analysis of high-throughput quantitative genetic interaction data. <i>Genome Biology</i> , 2012, 13, R123.	13.9	21
8176	RIDDLE: Reflective diffusion and local extension reveal functional associations for unannotated gene sets via proximity in a gene network. <i>Genome Biology</i> , 2012, 13, R125.	13.9	16
8177	Ray Meta: scalable de novo metagenome assembly and profiling. <i>Genome Biology</i> , 2012, 13, R122.	13.9	549
8178	Improving the prediction of the functional impact of cancer mutations by baseline tolerance transformation. <i>Genome Medicine</i> , 2012, 4, 89.	3.6	91
8179	Finding biomedical categories in Medlineâ€™. <i>Journal of Biomedical Semantics</i> , 2012, 3, S3.	0.9	6
8180	Ontology-based cross-species integration and analysis of <i>Saccharomyces cerevisiae</i> phenotypes. <i>Journal of Biomedical Semantics</i> , 2012, 3, S6.	0.9	6
8181	Towards improving phenotype representation in OWL. <i>Journal of Biomedical Semantics</i> , 2012, 3, S5.	0.9	4
8182	Towards an ontological representation of morbidity and mortality in Description Logics. <i>Journal of Biomedical Semantics</i> , 2012, 3, S7.	0.9	2
8183	Semantically enabling a genome-wide association study database. <i>Journal of Biomedical Semantics</i> , 2012, 3, 9.	0.9	8
8184	The Ontology for Parasite Lifecycle (OPL): towards a consistent vocabulary of lifecycle stages in parasitic organisms. <i>Journal of Biomedical Semantics</i> , 2012, 3, 5.	0.9	4
8185	An eUtils toolset and its use for creating a pipeline to link genomics and proteomics analyses to domain-specific biomedical literature. <i>Journal of Clinical Bioinformatics</i> , 2012, 2, 9.	1.2	5
8186	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
8187	Linking Genome Annotation Projects with Genetic Disorders using Ontologies. <i>Journal of Medical Systems</i> , 2012, 36, 11-23.	2.2	1
8188	Transcriptome and Network Changes in Climbers at Extreme Altitudes. <i>PLoS ONE</i> , 2012, 7, e31645.	1.1	21

#	ARTICLE	IF	CITATIONS
8189	Genome Analysis of a Highly Virulent Serotype 1 Strain of <i>Streptococcus pneumoniae</i> from West Africa. <i>PLoS ONE</i> , 2012, 7, e26742.	1.1	17
8190	Long-Term Survival of Hydrated Resting Eggs from <i>Brachionus plicatilis</i> . <i>PLoS ONE</i> , 2012, 7, e29365.	1.1	34
8191	Cloning and Characterization of Maize miRNAs Involved in Responses to Nitrogen Deficiency. <i>PLoS ONE</i> , 2012, 7, e29669.	1.1	142
8192	A Powerful Method for Transcriptional Profiling of Specific Cell Types in Eukaryotes: Laser-Assisted Microdissection and RNA Sequencing. <i>PLoS ONE</i> , 2012, 7, e29685.	1.1	104
8193	Expression of Extracellular Matrix Components Is Disrupted in the Immature and Adult Estrogen Receptor β -Null Mouse Ovary. <i>PLoS ONE</i> , 2012, 7, e29937.	1.1	18
8194	Polyglutamine Repeats Are Associated to Specific Sequence Biases That Are Conserved among Eukaryotes. <i>PLoS ONE</i> , 2012, 7, e30824.	1.1	32
8195	The Gene Expression Analysis of Blood Reveals S100A11 and AQP9 as Potential Biomarkers of Infective Endocarditis. <i>PLoS ONE</i> , 2012, 7, e31490.	1.1	46
8196	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
8197	iCanPlot: Visual Exploration of High-Throughput Omics Data Using Interactive Canvas Plotting. <i>PLoS ONE</i> , 2012, 7, e31690.	1.1	9
8198	Widespread mRNA Association with Cytoskeletal Motor Proteins and Identification and Dynamics of Myosin-Associated mRNAs in <i>S. cerevisiae</i> . <i>PLoS ONE</i> , 2012, 7, e31912.	1.1	16
8199	Function-Based Discovery of Significant Transcriptional Temporal Patterns in Insulin Stimulated Muscle Cells. <i>PLoS ONE</i> , 2012, 7, e32391.	1.1	11
8200	Dysregulation of Gene Expression in a Lysosomal Storage Disease Varies between Brain Regions Implicating Unexpected Mechanisms of Neuropathology. <i>PLoS ONE</i> , 2012, 7, e32419.	1.1	43
8201	High-Order SNP Combinations Associated with Complex Diseases: Efficient Discovery, Statistical Power and Functional Interactions. <i>PLoS ONE</i> , 2012, 7, e33531.	1.1	48
8202	Bagging Statistical Network Inference from Large-Scale Gene Expression Data. <i>PLoS ONE</i> , 2012, 7, e33624.	1.1	122
8203	Functional Annotation of Hierarchical Modularity. <i>PLoS ONE</i> , 2012, 7, e33744.	1.1	4
8204	Cell Cycle Gene Networks Are Associated with Melanoma Prognosis. <i>PLoS ONE</i> , 2012, 7, e34247.	1.1	32
8205	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
8206	Transcriptome Analysis Reveals Strain-Specific and Conserved Stemness Genes in <i>Schmidtea mediterranea</i> . <i>PLoS ONE</i> , 2012, 7, e34447.	1.1	48

#	ARTICLE	IF	CITATIONS
8207	Context-Specific Protein Network Miner “ An Online System for Exploring Context-Specific Protein Interaction Networks from the Literature. PLoS ONE, 2012, 7, e34480.	1.1	18
8208	Transcriptome Profiling of the Intoxication Response of <i>Tenebrio molitor</i> Larvae to <i>Bacillus thuringiensis</i> Cry3Aa Protoxin. PLoS ONE, 2012, 7, e34624.	1.1	60
8209	The Interaction Properties of the Human Rab GTPase Family “ A Comparative Analysis Reveals Determinants of Molecular Binding Selectivity. PLoS ONE, 2012, 7, e34870.	1.1	38
8210	Transcriptomics of In Vitro Immune-Stimulated Hemocytes from the Manila Clam <i>Ruditapes philippinarum</i> Using High-Throughput Sequencing. PLoS ONE, 2012, 7, e35009.	1.1	106
8211	SyStemCell: A Database Populated with Multiple Levels of Experimental Data from Stem Cell Differentiation Research. PLoS ONE, 2012, 7, e35230.	1.1	13
8212	Functional and Topological Properties in Hepatocellular Carcinoma Transcriptome. PLoS ONE, 2012, 7, e35510.	1.1	24
8213	Gene Expression Profiles of the NCI-60 Human Tumor Cell Lines Define Molecular Interaction Networks Governing Cell Migration Processes. PLoS ONE, 2012, 7, e35716.	1.1	28
8214	The Genome of <i>Ganderma lucidum</i> Provide Insights into Triterpene Biosynthesis and Wood Degradation. PLoS ONE, 2012, 7, e36146.	1.1	78
8215	Evolutionary Conservation and Network Structure Characterize Genes of Phenotypic Relevance for Mitosis in Human. PLoS ONE, 2012, 7, e36488.	1.1	5
8216	MGEx-Udb: A Mammalian Uterus Database for Expression-Based Cataloguing of Genes across Conditions, Including Endometriosis and Cervical Cancer. PLoS ONE, 2012, 7, e36776.	1.1	9
8217	WNP: A Novel Algorithm for Gene Products Annotation from Weighted Functional Networks. PLoS ONE, 2012, 7, e38767.	1.1	5
8218	Characteristic Gene Selection via Weighting Principal Components by Singular Values. PLoS ONE, 2012, 7, e38873.	1.1	17
8219	Effect of Chemical Mutagens and Carcinogens on Gene Expression Profiles in Human TK6 Cells. PLoS ONE, 2012, 7, e39205.	1.1	15
8220	Berry Flesh and Skin Ripening Features in <i>Vitis vinifera</i> as Assessed by Transcriptional Profiling. PLoS ONE, 2012, 7, e39547.	1.1	108
8221	Transcriptome Sequencing and Comparative Analysis of <i>Saccharina japonica</i> (Laminariales). PLoS ONE, 2012, 7, e39821.	1.1	93
8222	Different Genes Interact with Particulate Matter and Tobacco Smoke Exposure in Affecting Lung Function Decline in the General Population. PLoS ONE, 2012, 7, e40175.	1.1	40
8223	Concerted Perturbation Observed in a Hub Network in Alzheimer’s Disease. PLoS ONE, 2012, 7, e40498.	1.1	91
8224	Mining GO Annotations for Improving Annotation Consistency. PLoS ONE, 2012, 7, e40519.	1.1	33

#	ARTICLE	IF	CITATIONS
8225	A Least Angle Regression Model for the Prediction of Canonical and Non-Canonical miRNA-mRNA Interactions. PLoS ONE, 2012, 7, e40634.	1.1	20
8226	Comparative Transcriptomics of the Saprobic and Parasitic Growth Phases in <i>Coccidioides</i> spp. PLoS ONE, 2012, 7, e41034.	1.1	79
8227	Prediction and Analysis of the Protein Interactome in <i>Pseudomonas aeruginosa</i> to Enable Network-Based Drug Target Selection. PLoS ONE, 2012, 7, e41202.	1.1	33
8228	A Network Synthesis Model for Generating Protein Interaction Network Families. PLoS ONE, 2012, 7, e41474.	1.1	34
8229	Statistical Approaches to Use a Model Organism for Regulatory Sequences Annotation of Newly Sequenced Species. PLoS ONE, 2012, 7, e42489.	1.1	1
8230	A Comparison of Computational Methods for Identifying Virulence Factors. PLoS ONE, 2012, 7, e42517.	1.1	29
8231	Exploring Overlapping Functional Units with Various Structure in Protein Interaction Networks. PLoS ONE, 2012, 7, e43092.	1.1	20
8232	Cell-Free MicroRNA Expression Profiles in Malignant Effusion Associated with Patient Survival in Non-Small Cell Lung Cancer. PLoS ONE, 2012, 7, e43268.	1.1	53
8233	Identifying the Genetic Variation of Gene Expression Using Gene Sets: Application of Novel Gene Set eQTL Approach to PharmGKB and KEGG. PLoS ONE, 2012, 7, e43301.	1.1	6
8234	Gene Network Revealed Involvements of <i>Birc2</i> , <i>Birc3</i> and <i>Tnfrsf1a</i> in Anti-Apoptosis of Injured Peripheral Nerves. PLoS ONE, 2012, 7, e43436.	1.1	36
8235	Systems Analysis of a Mouse Xenograft Model Reveals Annexin A1 as a Regulator of Gene Expression in Tumor Stroma. PLoS ONE, 2012, 7, e43551.	1.1	3
8236	Identification and Comparative Profiling of miRNAs in an Early Flowering Mutant of Trifoliate Orange and Its Wild Type by Genome-Wide Deep Sequencing. PLoS ONE, 2012, 7, e43760.	1.1	38
8237	Comprehensive Binary Interaction Mapping of SH2 Domains via Fluorescence Polarization Reveals Novel Functional Diversification of ErbB Receptors. PLoS ONE, 2012, 7, e44471.	1.1	60
8238	An Insight into the Sialotranscriptome of the Cat Flea, <i>Ctenocephalides felis</i> . PLoS ONE, 2012, 7, e44612.	1.1	34
8239	Recruitment of Rpd3 to the Telomere Depends on the Protein Arginine Methyltransferase Hmt1. PLoS ONE, 2012, 7, e44656.	1.1	4
8240	Multi-Edge Gene Set Networks Reveal Novel Insights into Global Relationships between Biological Themes. PLoS ONE, 2012, 7, e45211.	1.1	10
8241	Analyzing Gene Expression from Whole Tissue vs. Different Cell Types Reveals the Central Role of Neurons in Predicting Severity of Alzheimer's Disease. PLoS ONE, 2012, 7, e45879.	1.1	6
8242	De Novo Foliar Transcriptome of <i>Chenopodium amaranticolor</i> and Analysis of Its Gene Expression During Virus-Induced Hypersensitive Response. PLoS ONE, 2012, 7, e45953.	1.1	30

#	ARTICLE	IF	CITATIONS
8243	Length Bias Correction in Gene Ontology Enrichment Analysis Using Logistic Regression. PLoS ONE, 2012, 7, e46128.	1.1	29
8244	PICARA, an Analytical Pipeline Providing Probabilistic Inference about A Priori Candidates Genes Underlying Genome-Wide Association QTL in Plants. PLoS ONE, 2012, 7, e46596.	1.1	23
8245	Identification of Gene Modules Associated with Drought Response in Rice by Network-Based Analysis. PLoS ONE, 2012, 7, e33748.	1.1	61
8246	Transcriptional Profiles of Mating-Responsive Genes from Testes and Male Accessory Glands of the Mediterranean Fruit Fly, <i>Ceratitis capitata</i> . PLoS ONE, 2012, 7, e46812.	1.1	40
8247	Non-Gaussian Distributions Affect Identification of Expression Patterns, Functional Annotation, and Prospective Classification in Human Cancer Genomes. PLoS ONE, 2012, 7, e46935.	1.1	24
8248	The Transcriptome Profile of the Mosquito <i>Culex quinquefasciatus</i> following Permethrin Selection. PLoS ONE, 2012, 7, e47163.	1.1	51
8249	SEED Servers: High-Performance Access to the SEED Genomes, Annotations, and Metabolic Models. PLoS ONE, 2012, 7, e48053.	1.1	169
8250	Wiki-Pi: A Web-Server of Annotated Human Protein-Protein Interactions to Aid in Discovery of Protein Function. PLoS ONE, 2012, 7, e49029.	1.1	67
8251	Comprehensive Human Transcription Factor Binding Site Map for Combinatory Binding Motifs Discovery. PLoS ONE, 2012, 7, e49086.	1.1	5
8252	Gene Size Matters. PLoS ONE, 2012, 7, e49093.	1.1	21
8253	Interactogeneous: Disease Gene Prioritization Using Heterogeneous Networks and Full Topology Scores. PLoS ONE, 2012, 7, e49634.	1.1	32
8254	Characterization of Head Transcriptome and Analysis of Gene Expression Involved in Caste Differentiation and Aggression in <i>Odontotermes formosanus</i> (Shiraki). PLoS ONE, 2012, 7, e50383.	1.1	41
8255	Structural and Functional Analysis of Multi-Interface Domains. PLoS ONE, 2012, 7, e50821.	1.1	5
8256	Pathway Analysis of Smoking Quantity in Multiple GWAS Identifies Cholinergic and Sensory Pathways. PLoS ONE, 2012, 7, e50913.	1.1	11
8257	RNA-Seq vs Dual- and Single-Channel Microarray Data: Sensitivity Analysis for Differential Expression and Clustering. PLoS ONE, 2012, 7, e50986.	1.1	71
8258	Computational Prediction of Protein-Protein Interactions in <i>Leishmania</i> Predicted Proteomes. PLoS ONE, 2012, 7, e51304.	1.1	32
8259	A Systems Approach to Rheumatoid Arthritis. PLoS ONE, 2012, 7, e51508.	1.1	26
8260	Labeling Nodes Using Three Degrees of Propagation. PLoS ONE, 2012, 7, e51947.	1.1	17

#	ARTICLE	IF	CITATIONS
8261	Development of Transcriptomic Resources for Interrogating the Biosynthesis of Monoterpene Indole Alkaloids in Medicinal Plant Species. <i>PLoS ONE</i> , 2012, 7, e52506.	1.1	150
8262	Analysis on the Pathogenesis of Symptomatic Pulmonary Embolism with Human Genomics. <i>International Journal of Medical Sciences</i> , 2012, 9, 380-386.	1.1	7
8263	Implications of TGF β ² on Transcriptome and Cellular Biofunctions of Palatal Mesenchyme. <i>Frontiers in Physiology</i> , 2012, 3, 85.	1.3	12
8265	An Overview of the Immunological Defenses in Fish Skin. <i>ISRN Immunology</i> , 2012, 2012, 1-29.	0.7	378
8266	Mining Low-Variance Biclusters to Discover Coregulation Modules in Sequencing Datasets. <i>Scientific Programming</i> , 2012, 20, 15-27.	0.5	1
8267	A Topology-Based Metric for Measuring Term Similarity in the Gene Ontology. <i>Advances in Bioinformatics</i> , 2012, 2012, 1-17.	5.7	44
8268	The Population Genomics of Sunflowers and Genomic Determinants of Protein Evolution Revealed by RNAseq. <i>Biology</i> , 2012, 1, 575-596.	1.3	34
8269	Using Multiple Phenotype Assays and Epistasis Testing to Enhance the Reliability of RNAi Screening and Identify Regulators of Muscle Protein Degradation. <i>Genes</i> , 2012, 3, 686-701.	1.0	5
8270	What mRNA Abundances Can Tell us about Metabolism. <i>Metabolites</i> , 2012, 2, 614-631.	1.3	42
8271	Metabolic Consequences of TGF β Stimulation in Cultured Primary Mouse Hepatocytes Screened from Transcript Data with ModeScore. <i>Metabolites</i> , 2012, 2, 983-1003.	1.3	2
8272	Statistical Inference and Reverse Engineering of Gene Regulatory Networks from Observational Expression Data. <i>Frontiers in Genetics</i> , 2012, 3, 8.	1.1	116
8273	Methods for Determining the Statistical Significance of Enrichment or Depletion of Gene Ontology Classifications under Weighted Membership. <i>Frontiers in Genetics</i> , 2012, 3, 24.	1.1	0
8274	Bioinformatic Resources of microRNA Sequences, Gene Targets, and Genetic Variation. <i>Frontiers in Genetics</i> , 2012, 3, 31.	1.1	17
8275	The Nematode <i>Caenorhabditis elegans</i> , Stress and Aging: Identifying the Complex Interplay of Genetic Pathways Following the Treatment with Humic Substances. <i>Frontiers in Genetics</i> , 2012, 3, 50.	1.1	10
8276	The Choice between MapMan and Gene Ontology for Automated Gene Function Prediction in Plant Science. <i>Frontiers in Genetics</i> , 2012, 3, 115.	1.1	71
8277	Benefits of using molecular structure and abundance in phylogenomic analysis. <i>Frontiers in Genetics</i> , 2012, 3, 172.	1.1	32
8278	The ontology-based answers (OBA) service: a connector for embedded usage of ontologies in applications. <i>Frontiers in Genetics</i> , 2012, 3, 197.	1.1	14
8279	An ontological analysis of some biological ontologies. <i>Frontiers in Genetics</i> , 2012, 3, 269.	1.1	1

#	ARTICLE	IF	CITATIONS
8280	Infection Strategies of Bacterial and Viral Pathogens through Pathogenâ€‘Human Proteinâ€‘Protein Interactions. <i>Frontiers in Microbiology</i> , 2012, 3, 46.	1.5	63
8281	An Interspecies Regulatory Network Inferred from Simultaneous RNA-seq of <i>Candida albicans</i> Invading Innate Immune Cells. <i>Frontiers in Microbiology</i> , 2012, 3, 85.	1.5	123
8282	Deciphering Novel Hostâ€‘Herpesvirus Interactions by Virion Proteomics. <i>Frontiers in Microbiology</i> , 2012, 3, 181.	1.5	26
8283	Effects of Aging and Anatomic Location on Gene Expression in Human Retina. <i>Frontiers in Aging Neuroscience</i> , 2012, 4, 8.	1.7	31
8284	Candidate genes in ocular dominance plasticity. <i>Frontiers in Neuroscience</i> , 2012, 6, 11.	1.4	9
8285	Understanding the Pathogenesis of Cytopathic and Noncytopathic Bovine Viral Diarrhea Virus Infection Using Proteomics. , 0, , .		2
8286	2D-NanoLC-ESI-MS/MS for Separation and Identification of Mouse Brain Membrane Proteins. , 2012, , .		0
8287	Centralities Based Analysis of Complex Networks. , 0, , .		44
8288	Unusual Viral Genomes. , 2012, , 115-125.		1
8289	Tumor Suppressor Maspin as a Rheostat in HDAC Regulation to Achieve the Fine-Tuning of Epithelial Homeostasis. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2012, 22, 249-258.	0.4	14
8290	A Critical Evaluation of Clinical Trials in Cancer and Pharmacogenomics. <i>Nature Precedings</i> , 2012, , .	0.1	0
8291	Using Self-Organizing Maps to Visualize, Filter and Cluster Multidimensional Bio-Omics Data. , 0, , .		4
8292	Subtractive libraries for prospecting differentially expressed genes in the soybean under water deficit. <i>Genetics and Molecular Biology</i> , 2012, 35, 304-314.	0.6	29
8293	iLoc-Gpos: A Multi-Layer Classifier for Predicting the Subcellular Localization of Singleplex and Multiplex Gram-Positive Bacterial Proteins. <i>Protein and Peptide Letters</i> , 2012, 19, 4-14.	0.4	138
8294	Contributions to an animal trait ontology ^{1,2} . <i>Journal of Animal Science</i> , 2012, 90, 2061-2066.	0.2	7
8295	Dynamic Subontology Evolution for Traditional Chinese Medicine Web Ontology. , 2012, , 135-169.		0
8296	Prediction of Ischemic Events on the Basis of Transcriptomic and Genomic Profiling in Patients Undergoing Carotid Endarterectomy. <i>Molecular Medicine</i> , 2012, 18, 669-675.	1.9	118
8297	Semantic E-Science for Traditional Chinese Medicine. , 2012, , 87-107.		2

#	ARTICLE	IF	CITATIONS
8298	AMDA 2.13: A major update for automated cross-platform microarray data analysis. <i>BioTechniques</i> , 2012, 53, 33-40.	0.8	6
8299	The Darwin Core extension for genebanks opens up new opportunities for sharing genebank datasets. <i>Biodiversity Informatics</i> , 2012, 8, .	3.0	12
8300	GeNet: A Graph-Based Genetic Programming Framework for the Reverse Engineering of Gene Regulatory Networks. <i>Lecture Notes in Computer Science</i> , 2012, , 97-109.	1.0	2
8301	Analysis of Gene Expression Data Using Biclustering Algorithms. , 0, , .		1
8302	The Investigation of Gene Regulation and Variation in Human Cancers and Other Diseases. , 2012, , .		0
8304	Protein-Protein Interactions and Disease. , 0, , .		1
8305	Application of functional genomic information to develop efficient EST-SSRs for the chicken (<i>Gallus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.3	13
8306	Methods for detection of horizontal transfer of transposable elements in complete genomes. <i>Genetics and Molecular Biology</i> , 2012, 35, 1078-1084.	0.6	21
8307	Gene-pair representation and incorporation of GO-based semantic similarity into classification of gene expression data. <i>Intelligent Data Analysis</i> , 2012, 16, 827-843.	0.4	0
8308	Hierarchical Modular Structure Identification with Its Applications in Gene Coexpression Networks. <i>Scientific World Journal, The</i> , 2012, 2012, 1-8.	0.8	27
8309	Clinical Research Data. , 2012, , 501-508.		0
8310	The gene expression profiles of induced pluripotent stem cells (iPSCs) generated by a non-integrating method are more similar to embryonic stem cells than those of iPSCs generated by an integrating method. <i>Genetics and Molecular Biology</i> , 2012, 35, 693-700.	0.6	15
8311	Pathway Detection from Protein Interaction Networks and Gene Expression Data Using Color-Coding Methods and A* Search Algorithms. <i>Scientific World Journal, The</i> , 2012, 2012, 1-14.	0.8	9
8312	A simple boiling-based DNA extraction for RAPD profiling of landfarm soil to provide representative metagenomic content. <i>Genetics and Molecular Research</i> , 2012, 11, 182-189.	0.3	4
8313	Biomarker Identification for Prostate Cancer and Lymph Node Metastasis from Microarray Data and Protein Interaction Network Using Gene Prioritization Method. <i>Scientific World Journal, The</i> , 2012, 2012, 1-15.	0.8	14
8314	A semantic web framework to integrate cancer omics data with biological knowledge. <i>BMC Bioinformatics</i> , 2012, 13, S10.	1.2	17
8315	Populous: a tool for building OWL ontologies from templates. <i>BMC Bioinformatics</i> , 2012, 13, S5.	1.2	25
8316	Camps 2.0: Exploring the sequence and structure space of prokaryotic, eukaryotic, and viral membrane proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 839-857.	1.5	13

#	ARTICLE	IF	CITATIONS
8317	Recent approaches to the prioritization of candidate disease genes. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 429-442.	6.6	59
8318	Systems vaccinology: learning to compute the behavior of vaccine induced immunity. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 193-205.	6.6	78
8319	Mass spectrometry-based proteomics: qualitative identification to activity-based protein profiling. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 141-162.	6.6	12
8320	Proteomic analysis of β 1 integrin adhesion complexes reveals β -subunit-dependent protein recruitment. Proteomics, 2012, 12, 2107-2114.	1.3	52
8321	Search engine processor: Filtering and organizing peptide spectrum matches. Proteomics, 2012, 12, 944-949.	1.3	107
8322	<scp>PRDB</scp>: <scp>P</scp>rotein <scp>R</scp>epeat <scp>D</scp>ata<scp>B</scp>ase. Proteomics, 2012, 12, 1333-1336.	1.3	12
8323	Interactome mapping for analysis of complex phenotypes: Insights from benchmarking binary interaction assays. Proteomics, 2012, 12, 1499-1518.	1.3	52
8324	Combining many interaction networks to predict gene function and analyze gene lists. Proteomics, 2012, 12, 1687-1696.	1.3	47
8325	Systems biology analysis of protein-drug interactions. Proteomics - Clinical Applications, 2012, 6, 102-116.	0.8	27
8326	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
8327	Computational design, construction, and characterization of a set of specificity determining residues in protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2426-2436.	1.5	4
8328	Clustering algorithm based on mutual K-nearest neighbor relationships. Statistical Analysis and Data Mining, 2012, 5, 100-113.	1.4	13
8329	Hierarchical multi-label classification based on over-sampling and hierarchy constraint for gene function prediction. IEEJ Transactions on Electrical and Electronic Engineering, 2012, 7, 183-189.	0.8	11
8330	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. Science, 2012, 337, 100-104.	6.0	626
8331	Comprehensive Description of the N-Glycoproteome of Mouse Pancreatic β -Cells and Human Islets. Journal of Proteome Research, 2012, 11, 1598-1608.	1.8	28
8332	clusterProfiler: an R Package for Comparing Biological Themes Among Gene Clusters. OMICS A Journal of Integrative Biology, 2012, 16, 284-287.	1.0	21,237
8333	Classificatory Theory in Data-intensive Science: The Case of Open Biomedical Ontologies. International Studies in the Philosophy of Science, 2012, 26, 47-65.	0.2	35
8334	Defining GM-CSF and Macrophage-CSF-Dependent Macrophage Responses by In Vitro Models. Journal of Immunology, 2012, 188, 5752-5765.	0.4	429

#	ARTICLE	IF	CITATIONS
8335	Next-Generation MicroRNA Expression Profiling Technology. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	5
8336	A Database of Annotated Promoters of Genes Associated with Common Respiratory and Related Diseases. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2012, 47, 112-119.	1.4	7
8337	Identification of Novel miR-21 Target Proteins in Multiple Myeloma Cells by Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 2078-2090.	1.8	66
8338	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 47-52.	9.4	893
8339	Analyzing Proteinâ€“Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2012, 11, 2014-2031.	1.8	145
8340	Deriving transcriptional programs and functional processes from gene expression databases. <i>Bioinformatics</i> , 2012, 28, 1122-1129.	1.8	3
8341	Gene Ontology-driven inference of proteinâ€“protein interactions using inducers. <i>Bioinformatics</i> , 2012, 28, 69-75.	1.8	76
8342	Bioinformatics for personal genome interpretation. <i>Briefings in Bioinformatics</i> , 2012, 13, 495-512.	3.2	62
8343	A strategy for building neuroanatomy ontologies. <i>Bioinformatics</i> , 2012, 28, 1262-1269.	1.8	28
8344	Detecting overlapping protein complexes in protein-protein interaction networks. <i>Nature Methods</i> , 2012, 9, 471-472.	9.0	1,129
8345	A Topology-Based Score for Pathway Enrichment. <i>Journal of Computational Biology</i> , 2012, 19, 563-573.	0.8	41
8346	Construction and characterization of a full-length cDNA library and identification of genes involved in salinity stress in wild eggplant (<i>Solanum torvum</i> Swartz). <i>Horticulture Environment and Biotechnology</i> , 2012, 53, 158-166.	0.7	4
8347	Functional assignment of metagenomic data: challenges and applications. <i>Briefings in Bioinformatics</i> , 2012, 13, 711-727.	3.2	150
8348	Transcript Profiling Using ESTs from <i>Paracoccidioides brasiliensis</i> in Models of Infection. <i>Methods in Molecular Biology</i> , 2012, 845, 381-396.	0.4	4
8349	miR-10a is aberrantly overexpressed in Nucleophosmin1 mutated acute myeloid leukaemia and its suppression induces cell death. <i>Molecular Cancer</i> , 2012, 11, 8.	7.9	63
8350	Rethinking Molecular Similarity: Comparing Compounds on the Basis of Biological Activity. <i>ACS Chemical Biology</i> , 2012, 7, 1399-1409.	1.6	181
8351	Genome-Scale Network Modeling. , 2012, , 1-23.		2
8352	SMAD4â€“dependent polysome RNA recruitment in human pancreatic cancer cells. <i>Molecular Carcinogenesis</i> , 2012, 51, 771-782.	1.3	5

#	ARTICLE	IF	CITATIONS
8353	Large-scale QSAR in Target Prediction and Phenotypic HTS Assessment. <i>Molecular Informatics</i> , 2012, 31, 508-514.	1.4	9
8354	Pediatric brainstem gangliogliomas show overexpression of neuropeptide prepronociceptin (PNO) by microarray and immunohistochemistry. <i>Pediatric Blood and Cancer</i> , 2012, 59, 1173-1179.	0.8	18
8355	Transcript profiling of CD16-positive monocytes reveals a unique molecular fingerprint. <i>European Journal of Immunology</i> , 2012, 42, 957-974.	1.6	80
8356	CNVd: Text mining-based copy number variation in disease database. <i>Human Mutation</i> , 2012, 33, E2375-E2381.	1.1	29
8357	Knockdown of metalloproteinase 1 inhibits NF- κ B signaling at different levels: The role of apoptosis induction of gastric cancer cells. <i>International Journal of Cancer</i> , 2012, 130, 2761-2770.	2.3	31
8358	Targeting of syndecan-1 by microRNA miR-10b promotes breast cancer cell motility and invasiveness via a Rho GTPase and E-cadherin-dependent mechanism. <i>International Journal of Cancer</i> , 2012, 131, 2.3 E884-96.		145
8359	Inhibition of the LSD1 (KDM1A) demethylase reactivates the all-trans-retinoic acid differentiation pathway in acute myeloid leukemia. <i>Nature Medicine</i> , 2012, 18, 605-611.	15.2	584
8360	Identification of novel ATP13A2 interactors and their role in α -synuclein misfolding and toxicity. <i>Human Molecular Genetics</i> , 2012, 21, 3785-3794.	1.4	66
8361	Gene Expression Profiling in the Lungs of Patients With Pulmonary Hypertension Associated With Pulmonary Fibrosis. <i>Chest</i> , 2012, 141, 661-673.	0.4	49
8362	Genetic inactivation of the polycomb repressive complex 2 in T cell acute lymphoblastic leukemia. <i>Nature Medicine</i> , 2012, 18, 298-302.	15.2	453
8363	ATM kinase inhibition in glial cells activates the innate immune response and causes neurodegeneration in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E656-64.	3.3	120
8364	Utilizing RNA-Seq data for <i>de novo</i> coexpression network inference. <i>Bioinformatics</i> , 2012, 28, 1592-1597.	1.8	112
8365	Analyzing Biological Data Using R: Methods for Graphs and Networks. <i>Methods in Molecular Biology</i> , 2012, 804, 343-373.	0.4	16
8366	Targeted Deletion of MicroRNA-22 Promotes Stress-Induced Cardiac Dilatation and Contractile Dysfunction. <i>Circulation</i> , 2012, 125, 2751-2761.	1.6	161
8367	Topology of functional networks predicts physical binding of proteins. <i>Bioinformatics</i> , 2012, 28, 2137-2145.	1.8	5
8368	Computational Framework for Analysis of Prey-Prey Associations in Interaction Proteomics Identifies Novel Human Protein-Protein Interactions and Networks. <i>Journal of Proteome Research</i> , 2012, 11, 4476-4487.	1.8	3
8369	Evolutionary Dynamics and Functional Specialization of Plant Paralogs Formed by Whole and Small-Scale Genome Duplications. <i>Molecular Biology and Evolution</i> , 2012, 29, 3541-3551.	3.5	86
8370	Different gene sets contribute to different symptom dimensions of depression and anxiety. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2012, 159B, 519-528.	1.1	14

#	ARTICLE	IF	CITATIONS
8371	Assembling models of embryo development: Image analysis and the construction of digital atlases. Birth Defects Research Part C: Embryo Today Reviews, 2012, 96, 109-120.	3.6	5
8372	Confined 3D microenvironment regulates early differentiation in human pluripotent stem cells. Biotechnology and Bioengineering, 2012, 109, 3119-3132.	1.7	44
8373	Automated Workflow for Large-Scale Selected Reaction Monitoring Experiments. Journal of Proteome Research, 2012, 11, 1644-1653.	1.8	20
8374	Genome sequence of foxtail millet (<i>Setaria italica</i>) provides insights into grass evolution and biofuel potential. Nature Biotechnology, 2012, 30, 549-554.	9.4	636
8375	Nonrandom mate choice in humans: insights from a genome scan. Molecular Ecology, 2012, 21, 587-596.	2.0	20
8376	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
8377	The yak genome and adaptation to life at high altitude. Nature Genetics, 2012, 44, 946-949.	9.4	708
8378	Mycobacterium tuberculosis and Clostridium difficile interactomes: demonstration of rapid development of computational system for bacterial interactome prediction. Microbial Informatics and Experimentation, 2012, 2, 4.	7.6	8
8379	Computational tools for prioritizing candidate genes: boosting disease gene discovery. Nature Reviews Genetics, 2012, 13, 523-536.	7.7	387
8380	Standardization in Synthetic Biology. Methods in Molecular Biology, 2012, 813, 23-43.	0.4	38
8381	Uncovering cis-regulatory sequence requirements for context-specific transcription factor binding. Genome Research, 2012, 22, 2018-2030.	2.4	98
8382	Staged-probability strategy of processing shotgun proteomic data to discover more functionally important proteins. Protein and Cell, 2012, 3, 140-147.	4.8	0
8383	Prioritization of candidate genes for attention deficit hyperactivity disorder by computational analysis of multiple data sources. Protein and Cell, 2012, 3, 526-534.	4.8	11
8384	Data Semantics on the Web. Journal on Data Semantics, 2012, 1, 1-9.	2.0	9
8385	KB-Rank: efficient protein structure and functional annotation identification via text query. Journal of Structural and Functional Genomics, 2012, 13, 101-110.	1.2	4
8386	Synergy of multi-label hierarchical ensembles, data fusion, and cost-sensitive methods for gene functional inference. Machine Learning, 2012, 88, 209-241.	3.4	67
8387	Experiment databases. Machine Learning, 2012, 87, 127-158.	3.4	62
8388	Exploiting BAC-end sequences for the mining, characterization and utility of new short sequences repeat (SSR) markers in Citrus. Molecular Biology Reports, 2012, 39, 5373-5386.	1.0	41

#	ARTICLE	IF	CITATIONS
8389	Gene expression profiling of <i>Sinapis alba</i> leaves under drought stress and rewatering growth conditions with Illumina deep sequencing. <i>Molecular Biology Reports</i> , 2012, 39, 5851-5857.	1.0	21
8390	Genome-wide pathway analysis of a genome-wide association study on psoriasis and Behçet's disease. <i>Molecular Biology Reports</i> , 2012, 39, 5953-5959.	1.0	36
8391	Analysis of 2,297 expressed sequence tags (ESTs) from a cDNA library of flax (<i>Linum usitatissimum</i> L.) bark tissue. <i>Molecular Biology Reports</i> , 2012, 39, 6289-6296.	1.0	24
8392	Generation, functional analysis and utility of <i>Citrus grandis</i> EST from a flower-derived cDNA library. <i>Molecular Biology Reports</i> , 2012, 39, 7221-7235.	1.0	14
8393	Pathway analysis of genome-wide association study for bone mineral density. <i>Molecular Biology Reports</i> , 2012, 39, 8099-8106.	1.0	11
8394	Transcriptional responses to drought stress in root and leaf of chickpea seedling. <i>Molecular Biology Reports</i> , 2012, 39, 8147-8158.	1.0	28
8395	High-throughput sequencing-based gene profiling on multi-staged fruit development of date palm (<i>Phoenix dactylifera</i> , L.). <i>Plant Molecular Biology</i> , 2012, 78, 617-626.	2.0	39
8396	Differential gene expression of rice roots inoculated with the diazotroph <i>Herbaspirillum seropedicae</i> . <i>Plant and Soil</i> , 2012, 356, 113-125.	1.8	61
8397	Mining of Candidate Maize Genes for Nitrogen Use Efficiency by Integrating Gene Expression and QTL Data. <i>Plant Molecular Biology Reporter</i> , 2012, 30, 297-308.	1.0	49
8398	Discovery, validation, and in silico functional characterization of EST-SSR markers in <i>Eucalyptus globulus</i> . <i>Tree Genetics and Genomes</i> , 2012, 8, 289-301.	0.6	28
8399	Uniform standards for genome databases in forest and fruit trees. <i>Tree Genetics and Genomes</i> , 2012, 8, 549-557.	0.6	20
8400	Citrus genomics. <i>Tree Genetics and Genomes</i> , 2012, 8, 611-626.	0.6	104
8401	Pathway-pathway network-based study of the therapeutic mechanisms by which salvianolic acid B regulates cardiovascular diseases. <i>Science Bulletin</i> , 2012, 57, 1672-1679.	1.7	9
8402	Differential DNA Methylation Status Between Human Preadipocytes and Mature Adipocytes. <i>Cell Biochemistry and Biophysics</i> , 2012, 63, 1-15.	0.9	29
8403	Identification of miRNAs and Their Target Genes Using Deep Sequencing and Degradome Analysis in Trifoliate Orange [<i>Poncirus trifoliata</i> (L.) Raf]. <i>Molecular Biotechnology</i> , 2012, 51, 44-57.	1.3	49
8404	Integration of MicroRNA Databases to Study MicroRNAs Associated with Multiple Sclerosis. <i>Molecular Neurobiology</i> , 2012, 45, 520-535.	1.9	58
8405	Information Resources for Cassava Research and Breeding. <i>Tropical Plant Biology</i> , 2012, 5, 140-151.	1.0	10
8406	Evaluation of multiple variate selection methods from a biological perspective: a nutrigenomics case study. <i>Genes and Nutrition</i> , 2012, 7, 387-397.	1.2	4

#	ARTICLE	IF	CITATIONS
8408	Frequent Pattern Discovery in Multiple Biological Networks: Patterns and Algorithms. <i>Statistics in Biosciences</i> , 2012, 4, 157-176.	0.6	4
8409	Determining distinct clusters in gene expression data using similarity in principal component subspaces. <i>International Journal of Advances in Engineering Sciences and Applied Mathematics</i> , 2012, 4, 41-51.	0.7	0
8410	Identification of an Hsp90 mutation that selectively disrupts cAMP/PKA signaling in <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 2012, 58, 149-163.	0.8	17
8411	Recovery from water stress affects grape leaf petiole transcriptome. <i>Planta</i> , 2012, 235, 1383-1396.	1.6	99
8412	Integrated analysis of transcriptome and lipid profiling reveals the co-influences of inositolâ€ˆcholine and Snf1 in controlling lipid biosynthesis in yeast. <i>Molecular Genetics and Genomics</i> , 2012, 287, 541-554.	1.0	16
8413	Gene expression profile of campylobacter jejuni-induced GBS in bama miniature pigs. <i>Cell and Tissue Research</i> , 2012, 348, 523-536.	1.5	0
8414	Predicting protein submitochondria locations by combining different descriptors into the general form of Chouâ€™s pseudo amino acid composition. <i>Amino Acids</i> , 2012, 43, 545-555.	1.2	83
8415	Genotypeâ€™phenotype correlation in interstitial 6q deletions: a report of 12 new cases. <i>Neurogenetics</i> , 2012, 13, 31-47.	0.7	48
8416	Transcriptomic Characterization of the Larval Stage in Gilthead Seabream (<i>Sparus aurata</i>) by 454 Pyrosequencing. <i>Marine Biotechnology</i> , 2012, 14, 423-435.	1.1	37
8417	Cultivar-specific kinetics of gene induction during downy mildew early infection in grapevine. <i>Functional and Integrative Genomics</i> , 2012, 12, 379-386.	1.4	54
8418	Functional roles for redox genes in ethanol sensitivity in <i>Drosophila</i> . <i>Functional and Integrative Genomics</i> , 2012, 12, 305-315.	1.4	14
8419	miR-15b and miR-16 regulate TNF mediated hepatocyte apoptosis via BCL2 in acute liver failure. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2012, 17, 702-716.	2.2	83
8420	Mitochondrial proteomicsâ€™a tool for the study of metabolic disorders. <i>Journal of Inherited Metabolic Disease</i> , 2012, 35, 715-726.	1.7	44
8421	Structural modelling and dynamics of proteins for insights into drug interactions. <i>Advanced Drug Delivery Reviews</i> , 2012, 64, 323-343.	6.6	32
8422	Rare and Common Variants in CARD14, Encoding an Epidermal Regulator of NF-kappaB, in Psoriasis. <i>American Journal of Human Genetics</i> , 2012, 90, 796-808.	2.6	306
8423	Evidence of function for conserved noncoding sequences in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2012, 193, 241-252.	3.5	13
8424	The transcriptome of the arbuscular mycorrhizal fungus <i>Glomus intraradices</i> (DAOM 197198) reveals functional tradeoffs in an obligate symbiont. <i>New Phytologist</i> , 2012, 193, 755-769.	3.5	305
8425	TreeMatrix: A Hybrid Visualization of Compound Graphs. <i>Computer Graphics Forum</i> , 2012, 31, 89-101.	1.8	30

#	ARTICLE	IF	CITATIONS
8426	Identification and functional validation of <i>CDH11</i> , <i>PCSK6</i> and <i>SH3GL3</i> as novel glioma invasion-associated candidate genes. <i>Neuropathology and Applied Neurobiology</i> , 2012, 38, 201-212.	1.8	49
8427	Cell and molecular biology of the spiny dogfish <i>Squalus acanthias</i> and little skate <i>Leucoraja erinacea</i> : insights from <i>in vitro</i> cultured cells. <i>Journal of Fish Biology</i> , 2012, 80, 2089-2111.	0.7	4
8428	Computational approaches to disease-gene prediction: rationale, classification and successes. <i>FEBS Journal</i> , 2012, 279, 678-696.	2.2	135
8429	Benzo[a]pyrene exposure influences the cardiac development and the expression of cardiovascular relative genes in zebrafish (<i>Danio rerio</i>) embryos. <i>Chemosphere</i> , 2012, 87, 369-375.	4.2	64
8430	Investigation of the relationship between SLA-1 and SLA-3 gene expression and susceptibility to <i>Escherichia coli</i> F18 in post-weaning pigs. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2012, 35, 23-30.	0.7	8
8431	Expression of genes associated with the antigen presentation and processing pathway are consistently regulated in early <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> infection. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2012, 35, 151-162.	0.7	40
8432	The NRF2-related interactome and regulome contain multifunctional proteins and fine-tuned autoregulatory loops. <i>FEBS Letters</i> , 2012, 586, 1795-1802.	1.3	95
8433	Transcription profiling of sparkling wine second fermentation. <i>International Journal of Food Microbiology</i> , 2012, 153, 176-182.	2.1	39
8434	Microarray-based bioinformatics analysis of osteoblasts on TiO ₂ nanotube layers. <i>Colloids and Surfaces B: Biointerfaces</i> , 2012, 93, 135-142.	2.5	27
8435	Visualizing the drug target landscape. <i>Drug Discovery Today</i> , 2012, 17, S3-S15.	3.2	9
8436	de novo analysis and functional classification of the transcriptome of the root lesion nematode, <i>Pratylenchus thornei</i> , after 454 GS FLX sequencing. <i>International Journal for Parasitology</i> , 2012, 42, 225-237.	1.3	40
8437	Analysis of functional and pathway association of differential co-expressed genes: A case study in drug addiction. <i>Journal of Biomedical Informatics</i> , 2012, 45, 30-36.	2.5	6
8438	BOAT: Automatic alignment of biomedical ontologies using term informativeness and candidate selection. <i>Journal of Biomedical Informatics</i> , 2012, 45, 337-349.	2.5	11
8439	Binding sites in membrane proteins – Diversity, druggability and prospects. <i>European Journal of Cell Biology</i> , 2012, 91, 326-339.	1.6	7
8440	<i>Trichoderma harzianum</i> expressed sequence tags for identification of genes with putative roles in mycoparasitism against <i>Fusarium solani</i> . <i>Biological Control</i> , 2012, 61, 134-140.	1.4	38
8441	Key strongylid nematodes of animals – Impact of next-generation transcriptomics on systems biology and biotechnology. <i>Biotechnology Advances</i> , 2012, 30, 469-488.	6.0	37
8442	Biochemical and transcriptional profiling to triage additional activities in a series of IGF-1R/IR inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2012, 20, 1961-1972.	1.4	2
8443	Transcriptome analysis of the citrus red mite, <i>Panonychus citri</i> , and its gene expression by exposure to insecticide/acaricide. <i>Insect Molecular Biology</i> , 2012, 21, 422-436.	1.0	30

#	ARTICLE	IF	CITATIONS
8444	From classification to epilepsy ontology and informatics. <i>Epilepsia</i> , 2012, 53, 28-32.	2.6	17
8445	Gene networks and haloperidol-induced catalepsy. <i>Genes, Brain and Behavior</i> , 2012, 11, 29-37.	1.1	26
8446	Dynamics of oscillatory phenotypes in <i>Saccharomyces cerevisiae</i> reveal a network of genome-wide transcriptional oscillators. <i>FEBS Journal</i> , 2012, 279, 1119-1130.	2.2	26
8447	Accurate evaluation and analysis of functional genomics data and methods. <i>Annals of the New York Academy of Sciences</i> , 2012, 1260, 95-100.	1.8	20
8448	The Proteome of the Locus Ceruleus in Parkinson's Disease: Relevance to Pathogenesis. <i>Brain Pathology</i> , 2012, 22, 485-498.	2.1	53
8449	InterStoreDB: A Generic Integration Resource for Genetic and Genomic Data. <i>Journal of Integrative Plant Biology</i> , 2012, 54, 345-355.	4.1	13
8450	Improved Estimation of the Noncentrality Parameter Distribution from a Large Number of t -Statistics, with Applications to False Discovery Rate Estimation in Microarray Data Analysis. <i>Biometrics</i> , 2012, 68, 1178-1187.	0.8	4
8451	Chronic psychosocial stressors and salivary biomarkers in emerging adults. <i>Psychoneuroendocrinology</i> , 2012, 37, 1158-1170.	1.3	10
8452	A combined DNA-microarray and mechanism-specific toxicity approach with zebrafish embryos to investigate the pollution of river sediments. <i>Reproductive Toxicology</i> , 2012, 33, 245-253.	1.3	31
8453	The use of evolutionary patterns in protein annotation. <i>Current Opinion in Structural Biology</i> , 2012, 22, 316-325.	2.6	28
8454	Insights into physiological traits of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BB-12 through membrane proteome analysis. <i>Journal of Proteomics</i> , 2012, 75, 1190-1200.	1.2	12
8455	Integrative analysis of the ubiquitin proteome isolated using Tandem Ubiquitin Binding Entities (TUBEs). <i>Journal of Proteomics</i> , 2012, 75, 2998-3014.	1.2	90
8456	Proteomic analysis of <i>Trichinella spiralis</i> proteins in intestinal epithelial cells after culture with their larvae by shotgun LC-MS/MS approach. <i>Journal of Proteomics</i> , 2012, 75, 2375-2383.	1.2	71
8457	Analysis of the nuclear proteome of the resurrection plant <i>Xerophyta viscosa</i> in response to dehydration stress using iTRAQ with 2DLC and tandem mass spectrometry. <i>Journal of Proteomics</i> , 2012, 75, 2361-2374.	1.2	42
8458	Identification of potential host proteins for influenza A virus based on topological and biological characteristics by proteome-wide network approach. <i>Journal of Proteomics</i> , 2012, 75, 2500-2513.	1.2	10
8459	Downregulation of Na ⁺ -NQR complex is essential for <i>Vibrio alginolyticus</i> in resistance to balofloxacin. <i>Journal of Proteomics</i> , 2012, 75, 2638-2648.	1.2	23
8460	Multi-kernel transfer learning based on Chou's PseAAC formulation for protein submitochondria localization. <i>Journal of Theoretical Biology</i> , 2012, 293, 121-130.	0.8	95
8461	Using the underlying biological organization of the <i>Mycobacterium tuberculosis</i> functional network for protein function prediction. <i>Infection, Genetics and Evolution</i> , 2012, 12, 922-932.	1.0	19

#	ARTICLE	IF	CITATIONS
8462	Functional bias of positively selected genes in <i>Streptococcus</i> genomes. <i>Infection, Genetics and Evolution</i> , 2012, 12, 274-277.	1.0	3
8463	Effect of human TGF- β 2 on the gene expression profile of <i>Schistosoma mansoni</i> adult worms. <i>Molecular and Biochemical Parasitology</i> , 2012, 183, 132-139.	0.5	20
8464	A cognitive phenotype for a polymorphism in the nicotinic receptor gene <i>CHRNA4</i> . <i>Neuroscience and Biobehavioral Reviews</i> , 2012, 36, 1331-1341.	2.9	37
8465	Developmental neurotoxicity of organophosphates targets cell cycle and apoptosis, revealed by transcriptional profiles in vivo and in vitro. <i>Neurotoxicology and Teratology</i> , 2012, 34, 232-241.	1.2	52
8466	Does mechanism matter? Unrelated neurotoxicants converge on cell cycle and apoptosis during neurodifferentiation. <i>Neurotoxicology and Teratology</i> , 2012, 34, 395-402.	1.2	8
8467	The genomic impact of 100 million years of social evolution in seven ant species. <i>Trends in Genetics</i> , 2012, 28, 14-21.	2.9	101
8468	High-resolution picture of a venom gland transcriptome: Case study with the marine snail <i>Conus</i> consors. <i>Toxicon</i> , 2012, 59, 34-46.	0.8	76
8469	A semi-supervised fuzzy clustering algorithm applied to gene expression data. <i>Pattern Recognition</i> , 2012, 45, 637-648.	5.1	61
8470	Gene expression in the ventral tegmental area of 5 pairs of rat lines selectively bred for high or low ethanol consumption. <i>Pharmacology Biochemistry and Behavior</i> , 2012, 102, 275-285.	1.3	41
8471	Possible connection between imidacloprid-induced changes in rice gene transcription profiles and susceptibility to the brown plant hopper <i>Nilaparvata lugens</i> Stål (Hemiptera: Delphacidae). <i>Pesticide Biochemistry and Physiology</i> , 2012, 102, 213-219.	1.6	19
8472	Transcriptome and gene expression analysis in cold-acclimated guayule (<i>Parthenium argentatum</i>) rubber-producing tissue. <i>Phytochemistry</i> , 2012, 79, 57-66.	1.4	40
8473	Computational tools for metabolic engineering. <i>Metabolic Engineering</i> , 2012, 14, 270-280.	3.6	93
8474	Microarray analysis of differential gene expression in sensitive and resistant pig to <i>Escherichia coli</i> F18. <i>Animal Genetics</i> , 2012, 43, 525-534.	0.6	30
8475	Changes in gene expression in a porcine preadipocyte cell line during differentiation. <i>Animal Genetics</i> , 2012, 43, 535-544.	0.6	11
8476	Dandruff/seborrheic dermatitis is characterized by an inflammatory genomic signature and possible immune dysfunction: transcriptional analysis of the condition and treatment effects of zinc pyrithione. <i>British Journal of Dermatology</i> , 2012, 166, 33-40.	1.4	34
8477	A GPU-Based Approach to Accelerate Computational Protein-DNA Docking. <i>Computing in Science and Engineering</i> , 2012, 14, 20-29.	1.2	6
8478	Discovering Functional Interdependence Relationship in PPI Networks for Protein Complex Identification. <i>IEEE Transactions on Biomedical Engineering</i> , 2012, 59, 899-908.	2.5	12
8479	Whole Transcriptome Analysis of the Coral <i>Acropora millepora</i> Reveals Complex Responses to CO ₂ -driven Acidification during the Initiation of Calcification. <i>Molecular Ecology</i> , 2012, 21, 2440-2454.	2.0	289

#	ARTICLE	IF	CITATIONS
8480	Genome-wide architecture of reproductive isolation in a naturally occurring hybrid zone between <i>Mus musculus musculus</i> and <i>M. m. domesticus</i> . <i>Molecular Ecology</i> , 2012, 21, 3032-3047.	2.0	137
8481	Bioinformatics meets parasitology. <i>Parasite Immunology</i> , 2012, 34, 265-275.	0.7	23
8482	Beyond the genome: recent advances in <i>Toxoplasma gondii</i> functional genomics. <i>Parasite Immunology</i> , 2012, 34, 80-89.	0.7	9
8483	Markov Chain Ontology Analysis (MCOA). <i>BMC Bioinformatics</i> , 2012, 13, 23.	1.2	13
8484	PupDB: a database of pupylated proteins. <i>BMC Bioinformatics</i> , 2012, 13, 40.	1.2	36
8485	A methodology for detecting the orthology signal in a PPI network at a functional complex level. <i>BMC Bioinformatics</i> , 2012, 13, S18.	1.2	14
8486	A systematic comparison of genome-scale clustering algorithms. <i>BMC Bioinformatics</i> , 2012, 13, S7.	1.2	55
8487	Genome plasticity and systems evolution in <i>Streptomyces</i> . <i>BMC Bioinformatics</i> , 2012, 13, S8.	1.2	61
8488	Overview of the ID, EPI and REL tasks of BioNLP Shared Task 2011. <i>BMC Bioinformatics</i> , 2012, 13, S2.	1.2	51
8489	Prediction of protein-protein interactions between viruses and human by an SVM model. <i>BMC Bioinformatics</i> , 2012, 13, S5.	1.2	83
8490	Inferring a protein interaction map of <i>Mycobacterium tuberculosis</i> based on sequences and interologs. <i>BMC Bioinformatics</i> , 2012, 13, S6.	1.2	19
8491	Comparative genomic analysis of the genus <i>Staphylococcus</i> including <i>Staphylococcus aureus</i> and its newly described sister species <i>Staphylococcus simiae</i> . <i>BMC Genomics</i> , 2012, 13, 38.	1.2	51
8492	Large-scale functional RNAi screen in <i>C. elegans</i> identifies genes that regulate the dysfunction of mutant polyglutamine neurons. <i>BMC Genomics</i> , 2012, 13, 91.	1.2	50
8493	A natural language interface plug-in for cooperative query answering in biological databases. <i>BMC Genomics</i> , 2012, 13, S4.	1.2	2
8494	Domain landscapes of somatic mutations in cancer. <i>BMC Genomics</i> , 2012, 13, S9.	1.2	51
8495	Seed selection strategy in global network alignment without destroying the entire structures of functional modules. <i>Proteome Science</i> , 2012, 10, S16.	0.7	3
8496	High performance transcription factor-DNA docking with GPU computing. <i>Proteome Science</i> , 2012, 10, S17.	0.7	18
8497	Regulatory interactions for iron homeostasis in <i>Aspergillus fumigatus</i> inferred by a Systems Biology approach. <i>BMC Systems Biology</i> , 2012, 6, 6.	3.0	37

#	ARTICLE	IF	CITATIONS
8498	Tracing dynamic biological processes during phase transition. BMC Systems Biology, 2012, 6, S12.	3.0	7
8499	The preservation of bidirectional promoter architecture in eukaryotes: what is the driving force?. BMC Systems Biology, 2012, 6, S21.	3.0	29
8500	An ovary transcriptome for all maturational stages of the striped bass (<i>Morone saxatilis</i>), a highly advanced perciform fish. BMC Research Notes, 2012, 5, 111.	0.6	47
8501	SpiroESTdb: a transcriptome database and online tool for sparganum expressed sequences tags. BMC Research Notes, 2012, 5, 130.	0.6	5
8502	Improving integrative searching of systems chemical biology data using semantic annotation. Journal of Cheminformatics, 2012, 4, 6.	2.8	27
8503	Target gene expression levels and competition between transfected and endogenous microRNAs are strong confounding factors in microRNA high-throughput experiments. Silence: A Journal of RNA Regulation, 2012, 3, 3.	8.0	30
8504	Open semantic annotation of scientific publications using DOMEQ. Journal of Biomedical Semantics, 2012, 3, S1.	0.9	30
8505	Logical Gene Ontology Annotations (GOAL): exploring gene ontology annotations with OWL. Journal of Biomedical Semantics, 2012, 3, S3.	0.9	11
8506	Implications of the solvent vehicles dimethylformamide and dimethylsulfoxide for establishing transcriptomic endpoints in the zebrafish embryo toxicity test. Environmental Toxicology and Chemistry, 2012, 31, 593-604.	2.2	30
8507	Electrophoretically driven SDS removal and protein fractionation in the shotgun analysis of membrane proteomes. Electrophoresis, 2012, 33, 316-324.	1.3	20
8508	Using the gene ontology to scan multilevel gene sets for associations in genome wide association studies. Genetic Epidemiology, 2012, 36, 3-16.	0.6	32
8509	Genome-wide and gene-based association implicates FRMD6 in alzheimer disease. Human Mutation, 2012, 33, 521-529.	1.1	32
8510	Facilitative effects of <i>Eucommia ulmoides</i> on fatty acid oxidation in hypertriglyceridaemic rats. Journal of the Science of Food and Agriculture, 2012, 92, 358-365.	1.7	19
8511	Scientific discovery as a combinatorial optimisation problem: How best to navigate the landscape of possible experiments?. BioEssays, 2012, 34, 236-244.	1.2	44
8512	Mechanisms underlying the radioprotective properties of $\hat{1}^3$ -tocotrienol: comparative gene expression profiling in tocol-treated endothelial cells. Genes and Nutrition, 2012, 7, 75-81.	1.2	28
8513	Amyloid pathway-based candidate gene analysis of [11C]PiB-PET in the Alzheimer's Disease Neuroimaging Initiative (ADNI) cohort. Brain Imaging and Behavior, 2012, 6, 1-15.	1.1	47
8514	Expressed sequence-tag analysis of ovaries of <i>Brachiaria brizantha</i> reveals genes associated with the early steps of embryo sac differentiation of apomictic plants. Plant Cell Reports, 2012, 31, 403-416.	2.8	28
8515	Fish welfare and genomics. Fish Physiology and Biochemistry, 2012, 38, 43-60.	0.9	44

#	ARTICLE	IF	CITATIONS
8516	Characterization of <i>Betula platyphylla</i> gene transcripts associated with early development of male inflorescence. <i>Molecular Biology Reports</i> , 2012, 39, 929-935.	1.0	7
8517	The application of gene co-expression network reconstruction based on CNVs and gene expression microarray data in breast cancer. <i>Molecular Biology Reports</i> , 2012, 39, 1627-1637.	1.0	16
8518	Generation and analysis of expressed sequence tags from the bone marrow of Chinese Sika deer. <i>Molecular Biology Reports</i> , 2012, 39, 2981-2990.	1.0	4
8519	EST dataset of pituitary and identification of somatolactin and novel genes in Chinese sturgeon, <i>Acipenser sinensis</i> . <i>Molecular Biology Reports</i> , 2012, 39, 4647-4653.	1.0	7
8520	SignatureClust: a tool for landmark gene-guided clustering. <i>Soft Computing</i> , 2012, 16, 411-418.	2.1	0
8521	How to Understand the Gene in the Twenty-First Century?. <i>Science and Education</i> , 2013, 22, 345-374.	1.7	17
8522	Genome-wide expression profiling of schizophrenia using a large combined cohort. <i>Molecular Psychiatry</i> , 2013, 18, 215-225.	4.1	88
8523	Nuclear proteome response to cell wall removal in rice (<i>Oryza sativa</i>). <i>Proteome Science</i> , 2013, 11, 26.	0.7	19
8524	Comparison of host cell gene expression in cowpox, monkeypox or vaccinia virus-infected cells reveals virus-specific regulation of immune response genes. <i>Virology Journal</i> , 2013, 10, 61.	1.4	43
8525	Gene Ontology consistent protein function prediction: the FALCON algorithm applied to six eukaryotic genomes. <i>Algorithms for Molecular Biology</i> , 2013, 8, 10.	0.3	9
8526	Configurable pattern-based evolutionary biclustering of gene expression data. <i>Algorithms for Molecular Biology</i> , 2013, 8, 4.	0.3	37
8527	Knowledge Driven Variable Selection (KDVS) – a new approach to enrichment analysis of gene signatures obtained from high-throughput data. <i>Source Code for Biology and Medicine</i> , 2013, 8, 2.	1.7	7
8528	MmPalateMiRNA, an R package compendium illustrating analysis of miRNA microarray data. <i>Source Code for Biology and Medicine</i> , 2013, 8, 1.	1.7	36
8529	Prediction of <i>Drosophila melanogaster</i> gene function using Support Vector Machines. <i>BioData Mining</i> , 2013, 6, 8.	2.2	10
8530	Protein biomarkers distinguish between high- and low-risk pediatric acute lymphoblastic leukemia in a tissue specific manner. <i>Journal of Hematology and Oncology</i> , 2013, 6, 52.	6.9	38
8531	Phosphoproteomics data classify hematological cancer cell lines according to tumor type and sensitivity to kinase inhibitors. <i>Genome Biology</i> , 2013, 14, R37.	13.9	60
8532	Premetazoan genome evolution and the regulation of cell differentiation in the choanoflagellate <i>Salpingoeca rosetta</i> . <i>Genome Biology</i> , 2013, 14, R15.	13.9	219
8533	Comparative transcriptome analysis to investigate the high starch accumulation of duckweed (<i>Landoltia punctata</i>) under nutrient starvation. <i>Biotechnology for Biofuels</i> , 2013, 6, 72.	6.2	80

#	ARTICLE	IF	CITATIONS
8534	Genome-wide comparative analysis revealed significant transcriptome changes in mice after <i>Toxoplasma gondii</i> infection. <i>Parasites and Vectors</i> , 2013, 6, 161.	1.0	23
8535	Transcriptome exploration of the sex pheromone gland of <i>Lutzomyia longipalpis</i> (Diptera): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.0	19
8536	A two-dimensional proteome map of the aflatoxigenic fungus <i>Aspergillus flavus</i> . <i>Proteomics</i> , 2013, 13, 1513-1518.	1.3	24
8537	A genome-wide analysis of transcripts in a 2BS.2RL wheat-rye translocation during Hessian fly infestation. <i>Genes and Genomics</i> , 2013, 35, 795-803.	0.5	5
8538	Mass spectrometry identification of granins and other proteins secreted by neuroblastoma cells. <i>Tumor Biology</i> , 2013, 34, 1773-1781.	0.8	13
8539	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. <i>Journal of Biomedical Semantics</i> , 2013, 4, 6.	0.9	26
8540	OPPL-Galaxy, a Galaxy tool for enhancing ontology exploitation as part of bioinformatics workflows. <i>Journal of Biomedical Semantics</i> , 2013, 4, 2.	0.9	5
8541	A task-based approach for Gene Ontology evaluation. <i>Journal of Biomedical Semantics</i> , 2013, 4, S4.	0.9	18
8542	Query enhancement through the practical application of ontology: the IEDB and OBI. <i>Journal of Biomedical Semantics</i> , 2013, 4, S6.	0.9	14
8543	Global Proteome Analysis of the NCI-60 Cell Line Panel. <i>Cell Reports</i> , 2013, 4, 609-620.	2.9	276
8544	Genome-wide pathway analysis of a genome-wide association study on multiple sclerosis. <i>Molecular Biology Reports</i> , 2013, 40, 2557-2564.	1.0	20
8545	Pathway analysis of genome-wide association studies for Parkinson's disease. <i>Molecular Biology Reports</i> , 2013, 40, 2599-2607.	1.0	21
8546	Toxicogenomic Studies of Human Neural Cells Following Exposure to Organophosphorus Chemical Warfare Nerve Agent VX. <i>Neurochemical Research</i> , 2013, 38, 916-934.	1.6	10
8547	Selection Shapes the Robustness of Ligand-Binding Amino Acids. <i>Journal of Molecular Evolution</i> , 2013, 76, 343-349.	0.8	5
8548	Gene Expression Analysis in Cardiac Tissues From Infants Identifies Candidate Agents for Tetralogy of Fallot. <i>Pediatric Cardiology</i> , 2013, 34, 1637-1644.	0.6	5
8549	Taxonomic Profiling and Metagenome Analysis of a Microbial Community from a Habitat Contaminated with Industrial Discharges. <i>Microbial Ecology</i> , 2013, 66, 533-550.	1.4	39
8551	Transcriptome analyses and virus induced gene silencing identify genes in the Rpp4-mediated Asian soybean rust resistance pathway. <i>Functional Plant Biology</i> , 2013, 40, 1029.	1.1	57
8552	Sulfur Amino Acids Regulate Translational Capacity and Metabolic Homeostasis through Modulation of tRNA Thiolation. <i>Cell</i> , 2013, 154, 416-429.	13.5	189

#	ARTICLE	IF	CITATIONS
8553	Diagnostics in Plant Breeding. , 2013, , .		2
8555	Basic nuclear processes affected by histone acetyltransferases and histone deacetylase inhibitors. Epigenomics, 2013, 5, 379-396.	1.0	28
8556	Screening of a Botrytis cinerea one-hybrid library reveals a Cys2His2 transcription factor involved in the regulation of secondary metabolism gene clusters. Fungal Genetics and Biology, 2013, 52, 9-19.	0.9	39
8557	Bioinformatics Research and Applications. Lecture Notes in Computer Science, 2013, , .	1.0	0
8558	In Silico Systems Biology. Methods in Molecular Biology, 2013, , .	0.4	8
8559	Discovery of functional protein groups by clustering community links and integration of ontological knowledge. Expert Systems With Applications, 2013, 40, 5101-5112.	4.4	11
8561	Emerging Intelligent Computing Technology and Applications. Communications in Computer and Information Science, 2013, , .	0.4	1
8562	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. Nature Genetics, 2013, 45, 891-898.	9.4	350
8563	Mapping the functional yeast ABC transporter interactome. Nature Chemical Biology, 2013, 9, 565-572.	3.9	93
8564	Proximity Measures for Clustering Gene Expression Microarray Data: A Validation Methodology and a Comparative Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 845-857.	1.9	42
8565	MicroRNA Cancer Regulation. Advances in Experimental Medicine and Biology, 2013, , .	0.8	17
8566	MicroRNA Protocols. Methods in Molecular Biology, 2013, , .	0.4	2
8567	The human oviduct transcriptome reveals an anti-inflammatory, anti-angiogenic, secretory and matrix-stable environment during embryo transit. Reproductive BioMedicine Online, 2013, 27, 423-435.	1.1	31
8568	Prediction and characterization of novel microRNA<sc>s from brown plant hopper, <i><sc>Nilaparvata lugens</sc></i> (<sc>S</sc>tA¥l) (<sc>H</sc>emiptera:) Tj ETQq1 1 0.784314 rgBT /Ovarlock 10 Tf 50 2 17		
8569	Transcriptome analysis of venom glands from a single fishing spider Dolomedes mizhoanus. Toxicon, 2013, 73, 23-32.	0.8	24
8570	Systems Biology Characterization of Engineered Tissues. Annual Review of Biomedical Engineering, 2013, 15, 55-70.	5.7	13
8571	Identification of SNP markers for inferring phylogeny in temperate bamboos (P oaceae: B ambusoideae) using RAD sequencing. Molecular Ecology Resources, 2013, 13, 938-945.	2.2	53
8572	Improving an evolutionary multi-objective algorithm for the biclustering of gene expression data. , 2013, , .		3

#	ARTICLE	IF	CITATIONS
8573	Interspecific bacterial sensing through airborne signals modulates locomotion and drug resistance. <i>Nature Communications</i> , 2013, 4, 1809.	5.8	102
8574	Genomic Signatures of Pregnancy-Associated Breast Cancer Epithelia and Stroma and their Regulation by Estrogens and Progesterone. <i>Hormones and Cancer</i> , 2013, 4, 140-153.	4.9	46
8575	eFindSite: Improved prediction of ligand binding sites in protein models using meta-threading, machine learning and auxiliary ligands. <i>Journal of Computer-Aided Molecular Design</i> , 2013, 27, 551-567.	1.3	66
8576	A Novel Biclustering Algorithm for the Discovery of Meaningful Biological Correlations between microRNAs and their Target Genes. <i>BMC Bioinformatics</i> , 2013, 14, S8.	1.2	38
8577	How to inherit statistically validated annotation within BAR+ protein clusters. <i>BMC Bioinformatics</i> , 2013, 14, S4.	1.2	8
8578	Concomitant prediction of function and fold at the domain level with GO-based profiles. <i>BMC Bioinformatics</i> , 2013, 14, S12.	1.2	4
8579	Protein function prediction by massive integration of evolutionary analyses and multiple data sources. <i>BMC Bioinformatics</i> , 2013, 14, S1.	1.2	72
8580	Three-Level Prediction of Protein Function by Combining Profile-Sequence Search, Profile-Profile Search, and Domain Co-Occurrence Networks. <i>BMC Bioinformatics</i> , 2013, 14, S3.	1.2	23
8581	Protein function prediction using domain families. <i>BMC Bioinformatics</i> , 2013, 14, S5.	1.2	77
8582	Homology-based inference sets the bar high for protein function prediction. <i>BMC Bioinformatics</i> , 2013, 14, S7.	1.2	38
8583	Characterizing the state of the art in the computational assignment of gene function: lessons from the first critical assessment of functional annotation (CAFA). <i>BMC Bioinformatics</i> , 2013, 14, S15.	1.2	53
8584	Function prediction from networks of local evolutionary similarity in protein structure. <i>BMC Bioinformatics</i> , 2013, 14, S6.	1.2	9
8585	MS-k NN: protein function prediction by integrating multiple data sources. <i>BMC Bioinformatics</i> , 2013, 14, S8.	1.2	74
8586	Combining heterogeneous data sources for accurate functional annotation of proteins. <i>BMC Bioinformatics</i> , 2013, 14, S10.	1.2	41
8587	Identifying cross-category relations in gene ontology and constructing genome-specific term association networks. <i>BMC Bioinformatics</i> , 2013, 14, S15.	1.2	14
8588	CELDA – an ontology for the comprehensive representation of cells in complex systems. <i>BMC Bioinformatics</i> , 2013, 14, 228.	1.2	15
8589	bioNerDS: exploring bioinformatics™ database and software use through literature mining. <i>BMC Bioinformatics</i> , 2013, 14, 194.	1.2	23
8590	Exploring the transcription factor activity in high-throughput gene expression data using RLQ analysis. <i>BMC Bioinformatics</i> , 2013, 14, 178.	1.2	8

#	ARTICLE	IF	CITATIONS
8591	Wide coverage biomedical event extraction using multiple partially overlapping corpora. BMC Bioinformatics, 2013, 14, 175.	1.2	35
8592	Investigating the concordance of Gene Ontology terms reveals the intra- and inter-platform reproducibility of enrichment analysis. BMC Bioinformatics, 2013, 14, 143.	1.2	21
8593	Eliciting candidate anatomical routes for protein interactions: a scenario from endocrine physiology. BMC Bioinformatics, 2013, 14, 131.	1.2	2
8594	Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. BMC Bioinformatics, 2013, 14, 128.	1.2	5,305
8595	STOP using just GO: a multi-ontology hypothesis generation tool for high throughput experimentation. BMC Bioinformatics, 2013, 14, 53.	1.2	17
8596	A new unsupervised gene clustering algorithm based on the integration of biological knowledge into expression data. BMC Bioinformatics, 2013, 14, 42.	1.2	20
8597	The evolutionary rate of antibacterial drug targets. BMC Bioinformatics, 2013, 14, 36.	1.2	14
8598	Predicting PDZ domain mediated protein interactions from structure. BMC Bioinformatics, 2013, 14, 27.	1.2	32
8599	Negated bio-events: analysis and identification. BMC Bioinformatics, 2013, 14, 14.	1.2	52
8600	BioCause: Annotating and analysing causality in the biomedical domain. BMC Bioinformatics, 2013, 14, 2.	1.2	58
8601	SNPranker 2.0: a gene-centric data mining tool for diseases associated SNP prioritization in GWAS. BMC Bioinformatics, 2013, 14, S9.	1.2	23
8602	Screening and evaluation of traditional Chinese medicine by microarray expression analysis. Journal of Ethnopharmacology, 2013, 147, 564-569.	2.0	10
8603	Identification of <i>Lens culinaris</i> defense genes responsive to the anthracnose pathogen <i>Colletotrichum truncatum</i> . BMC Genetics, 2013, 14, 31.	2.7	27
8604	WS-SNPs&GO: a web server for predicting the deleterious effect of human protein variants using functional annotation. BMC Genomics, 2013, 14, S6.	1.2	248
8605	Multiscale modeling of the causal functional roles of nsSNPs in a genome-wide association study: application to hypoxia. BMC Genomics, 2013, 14, S9.	1.2	6
8606	Differential impacts of juvenile hormone, soldier head extract and alternate caste phenotypes on host and symbiont transcriptome composition in the gut of the termite <i>Reticulitermes flavipes</i> . BMC Genomics, 2013, 14, 491.	1.2	16
8607	KONAGAbase: a genomic and transcriptomic database for the diamondback moth, <i>Plutella xylostella</i> . BMC Genomics, 2013, 14, 464.	1.2	47
8608	Global transcriptome profiles of <i>Camellia sinensis</i> during cold acclimation. BMC Genomics, 2013, 14, 415.	1.2	268

#	ARTICLE	IF	CITATIONS
8609	Skin transcriptome profiles associated with coat color in sheep. <i>BMC Genomics</i> , 2013, 14, 389.	1.2	65
8610	Genomic basis of ecological niche divergence among cryptic sister species of non-biting midges. <i>BMC Genomics</i> , 2013, 14, 384.	1.2	25
8611	Expression profiling of genes regulated by Fra-1/AP-1 transcription factor during bleomycin-induced pulmonary fibrosis. <i>BMC Genomics</i> , 2013, 14, 381.	1.2	19
8612	Alternative splicing tends to avoid partial removals of protein-protein interaction sites. <i>BMC Genomics</i> , 2013, 14, 379.	1.2	4
8613	Structural and functional annotation of the porcine immunome. <i>BMC Genomics</i> , 2013, 14, 332.	1.2	203
8614	Comparative transcriptome analysis and marker development of two closely related Primrose species (<i>Primula poissonii</i> and <i>Primula wilsonii</i>). <i>BMC Genomics</i> , 2013, 14, 329.	1.2	62
8615	Interfacing cellular networks of <i>S. cerevisiae</i> and <i>E. coli</i> : Connecting dynamic and genetic information. <i>BMC Genomics</i> , 2013, 14, 324.	1.2	27
8616	Transcription profile of soybean-root-knot nematode interaction reveals a key role of phytohormones in the resistance reaction. <i>BMC Genomics</i> , 2013, 14, 322.	1.2	56
8617	Discovering putative prion sequences in complete proteomes using probabilistic representations of Q/N-rich domains. <i>BMC Genomics</i> , 2013, 14, 316.	1.2	73
8618	Translational signatures and mRNA levels are highly correlated in human stably expressed genes. <i>BMC Genomics</i> , 2013, 14, 268.	1.2	6
8619	Transcriptional profiling of bud dormancy induction and release in oak by next-generation sequencing. <i>BMC Genomics</i> , 2013, 14, 236.	1.2	82
8620	Antennal transcriptome analysis of the chemosensory gene families in the tree killing bark beetles, <i>Ips typographus</i> and <i>Dendroctonus ponderosae</i> (Coleoptera: Curculionidae: Scolytinae). <i>BMC Genomics</i> , 2013, 14, 198.	1.2	216
8621	Dynamic regulation of epigenomic landscapes during hematopoiesis. <i>BMC Genomics</i> , 2013, 14, 193.	1.2	41
8622	De novo assembly and characterization of <i>Camelina sativa</i> transcriptome by paired-end sequencing. <i>BMC Genomics</i> , 2013, 14, 146.	1.2	83
8623	Biclustering for the comprehensive search of correlated gene expression patterns using clustered seed expansion. <i>BMC Genomics</i> , 2013, 14, 144.	1.2	22
8624	Genome-wide detection of copy number variations using high-density SNP genotyping platforms in Holsteins. <i>BMC Genomics</i> , 2013, 14, 131.	1.2	87
8625	Neurocarta: aggregating and sharing disease-gene relations for the neurosciences. <i>BMC Genomics</i> , 2013, 14, 129.	1.2	20
8626	Comparative transcriptomics of early dipteran development. <i>BMC Genomics</i> , 2013, 14, 123.	1.2	41

#	ARTICLE	IF	CITATIONS
8627	Learning contextual gene set interaction networks of cancer with condition specificity. BMC Genomics, 2013, 14, 110.	1.2	2
8628	Insights into the evolution of Darwin's finches from comparative analysis of the <i>Geospiza magnirostris</i> genome sequence. BMC Genomics, 2013, 14, 95.	1.2	38
8629	Draft genome sequence of the rubber tree <i>Hevea brasiliensis</i> . BMC Genomics, 2013, 14, 75.	1.2	222
8630	Transcriptional profiling of the <i>Arabidopsis</i> abscission mutant <i>hae hsl2</i> by RNA-Seq. BMC Genomics, 2013, 14, 37.	1.2	78
8631	Transcriptomic profiling of the salt-stress response in the wild recretohalophyte <i>Reaumuria trigyna</i> . BMC Genomics, 2013, 14, 29.	1.2	147
8632	Genetic variation and expression diversity between grain and sweet sorghum lines. BMC Genomics, 2013, 14, 18.	1.2	32
8633	Common bean (<i>Phaseolus vulgaris</i> L.) PvTIFY orchestrates global changes in transcript profile response to jasmonate and phosphorus deficiency. BMC Plant Biology, 2013, 13, 26.	1.6	48
8634	Mutation spectrum in human colorectal cancers and potential functional relevance. BMC Medical Genetics, 2013, 14, 32.	2.1	13
8635	Finding type 2 diabetes causal single nucleotide polymorphism combinations and functional modules from genome-wide association data. BMC Medical Informatics and Decision Making, 2013, 13, S3.	1.5	4
8636	Vitamin D receptor ChIP-seq in primary CD4+ cells: relationship to serum 25-hydroxyvitamin D levels and autoimmune disease. BMC Medicine, 2013, 11, 163.	2.3	59
8637	Serum biomarkers for neurofibromatosis type 1 and early detection of malignant peripheral nerve-sheath tumors. BMC Medicine, 2013, 11, 109.	2.3	44
8638	A novel function prediction approach using protein overlap networks. BMC Systems Biology, 2013, 7, 61.	3.0	13
8639	Mining breast cancer genes with a network based noise-tolerant approach. BMC Systems Biology, 2013, 7, 49.	3.0	10
8640	Maximizing capture of gene co-expression relationships through pre-clustering of input expression samples: an <i>Arabidopsis</i> case study. BMC Systems Biology, 2013, 7, 44.	3.0	22
8641	Multilevel omic data integration in cancer cell lines: advanced annotation and emergent properties. BMC Systems Biology, 2013, 7, 14.	3.0	55
8642	Disentangling function from topology to infer the network properties of disease genes. BMC Systems Biology, 2013, 7, 5.	3.0	20
8643	Genome-wide expression profiling and functional characterization of SCA28 lymphoblastoid cell lines reveal impairment in cell growth and activation of apoptotic pathways. BMC Medical Genomics, 2013, 6, 22.	0.7	14
8644	Next-generation text-mining mediated generation of chemical response-specific gene sets for interpretation of gene expression data. BMC Medical Genomics, 2013, 6, 2.	0.7	15

#	ARTICLE	IF	CITATIONS
8645	HDAM: a resource of human disease associated mutations from next generation sequencing studies. BMC Medical Genomics, 2013, 6, S16.	0.7	3
8646	Discovery-2: an interactive resource for the rational selection and comparison of putative drug target proteins in malaria. Malaria Journal, 2013, 12, 116.	0.8	3
8647	Selection of genes for gene-environment interaction studies: a candidate pathway-based strategy using asthma as an example. Environmental Health, 2013, 12, 56.	1.7	11
8648	Comparison of global responses to mild deficiency and excess copper levels in Arabidopsis seedlings. Metallomics, 2013, 5, 1234.	1.0	28
8649	The genetics of alcohol dependence. Annals of the New York Academy of Sciences, 2013, 1282, 39-70.	1.8	84
8650	Proximity Measures and Results Validation in Biclustering – A Survey. Lecture Notes in Computer Science, 2013, , 206-217.	1.0	9
8651	A review of the infection, genetics, and evolution of Neospora caninum: From the past to the present. Infection, Genetics and Evolution, 2013, 13, 133-150.	1.0	111
8652	Dictyostelium discoideum Protocols. Methods in Molecular Biology, 2013, , .	0.4	18
8653	Computational Toxicology. Methods in Molecular Biology, 2013, , .	0.4	12
8654	Effects of sustained swimming on the red and white muscle transcriptome of rainbow trout (Oncorhynchus mykiss) fed a carbohydrate-rich diet. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2013, 166, 510-521.	0.8	43
8655	Biomarkers. , 2013, , 123-124.		0
8656	Mechanism of Roux-en-Y Gastric Bypass Treatment for Type 2 Diabetes in Rats. Journal of Gastrointestinal Surgery, 2013, 17, 1073-1083.	0.9	8
8657	Altered miRNA Expression is Associated with Differentiation, Invasion, and Metastasis of Esophageal Squamous Cell Carcinoma (ESCC) in Patients from Huaian, China. Cell Biochemistry and Biophysics, 2013, 67, 657-668.	0.9	74
8658	Genome-Wide Pathway Analysis in Major Depressive Disorder. Journal of Molecular Neuroscience, 2013, 51, 428-436.	1.1	27
8659	Computational Intelligence in Intelligent Data Analysis. Studies in Computational Intelligence, 2013, , .	0.7	3
8660	Proteomic analysis of schistosomiasis japonica vaccine candidate antigens recognized by UV-attenuated cercariae-immunized porcine serum IgG2. Parasitology Research, 2013, 112, 2791-2803.	0.6	10
8661	Digital gene expression analysis of early root infection resistance to Sporisorium reilianum f. sp. zeae in maize. Molecular Genetics and Genomics, 2013, 288, 21-37.	1.0	20
8662	Gene-smoking interactions in multiple Rho-GTPase pathway genes in an early-onset coronary artery disease cohort. Human Genetics, 2013, 132, 1371-1382.	1.8	10

#	ARTICLE	IF	CITATIONS
8663	Candidate Agents for Papillary Thyroid Cancer Identified by Gene Expression Analysis. <i>Pathology and Oncology Research</i> , 2013, 19, 597-604.	0.9	3
8664	A pathway approach to investigate the function and regulation of SREBPs. <i>Genes and Nutrition</i> , 2013, 8, 289-300.	1.2	50
8665	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
8666	ROCK: a resource for integrative breast cancer data analysis. <i>Breast Cancer Research and Treatment</i> , 2013, 139, 907-921.	1.1	30
8667	A Novel Knowledge Representation Framework for the Statistical Validation of Quantitative Imaging Biomarkers. <i>Journal of Digital Imaging</i> , 2013, 26, 614-629.	1.6	6
8668	Quantitative Imaging Biomarker Ontology (QIBO) for Knowledge Representation of Biomedical Imaging Biomarkers. <i>Journal of Digital Imaging</i> , 2013, 26, 630-641.	1.6	12
8669	A predicted functional gene network for the plant pathogen <i>Phytophthora infestans</i> as a framework for genomic biology. <i>BMC Genomics</i> , 2013, 14, 483.	1.2	20
8670	Term extraction from sparse, ungrammatical domain-specific documents. <i>Expert Systems With Applications</i> , 2013, 40, 2530-2540.	4.4	19
8671	Getting the most out of parasitic helminth transcriptomes using HelmDB: Implications for biology and biotechnology. <i>Biotechnology Advances</i> , 2013, 31, 1109-1119.	6.0	23
8672	Heterogeneity of the biological properties and gene expression profiles of murine bone marrow stromal cells. <i>International Journal of Biochemistry and Cell Biology</i> , 2013, 45, 2431-2443.	1.2	29
8673	Whole-genome sequencing reveals untapped genetic potential in Africa's indigenous cereal crop sorghum. <i>Nature Communications</i> , 2013, 4, 2320.	5.8	405
8674	Systems Biology. , 2013, , .		9
8675	The emergence of Semantic Systems Biology. <i>New Biotechnology</i> , 2013, 30, 286-290.	2.4	3
8676	Reconstruction of Signaling Network from Protein Interactions Based on Function Annotations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 514-521.	1.9	3
8677	Interpreting the Omics Era's Data. <i>Smart Innovation, Systems and Technologies</i> , 2013, , 79-100.	0.5	7
8678	Computational studies on Alzheimer's disease associated pathways and regulatory patterns using microarray gene expression and network data: Revealed association with aging and other diseases. <i>Journal of Theoretical Biology</i> , 2013, 334, 109-121.	0.8	33
8679	Candidate Genes Expressed in Human Islets and Their Role in the Pathogenesis of Type 1 Diabetes. <i>Current Diabetes Reports</i> , 2013, 13, 633-641.	1.7	30
8680	Characterization of the EGFR interactome reveals associated protein complex networks and intracellular receptor dynamics. <i>Proteomics</i> , 2013, 13, 3131-3144.	1.3	54

#	ARTICLE	IF	CITATIONS
8681	The sacred lotus genome provides insights into the evolution of flowering plants. <i>Plant Journal</i> , 2013, 76, 557-567.	2.8	75
8682	Tethering preferences of domain families co-occurring in multi-domain proteins. <i>Molecular BioSystems</i> , 2013, 9, 1708.	2.9	1
8683	A transcriptomic investigation of handicap models in sexual selection. <i>Behavioral Ecology and Sociobiology</i> , 2013, 67, 221-234.	0.6	9
8684	Modelling Molecular Mechanisms: A Framework of Scientific Reasoning to Construct Molecular-Level Explanations for Cellular Behaviour. <i>Science and Education</i> , 2013, 22, 93-118.	1.7	75
8685	Information recovery in molecular biology: causal modelling of regulated promoter switching experiments. <i>Journal of Mathematical Biology</i> , 2013, 67, 105-122.	0.8	3
8687	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
8688	Accelerated protein evolution analysis reveals genes and pathways associated with the evolution of mammalian longevity. <i>Age</i> , 2013, 35, 301-314.	3.0	54
8689	Identification of drug candidate for osteoporosis by computational bioinformatics analysis of gene expression profile. <i>European Journal of Medical Research</i> , 2013, 18, 5.	0.9	8
8690	Agent-based Modeling. , 2013, , 13-13.		0
8691	Bayesian Decision Analysis. , 2013, , 71-71.		0
8692	Transcriptome profiling of the developing postnatal mouse testis using next-generation sequencing. <i>Science China Life Sciences</i> , 2013, 56, 1-12.	2.3	42
8693	Rank-based genome-wide analysis reveals the association of Ryanodine receptor-2 gene variants with childhood asthma among human populations. <i>Human Genomics</i> , 2013, 7, 16.	1.4	46
8694	Genome-wide signatures of convergent evolution in echolocating mammals. <i>Nature</i> , 2013, 502, 228-231.	13.7	321
8695	Insights into the immuno-molecular biology of <i>Angiostrongylus vasorum</i> through transcriptomicsâ€™ Prospects for new interventions. <i>Biotechnology Advances</i> , 2013, 31, 1486-1500.	6.0	18
8696	Metagenomic insights into microbial metabolism affecting arsenic dispersion in <sc>M</sc>editerranean marine sediments. <i>Molecular Ecology</i> , 2013, 22, 4870-4883.	2.0	36
8697	The impact of temperature on marine phytoplankton resource allocation and metabolism. <i>Nature Climate Change</i> , 2013, 3, 979-984.	8.1	358
8698	Functional Genomics, Proteomics, Metabolomics and Bioinformatics for Systems Biology. , 2013, , 3-41.		5
8699	A grammatical evolution algorithm for generation of Hierarchical Multi-Label Classification rules. , 2013, , .		6

#	ARTICLE	IF	CITATIONS
8700	Draft Assembly of the Symbiodinium minutum Nuclear Genome Reveals Dinoflagellate Gene Structure. <i>Current Biology</i> , 2013, 23, 1399-1408.	1.8	488
8701	Deciphering the host-pathogen protein interface in chikungunya virus-mediated sickness. <i>Archives of Virology</i> , 2013, 158, 1159-1172.	0.9	14
8702	Genome-wide computational identification of bicistronic mRNA in humans. <i>Amino Acids</i> , 2013, 44, 597-606.	1.2	2
8703	Hierarchical Dirichlet process model for gene expression clustering. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2013, 2013, 5.	1.4	13
8704	Molecular and Functional Alterations in a Mouse Cardiac Model of Friedreich Ataxia. <i>American Journal of Pathology</i> , 2013, 183, 745-757.	1.9	62
8705	2 α -Hydroxy C16-Ceramide Induces Apoptosis-Associated Proteomic Changes in C6 Glioma Cells. <i>Journal of Proteome Research</i> , 2013, 12, 4366-4375.	1.8	14
8706	Clonal evolution of high-grade serous ovarian carcinoma from primary to recurrent disease. <i>Journal of Pathology</i> , 2013, 229, 515-524.	2.1	88
8707	The Contribution of New Technologies Toward Understanding Plant-Fungus Symbioses. , 2013, , 201-214.		2
8708	Complete genome sequence of invertebrate iridescent virus 22 isolated from a blackfly larva. <i>Journal of General Virology</i> , 2013, 94, 2112-2116.	1.3	22
8709	Transcriptome responses in the rectal gland of fed and fasted spiny dogfish shark (<i>Squalus acanthias</i>) determined by suppression subtractive hybridization. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2013, 8, 334-343.	0.4	8
8710	Insulin Biosynthetic Interaction Network Component, TMEM24, Facilitates Insulin Reserve Pool Release. <i>Cell Reports</i> , 2013, 4, 921-930.	2.9	38
8711	PainNetworks: A web-based resource for the visualisation of pain-related genes in the context of their network associations. <i>Pain</i> , 2013, 154, 2586e1-2586e12.	2.0	50
8712	Gene coexpression network analysis identifies genes and biological processes shared among anterior pituitary and brain areas that affect estrous behavior in dairy cows. <i>Journal of Dairy Science</i> , 2013, 96, 2583-2595.	1.4	15
8713	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
8714	State of the art and open challenges in community-driven knowledge curation. <i>Journal of Biomedical Informatics</i> , 2013, 46, 1-4.	2.5	23
8715	A simulation to analyze feature selection methods utilizing gene ontology for gene expression classification. <i>Journal of Biomedical Informatics</i> , 2013, 46, 1044-1059.	2.5	13
8716	ADAR Regulates RNA Editing, Transcript Stability, and Gene Expression. <i>Cell Reports</i> , 2013, 5, 849-860.	2.9	169
8717	Methylmercury exposure increases lipocalin related (lpr) and decreases activated in blocked unfolded protein response (abu) genes and specific miRNAs in <i>Caenorhabditis elegans</i> . <i>Toxicology Letters</i> , 2013, 222, 189-196.	0.4	22

#	ARTICLE	IF	CITATIONS
8718	The DNA Methylomes of Serous Borderline Tumors Reveal Subgroups With Malignant- or Benign-Like Profiles. <i>American Journal of Pathology</i> , 2013, 182, 668-677.	1.9	13
8719	Long-term strain improvements accumulate mutations in regulatory elements responsible for hyper-production of cellulolytic enzymes. <i>Scientific Reports</i> , 2013, 3, 1569.	1.6	104
8720	Hierarchical multi-label gene function prediction using adaptive mutation in crowding niching. , 2013, , .		5
8721	Identifying Spurious Interactions and Predicting Missing Interactions in the Protein-Protein Interaction Networks via a Generative Network Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 219-225.	1.9	16
8722	An EST database of the Caribbean fruit fly, <i>Anastrepha suspensa</i> (Diptera: Tephritidae). <i>Gene</i> , 2013, 517, 212-217.	1.0	10
8723	Teaching the bioinformatics of signaling networks: an integrated approach to facilitate multi-disciplinary learning. <i>Briefings in Bioinformatics</i> , 2013, 14, 618-632.	3.2	15
8724	TMT-HCC: A tool for text mining the biomedical literature for hepatocellular carcinoma (HCC) biomarkers identification. <i>Computer Methods and Programs in Biomedicine</i> , 2013, 112, 640-648.	2.6	9
8725	YGA: Identifying distinct biological features between yeast gene sets. <i>Gene</i> , 2013, 518, 26-34.	1.0	6
8726	Genomic architecture of bovine κ -casein and λ -lactoglobulin. <i>Journal of Dairy Science</i> , 2013, 96, 5333-5343.	1.4	30
8727	In vivo regulation of gene transcription by alpha- and gamma-tocopherol in murine T lymphocytes. <i>Archives of Biochemistry and Biophysics</i> , 2013, 538, 111-119.	1.4	31
8728	Predicting the host protein interactors of Chandipura virus using a structural similarity-based approach. <i>Pathogens and Disease</i> , 2013, 69, n/a-n/a.	0.8	14
8729	Effects of bisphosphonate treatment on DNA methylation in osteonecrosis of the jaw. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2013, 757, 104-113.	0.9	10
8730	Flexible and robust co-regularized multi-domain graph clustering. , 2013, , .		48
8731	Applied ontologies and standards for service robots. <i>Robotics and Autonomous Systems</i> , 2013, 61, 1215-1223.	3.0	88
8732	Evolutionarily conserved motifs and modules in mitochondrial protein-protein interaction networks. <i>Mitochondrion</i> , 2013, 13, 668-675.	1.6	15
8733	Collaborative matrix factorization with multiple similarities for predicting drug-target interactions. , 2013, , .		222
8735	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	9.4	2,641
8736	Cyanidin is an agonistic ligand for peroxisome proliferator-activated receptor-alpha reducing hepatic lipid. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2013, 1831, 698-708.	1.2	68

#	ARTICLE	IF	CITATIONS
8737	Pattern Recognition in Bioinformatics. Lecture Notes in Computer Science, 2013, , .	1.0	1
8738	DGldb: mining the druggable genome. Nature Methods, 2013, 10, 1209-1210.	9.0	443
8739	Comparative Proteomics Reveal Diverse Functions and Dynamic Changes of <i>Bombyx mori</i> Silk Proteins Spun from Different Development Stages. Journal of Proteome Research, 2013, 12, 5213-5222.	1.8	75
8740	Expression Profile of Inflammatory Breast Cancer. Bulletin of Experimental Biology and Medicine, 2013, 155, 667-672.	0.3	9
8742	Radiation Proteomics. Advances in Experimental Medicine and Biology, 2013, , .	0.8	6
8743	Pathway analysis of a genome-wide association study in schizophrenia. Gene, 2013, 525, 107-115.	1.0	46
8744	Suitability of Illumina deep mRNA sequencing for reliable gene expression profiling in a non-model conifer species (<i>Pseudotsuga menziesii</i>). Tree Genetics and Genomes, 2013, 9, 1513-1527.	0.6	2
8745	Sleep-wake dynamics under extended light and extended dark conditions in adult zebrafish. Behavioural Brain Research, 2013, 256, 377-390.	1.2	36
8746	A Spatio-Temporal Understanding of Growth Regulation during the Salt Stress Response in Arabidopsis. Plant Cell, 2013, 25, 2132-2154.	3.1	351
8747	Identification of a miRNA signature in neutrophils after traumatic injury. Acta Biochimica Et Biophysica Sinica, 2013, 45, 938-945.	0.9	27
8748	Dynamic transcriptomes of human myeloid leukemia cells. Genomics, 2013, 102, 250-256.	1.3	32
8749	Human interactome resource and gene set linkage analysis for the functional interpretation of biologically meaningful gene sets. Bioinformatics, 2013, 29, 2024-2031.	1.8	14
8750	The Arabidopsis NAC Transcription Factor ANAC096 Cooperates with bZIP-Type Transcription Factors in Dehydration and Osmotic Stress Responses. Plant Cell, 2013, 25, 4708-4724.	3.1	240
8751	GPCR ontology: development and application of a G protein-coupled receptor pharmacology knowledge framework. Bioinformatics, 2013, 29, 3211-3219.	1.8	24
8752	Rule extraction in gene-disease relationship discovery. Gene, 2013, 518, 132-138.	1.0	7
8753	Discovering disease-disease associations by fusing systems-level molecular data. Scientific Reports, 2013, 3, 3202.	1.6	96
8754	Network2Canvas: network visualization on a canvas with enrichment analysis. Bioinformatics, 2013, 29, 1872-1878.	1.8	34
8755	Transcriptional profiling technology for studying vaccine responses: An untapped goldmine. Methods, 2013, 60, 269-274.	1.9	10

#	ARTICLE	IF	CITATIONS
8757	Inconsistency in large pharmacogenomic studies. <i>Nature</i> , 2013, 504, 389-393.	13.7	467
8758	Sieving through the cancer secretome. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2360-2371.	1.1	28
8759	The Comprehensive Antibiotic Resistance Database. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3348-3357.	1.4	1,615
8760	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20645-20650.	3.3	260
8761	Expression of Polycomb Targets Predicts Breast Cancer Prognosis. <i>Molecular and Cellular Biology</i> , 2013, 33, 3951-3961.	1.1	38
8762	Data Mining for Systems Biology. <i>Methods in Molecular Biology</i> , 2013, , .	0.4	2
8764	ERF115 Controls Root Quiescent Center Cell Division and Stem Cell Replenishment. <i>Science</i> , 2013, 342, 860-863.	6.0	263
8765	INSECT: IN-silico SEarch for Co-occurring Transcription factors. <i>Bioinformatics</i> , 2013, 29, 2852-2858.	1.8	13
8766	Beyond the ENCODE project: using genomics and epigenomics strategies to study enhancer evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130022.	1.8	14
8767	Widespread Aggregation and Neurodegenerative Diseases Are Associated with Supersaturated Proteins. <i>Cell Reports</i> , 2013, 5, 781-790.	2.9	245
8768	Genome-Wide Binding Analysis of the Transcription Activator IDEAL PLANT ARCHITECTURE1 Reveals a Complex Network Regulating Rice Plant Architecture. <i>Plant Cell</i> , 2013, 25, 3743-3759.	3.1	588
8769	Fundamentals and Application of New Bioproduction Systems. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2013, , .	0.6	4
8770	COPRED: prediction of fold, GO molecular function and functional residues at the domain level. <i>Bioinformatics</i> , 2013, 29, 1811-1812.	1.8	1
8771	iLoc-Animal: a multi-label learning classifier for predicting subcellular localization of animal proteins. <i>Molecular BioSystems</i> , 2013, 9, 634.	2.9	245
8772	Balanced Caloric Macronutrient Composition Downregulates Immunological Gene Expression in Human Blood Cells—Adipose Tissue Diverges. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 41-52.	1.0	12
8773	A system biology approach to identify regulatory pathways underlying the neuroendocrine control of female puberty in rats and nonhuman primates. <i>Hormones and Behavior</i> , 2013, 64, 175-186.	1.0	43
8774	Genome-wide survey of repetitive DNA elements in the button mushroom <i>Agaricus bisporus</i> . <i>Fungal Genetics and Biology</i> , 2013, 55, 6-21.	0.9	37
8775	Changes in gene expression within the ventral tegmental area following repeated excessive binge-like alcohol drinking by alcohol-preferring (P) rats. <i>Alcohol</i> , 2013, 47, 367-380.	0.8	45

#	ARTICLE	IF	CITATIONS
8776	Models and Algorithms for Genome Evolution. Computational Biology, 2013, , .	0.1	7
8777	ppiPre: predicting protein-protein interactions by combining heterogeneous features. BMC Systems Biology, 2013, 7, S8.	3.0	17
8778	Analysis of altered <sc>microRNA</sc> expression profiles in peripheral blood mononuclear cells from patients with primary biliary cirrhosis. Journal of Gastroenterology and Hepatology (Australia), 2013, 28, 543-550.	1.4	38
8779	Differential proteomic profiling in human spermatozoa that did or did not result in pregnancy via IVF and AID. Proteomics - Clinical Applications, 2013, 7, 850-858.	0.8	44
8780	Predicting effective drug combinations via network propagation. , 2013, , .		2
8781	Expressed sequence tag analysis of the emu (Dromaius novaehollandiae) pituitary by 454 GS Junior pyrosequencing. Poultry Science, 2013, 92, 90-96.	1.5	0
8783	Evaluation of research in biomedical ontologies. Briefings in Bioinformatics, 2013, 14, 696-712.	3.2	60
8784	Brain and Health Informatics. Lecture Notes in Computer Science, 2013, , .	1.0	2
8785	<i><sc>TIME FOR COFFEE</sc></i> is an essential component in the maintenance of metabolic homeostasis in <i><sc>A</sc>rabidopsis thaliana</i>. Plant Journal, 2013, 76, 188-200.	2.8	79
8786	A Framework for Measuring Ontology Usage on the Web. Computer Journal, 2013, 56, 1083-1101.	1.5	13
8787	The <sc>B</sc>asic <sc>F</sc>ormal <sc>O</sc>ntology as a Reference Framework for Modeling the Evolution of Administrative Units. Transactions in GIS, 2013, 17, 206-226.	1.0	12
8788	Benchmarking technology infrastructures for embarrassingly and non-embarrassingly parallel problems in biomedical domain. , 2013, , .		1
8789	Proteomic analysis of Girdin-interacting proteins in migrating new neurons in the postnatal mouse brain. Biochemical and Biophysical Research Communications, 2013, 442, 16-21.	1.0	4
8790	Transcriptome-wide identification of RNA binding sites by CLIP-seq. Methods, 2013, 63, 32-40.	1.9	28
8791	Evidence for Postinitiation Regulation of mRNA Biogenesis in Tuberculosis. Journal of Immunology, 2013, 190, 2747-2755.	0.4	4
8792	Literature mining associations of diseases using gene ontology. , 2013, , .		2
8793	Review of processing and analysis methods for DNA methylation array data. British Journal of Cancer, 2013, 109, 1394-1402.	2.9	164
8796	Drug Uptake, Lipid Rafts, and Vesicle Trafficking Modulate Resistance to an Anticancer Lysophosphatidylcholine Analogue in Yeast. Journal of Biological Chemistry, 2013, 288, 8405-8418.	1.6	41

#	ARTICLE	IF	CITATIONS
8797	Enrichment analysis applied to disease prognosis. <i>Journal of Biomedical Semantics</i> , 2013, 4, 21.	0.9	2
8798	Topology of molecular interaction networks. <i>BMC Systems Biology</i> , 2013, 7, 90.	3.0	119
8799	Inferring the effective TOR-dependent network: a computational study in yeast. <i>BMC Systems Biology</i> , 2013, 7, 84.	3.0	3
8800	Identification of differentially expressed genes in American cockroach ovaries and testes by suppression subtractive hybridization and the prediction of its miRNAs. <i>Molecular Genetics and Genomics</i> , 2013, 288, 627-638.	1.0	8
8801	Semantic integration of gene expression analysis tools and data sources using software connectors. <i>BMC Genomics</i> , 2013, 14, S2.	1.2	4
8802	afterParty: turning raw transcriptomes into permanent resources. <i>BMC Bioinformatics</i> , 2013, 14, 301.	1.2	8
8803	Function of dynamic models in systems biology: linking structure to behaviour. <i>Journal of Biomedical Semantics</i> , 2013, 4, 24.	0.9	4
8804	The genome and transcriptome of <i>Haemonchus contortus</i> , a key model parasite for drug and vaccine discovery. <i>Genome Biology</i> , 2013, 14, R88.	13.9	293
8805	A genome-wide MeSH-based literature mining system predicts implicit gene-to-gene relationships and networks. <i>BMC Systems Biology</i> , 2013, 7, S9.	3.0	32
8806	Identification of novel microRNA regulatory pathways associated with heterogeneous prostate cancer. <i>BMC Systems Biology</i> , 2013, 7, S6.	3.0	37
8807	The Gene Ontology (GO) Cellular Component Ontology: integration with SAO (Subcellular Anatomy) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	0.9	44
8808	Using ontologies to study cell transitions. <i>Journal of Biomedical Semantics</i> , 2013, 4, 25.	0.9	2
8809	An integrated transcriptome and epigenome analysis identifies a novel candidate gene for pancreatic cancer. <i>BMC Medical Genomics</i> , 2013, 6, 33.	0.7	31
8810	SCLpredT: Ab initio and homology-based prediction of subcellular localization by N-to-1 neural networks. <i>SpringerPlus</i> , 2013, 2, 502.	1.2	9
8811	The Vertebrate Trait Ontology: a controlled vocabulary for the annotation of trait data across species. <i>Journal of Biomedical Semantics</i> , 2013, 4, 13.	0.9	42
8812	Unsupervised automated high throughput phenotyping of RNAi time-lapse movies. <i>BMC Bioinformatics</i> , 2013, 14, 292.	1.2	21
8813	Drug repositioning for orphan genetic diseases through Conserved Anticoexpressed Gene Clusters (CAGCs). <i>BMC Bioinformatics</i> , 2013, 14, 288.	1.2	11
8814	Bolbase: a comprehensive genomics database for <i>Brassica oleracea</i> . <i>BMC Genomics</i> , 2013, 14, 664.	1.2	99

#	ARTICLE	IF	CITATIONS
8815	Using PPI network autocorrelation in hierarchical multi-label classification trees for gene function prediction. <i>BMC Bioinformatics</i> , 2013, 14, 285.	1.2	41
8816	Pathprinting: An integrative approach to understand the functional basis of disease. <i>Genome Medicine</i> , 2013, 5, 68.	3.6	13
8817	Genome-wide modeling of complex phenotypes in <i>Caenorhabditis elegans</i> and <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2013, 14, 580.	1.2	1
8818	Fuzzy clustering of CPP family in plants with evolution and interaction analyses. <i>BMC Bioinformatics</i> , 2013, 14, S10.	1.2	28
8819	The ovarian transcriptome of the cattle tick, <i>Rhipicephalus (Boophilus) microplus</i> , feeding upon a bovine host infected with <i>Babesia bovis</i> . <i>Parasites and Vectors</i> , 2013, 6, 276.	1.0	31
8820	Pathway-based outlier method reveals heterogeneous genomic structure of autism in blood transcriptome. <i>BMC Medical Genomics</i> , 2013, 6, 34.	0.7	24
8821	DaGO-Fun: tool for Gene Ontology-based functional analysis using term information content measures. <i>BMC Bioinformatics</i> , 2013, 14, 284.	1.2	33
8822	Single nucleotide polymorphisms and haplotypes associated with feed efficiency in beef cattle. <i>BMC Genetics</i> , 2013, 14, 94.	2.7	52
8823	A modular framework for biomedical concept recognition. <i>BMC Bioinformatics</i> , 2013, 14, 281.	1.2	53
8824	Learning a Markov Logic network for supervised gene regulatory network inference. <i>BMC Bioinformatics</i> , 2013, 14, 273.	1.2	12
8825	Experimental characterization of the human non-sequence-specific nucleic acid interactome. <i>Genome Biology</i> , 2013, 14, R81.	13.9	7
8826	IDOMAL: the malaria ontology revisited. <i>Journal of Biomedical Semantics</i> , 2013, 4, 16.	0.9	12
8827	Whole transcriptome sequencing identifies tumor-specific mutations in human oral squamous cell carcinoma. <i>BMC Medical Genomics</i> , 2013, 6, 28.	0.7	26
8828	Transcriptomic analysis highlights epigenetic and transcriptional regulation during zygotic embryo development of <i>Pinus pinaster</i> . <i>BMC Plant Biology</i> , 2013, 13, 123.	1.6	37
8829	Protein function prediction by collective classification with explicit and implicit edges in protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2013, 14, S4.	1.2	15
8830	Microarray profiling reveals suppressed interferon stimulated gene program in fibroblasts from scleroderma-associated interstitial lung disease. <i>Respiratory Research</i> , 2013, 14, 80.	1.4	81
8831	The predicted secretome and transmembranome of the poultry red mite <i>Dermanyssus gallinae</i> . <i>Parasites and Vectors</i> , 2013, 6, 259.	1.0	32
8832	Genes involved in thoracic exoskeleton formation during the pupal-to-adult molt in a social insect model, <i>Apis mellifera</i> . <i>BMC Genomics</i> , 2013, 14, 576.	1.2	28

#	ARTICLE	IF	CITATIONS
8833	Systematic review of genome-wide gene expression studies of bipolar disorder. <i>BMC Psychiatry</i> , 2013, 13, 213.	1.1	70
8834	Molecular fingerprinting reflects different histotypes and brain region in low grade gliomas. <i>BMC Cancer</i> , 2013, 13, 387.	1.1	13
8835	Vitamin B6 reduces hippocampal apoptosis in experimental pneumococcal meningitis. <i>BMC Infectious Diseases</i> , 2013, 13, 393.	1.3	22
8836	MicroRNAs implicated in dysregulation of gene expression following human lung transplantation. <i>Translational Respiratory Medicine</i> , 2013, 1, .	3.8	22
8837	Mining differential top-k co-expression patterns from time course comparative gene expression datasets. <i>BMC Bioinformatics</i> , 2013, 14, 230.	1.2	27
8838	Interspecies protein-protein interaction network construction for characterization of host-pathogen interactions: a <i>Candida albicans</i> -zebrafish interaction study. <i>BMC Systems Biology</i> , 2013, 7, 79.	3.0	32
8839	GOParGenPy: a high throughput method to generate Gene Ontology data matrices. <i>BMC Bioinformatics</i> , 2013, 14, 242.	1.2	5
8840	Label-free mass spectrometry proteome quantification of human embryonic kidney cells following 24 hours of sialic acid overproduction. <i>Proteome Science</i> , 2013, 11, 38.	0.7	13
8841	Dovetailing biology and chemistry: integrating the Gene Ontology with the ChEBI chemical ontology. <i>BMC Genomics</i> , 2013, 14, 513.	1.2	45
8842	Systems perspectives on erythromycin biosynthesis by comparative genomic and transcriptomic analyses of <i>S. erythraea</i> E3 and NRRL23338 strains. <i>BMC Genomics</i> , 2013, 14, 523.	1.2	39
8843	Wheat resistome in response to barley yellow dwarf virus infection. <i>Functional and Integrative Genomics</i> , 2013, 13, 155-165.	1.4	18
8844	Obligate mutualism within a host drives the extreme specialization of a fig wasp genome. <i>Genome Biology</i> , 2013, 14, R141.	13.9	85
8845	The genome of <i>Romanomermis culicivorax</i> : revealing fundamental changes in the core developmental genetic toolkit in Nematoda. <i>BMC Genomics</i> , 2013, 14, 923.	1.2	43
8846	Conceptualization of molecular findings by mining gene annotations. <i>BMC Proceedings</i> , 2013, 7, S2.	1.8	5
8847	A multi-omic analysis of an <i>Enterococcus faecium</i> mutant reveals specific genetic mutations and dramatic changes in mRNA and protein expression. <i>BMC Microbiology</i> , 2013, 13, 304.	1.3	14
8848	Comparative inner ear transcriptome analysis between the <i>Rickettsia</i> 's big-footed bats (<i>Myotis ricketti</i>) and the greater short-nosed fruit bats (<i>Cynopterus sphinx</i>). <i>BMC Genomics</i> , 2013, 14, 916.	1.2	25
8849	A new computational strategy for predicting essential genes. <i>BMC Genomics</i> , 2013, 14, 910.	1.2	34
8850	A mesh generation and machine learning framework for <i>Drosophila</i> gene expression pattern image analysis. <i>BMC Bioinformatics</i> , 2013, 14, 372.	1.2	8

#	ARTICLE	IF	CITATIONS
8851	Population genomics of the endangered giant Galápagos tortoise. <i>Genome Biology</i> , 2013, 14, R136.	13.9	32
8852	Establishing an osteosarcoma associated protein-protein interaction network to explore the pathogenesis of osteosarcoma. <i>European Journal of Medical Research</i> , 2013, 18, 57.	0.9	3
8853	Integrating human omics data to prioritize candidate genes. <i>BMC Medical Genomics</i> , 2013, 6, 57.	0.7	36
8854	Whole transcriptome characterization of the effects of dehydration and rehydration on <i>Cladonia rangiferina</i> , the grey reindeer lichen. <i>BMC Genomics</i> , 2013, 14, 870.	1.2	31
8855	Transcriptome analysis of leaf and root of rice seedling to acute dehydration. <i>Rice</i> , 2013, 6, 38.	1.7	42
8856	Genome-wide characterization of microRNA in foxtail millet (<i>Setaria italica</i>). <i>BMC Plant Biology</i> , 2013, 13, 212.	1.6	47
8857	Fermentation stage-dependent adaptations of <i>Bacillus licheniformis</i> during enzyme production. <i>Microbial Cell Factories</i> , 2013, 12, 120.	1.9	19
8858	Exploring the "dark matter" of a mammalian proteome by protein structure and function modeling. <i>Proteome Science</i> , 2013, 11, 47.	0.7	9
8859	Prediction of protein interaction types based on sequence and network features. <i>BMC Systems Biology</i> , 2013, 7, S5.	3.0	5
8860	PPSampler2: Predicting protein complexes more accurately and efficiently by sampling. <i>BMC Systems Biology</i> , 2013, 7, S14.	3.0	27
8861	GeneTopics - interpretation of gene sets via literature-driven topic models. <i>BMC Systems Biology</i> , 2013, 7, S10.	3.0	10
8862	Dynamic protein interaction modules in human hepatocellular carcinoma progression. <i>BMC Systems Biology</i> , 2013, 7, S2.	3.0	22
8863	The neurological disease ontology. <i>Journal of Biomedical Semantics</i> , 2013, 4, 42.	0.9	32
8864	Gene-gene interaction network analysis of ovarian cancer using TCGA data. <i>Journal of Ovarian Research</i> , 2013, 6, 88.	1.3	15
8865	Gene expression profiling analysis of hepatocellular carcinoma. <i>European Journal of Medical Research</i> , 2013, 18, 44.	0.9	3
8866	A novel phenotypic dissimilarity method for image-based high-throughput screens. <i>BMC Bioinformatics</i> , 2013, 14, 336.	1.2	15
8867	Catastrophic chaos theory: predicting recovery of health or death. <i>Artificial Life and Robotics</i> , 2013, 18, 127-132.	0.7	3
8868	A systems biology approach using metabolomic data reveals genes and pathways interacting to modulate divergent growth in cattle. <i>BMC Genomics</i> , 2013, 14, 798.	1.2	76

#	ARTICLE	IF	CITATIONS
8869	Genomic divergence between nine- and three-spined sticklebacks. <i>BMC Genomics</i> , 2013, 14, 756.	1.2	42
8870	The strength of genetic interactions scales weakly with mutational effects. <i>Genome Biology</i> , 2013, 14, R76.	13.9	17
8871	Enhanced XAO: the ontology of <i>Xenopus</i> anatomy and development underpins more accurate annotation of gene expression and queries on Xenbase. <i>Journal of Biomedical Semantics</i> , 2013, 4, 31.	0.9	33
8872	The <i>Drosophila</i> phenotype ontology. <i>Journal of Biomedical Semantics</i> , 2013, 4, 30.	0.9	22
8873	Proteomics methods for subcellular proteome analysis. <i>FEBS Journal</i> , 2013, 280, 5626-5634.	2.2	87
8874	Agrigenomics for Microalgal Biofuel Production: An Overview of Various Bioinformatics Resources and Recent Studies to Link OMICS to Bioenergy and Bioeconomy. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 537-549.	1.0	41
8875	Utilizing Both Topological and Attribute Information for Protein Complex Identification in PPI Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 780-792.	1.9	44
8876	Tetraploid Rangpur lime rootstock increases drought tolerance via enhanced constitutive root abscisic acid production. <i>Plant, Cell and Environment</i> , 2013, 36, 856-868.	2.8	167
8877	Drug target inference through pathway analysis of genomics data. <i>Advanced Drug Delivery Reviews</i> , 2013, 65, 966-972.	6.6	25
8878	DYNAMICALLY SEARCHING FOR A DOMAIN FOR PROTEIN FUNCTION PREDICTION. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1350008.	0.3	2
8879	Application of <i>Cydia pomonella</i> expressed sequence tags: Identification and expression of three general odorant binding proteins in codling moth. <i>Insect Science</i> , 2013, 20, 559-574.	1.5	16
8880	Towards Precision Medicine: Advances in Computational Approaches for the Analysis of Human Variants. <i>Journal of Molecular Biology</i> , 2013, 425, 4047-4063.	2.0	122
8881	Searching for a needle in a stack of needles: challenges in metaproteomics data analysis. <i>Molecular BioSystems</i> , 2013, 9, 578-585.	2.9	93
8882	Expression Profiling of Intestinal Tissues Implicates Tissue-Specific Genes and Pathways Essential for Thyroid Hormone-Induced Adult Stem Cell Development. <i>Endocrinology</i> , 2013, 154, 4396-4407.	1.4	42
8883	PPIExtractor: A Protein Interaction Extraction and Visualization System for Biomedical Literature. <i>IEEE Transactions on Nanobioscience</i> , 2013, 12, 173-181.	2.2	14
8884	Network-Based Penalized Regression With Application to Genomic Data. <i>Biometrics</i> , 2013, 69, 582-593.	0.8	36
8885	Recommendations for the design and analysis of epigenome-wide association studies. <i>Nature Methods</i> , 2013, 10, 949-955.	9.0	345
8886	Comparative antigen-induced gene expression profiles unveil novel aspects of susceptibility/resistance to adjuvant arthritis in rats. <i>Molecular Immunology</i> , 2013, 56, 531-539.	1.0	7

#	ARTICLE	IF	CITATIONS
8887	Assessment of crosstalks between the Snf1 kinase complex and sphingolipid metabolism in <i>S. cerevisiae</i> via systems biology approaches. <i>Molecular BioSystems</i> , 2013, 9, 2914.	2.9	7
8888	Transcriptional profiling by RNA-Seq of peri-attachment porcine embryos generated by a variety of assisted reproductive technologies. <i>Physiological Genomics</i> , 2013, 45, 577-589.	1.0	19
8889	Identifying Protein Complexes Based on Multiple Topological Structures in PPI Networks. <i>IEEE Transactions on Nanobioscience</i> , 2013, 12, 165-172.	2.2	20
8890	Transcriptome analysis of a spontaneous reddish mutant in Miyagawa Wase Satsuma mandarin. <i>Journal of the Korean Society for Applied Biological Chemistry</i> , 2013, 56, 391-399.	0.9	3
8891	Predicting drug-target interactions through integrative analysis of chemogenetic assays in yeast. <i>Molecular BioSystems</i> , 2013, 9, 768.	2.9	6
8892	Prioritized functional analysis of biological experiments using resampling and noise control methodologies. , 2013, , .		5
8893	Community-Driven and Ontology-Based Biological Knowledge Management: A Hybrid Approach to Harnessing Collective Intelligence. , 2013, , .		0
8894	Gelsius: A Literature-Based Workflow for Determining Quantitative Associations between Genes and Biological Processes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 619-631.	1.9	2
8895	COMBat: Visualizing co-occurrence of annotation terms. , 2013, , .		2
8896	A mechanical perforation procedure for embryo biopsy. , 2013, , .		3
8897	Characterization of drug-induced transcriptional modules: towards drug repositioning and functional understanding. <i>Molecular Systems Biology</i> , 2013, 9, 662.	3.2	110
8898	PUPPI: A pathway analysis method using protein-protein interaction network for case-control data. , 2013, , .		2
8899	Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. <i>Molecular Systems Biology</i> , 2013, 9, 637.	3.2	267
8900	Directed Multistep Biocatalysis Using Tailored Permeabilized Cells. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2013, 137, 185-234.	0.6	15
8901	Systems-based understanding of pharmacological responses with combinations of multidisciplinary methodologies. <i>Biopharmaceutics and Drug Disposition</i> , 2013, 34, 489-507.	1.1	8
8902	The Formation of a Neural Fear Network in Posttraumatic Stress Disorder. <i>Clinical Psychological Science</i> , 2013, 1, 452-469.	2.4	30
8903	Zebrafish Expression Ontology of Gene Sets (ZEOGS): A Tool to Analyze Enrichment of Zebrafish Anatomical Terms in Large Gene Sets. <i>Zebrafish</i> , 2013, 10, 303-315.	0.5	17
8904	Mining featured biomarkers associated with prostatic carcinoma based on bioinformatics. <i>Biomarkers</i> , 2013, 18, 580-586.	0.9	0

#	ARTICLE	IF	CITATIONS
8905	Evaluation of the combinative application of SDS and sodium deoxycholate to the LC-MS-based shotgun analysis of membrane proteomes. <i>Journal of Separation Science</i> , 2013, 36, 3026-3034.	1.3	9
8906	Toward knowledge support for analysis and interpretation of complex traits. <i>Genome Biology</i> , 2013, 14, 214.	13.9	7
8907	Semantics-driven modelling of user preferences for information retrieval in the biomedical domain. <i>Informatics for Health and Social Care</i> , 2013, 38, 150-170.	1.4	6
8909	Application of Machine Learning to Proteomics Data: Classification and Biomarker Identification in Postgenomics Biology. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 595-610.	1.0	171
8910	Rank-based interolog mapping for predicting proteinprotein interactions between genomes. , 2013, , .		0
8911	Power graph compression reveals dominant relationships in genetic transcription networks. <i>Molecular BioSystems</i> , 2013, 9, 2681.	2.9	9
8912	Applications of systems biology in cancer immunotherapy: from target discovery to biomarkers of clinical outcome. <i>Expert Review of Clinical Pharmacology</i> , 2013, 6, 387-401.	1.3	17
8913	Deep Coverage of the Escherichia coli Proteome Enables the Assessment of False Discovery Rates in Simple Proteogenomic Experiments. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3420-3430.	2.5	71
8914	Biotin labeling and receptor analysis of huwentoxin-I. <i>Analytical Methods</i> , 2013, 5, 3888.	1.3	2
8915	Annotation and reâ€sequencing of genes from de novo transcriptome assembly of <i>Abies alba</i> (Pinaceae). <i>Applications in Plant Sciences</i> , 2013, 1, 1200179.	0.8	17
8916	Multiscale gene sets from protein interaction networks. , 2013, , .		0
8917	A systems medicine research approach for studying alcohol addiction. <i>Addiction Biology</i> , 2013, 18, 883-896.	1.4	76
8918	Trelliscope: A system for detailed visualization in the deep analysis of large complex data. , 2013, , .		10
8919	A genetic algorithms framework for estimating individual gene contributions in signaling pathways. , 2013, , .		1
8920	Long non-coding RNAs function annotation: a global prediction method based on bi-colored networks. <i>Nucleic Acids Research</i> , 2013, 41, e35-e35.	6.5	174
8921	Integrative variable selection via Bayesian model uncertainty. <i>Statistics in Medicine</i> , 2013, 32, 4938-4953.	0.8	31
8922	Immune gene discovery by expressed sequence tag (EST) analysis of hemocytes in the ridgetail white prawn <i>Exopalaemon carinicauda</i> . <i>Fish and Shellfish Immunology</i> , 2013, 34, 173-182.	1.6	27
8923	Transcription factors expressed in embryonic and adult olfactory bulb neural stem cells reveal distinct proliferation, differentiation and epigenetic control. <i>Genomics</i> , 2013, 101, 12-19.	1.3	16

#	ARTICLE	IF	CITATIONS
8924	Systems biology of pathogen-host interaction: Networks of protein-protein interaction within pathogens and pathogen-human interactions in the post-genomic era. <i>Biotechnology Journal</i> , 2013, 8, 85-96.	1.8	39
8925	OrchidBase 2.0: Comprehensive Collection of Orchidaceae Floral Transcriptomes. <i>Plant and Cell Physiology</i> , 2013, 54, e7-e7.	1.5	76
8926	DNA Methylation Alterations Exhibit Intraindividual Stability and Interindividual Heterogeneity in Prostate Cancer Metastases. <i>Science Translational Medicine</i> , 2013, 5, 169ra10.	5.8	231
8927	Multiple Phytohormone Signals Control the Transcriptional Response to Soybean Aphid Infestation in Susceptible and Resistant Soybean Plants. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 116-129.	1.4	114
8928	A gene ontology inferred from molecular networks. <i>Nature Biotechnology</i> , 2013, 31, 38-45.	9.4	184
8929	Cancer pharmacogenomics: strategies and challenges. <i>Nature Reviews Genetics</i> , 2013, 14, 23-34.	7.7	192
8930	Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 2013, 493, 526-531.	13.7	564
8931	Exome-based linkage disequilibrium maps of individual genes: functional clustering and relationship to disease. <i>Human Genetics</i> , 2013, 132, 233-243.	1.8	15
8932	Crystal Structure of Rice Importin-1 α and Structural Basis of Its Interaction with Plant-Specific Nuclear Localization Signals. <i>Plant Cell</i> , 2013, 24, 5074-5088.	3.1	60
8933	A pharmacological organization of G protein-coupled receptors. <i>Nature Methods</i> , 2013, 10, 140-146.	9.0	89
8934	Interactions of miR-323/miR-326/miR-329 and miR-130a/miR-155/miR-210 as prognostic indicators for clinical outcome of glioblastoma patients. <i>Journal of Translational Medicine</i> , 2013, 11, 10.	1.8	162
8935	Detection and interpretation of genomic structural variation in health and disease. <i>Expert Review of Molecular Diagnostics</i> , 2013, 13, 61-82.	1.5	13
8936	Genome-wide Chromatin State Transitions Associated with Developmental and Environmental Cues. <i>Cell</i> , 2013, 152, 642-654.	13.5	473
8937	Semantic Web meets Integrative Biology: a survey. <i>Briefings in Bioinformatics</i> , 2013, 14, 109-125.	3.2	50
8938	Chromosome 18 Transcriptome Profiling and Targeted Proteome Mapping in Depleted Plasma, Liver Tissue and HepG2 Cells. <i>Journal of Proteome Research</i> , 2013, 12, 123-134.	1.8	59
8939	Setting Up an Intronic miRNA Database. <i>Methods in Molecular Biology</i> , 2013, 936, 69-76.	0.4	6
8940	Deciphering gene expression program of MAP3K1 in mouse eyelid morphogenesis. <i>Developmental Biology</i> , 2013, 374, 96-107.	0.9	13
8941	Exploring local immunological adaptation of two stickleback ecotypes by experimental infection and transcriptome-wide digital gene expression analysis. <i>Molecular Ecology</i> , 2013, 22, 774-786.	2.0	79

#	ARTICLE	IF	CITATIONS
8942	Discovery of Potential Bladder Cancer Biomarkers by Comparative Urine Proteomics and Analysis. <i>Clinical Genitourinary Cancer</i> , 2013, 11, 56-62.	0.9	70
8943	Discovery of Cell Compartment Specific Protein-Protein Interactions using Affinity Purification Combined with Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2013, 12, 272-281.	1.8	28
8944	ALKBH5 Is a Mammalian RNA Demethylase that Impacts RNA Metabolism and Mouse Fertility. <i>Molecular Cell</i> , 2013, 49, 18-29.	4.5	2,549
8945	Functional genomic analysis of chromosomal aberrations in a compendium of 8000 cancer genomes. <i>Genome Research</i> , 2013, 23, 217-227.	2.4	139
8946	Identification of the major proteins of an immune modulating fraction from adult <i>Fasciola hepatica</i> released by Nonidet P40. <i>Veterinary Parasitology</i> , 2013, 191, 379-385.	0.7	24
8947	Enrichment Analysis of miRNA Targets. <i>Methods in Molecular Biology</i> , 2013, 936, 91-103.	0.4	12
8948	Detecting the knowledge structure of bioinformatics by mining full-text collections. <i>Scientometrics</i> , 2013, 96, 183-201.	1.6	66
8949	Linking the signaling cascades and dynamic regulatory networks controlling stress responses. <i>Genome Research</i> , 2013, 23, 365-376.	2.4	71
8950	Distinct Metabolic Flow Enables Large-Scale Purification of Mouse and Human Pluripotent Stem Cell-Derived Cardiomyocytes. <i>Cell Stem Cell</i> , 2013, 12, 127-137.	5.2	860
8951	Unravelling the enigma of selective vulnerability in neurodegeneration: motor neurons resistant to degeneration in ALS show distinct gene expression characteristics and decreased susceptibility to excitotoxicity. <i>Acta Neuropathologica</i> , 2013, 125, 95-109.	3.9	133
8952	Gene set analysis of GWAS data for human longevity highlights the relevance of the insulin/IGF-1 signaling and telomere maintenance pathways. <i>Age</i> , 2013, 35, 235-249.	3.0	105
8953	Phyletic Profiling with Cliques of Orthologs Is Enhanced by Signatures of Paralogy Relationships. <i>PLoS Computational Biology</i> , 2013, 9, e1002852.	1.5	29
8954	DNA Damage and Transcriptional Changes in the Gills of <i>Mytilus galloprovincialis</i> Exposed to Nanomolar Doses of Combined Metal Salts (Cd, Cu, Hg). <i>PLoS ONE</i> , 2013, 8, e54602.	1.1	68
8955	Microarray Analysis Reveals Novel Features of the Muscle Aging Process in Men and Women. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2013, 68, 1035-1044.	1.7	50
8956	Genetics and epigenetics of rheumatoid arthritis. <i>Nature Reviews Rheumatology</i> , 2013, 9, 141-153.	3.5	325
8957	Microarray-based analysis of gene regulation by transcription factors and microRNAs in glioma. <i>Neurological Sciences</i> , 2013, 34, 1283-1289.	0.9	20
8958	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
8959	Loss, replacement and gain of proteins at the origin of the mitochondria. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2013, 1827, 224-231.	0.5	45

#	ARTICLE	IF	CITATIONS
8960	Predicting the Functional, Molecular, and Phenotypic Consequences of Amino Acid Substitutions using Hidden Markov Models. <i>Human Mutation</i> , 2013, 34, 57-65.	1.1	1,057
8961	Systems biology approaches to finding novel pain mediators. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013, 5, 11-35.	6.6	42
8962	Patient-Specific Modelling in Drug Design, Development and Selection Including its Role in Clinical Decision-Making. <i>Chemical Biology and Drug Design</i> , 2013, 81, 5-12.	1.5	9
8963	A DNA-Centric Protein Interaction Map of Ultraconserved Elements Reveals Contribution of Transcription Factor Binding Hubs to Conservation. <i>Cell Reports</i> , 2013, 5, 531-545.	2.9	26
8964	Semantically predicting protein functions based on protein functional connectivity. <i>Computational Biology and Chemistry</i> , 2013, 44, 9-14.	1.1	4
8965	Pinda: A Web service for detection and analysis of intraspecies gene duplication events. <i>Computer Methods and Programs in Biomedicine</i> , 2013, 111, 711-714.	2.6	5
8966	Multiphasic adaptation of the transcriptome of <i>Saccharomyces cerevisiae</i> to heat stress. <i>Food Research International</i> , 2013, 54, 1103-1112.	2.9	9
8967	Co-expression network with protein-protein interaction and transcription regulation in malaria parasite <i>Plasmodium falciparum</i> . <i>Gene</i> , 2013, 518, 7-16.	1.0	8
8968	Unsupervised biomedical named entity recognition: Experiments with clinical and biological texts. <i>Journal of Biomedical Informatics</i> , 2013, 46, 1088-1098.	2.5	169
8969	Novel Dedifferentiated Liposarcoma Xenograft Models Reveal PTEN Down-Regulation as a Malignant Signature and Response to PI3K Pathway Inhibition. <i>American Journal of Pathology</i> , 2013, 182, 1400-1411.	1.9	31
8970	Integrating Genomic, Epigenomic, and Transcriptomic Features Reveals Modular Signatures Underlying Poor Prognosis in Ovarian Cancer. <i>Cell Reports</i> , 2013, 4, 542-553.	2.9	88
8971	The Roles of FMRP-Regulated Genes in Autism Spectrum Disorder: Single- and Multiple-Hit Genetic Etiologies. <i>American Journal of Human Genetics</i> , 2013, 93, 825-839.	2.6	60
8972	Interestingness measures and strategies for mining multi-ontology multi-level association rules from gene ontology annotations for the discovery of new GO relationships. <i>Journal of Biomedical Informatics</i> , 2013, 46, 849-856.	2.5	30
8974	Gene set control analysis predicts hematopoietic control mechanisms from genome-wide transcription factor binding data. <i>Experimental Hematology</i> , 2013, 41, 354-366.e14.	0.2	15
8975	Expanding the bovine milk proteome through extensive fractionation. <i>Journal of Dairy Science</i> , 2013, 96, 7854-7866.	1.4	26
8976	Sampling strategy for protein complex prediction using cluster size frequency. <i>Gene</i> , 2013, 518, 152-158.	1.0	32
8977	Transcriptome analysis of HIV-infected peripheral blood monocytes: Gene transcripts and networks associated with neurocognitive functioning. <i>Journal of Neuroimmunology</i> , 2013, 265, 96-105.	1.1	23
8978	Bagging with CTD - A Novel Signature for the Hierarchical Prediction of Secreted Protein Trafficking in Eukaryotes. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 385-390.	3.0	3

#	ARTICLE	IF	CITATIONS
8979	FOXC1 in human trabecular meshwork cells is involved in regulatory pathway that includes miR-204, MEIS2, and ITGÎ ²¹ . <i>Experimental Eye Research</i> , 2013, 111, 112-121.	1.2	46
8980	Modelling knowledge strategy for solving the DNA sequence annotation problem through CommonKADS methodology. <i>Expert Systems With Applications</i> , 2013, 40, 3943-3952.	4.4	7
8981	Crustacean oxi-reductases protein sequences derived from a functional genomic project potentially involved in ecdysteroid hormones metabolism â€œ A starting point for function examination. <i>General and Comparative Endocrinology</i> , 2013, 194, 71-80.	0.8	26
8982	The Functional Genomics Network in the evolution of biological text mining over the past decade. <i>New Biotechnology</i> , 2013, 30, 278-285.	2.4	10
8983	Functional genomics of pain in analgesic drug development and therapy. , 2013, 139, 60-70.		61
8984	Cell cycle genes co-expression in multiple myeloma and plasma cell leukemia. <i>Genomics</i> , 2013, 102, 243-249.	1.3	15
8985	Predicting acidic and alkaline enzymes by incorporating the average chemical shift and gene ontology informations into the general form of Chou's PseAAC. <i>Process Biochemistry</i> , 2013, 48, 1048-1053.	1.8	38
8986	Analysis of salivary gland transcripts of the sand fly <i>Lutzomyia ayacuchensis</i> , a vector of Andean-type cutaneous leishmaniasis. <i>Infection, Genetics and Evolution</i> , 2013, 13, 56-66.	1.0	43
8987	On the geometric modeling approach to empirical null distribution estimation for empirical Bayes modeling of multiple hypothesis testing. <i>Computational Biology and Chemistry</i> , 2013, 43, 17-22.	1.1	2
8988	The Pathogen-annotated Tracking Resource Network (PATRN) system: A web-based resource to aid food safety, regulatory science, and investigations of foodborne pathogens and disease. <i>Food Microbiology</i> , 2013, 34, 303-318.	2.1	11
8989	How AIS can progress along with ontology research in IS. <i>International Journal of Accounting Information Systems</i> , 2013, 14, 21-38.	2.6	17
8990	Gene expression profile of hepatopancreas from grass shrimp <i>Palaemonetes pugio</i> exposed to cyclic hypoxia. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2013, 8, 1-10.	0.4	21
8991	Pathway analysis of genome-wide association study on asthma. <i>Human Immunology</i> , 2013, 74, 256-260.	1.2	17
8992	RAPID: Fast and accurate sequence-based prediction of intrinsic disorder content on proteomic scale. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1671-1680.	1.1	49
8993	Peri-pubertal gonadotropin-releasing hormone agonist treatment affects sex biased gene expression of amygdala in sheep. <i>Psychoneuroendocrinology</i> , 2013, 38, 3115-3127.	1.3	9
8994	Ubiquitin C-terminal Hydrolase 37, a novel predictor for hepatocellular carcinoma recurrence, promotes cell migration and invasion via interacting and deubiquitinating PRP19. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2013, 1833, 559-572.	1.9	56
8995	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
8996	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

#	ARTICLE	IF	CITATIONS
8997	WHEN CLOUD COMPUTING MEETS BIOINFORMATICS: A REVIEW. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1330002.	0.3	13
8998	Microsatellite analyses across three diverse vertebrate transcriptomes (<i>Acipenser fulvescens</i> ,) Tj ETQq1 1 0.784314,rgBT /Overlock 10 T	0.9	11
8999	Identification of Lysine Succinylation Substrates and the Succinylation Regulatory Enzyme CobB in <i>Escherichia coli</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3509-3520.	2.5	236
9000	Microarray Analysis of the Semicompatible, Pathogenic Response and Recovery of Leafy Spurge (<i>Euphorbia esula</i>) Inoculated with the Cassava Bacterial Blight Pathogen <i>Xanthomonas axonopodispv.manihotis</i> . <i>Weed Science</i> , 2013, 61, 428-436.	0.8	2
9001	Automating the construction of gene ontologies. <i>Nature Biotechnology</i> , 2013, 31, 34-35.	9.4	12
9002	Molecular programme of senescence in dry and fleshy fruits. <i>Journal of Experimental Botany</i> , 2013, 65, 4515-4526.	2.4	47
9003	Prediction of the pro-longevity or anti-longevity effect of <i>Caenorhabditis Elegans</i> genes based on Bayesian classification methods. , 2013, , .		12
9004	Early <i>Trichinella spiralis</i> and <i>Trichinella nativa</i> infections induce similar gene expression profiles in rat jejunal mucosa. <i>Experimental Parasitology</i> , 2013, 135, 363-369.	0.5	1
9005	Exploring charged biased regions in the human proteome. <i>Gene</i> , 2013, 515, 277-280.	1.0	9
9006	A pattern-oriented specification of gene network inference processes. <i>Computers in Biology and Medicine</i> , 2013, 43, 1415-1427.	3.9	3
9007	An effective, practical and low computational cost framework for the integration of heterogeneous data to predict functional associations between proteins by means of Artificial Neural Networks. <i>Neurocomputing</i> , 2013, 121, 64-78.	3.5	3
9008	Protein function prediction using neighbor relativity in proteinâ€“protein interaction network. <i>Computational Biology and Chemistry</i> , 2013, 43, 11-16.	1.1	22
9009	Web-based visualisation and analysis of 3D electron-microscopy data from EMDB and PDB. <i>Journal of Structural Biology</i> , 2013, 184, 173-181.	1.3	34
9010	Dysfunctional co-expression network analysis of familial hypercholesterolemia. <i>Journal of Cardiology</i> , 2013, 62, 58-62.	0.8	2
9011	Moving H5N1 studies into the era of systems biology. <i>Virus Research</i> , 2013, 178, 151-167.	1.1	14
9012	Identification of Small Exonic CNV from Whole-Exome Sequence Data and Application to Autism Spectrum Disorder. <i>American Journal of Human Genetics</i> , 2013, 93, 607-619.	2.6	136
9013	Differential regulation of extracellular matrix constituents in myocardial remodeling with and without heart failure following pressure overload. <i>Matrix Biology</i> , 2013, 32, 133-142.	1.5	17
9014	Transcriptome analysis of normal and mantled developing oil palm flower and fruit. <i>Genomics</i> , 2013, 101, 306-312.	1.3	36

#	ARTICLE	IF	CITATIONS
9015	A two-sorted logic for structurally modeling systems. <i>Progress in Biophysics and Molecular Biology</i> , 2013, 113, 141-178.	1.4	19
9016	Towards an integrative soil health assessment strategy: A three tier (integrative biomarker response) approach with <i>Eisenia fetida</i> applied to soils subjected to chronic metal pollution. <i>Science of the Total Environment</i> , 2013, 442, 344-365.	3.9	44
9017	BDgene: A Genetic Database for Bipolar Disorder and Its Overlap With Schizophrenia and Major Depressive Disorder. <i>Biological Psychiatry</i> , 2013, 74, 727-733.	0.7	47
9018	Maize toxin degrades peritrophic matrix proteins and stimulates compensatory transcriptome responses in fall armyworm midgut. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 280-291.	1.2	45
9019	Screening Preeclamptic Cord Plasma for Proteins Associated with Decreased Breast Cancer Susceptibility. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 335-344.	3.0	7
9020	Immature myeloid cells derived from mouse placentas and malignant tumors demonstrate similar proangiogenic transcriptional signatures. <i>Fertility and Sterility</i> , 2013, 99, 910-917.e2.	0.5	8
9021	Using radial basis function on the general form of Chou's pseudo amino acid composition and PSSM to predict subcellular locations of proteins with both single and multiple sites. <i>BioSystems</i> , 2013, 113, 50-57.	0.9	79
9022	Spotlight: Assembly of protein complexes by integrating graph clustering methods. <i>Gene</i> , 2013, 518, 42-51.	1.0	1
9023	Identification of susceptibility modules for coronary artery disease using a genome wide integrated network analysis. <i>Gene</i> , 2013, 531, 347-354.	1.0	17
9024	Subcellular fractionation enhances proteome coverage of pancreatic duct cells. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 791-797.	1.1	17
9025	Deep parallel sequencing reveals conserved and novel miRNAs in gill and hepatopancreas of giant freshwater prawn. <i>Fish and Shellfish Immunology</i> , 2013, 35, 1061-1069.	1.6	22
9026	Pitx1 broadly associates with limb enhancers and is enriched on hindlimb cis-regulatory elements. <i>Developmental Biology</i> , 2013, 374, 234-244.	0.9	51
9027	Molecular crosstalk between a chemical and a biological stressor and consequences on disease manifestation in rainbow trout. <i>Aquatic Toxicology</i> , 2013, 127, 2-8.	1.9	17
9028	Changes in the seminal plasma proteome of adolescents before and after varicocelelectomy. <i>Fertility and Sterility</i> , 2013, 100, 667-672.	0.5	36
9029	Computational identification of operon-like transcriptional loci in eukaryotes. <i>Computers in Biology and Medicine</i> , 2013, 43, 738-743.	3.9	1
9030	Identification and expression analysis of key enzymes of the terpenoids biosynthesis pathway of a liverwort <i>Plagiochasma appendiculatum</i> by EST analysis. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 107-118.	1.0	14
9031	De-novo characterization of the soft-shelled turtle <i>Pelodiscus sinensis</i> transcriptome using Illumina RNA-Seq technology. <i>Journal of Zhejiang University: Science B</i> , 2013, 14, 58-67.	1.3	18
9032	Differentially regulated gene expression associated with hepatitis C virus clearance. <i>Journal of General Virology</i> , 2013, 94, 534-542.	1.3	8

#	ARTICLE	IF	CITATIONS
9033	OralCard: A bioinformatic tool for the study of oral proteome. Archives of Oral Biology, 2013, 58, 762-772.	0.8	23
9034	Exploring biological processes involved in embryonic stem cell differentiation by analyzing proteomic data. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1063-1069.	1.1	12
9035	Reuse of public genome-wide gene expression data. Nature Reviews Genetics, 2013, 14, 89-99.	7.7	328
9036	Towards a bioinformatics of patterning: a computational approach to understanding regulative morphogenesis. Biology Open, 2013, 2, 156-169.	0.6	28
9037	Integrative pathway dissection of molecular mechanisms of moxLDL-induced vascular smooth muscle phenotype transformation. BMC Cardiovascular Disorders, 2013, 13, 4.	0.7	48
9038	A diverse array of genetic factors contribute to the pathogenesis of Systemic Lupus Erythematosus. Orphanet Journal of Rare Diseases, 2013, 8, 2.	1.2	53
9039	Selecting age-related functional characteristics in the human gut microbiome. Microbiome, 2013, 1, 2.	4.9	45
9041	Systems Biology of Caenorhabditis elegans. , 2013, , 367-390.		0
9042	Statistical Methods for Microarray Data Analysis. Methods in Molecular Biology, 2013, , .	0.4	2
9043	A fast approach to global alignment of protein-protein interaction networks. BMC Research Notes, 2013, 6, 35.	0.6	18
9044	Global Alignment of Protein-Protein Interaction Networks. Methods in Molecular Biology, 2013, 939, 21-34.	0.4	7
9045	Analysis Strategy of Protein-Protein Interaction Networks. Methods in Molecular Biology, 2013, 939, 141-181.	0.4	4
9046	Gene Set/Pathway Enrichment Analysis. Methods in Molecular Biology, 2013, 939, 201-213.	0.4	35
9047	High mortality of juvenile gilthead sea bream (Sparus aurata) from photobacteriosis is associated with alternative macrophage activation and anti-inflammatory response: Results of gene expression profiling of early responses in the head kidney. Fish and Shellfish Immunology, 2013, 34, 1269-1278.	1.6	22
9049	A semantic metrics suite for evaluating modular ontologies. Information Systems, 2013, 38, 745-770.	2.4	22
9050	Quantification and functional analysis of modular protein evolution in a dense phylogenetic tree. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 898-907.	1.1	29
9051	Lipopolysaccharide induces a stromal-epithelial signalling axis in a rat model of chronic periodontitis. Journal of Clinical Periodontology, 2013, 40, 8-17.	2.3	31
9052	Saccharinae Bioinformatics Resources. , 2013, , 303-330.		0

#	ARTICLE	IF	CITATIONS
9053	Technologies and challenges in large-scale phosphoproteomics. <i>Proteomics</i> , 2013, 13, 910-931.	1.3	142
9054	Finding the targets of a drug by integration of gene expression data with a protein interaction network. <i>Molecular BioSystems</i> , 2013, 9, 1676.	2.9	59
9055	In Vivo SILAC-Based Proteomics Reveals Phosphoproteome Changes during Mouse Skin Carcinogenesis. <i>Cell Reports</i> , 2013, 3, 552-566.	2.9	90
9056	Simultaneously Learning DNA Motif Along with Its Position and Sequence Rank Preferences Through Expectation Maximization Algorithm. <i>Journal of Computational Biology</i> , 2013, 20, 237-248.	0.8	10
9057	The contribution of intrinsic disorder prediction to the elucidation of protein function. <i>Current Opinion in Structural Biology</i> , 2013, 23, 467-472.	2.6	45
9058	CartograTree: connecting tree genomes, phenotypes and environment. <i>Molecular Ecology Resources</i> , 2013, 13, 528-537.	2.2	9
9059	Transcriptome analysis of Inbred Long Sleep and Inbred Short Sleep mice. <i>Genes, Brain and Behavior</i> , 2013, 12, 263-274.	1.1	15
9060	Host-Pathogen Interactions. , 2013, , 107-126.		1
9061	Proteomics: from single molecules to biological pathways. <i>Cardiovascular Research</i> , 2013, 97, 612-622.	1.8	71
9062	Antipsychotics activate the TGF β 2 pathway effector SMAD3. <i>Molecular Psychiatry</i> , 2013, 18, 347-357.	4.1	15
9063	A disease-drug-phenotype matrix inferred by walking on a functional domain network. <i>Molecular BioSystems</i> , 2013, 9, 1686.	2.9	10
9064	Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. <i>Science</i> , 2013, 339, 1207-1210.	6.0	439
9065	Bioinformatics tools for secretome analysis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2442-2453.	1.1	93
9066	Fractal nature of protein surface roughness: a note on quantification of change of surface roughness in active sites, before and after binding. <i>Journal of Molecular Recognition</i> , 2013, 26, 201-214.	1.1	10
9067	Peregrine and saker falcon genome sequences provide insights into evolution of a predatory lifestyle. <i>Nature Genetics</i> , 2013, 45, 563-566.	9.4	141
9068	Access Guide to Human Proteinpedia. <i>Current Protocols in Bioinformatics</i> , 2013, 41, Unit 1.21.	25.8	19
9069	The plover neurotranscriptome assembly: transcriptomic analysis in an ecological model species without a reference genome. <i>Molecular Ecology Resources</i> , 2013, 13, 696-705.	2.2	26
9070	The neuron-specific chromatin regulatory subunit BAF53b is necessary for synaptic plasticity and memory. <i>Nature Neuroscience</i> , 2013, 16, 552-561.	7.1	213

#	ARTICLE	IF	CITATIONS
9071	Diet-Induced Developmental Acceleration Independent of TOR and Insulin in <i>C.Âlegans</i> . <i>Cell</i> , 2013, 153, 240-252.	13.5	260
9072	An enteral leucine supply modulates human duodenal mucosal proteome and decreases the expression of enzymes involved in fatty acid beta-oxidation. <i>Journal of Proteomics</i> , 2013, 78, 535-544.	1.2	21
9073	Expression Profiling in Glaucomatous Human Lamina Cribrosa Cells Based on Graph-clustering Approach. <i>Current Eye Research</i> , 2013, 38, 767-773.	0.7	3
9074	Computational Approaches to RNAi and Gene Silencing. , 2013, , 169-194.		0
9075	Genome-Scale Model Management and Comparison. <i>Methods in Molecular Biology</i> , 2013, 985, 3-16.	0.4	1
9076	Network-based drug repositioning. <i>Molecular BioSystems</i> , 2013, 9, 1268.	2.9	135
9077	Impact of Experimental Noise and Annotation Imprecision on Data Quality in Microarray Experiments. <i>Methods in Molecular Biology</i> , 2013, 972, 155-176.	0.4	4
9078	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
9079	Development and evaluation of an entirely solution-based combinative sample preparation method for membrane proteomics. <i>Analytical Biochemistry</i> , 2013, 432, 41-48.	1.1	18
9080	Discovery of microRNA Regulatory Networks by Integrating Multidimensional High-Throughput Data. <i>Advances in Experimental Medicine and Biology</i> , 2013, 774, 251-266.	0.8	5
9081	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013, 9, 652.	3.2	61
9082	STK38 is a critical upstream regulator of MYCâ€™s oncogenic activity in human B-cell lymphoma. <i>Oncogene</i> , 2013, 32, 5283-5291.	2.6	58
9083	Gene-pair expression signatures reveal lineage control. <i>Nature Methods</i> , 2013, 10, 577-583.	9.0	129
9084	The role of structural bioinformatics resources in the era of integrative structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 710-721.	2.5	17
9085	Transcriptome sequencing, annotation and expression analysis of <i>Nannochloropsis</i> sp. at different growth phases. <i>Gene</i> , 2013, 523, 117-121.	1.0	39
9086	LiverAtlas: a unique integrated knowledge database for systemsâ€level research of liver and hepatic disease. <i>Liver International</i> , 2013, 33, 1239-1248.	1.9	20
9087	One Stop Shop for Everything Dictyostelium: dictyBase and the Dicty Stock Center in 2012. <i>Methods in Molecular Biology</i> , 2013, 983, 59-92.	0.4	151
9088	Transcriptional Profiling of Dictyostelium with RNA Sequencing. <i>Methods in Molecular Biology</i> , 2013, 983, 139-171.	0.4	17

#	ARTICLE	IF	CITATIONS
9089	De novo sequencing and comparative analysis of expressed sequence tags from gynodioecious fig (<i>Ficus carica</i> L.) fruits: caprifig and common fig. <i>Tree Genetics and Genomes</i> , 2013, 9, 1075-1088.	0.6	28
9090	The Coevolutionary Roots of Biochemistry and Cellular Organization Challenge the RNA World Paradigm. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2013, 23, 152-177.	1.0	40
9091	RNA-seq based transcriptome analysis of <i>Lactuca sativa</i> infected by the fungal necrotroph <i>Botrytis cinerea</i> . <i>Plant, Cell and Environment</i> , 2013, 36, 1992-2007.	2.8	129
9092	Designing a Multicellular Organotypic 3D Liver Model with a Detachable, Nanoscale Polymeric Space of Disse. <i>Tissue Engineering - Part C: Methods</i> , 2013, 19, 875-884.	1.1	33
9093	The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. <i>Nature Genetics</i> , 2013, 45, 701-706.	9.4	409
9094	Principles of transcriptome analysis and gene expression quantification: an RNA-seq tutorial. <i>Molecular Ecology Resources</i> , 2013, 13, 559-572.	2.2	167
9095	Large-Scale Characterization of the Murine Cardiac Proteome. <i>Methods in Molecular Biology</i> , 2013, 1005, 1-10.	0.4	2
9096	Are long-lived trees poised for evolutionary change? Single locus effects in the evolution of gene expression networks in spruce. <i>Molecular Ecology</i> , 2013, 22, 2369-2379.	2.0	20
9097	DNA Sequencing and the Evolution of the "Omics", 2013, , 251-305.		2
9098	Translational Bioinformatics for Genomic Medicine. , 2013, , 272-286.		4
9099	Inferring ancient divergences requires genes with strong phylogenetic signals. <i>Nature</i> , 2013, 497, 327-331.	13.7	541
9100	Laser microdissection and microarray analysis of <i>Truber melanosporum</i> ectomycorrhizas reveal functional heterogeneity between mantle and Hartig net compartments. <i>Environmental Microbiology</i> , 2013, 15, 1853-1869.	1.8	62
9101	Biodiversity data should be published, cited, and peer reviewed. <i>Trends in Ecology and Evolution</i> , 2013, 28, 454-461.	4.2	193
9102	Inferring pathway crosstalk networks using gene set co-expression signatures. <i>Molecular BioSystems</i> , 2013, 9, 1822.	2.9	24
9103	Gut transcriptome of replete adult female cattle ticks, <i>Rhipicephalus (Boophilus) microplus</i> , feeding upon a <i>Babesia bovis</i> -infected bovine host. <i>Parasitology Research</i> , 2013, 112, 3075-3090.	0.6	37
9104	Analysis of the inheritance pattern of a Chinese family with pheochromocytomas through whole exome sequencing. <i>Gene</i> , 2013, 526, 164-169.	1.0	6
9105	Identification of stromal differentially expressed proteins in the colon carcinoma by quantitative proteomics. <i>Electrophoresis</i> , 2013, 34, 1679-1692.	1.3	46
9106	Genome-wide inference of natural selection on human transcription factor binding sites. <i>Nature Genetics</i> , 2013, 45, 723-729.	9.4	121

#	ARTICLE	IF	CITATIONS
9107	A novel insight into Gene Ontology semantic similarity. <i>Genomics</i> , 2013, 101, 368-375.	1.3	57
9108	A SURVEY OF COMPUTATIONAL METHODS FOR PROTEIN COMPLEX PREDICTION FROM PROTEIN INTERACTION NETWORKS. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1230002.	0.3	106
9109	Predicting Protein-Protein Interactions from Multimodal Biological Data Sources via Nonnegative Matrix Tri-Factorization. <i>Journal of Computational Biology</i> , 2013, 20, 344-358.	0.8	55
9110	Identification of somatic mutations in human prostate cancer by RNA-Seq. <i>Gene</i> , 2013, 519, 343-347.	1.0	24
9111	Understanding the Biological Context of NS5A-Host Interactions in HCV Infection: A Network-Based Approach. <i>Journal of Proteome Research</i> , 2013, 12, 2537-2551.	1.8	33
9112	genEnsemble: A new model for the combination of classifiers and integration of biological knowledge applied to genomic data. <i>Expert Systems With Applications</i> , 2013, 40, 52-63.	4.4	6
9113	Molecular models of the cardiorenal syndrome. <i>Electrophoresis</i> , 2013, 34, 1649-1656.	1.3	3
9114	Some remarks on predicting multi-label attributes in molecular biosystems. <i>Molecular BioSystems</i> , 2013, 9, 1092.	2.9	393
9115	Screening and Expression of Genes from Metagenomes. <i>Advances in Applied Microbiology</i> , 2013, 83, 1-68.	1.3	43
9116	Pathway Databases: Making Chemical and Biological Sense of the Genomic Data Flood. <i>Chemistry and Biology</i> , 2013, 20, 629-635.	6.2	20
9117	The mutational landscape of adenoid cystic carcinoma. <i>Nature Genetics</i> , 2013, 45, 791-798.	9.4	394
9118	Identification of significant features in <scp>DNA</scp> microarray data. <i>Wiley Interdisciplinary Reviews: Computational Statistics</i> , 2013, 5, 309-325.	2.1	10
9119	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. <i>Science</i> , 2013, 340, 1467-1471.	6.0	750
9120	CONVERGENCE AND DIVERGENCE DURING THE ADAPTATION TO SIMILAR ENVIRONMENTS BY AN AUSTRALIAN GROUNDSEL. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2515-2529.	1.1	66
9121	Graphical Identification of Cancer-Associated Gene Subnetworks Based on Small Proteomics Data Sets. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 393-397.	1.0	1
9122	Integration of Genomic Information with Biological Networks Using Cytoscape. <i>Methods in Molecular Biology</i> , 2013, 1021, 37-61.	0.4	50
9123	Comparative metatranscriptomic signatures of wood and paper feeding in the gut of the termite <i>Reticulitermes flavipes</i> (Insecta: Isoptera: Termitidae). <i>Insect Molecular Biology</i> , 2013, 22, 155-171.	1.0	58
9124	Transcriptional profiling of <i>Neurospora crassa</i> Δmak-2 reveals that mitogen-activated protein kinase MAK-2 participates in the phosphate signaling pathway. <i>Fungal Genetics and Biology</i> , 2013, 60, 140-149.	0.9	33

#	ARTICLE	IF	CITATIONS
9125	Nonnegative matrix factorization for the improvement in sensitivity of discovering potentially disease-related genes. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2013, 126, 100-107.	1.8	4
9126	Transcriptome of the <i>Lymantria dispar</i> (Gypsy Moth) Larval Midgut in Response to Infection by <i>Bacillus thuringiensis</i> . <i>PLoS ONE</i> , 2013, 8, e61190.	1.1	46
9127	Functional Annotation of Plant Genomes. , 2013, , 155-176.		0
9128	Multi-stage filtering for improving confidence level and determining dominant clusters in clustering algorithms of gene expression data. <i>Computers in Biology and Medicine</i> , 2013, 43, 1120-1133.	3.9	7
9129	Transcript profiling of common bean nodules subjected to oxidative stress. <i>Physiologia Plantarum</i> , 2013, 149, 389-407.	2.6	8
9130	Efficient isolation of polymorphic microsatellites from high-throughput sequence data based on number of repeats. <i>Marine Genomics</i> , 2013, 11, 11-16.	0.4	8
9131	Optimal dictionaries of the final information on the basis of the solvability criterion and their applications in bioinformatics. <i>Pattern Recognition and Image Analysis</i> , 2013, 23, 319-327.	0.6	36
9133	Elucidating the Role of microRNAs in Cancer Through Data Mining Techniques. <i>Advances in Experimental Medicine and Biology</i> , 2013, 774, 291-315.	0.8	6
9134	Functional Classification of Cellular Proteome Profiles Support the Identification of Drug Resistance Signatures in Melanoma Cells. <i>Journal of Proteome Research</i> , 2013, 12, 3264-3276.	1.8	24
9135	Plant Databases and Data Analysis Tools. , 2013, , 313-325.		0
9136	Ontology as a Service (OaaS): a case for sub-ontology merging on the cloud. <i>Journal of Supercomputing</i> , 2013, 65, 185-216.	2.4	27
9137	mirTools 2.0 for non-coding RNA discovery, profiling, and functional annotation based on high-throughput sequencing. <i>RNA Biology</i> , 2013, 10, 1087-1092.	1.5	84
9138	Identification of Autocrine Growth Factors Secreted by CHO Cells for Applications in Single-Cell Cloning Media. <i>Journal of Proteome Research</i> , 2013, 12, 3496-3510.	1.8	42
9139	Visualization and Analysis of Biological Networks. <i>Methods in Molecular Biology</i> , 2013, 1021, 63-88.	0.4	21
9140	Ground tit genome reveals avian adaptation to living at high altitudes in the Tibetan plateau. <i>Nature Communications</i> , 2013, 4, 2071.	5.8	229
9141	Molecular pathways involved in the improvement of non-alcoholic fatty liver disease. <i>Journal of Molecular Endocrinology</i> , 2013, 51, 167-179.	1.1	15
9143	Mass Spectrometry Data Analysis in Proteomics. <i>Methods in Molecular Biology</i> , 2013, , .	0.4	11
9144	Genomic and Proteomic Dissection of the Ubiquitous Plant Pathogen, <i>Armillaria mellea</i> : Toward a New Infection Model System. <i>Journal of Proteome Research</i> , 2013, 12, 2552-2570.	1.8	85

#	ARTICLE	IF	CITATIONS
9145	Genetic characterization of a core collection of flax (<i>Linum usitatissimum</i> L.) suitable for association mapping studies and evidence of divergent selection between fiber and linseed types. <i>BMC Plant Biology</i> , 2013, 13, 78.	1.6	101
9146	TFEB controls cellular lipid metabolism through a starvation-induced autoregulatory loop. <i>Nature Cell Biology</i> , 2013, 15, 647-658.	4.6	796
9149	Evaluation of the OQuaRE framework for ontology quality. <i>Expert Systems With Applications</i> , 2013, 40, 2696-2703.	4.4	45
9150	Uniform Curation Protocol of Metazoan Signaling Pathways to Predict Novel Signaling Components. <i>Methods in Molecular Biology</i> , 2013, 1021, 285-297.	0.4	0
9151	Sub-lethal coral stress: Detecting molecular responses of coral populations to environmental conditions over space and time. <i>Aquatic Toxicology</i> , 2013, 128-129, 135-146.	1.9	18
9152	Glucocorticoid-Dependent Hippocampal Transcriptome in Male Rats: Pathway-Specific Alterations With Aging. <i>Endocrinology</i> , 2013, 154, 2807-2820.	1.4	30
9153	A conceptual basis to encode and detect organic functional groups in XML. <i>Journal of Molecular Graphics and Modelling</i> , 2013, 43, 1-10.	1.3	7
9154	Regulation of SIRT1 by Oxidative Stress-Responsive miRNAs and a Systematic Approach to Identify Its Role in the Endothelium. <i>Antioxidants and Redox Signaling</i> , 2013, 19, 1522-1538.	2.5	78
9155	HDAC inhibitors induce tumor-cell-selective pro-apoptotic transcriptional responses. <i>Cell Death and Disease</i> , 2013, 4, e519-e519.	2.7	150
9156	Differences in gene expression profiles and carcinogenesis pathways involved in cisplatin resistance of four types of cancer. <i>Oncology Reports</i> , 2013, 30, 596-614.	1.2	5
9157	Multiple Reaction Monitoring of Multiple Low-Abundance Transcription Factors in Whole Lung Cancer Cell Lysates. <i>Journal of Proteome Research</i> , 2013, 12, 2582-2596.	1.8	13
9158	Paleoproteomic study of the Iceman's brain tissue. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 3709-3722.	2.4	44
9159	A Context-Driven Gene Prioritization Method for Web-Based Functional Genomics. <i>Lecture Notes in Computer Science</i> , 2013, , 161-172.	1.0	0
9160	An ontology-centric architecture for extensible scientific data management systems. <i>Future Generation Computer Systems</i> , 2013, 29, 641-653.	4.9	31
9161	Analysis of microRNA expression profile induced by AICAR in mouse hepatocytes. <i>Gene</i> , 2013, 512, 364-372.	1.0	18
9162	Efficient semantic network construction with application to PubMed search. <i>Knowledge-Based Systems</i> , 2013, 39, 185-193.	4.0	6
9163	Predicting Gene Function from Uncontrolled Expression Variation among Individual Wild-Type <i>Arabidopsis</i> Plants. <i>Plant Cell</i> , 2013, 25, 2865-2877.	3.1	50
9164	Predicting drug-target interaction networks of human diseases based on multiple feature information. <i>Pharmacogenomics</i> , 2013, 14, 1701-1707.	0.6	13

#	ARTICLE	IF	CITATIONS
9165	Enlarging Cells Initiating Apomixis in <i>Hieracium praealtum</i> prior to Entering Mitosis. <i>Plant Physiology</i> , 2013, 163, 216-231.	2.3	78
9166	Diagnosis of β -Lactam Resistance in <i>Acinetobacter baumannii</i> Using Shotgun Proteomics and LC-Nano-Electrospray Ionization Ion Trap Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 2802-2808.	3.2	24
9167	Evolution of the Correlation between Expression Divergence and Protein Divergence in Mammals. <i>Genome Biology and Evolution</i> , 2013, 5, 1324-1335.	1.1	39
9170	Reverse causal reasoning: applying qualitative causal knowledge to the interpretation of high-throughput data. <i>BMC Bioinformatics</i> , 2013, 14, 340.	1.2	92
9171	MaTSE: the gene expression time-series explorer. <i>BMC Bioinformatics</i> , 2013, 14, S1.	1.2	57
9172	SPIEDw: a searchable platform-independent expression database web tool. <i>BMC Genomics</i> , 2013, 14, 765.	1.2	31
9173	Altered microRNA expression profile during epithelial wound repair in bronchial epithelial cells. <i>BMC Pulmonary Medicine</i> , 2013, 13, 63.	0.8	14
9174	Integrating domain similarity to improve protein complexes identification in TAP-MS data. <i>Proteome Science</i> , 2013, 11, S2.	0.7	6
9175	M-Finder: Uncovering functionally associated proteins from interactome data integrated with GO annotations. <i>Proteome Science</i> , 2013, 11, S3.	0.7	34
9176	HMPAS: Human Membrane Protein Analysis System. <i>Proteome Science</i> , 2013, 11, S7.	0.7	10
9177	Determining the Semantic Similarities Among Gene Ontology Terms. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2013, 17, 512-525.	3.9	17
9178	RDAVIDWebService: a versatile interface to DAVID. <i>Bioinformatics</i> , 2013, 29, 2810-2811.	1.8	191
9180	Three EST-SSR Markers Associated with QTL for the Growth of the Clam <i>Meretrix meretrix</i> Revealed by Selective Genotyping. <i>Marine Biotechnology</i> , 2013, 15, 16-25.	1.1	27
9181	Characterization of the Pearl Oyster (<i>Pinctada martensii</i>) Mantle Transcriptome Unravels Biomaterialization Genes. <i>Marine Biotechnology</i> , 2013, 15, 175-187.	1.1	83
9182	MicroRNA-384-5p regulates ischemia-induced cardioprotection by targeting phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit delta (PI3K p110 δ). <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2013, 18, 260-270.	2.2	37
9183	Comparison of nanowire pellicles for plasma membrane enrichment: coating nanowires on cell. <i>Journal of Nanoparticle Research</i> , 2013, 15, 2133.	0.8	1
9187	Tools for the functional interpretation of metabolomic experiments. <i>Briefings in Bioinformatics</i> , 2013, 14, 737-744.	3.2	56
9188	Predict Subcellular Locations of Singleplex and Multiplex Proteins by Semi-Supervised Learning and Dimension-Reducing General Mode of Chou's PseAAC. <i>IEEE Transactions on Nanobioscience</i> , 2013, 12, 311-320.	2.2	64

#	ARTICLE	IF	CITATIONS
9190	The TissueNet database of human tissue protein-protein interactions. <i>Nucleic Acids Research</i> , 2013, 41, D841-D844.	6.5	54
9191	Genome Sequence of the Banana Pathogen <i>Dickeya zeae</i> Strain MS1, Which Causes Bacterial Soft Rot. <i>Genome Announcements</i> , 2013, 1, .	0.8	14
9192	Protein Function Prediction Using Multilabel Ensemble Classification. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1045-1057.	1.9	46
9193	Function-Function Correlated Multi-label Protein Function Prediction over Interaction Networks. <i>Journal of Computational Biology</i> , 2013, 20, 322-343.	0.8	23
9194	Comparative Genomics Analysis of <i>Trichoderma reesei</i> Strains. <i>Industrial Biotechnology</i> , 2013, 9, 352-367.	0.5	34
9195	Evolutionary and ontogenetic changes in RNA editing in human, chimpanzee, and macaque brains. <i>Rna</i> , 2013, 19, 1693-1702.	1.6	41
9196	Gene expression within the extended amygdala of 5 pairs of rat lines selectively bred for high or low ethanol consumption. <i>Alcohol</i> , 2013, 47, 517-529.	0.8	38
9197	Functional genomics in the study of yeast cell polarity: moving in the right direction. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130118.	1.8	9
9198	Accelerated Evolution of Innate Immunity Proteins in Social Insects: Adaptive Evolution or Relaxed Constraint?. <i>Molecular Biology and Evolution</i> , 2013, 30, 1665-1674.	3.5	59
9199	Candidate genes and biological pathways associated with carcass quality traits in beef cattle. <i>Canadian Journal of Animal Science</i> , 2013, 93, 295-306.	0.7	12
9200	Signs of Adaptation to Local pH Conditions across an Environmental Mosaic in the California Current Ecosystem. <i>Integrative and Comparative Biology</i> , 2013, 53, 857-870.	0.9	67
9201	Arabidopsis Copper Transport Protein COPT2 Participates in the Cross Talk between Iron Deficiency Responses and Low-Phosphate Signaling. <i>Plant Physiology</i> , 2013, 162, 180-194.	2.3	113
9202	Application of omics technologies to biomarker discovery in inflammatory lung diseases. <i>European Respiratory Journal</i> , 2013, 42, 802-825.	3.1	234
9203	Transcriptome Analysis of Japanese Pear (<i>Pyrus pyrifolia</i> Nakai) Flower Buds Transitioning Through Endodormancy. <i>Plant and Cell Physiology</i> , 2013, 54, 1132-1151.	1.5	147
9204	Transcriptional hierarchies regulating early blood cell development. <i>Blood Cells, Molecules, and Diseases</i> , 2013, 51, 239-247.	0.6	18
9205	Integrated gene co-expression network analysis in the growth phase of <i>Mycobacterium tuberculosis</i> reveals new potential drug targets. <i>Molecular BioSystems</i> , 2013, 9, 2798.	2.9	22
9206	Comprehensive identification of mutational cancer driver genes across 12 tumor types. <i>Scientific Reports</i> , 2013, 3, 2650.	1.6	437
9207	De novo transcriptome profiling uncovers a drastic downregulation of photosynthesis upon nitrogen deprivation in the nonmodel green alga <i>Botryosphaerella sudeticus</i> . <i>BMC Genomics</i> , 2013, 14, 715.	1.2	23

#	ARTICLE	IF	CITATIONS
9208	Status of Large-scale Analysis of Post-translational Modifications by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3444-3452.	2.5	491
9209	Active learning of causal Bayesian networks using ontologies: A case study. , 2013, , .		5
9210	Hierarchical Clustering of High- Throughput Expression Data Based on General Dependences. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1080-1085.	1.9	14
9211	Proteomic Analysis of Tegument-Exposed Proteins of Female and Male <i>Schistosoma japonicum</i> Worms. <i>Journal of Proteome Research</i> , 2013, 12, 5260-5270.	1.8	46
9213	The ontology of craniofacial development and malformation for translational craniofacial research. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , 2013, 163, 232-245.	0.7	18
9214	Shotgun proteomic analysis of wing discs from the domesticated silkworm (<i>Bombyx mori</i>) during metamorphosis. <i>Amino Acids</i> , 2013, 45, 1231-1241.	1.2	11
9215	A Systems Biology Framework Identifies Molecular Underpinnings of Coronary Heart Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 1427-1434.	1.1	157
9216	Transcriptome Responses to Combinations of Stresses in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2013, 161, 1783-1794.	2.3	478
9217	Combining Filter-Aided Sample Preparation and Pseudoshotgun Technology To Profile the Proteome of a Low Number of Early Passage Human Melanoma Cells. <i>Journal of Proteome Research</i> , 2013, 12, 1040-1048.	1.8	33
9218	NETAL: a new graph-based method for global alignment of protein-protein interaction networks. <i>Bioinformatics</i> , 2013, 29, 1654-1662.	1.8	151
9219	Identifying overlapping functional modules in biological networks by Markov random walk. , 2013, , .		0
9220	Identification of Potential Target Genes of Butyrate in Dimethylhydrazine-Induced Colorectal Cancer in Mice. <i>Nutrition and Cancer</i> , 2013, 65, 1171-1183.	0.9	7
9221	SecretePipe: A Screening Pipeline for Secreted Proteins with Competence to Identify Potential Membrane-Bound Shed Markers. <i>Journal of Proteome Research</i> , 2013, 12, 1235-1244.	1.8	4
9222	Global Network Alignment In The Context Of Aging. , 2013, , .		18
9223	Hepatic gene expression analysis of mice exposed to raw water from Meiliang Bay, Lake Taihu, China. <i>Journal of Applied Toxicology</i> , 2013, 33, 1416-1423.	1.4	2
9224	Prioritising risk pathways of complex human diseases based on functional profiling. <i>European Journal of Human Genetics</i> , 2013, 21, 666-672.	1.4	1
9225	Hepatic Differentiation and Maturation of Human Embryonic Stem Cells Cultured in a Perfused Three-Dimensional Bioreactor. <i>Stem Cells and Development</i> , 2013, 22, 581-594.	1.1	56
9226	<i>i</i> -value-based regulatory motif discovery using positional weight matrices. <i>Genome Research</i> , 2013, 23, 181-194.	2.4	64

#	ARTICLE	IF	CITATIONS
9227	Informatics and clinical genome sequencing: opening the black box. <i>Genetics in Medicine</i> , 2013, 15, 165-171.	1.1	33
9228	Classificatory Theory in Biology. <i>Biological Theory</i> , 2013, 7, 338-345.	0.8	16
9229	Genome-wide detection of sRNA targets with rNAV. , 2013, , .		6
9230	L4 Ontology. , 0, , .		0
9231	A unified structural/terminological interoperability framework based on LexEVS: application to TRANSFoRM. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2013, 20, 986-994.	2.2	37
9232	Evaluation of gene ontology semantic similarities on protein interaction datasets. <i>International Journal of Bioinformatics Research and Applications</i> , 2013, 9, 173.	0.1	2
9233	Integrating Biological and Engineering Ontologies. , 2013, , .		6
9234	Elucidating Human Phosphatase-Substrate Networks. <i>Science Signaling</i> , 2013, 6, rs10.	1.6	145
9235	Network models of genome-wide association studies uncover the topological centrality of protein interactions in complex diseases. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2013, 20, 619-629.	2.2	43
9236	Inferring Gene Function and Network Organization in <i>Drosophila</i> Signaling by Combined Analysis of Pleiotropy and Epistasis. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 807-814.	0.8	16
9237	Quantification of the N-glycosylated Secretome by Super-SILAC During Breast Cancer Progression and in Human Blood Samples. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 158-171.	2.5	108
9238	Unbiased label-free quantitative proteomic profiling and enriched proteomic pathways in seminal plasma of adult men before and after varicocelectomy. <i>Human Reproduction</i> , 2013, 28, 33-46.	0.4	48
9239	Systems biology of Ewing sarcoma: a network model of EWS-FLI1 effect on proliferation and apoptosis. <i>Nucleic Acids Research</i> , 2013, 41, 8853-8871.	6.5	45
9240	Gene Expression Biomarkers and Longevity. <i>Annual Review of Gerontology and Geriatrics</i> , 2013, 33, 233-258.	0.5	1
9241	PRISM offers a comprehensive genomic approach to transcription factor function prediction. <i>Genome Research</i> , 2013, 23, 889-904.	2.4	32
9242	Characterization of genome-wide transcriptional changes in liver and adipose tissues of ZDF (<i>fa/fa</i>) rats fed R- α -lipoic acid by next-generation sequencing. <i>Physiological Genomics</i> , 2013, 45, 1136-1143.	1.0	29
9243	Identification of gene sets and pathways associated with lactation performance in mice. <i>Physiological Genomics</i> , 2013, 45, 171-181.	1.0	15
9244	Functional Heterogeneity of Cancer-Associated Fibroblasts from Human Colon Tumors Shows Specific Prognostic Gene Expression Signature. <i>Clinical Cancer Research</i> , 2013, 19, 5914-5926.	3.2	146

#	ARTICLE	IF	CITATIONS
9245	Cooperative Effects of 17 β -Estradiol and Oocyte-Derived Paracrine Factors on the Transcriptome of Mouse Cumulus Cells. <i>Endocrinology</i> , 2013, 154, 4859-4872.	1.4	27
9246	Dynamic networks reveal key players in aging. , 2013, , .		1
9247	DNA damage induces targeted, genome-wide variation of poly(A) sites in budding yeast. <i>Genome Research</i> , 2013, 23, 1690-1703.	2.4	50
9248	Co-regulation in embryonic stem cells via context-dependent binding of transcription factors. <i>Bioinformatics</i> , 2013, 29, 2162-2168.	1.8	14
9249	Ontology-aware classification of tissue and cell-type signals in gene expression profiles across platforms and technologies. <i>Bioinformatics</i> , 2013, 29, 3036-3044.	1.8	27
9250	Heuristic approaches for time-lagged biclustering. , 2013, , .		1
9251	Multitask learning for hostâ€“pathogen protein interactions. <i>Bioinformatics</i> , 2013, 29, i217-i226.	1.8	72
9252	Latent factor analysis facilitates modelling of oncogenic genes for colon adenocarcinoma. <i>IET Systems Biology</i> , 2013, 7, 165-169.	0.8	2
9253	Gene expression rate comparison for multiple highâ€“throughput datasets. <i>IET Systems Biology</i> , 2013, 7, 135-142.	0.8	3
9254	Ontology for Vector Surveillance and Management. <i>Journal of Medical Entomology</i> , 2013, 50, 1-14.	0.9	12
9255	Construction and analysis of single nucleotide polymorphismâ€“single nucleotide polymorphism interaction networks. <i>IET Systems Biology</i> , 2013, 7, 170-181.	0.8	0
9256	In silico analysis of autoimmune diseases and genetic relationships to vaccination against infectious diseases. , 2013, , .		0
9257	Mining spatially cohesive itemsets in protein molecular structures. , 2013, , .		2
9258	Identifying protein complexes in AP-MS data with negative evidence via soft Markov clustering. , 2013, , .		0
9259	Improving the Prediction of Kinase Binding Affinity Using Homology Models. , 2013, , .		2
9260	Ets-1 regulates its target genes mainly by DNA methylation in human ovarian cancer. <i>Journal of Obstetrics and Gynaecology</i> , 2013, 33, 877-881.	0.4	3
9261	bc-GenExMiner 3.0: new mining module computes breast cancer gene expression correlation analyses. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bas060-bas060.	1.4	211
9262	Managing the data deluge: data-driven GO category assignment improves while complexity of functional annotation increases. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat041.	1.4	23

#	ARTICLE	IF	CITATIONS
9263	DBATE: database of alternative transcripts expression. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat050.	1.4	11
9264	Chronic Hepatitis E Virus Infection Is Specifically Associated With an Interferon-Related Transcriptional Program. Journal of Infectious Diseases, 2013, 207, 125-132.	1.9	42
9265	ResponseNet2.0: revealing signaling and regulatory pathways connecting your proteins and genesâ€”now with human data. Nucleic Acids Research, 2013, 41, W198-W203.	6.5	25
9266	Prediction of Drugs Target Groups Based on ChEBI Ontology. BioMed Research International, 2013, 2013, 1-6.	0.9	4
9267	Signal Propagation in Protein Interaction Network during Colorectal Cancer Progression. BioMed Research International, 2013, 2013, 1-9.	0.9	53
9268	A Network-Based Systematic Study for the Mechanism of the Treatment of Zheng's Related to Cough Variant Asthma. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-15.	0.5	10
9269	Aberrant DNA Methylation at Genes Associated with a Stem Cell-like Phenotype in Cholangiocarcinoma Tumors. Cancer Prevention Research, 2013, 6, 1348-1355.	0.7	24
9270	Chapter 15: Disease Gene Prioritization. PLoS Computational Biology, 2013, 9, e1002902.	1.5	65
9271	A Genome-Wide Systematic Analysis Reveals Different and Predictive Proliferation Expression Signatures of Cancerous vs. Non-Cancerous Cells. PLoS Genetics, 2013, 9, e1003806.	1.5	23
9272	FSRD: fungal stress response database. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat037-bat037.	1.4	28
9273	MicroRNA Expression Profile of Pulmonary Artery Smooth Muscle Cells and the Effect of Letâ€”d in Chronic Thromboembolic Pulmonary Hypertension. Pulmonary Circulation, 2013, 3, 654-664.	0.8	32
9274	Computational Assessment of the Cooperativity between RNA Binding Proteins and MicroRNAs in Transcript Decay. PLoS Computational Biology, 2013, 9, e1003075.	1.5	30
9275	Role of GÎ±(olf) in familial and sporadic adult-onset primary dystonia. Human Molecular Genetics, 2013, 22, 2510-2519.	1.4	97
9276	Microarray Analysis of mRNA and MicroRNA Expression Profile Reveals the Role of Sitosterol-D-glucoside in the Proliferation of Neural Stem Cell. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-12.	0.5	7
9277	An Integrative Platform of TCM Network Pharmacology and Its Application on a Herbal Formula, Qing-Luo-Yin. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-12.	0.5	118
9278	Transcriptome-Wide Single Nucleotide Polymorphisms (SNPs) for Abalone (<i>Haliotis midae</i>): Validation and Application Using GoldenGate Medium-Throughput Genotyping Assays. International Journal of Molecular Sciences, 2013, 14, 19341-19360.	1.8	30
9279	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	1.5	105
9280	Dynamics of the <i>Saccharomyces cerevisiae</i> Transcriptome during Bread Dough Fermentation. Applied and Environmental Microbiology, 2013, 79, 7325-7333.	1.4	24

#	ARTICLE	IF	CITATIONS
9281	Global Alignment of Pairwise Protein Interaction Networks for Maximal Common Conserved Patterns. <i>International Journal of Genomics</i> , 2013, 2013, 1-11.	0.8	5
9282	Profiling, Bioinformatic, and Functional Data on the Developing Olfactory/GnRH System Reveal Cellular and Molecular Pathways Essential for This Process and Potentially Relevant for the Kallmann Syndrome. <i>Frontiers in Endocrinology</i> , 2013, 4, 203.	1.5	9
9283	A contribution to the study of plant development evolution based on gene co-expression networks. <i>Frontiers in Plant Science</i> , 2013, 4, 291.	1.7	22
9284	Identification of Genes Critical for Resistance to Infection by West Nile Virus Using RNA-Seq Analysis. <i>Viruses</i> , 2013, 5, 1664-1681.	1.5	25
9285	A Module Analysis Approach to Investigate Molecular Mechanism of TCM Formula: A Trial on Shu-feng-jie-du Formula. <i>Evidence-based Complementary and Alternative Medicine</i> , 2013, 2013, 1-14.	0.5	18
9286	From Hub Proteins to Hub Modules: The Relationship Between Essentiality and Centrality in the Yeast Interactome at Different Scales of Organization. <i>PLoS Computational Biology</i> , 2013, 9, e1002910.	1.5	58
9287	Deciphering the calcitriol-induced transcriptomic response in keratinocytes: presentation of novel target genes. <i>Journal of Molecular Endocrinology</i> , 2013, 50, 131-149.	1.1	11
9288	Information Content-Based Gene Ontology Semantic Similarity Approaches: Toward a Unified Framework Theory. <i>BioMed Research International</i> , 2013, 2013, 1-11.	0.9	43
9289	Discovery of Anthelmintic Drug Targets and Drugs Using Chokepoints in Nematode Metabolic Pathways. <i>PLoS Pathogens</i> , 2013, 9, e1003505.	2.1	69
9290	Prioritization of Disease Susceptibility Genes Using LSM/SVD. <i>IEEE Transactions on Biomedical Engineering</i> , 2013, 60, 3410-3417.	2.5	10
9291	A Semiautomated Framework for Integrating Expert Knowledge into Disease Marker Identification. <i>Disease Markers</i> , 2013, 35, 513-523.	0.6	3
9292	Integrated Enrichment Analysis of Variants and Pathways in Genome-Wide Association Studies Indicates Central Role for IL-2 Signaling Genes in Type 1 Diabetes, and Cytokine Signaling Genes in Crohn's Disease. <i>PLoS Genetics</i> , 2013, 9, e1003770.	1.5	67
9293	Impacts of Population Structure and Analytical Models in Genome-Wide Association Studies of Complex Traits in Forest Trees: A Case Study in <i>Eucalyptus globulus</i> . <i>PLoS ONE</i> , 2013, 8, e81267.	1.1	82
9294	Regulation of Sulphur Assimilation Is Essential for Virulence and Affects Iron Homeostasis of the Human-Pathogenic Mould <i>Aspergillus fumigatus</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003573.	2.1	81
9295	In Vitro Perturbations of Targets in Cancer Hallmark Processes Predict Rodent Chemical Carcinogenesis. <i>Toxicological Sciences</i> , 2013, 131, 40-55.	1.4	67
9296	The <i>Tarenaya hassleriana</i> Genome Provides Insight into Reproductive Trait and Genome Evolution of Crucifers. <i>Plant Cell</i> , 2013, 25, 2813-2830.	3.1	95
9297	Protein Complex-Based Analysis Framework for High-Throughput Data Sets. <i>Science Signaling</i> , 2013, 6, rs5.	1.6	110
9298	A Comprehensive Survey of Small-Molecule Binding Pockets in Proteins. <i>PLoS Computational Biology</i> , 2013, 9, e1003302.	1.5	103

#	ARTICLE	IF	CITATIONS
9299	De Novo Transcriptome Sequencing Reveals Important Molecular Networks and Metabolic Pathways of the Plant, <i>Chlorophytum borivillianum</i> . PLoS ONE, 2013, 8, e83336.	1.1	65
9300	Expression Sensitivity Analysis of Human Disease Related Genes. BioMed Research International, 2013, 2013, 1-8.	0.9	0
9301	Multiple Statistical Methods for Assessing Differential Gene Expression in Microarray Data of Diabetic Model Rats to Predict the Molecular Mechanism of Atorvastatin on Anti-Atherogenesis. Experimental and Clinical Endocrinology and Diabetes, 2013, 121, 272-279.	0.6	6
9302	A Systemsâ€™ Biology Approach to Study MicroRNA-Mediated Gene Regulatory Networks. BioMed Research International, 2013, 2013, 1-15.	0.9	32
9303	Pathogenicity associated genes in <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> race 4. South African Journal of Science, 2013, 109, 10.	0.3	32
9304	Systems Biology as a Comparative Approach to Understand Complex Gene Expression in Neurological Diseases. Behavioral Sciences (Basel, Switzerland), 2013, 3, 253-272.	1.0	23
9305	Integration of Data from Omic Studies with the Literature-Based Discovery towards Identification of Novel Treatments for Neovascularization in Diabetic Retinopathy. BioMed Research International, 2013, 2013, 1-7.	0.9	5
9306	A CTD-Pfizer collaboration: manual curation of 88 000 scientific articles text mined for drug-disease and drug-phenotype interactions. Database: the Journal of Biological Databases and Curation, 2013, bat080-bat080.	1.4	88
9307	Fusion of Large-Scale Genomic Knowledge and Frequency Data Computationally Prioritizes Variants in Epilepsy. PLoS Genetics, 2013, 9, e1003797.	1.5	22
9308	Genome scale transcriptional response diversity among ten ecotypes of <i>Arabidopsis thaliana</i> during heat stress. Frontiers in Plant Science, 2013, 4, 532.	1.7	43
9309	Novel Integrative Genomics Approach for Associating GWAS Information with Intrinsic Subtypes of Breast Cancer. Cancer Informatics, 2013, 12, CIN.S11452.	0.9	4
9310	Transcript Expression Patterns Illuminate the Mechanistic Background of Hormesis in <i>Caenorhabditis Elegans</i> Maupas. Dose-Response, 2013, 11, dose-response.1.	0.7	5
9311	Sequential Waves of Gene Expression in Patients with Clinically Defined Dengue Illnesses Reveal Subtle Disease Phases and Predict Disease Severity. PLoS Neglected Tropical Diseases, 2013, 7, e2298.	1.3	64
9312	Gene Set Signature of Reversal Reaction Type I in Leprosy Patients. PLoS Genetics, 2013, 9, e1003624.	1.5	32
9313	A Web Application and Database for Agriculture Genetic Diversity and Association Studies. International Journal of Bio-Science and Bio-Technology, 2013, 5, 33-42.	0.2	22
9314	From Linear Operators to Computational Biology. , 2013, , .		1
9315	Unsupervised Clustering of Subcellular Protein Expression Patterns in High-Throughput Microscopy Images Reveals Protein Complexes and Functional Relationships between Proteins. PLoS Computational Biology, 2013, 9, e1003085.	1.5	33
9316	Integrative Analysis Using Module-Guided Random Forests Reveals Correlated Genetic Factors Related to Mouse Weight. PLoS Computational Biology, 2013, 9, e1002956.	1.5	24

#	ARTICLE	IF	CITATIONS
9317	Towards Systematic Discovery of Signaling Networks in Budding Yeast Filamentous Growth Stress Response Using Interventional Phosphorylation Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003077.	1.5	15
9318	Specialization of Gene Expression during Mouse Brain Development. <i>PLoS Computational Biology</i> , 2013, 9, e1003185.	1.5	29
9319	On the Importance of Polar Interactions for Complexes Containing Intrinsically Disordered Proteins. <i>PLoS Computational Biology</i> , 2013, 9, e1003192.	1.5	57
9320	Assessing Computational Methods for Transcription Factor Target Gene Identification Based on ChIP-seq Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003342.	1.5	55
9321	Congruence of Additive and Non-Additive Effects on Gene Expression Estimated from Pedigree and SNP Data. <i>PLoS Genetics</i> , 2013, 9, e1003502.	1.5	79
9322	Impact of Natural Genetic Variation on Gene Expression Dynamics. <i>PLoS Genetics</i> , 2013, 9, e1003514.	1.5	35
9323	Network-Based Inference Framework for Identifying Cancer Genes from Gene Expression Data. <i>BioMed Research International</i> , 2013, 2013, 1-12.	0.9	10
9324	A Systematic Analysis of Host Factors Reveals a Med23-Interferon- β Regulatory Axis against Herpes Simplex Virus Type 1 Replication. <i>PLoS Pathogens</i> , 2013, 9, e1003514.	2.1	88
9325	Candidate genes and single nucleotide polymorphisms associated with variation in residual feed intake in beef cattle. <i>Journal of Animal Science</i> , 2013, 91, 3502-3513.	0.2	44
9326	A Compendium of <i>Caenorhabditis elegans</i> RNA Binding Proteins Predicts Extensive Regulation at Multiple Levels. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 297-304.	0.8	31
9327	Redefinition of Decision Rules Based on the Importance of Elementary Conditions Evaluation. <i>Fundamenta Informaticae</i> , 2013, 123, 171-197.	0.3	6
9328	Genome-Wide Assessment of the Association of Rare and Common Copy Number Variations to Testicular Germ Cell Cancer. <i>Frontiers in Endocrinology</i> , 2013, 4, 2.	1.5	14
9329	Identification of Recurrence Related microRNAs in Hepatocellular Carcinoma after Surgical Resection. <i>International Journal of Molecular Sciences</i> , 2013, 14, 1105-1118.	1.8	23
9330	Genomics of an emerging clone of <i>Salmonella</i> serovar Typhimurium ST313 from Nigeria and the Democratic Republic of Congo. <i>Journal of Infection in Developing Countries</i> , 2013, 7, 696-706.	0.5	30
9331	Functional Knowledge Transfer for High-accuracy Prediction of Under-studied Biological Processes. <i>PLoS Computational Biology</i> , 2013, 9, e1002957.	1.5	62
9332	Exploring Fold Space Preferences of New-born and Ancient Protein Superfamilies. <i>PLoS Computational Biology</i> , 2013, 9, e1003325.	1.5	31
9333	Transcriptome Analyses of Inhibitor-treated Schistosome Females Provide Evidence for Cooperating Src-kinase and TGF β Receptor Pathways Controlling Mitosis and Eggshell Formation. <i>PLoS Pathogens</i> , 2013, 9, e1003448.	2.1	46
9334	Irf8-Regulated Genomic Responses Drive Pathological Inflammation during Cerebral Malaria. <i>PLoS Pathogens</i> , 2013, 9, e1003491.	2.1	63

#	ARTICLE	IF	CITATIONS
9335	GOLink: Finding Cooccurring Terms across Gene Ontology Namespaces. <i>International Journal of Genomics</i> , 2013, 2013, 1-10.	0.8	3
9336	Transcriptome Profiling of <i>Giardia intestinalis</i> Using Strand-specific RNA-Seq. <i>PLoS Computational Biology</i> , 2013, 9, e1003000.	1.5	56
9337	Simultaneous Identification of Multiple Driver Pathways in Cancer. <i>PLoS Computational Biology</i> , 2013, 9, e1003054.	1.5	231
9338	Biases in the Experimental Annotations of Protein Function and Their Effect on Our Understanding of Protein Function Space. <i>PLoS Computational Biology</i> , 2013, 9, e1003063.	1.5	103
9339	Ten Quick Tips for Using the Gene Ontology. <i>PLoS Computational Biology</i> , 2013, 9, e1003343.	1.5	45
9340	Odoriferous Defensive Stink Gland Transcriptome to Identify Novel Genes Necessary for Quinone Synthesis in the Red Flour Beetle, <i>Tribolium castaneum</i> . <i>PLoS Genetics</i> , 2013, 9, e1003596.	1.5	60
9341	Silicon Era of Carbon-Based Life: Application of Genomics and Bioinformatics in Crop Stress Research. <i>International Journal of Molecular Sciences</i> , 2013, 14, 11444-11483.	1.8	8
9342	Assessing identity, redundancy and confounds in Gene Ontology annotations over time. <i>Bioinformatics</i> , 2013, 29, 476-482.	1.8	47
9343	Identifying proteins controlling key disease signaling pathways. <i>Bioinformatics</i> , 2013, 29, i227-i236.	1.8	28
9344	MIG: Multi-Image Genome viewer. <i>Bioinformatics</i> , 2013, 29, 2477-2478.	1.8	15
9345	Human Monogenic Disease Genes Have Frequently Functionally Redundant Paralogs. <i>PLoS Computational Biology</i> , 2013, 9, e1003073.	1.5	49
9346	Reconstruction and Validation of a Genome-Scale Metabolic Model for the Filamentous Fungus <i>Neurospora crassa</i> Using FARM. <i>PLoS Computational Biology</i> , 2013, 9, e1003126.	1.5	70
9347	Brain: biomedical knowledge manipulation. <i>Bioinformatics</i> , 2013, 29, 1238-1239.	1.8	5
9348	Visual Data Mining of Biological Networks: One Size Does Not Fit All. <i>PLoS Computational Biology</i> , 2013, 9, e1002833.	1.5	19
9349	Combinatorial Clustering of Residue Position Subsets Predicts Inhibitor Affinity across the Human Kinome. <i>PLoS Computational Biology</i> , 2013, 9, e1003087.	1.5	14
9350	Simple Topological Features Reflect Dynamics and Modularity in Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1003243.	1.5	36
9351	Integrated Module and Gene-Specific Regulatory Inference Implicates Upstream Signaling Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1003252.	1.5	78
9352	Inferring Developmental Stage Composition from Gene Expression in Human Malaria. <i>PLoS Computational Biology</i> , 2013, 9, e1003392.	1.5	45

#	ARTICLE	IF	CITATIONS
9353	A context-sensitive framework for the analysis of human signalling pathways in molecular interaction networks. <i>Bioinformatics</i> , 2013, 29, i210-i216.	1.8	8
9354	Proteins Involved in Distinct Phases of Cold Hardening Process in Frost Resistant Winter Barley (<i>Hordeum vulgare</i> L.) cv Luxor. <i>International Journal of Molecular Sciences</i> , 2013, 14, 8000-8024.	1.8	43
9355	Systematically Differentiating Functions for Alternatively Spliced Isoforms through Integrating RNA-seq Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003314.	1.5	78
9356	X-linked dystonia parkinsonism syndrome (XDP, lubag): disease-specific sequence change DSC3 in TAF1/DYT3 affects genes in vesicular transport and dopamine metabolism. <i>Human Molecular Genetics</i> , 2013, 22, 941-951.	1.4	35
9357	Proteome-wide Prediction of Self-interacting Proteins Based on Multiple Properties. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1689-1700.	2.5	31
9358	Inactivation of Serum Response Factor Contributes To Decrease Vascular Muscular Tone and Arterial Stiffness in Mice. <i>Circulation Research</i> , 2013, 112, 1035-1045.	2.0	43
9359	BGDB: a database of bivalent genes. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat057.	1.4	17
9360	The Genomic and Transcriptomic Landscape of a HeLa Cell Line. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1213-1224.	0.8	355
9361	Topologically inferring risk-active pathways toward precise cancer classification by directed random walk. <i>Bioinformatics</i> , 2013, 29, 2169-2177.	1.8	60
9362	Information-theoretic evaluation of predicted ontological annotations. <i>Bioinformatics</i> , 2013, 29, i53-i61.	1.8	97
9363	Prevalent Role of Gene Features in Determining Evolutionary Fates of Whole-Genome Duplication Duplicated Genes in Flowering Plants Å Å. <i>Plant Physiology</i> , 2013, 161, 1844-1861.	2.3	80
9364	PRIME Update: Innovative Content for Plant Metabolomics and Integration of Gene Expression and Metabolite Accumulation. <i>Plant and Cell Physiology</i> , 2013, 54, e5-e5.	1.5	76
9365	Inferring gene networks from discrete expression data. <i>Biostatistics</i> , 2013, 14, 708-722.	0.9	12
9366	Use of Gene Ontology Annotation to understand the peroxisome proteome in humans. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bas062.	1.4	17
9367	hLGDB: a database of human lysosomal genes and their regulation. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat024.	1.4	48
9368	The gut microbiota and mucosal homeostasis. <i>Gut Microbes</i> , 2013, 4, 118-124.	4.3	111
9369	Ensuring the statistical soundness of competitive gene set approaches: gene filtering and genome-scale coverage are essential. <i>Nucleic Acids Research</i> , 2013, 41, e82-e82.	6.5	24
9370	High expression of glycolytic and pigment proteins is associated with worse clinical outcome in stage III melanoma. <i>Melanoma Research</i> , 2013, 23, 452-460.	0.6	24

#	ARTICLE	IF	CITATIONS
9371	Caveolin-1 is a negative regulator of tumor growth in glioblastoma and modulates chemosensitivity to temozolomide. <i>Cell Cycle</i> , 2013, 12, 1510-1520.	1.3	45
9372	Deep sequencing reveals complex mechanisms of diapause preparation in the invasive mosquito, <i>Aedes albopictus</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20130143.	1.2	134
9373	Multi-scale computational models of the airways to unravel the pathophysiological mechanisms in asthma and chronic obstructive pulmonary disease (AirPROM). <i>Interface Focus</i> , 2013, 3, 20120057.	1.5	40
9374	An integrative, translational approach to understanding rare and orphan genetically based diseases. <i>Interface Focus</i> , 2013, 3, 20120055.	1.5	16
9375	Insights from a Chimpanzee Adipose Stromal Cell Population: Opportunities for Adult Stem Cells to Expand Primate Functional Genomics. <i>Genome Biology and Evolution</i> , 2013, 5, 1995-2005.	1.1	2
9376	Exploring biological data: Mappings between ontology- and cluster-based representations. <i>Information Visualization</i> , 2013, 12, 291-307.	1.2	2
9377	Construction of protein phosphorylation networks by data mining, text mining and ontology integration: analysis of the spindle checkpoint. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat038.	1.4	15
9378	Effect of Growth Factors on the Proliferation and Gene Expression of Human Meibomian Gland Epithelial Cells. , 2013, 54, 2541.		42
9379	DKK2 Mediates Osteolysis, Invasiveness, and Metastatic Spread in Ewing Sarcoma. <i>Cancer Research</i> , 2013, 73, 967-977.	0.4	56
9380	Branching process deconvolution algorithm reveals a detailed cell-cycle transcription program. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E968-77.	3.3	8
9381	In vitro-differentiated neural cell cultures progress towards donor-identical brain tissue. <i>Human Molecular Genetics</i> , 2013, 22, 3534-3546.	1.4	19
9382	Accelerated Evolution after Gene Duplication: A Time-Dependent Process Affecting Just One Copy. <i>Molecular Biology and Evolution</i> , 2013, 30, 1830-1842.	3.5	116
9383	OntoQuery: easy-to-use web-based OWL querying. <i>Bioinformatics</i> , 2013, 29, 2955-2957.	1.8	7
9384	Genome-Wide Functional and Stress Response Profiling Reveals Toxic Mechanism and Genes Required for Tolerance to Benzo[a]pyrene in <i>S. cerevisiae</i> . <i>Frontiers in Genetics</i> , 2012, 3, 316.	1.1	26
9385	Computational Translation of Nonmammalian Species Data to Mammalian Species to Meet REACH and Next Generation Risk Assessment Needs. , 2013, , 113-136.		1
9386	The Mouse Genome Database: Genotypes, Phenotypes, and Models of Human Disease. <i>Nucleic Acids Research</i> , 2013, 41, D885-D891.	6.5	61
9387	The Plant Ontology as a Tool for Comparative Plant Anatomy and Genomic Analyses. <i>Plant and Cell Physiology</i> , 2013, 54, e1-e1.	1.5	131
9388	Predicting Therapeutic Targets with Integration of Heterogeneous Data Sources. <i>Lecture Notes in Computer Science</i> , 2013, , 149-158.	1.0	0

#	ARTICLE	IF	CITATIONS
9389	Integrated Analysis of Dysregulated lncRNA Expression in Fetal Cardiac Tissues with Ventricular Septal Defect. PLoS ONE, 2013, 8, e77492.	1.1	41
9390	Phylogenetic Portrait of the Saccharomyces cerevisiae Functional Genome. G3: Genes, Genomes, Genetics, 2013, 3, 1335-1340.	0.8	4
9391	GRN2SBML: automated encoding and annotation of inferred gene regulatory networks complying with SBML. Bioinformatics, 2013, 29, 2216-2217.	1.8	4
9392	The Comparative Toxicogenomics Database: update 2013. Nucleic Acids Research, 2013, 41, D1104-D1114.	6.5	371
9393	Model-based approaches to synthesize microarray data: a unifying review using mixture of SEMs. Statistical Methods in Medical Research, 2013, 22, 567-582.	0.7	0
9394	Identification of well-differentiated gene expressions between Han Chinese and Japanese using genome-wide microarray data analysis. Journal of Medical Genetics, 2013, 50, 534-542.	1.5	4
9395	The ConsensusPathDB interaction database: 2013 update. Nucleic Acids Research, 2013, 41, D793-D800.	6.5	728
9396	EDAM: an ontology of bioinformatics operations, types of data and identifiers, topics and formats. Bioinformatics, 2013, 29, 1325-1332.	1.8	215
9397	Genome-wide survey of DNA-binding proteins in Arabidopsis thaliana : analysis of distribution and functions. Nucleic Acids Research, 2013, 41, 7212-7219.	6.5	14
9398	MS risk genes are transcriptionally regulated in CSF leukocytes at relapse. Multiple Sclerosis Journal, 2013, 19, 403-410.	1.4	9
9399	Popular Computational Methods to Assess Multiprotein Complexes Derived From Label-Free Affinity Purification and Mass Spectrometry (AP-MS) Experiments. Molecular and Cellular Proteomics, 2013, 12, 1-13.	2.5	46
9400	Integrative analysis of C. elegans modENCODE CHIP-seq data sets to infer gene regulatory interactions. Genome Research, 2013, 23, 941-953.	2.4	30
9401	Comparative Analysis of Transcriptional Gene Regulation Indicates Similar Physiologic Response in Mouse Tissues at Low Absorbed Doses from Intravenously Administered 211At. Journal of Nuclear Medicine, 2013, 54, 990-998.	2.8	27
9402	FlyAtlas: database of gene expression in the tissues of Drosophila melanogaster. Nucleic Acids Research, 2013, 41, D744-D750.	6.5	162
9403	Acetylation dynamics of human nuclear proteins during the ionizing radiation-induced DNA damage response. Cell Cycle, 2013, 12, 1688-1695.	1.3	27
9404	Imbalanced network biomarkers for traditional Chinese medicine Syndrome in gastritis patients. Scientific Reports, 2013, 3, 1543.	1.6	87
9405	Genome Maps, a new generation genome browser. Nucleic Acids Research, 2013, 41, W41-W46.	6.5	27
9406	String Similarity Metrics for Ontology Alignment. Lecture Notes in Computer Science, 2013, , 294-309.	1.0	92

#	ARTICLE	IF	CITATIONS
9407	Extensive Transcript Diversity and Novel Upstream Open Reading Frame Regulation in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 343-352.	0.8	59
9408	Impaired replication elongation in <i>Tetrahymena</i> mutants deficient in histone H3 Lys 27 monomethylation. <i>Genes and Development</i> , 2013, 27, 1662-1679.	2.7	64
9409	Systems Pharmacology of Adverse Event Mitigation by Drug Combinations. <i>Science Translational Medicine</i> , 2013, 5, 206ra140.	5.8	105
9410	Pulmonary Hypertension and Pregnancy: Management and Outcome. <i>Journal of Pulmonary & Respiratory Medicine</i> , 2013, , .	0.1	1
9411	JBioWH: an open-source Java framework for bioinformatics data integration. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat051-bat051.	1.4	8
9412	A guide to best practices for Gene Ontology (GO) manual annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat054-bat054.	1.4	135
9413	3' UTR-isoform choice has limited influence on the stability and translational efficiency of most mRNAs in mouse fibroblasts. <i>Genome Research</i> , 2013, 23, 2078-2090.	2.4	186
9414	Analysis of disease-associated objects at the Rat Genome Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat046.	1.4	11
9415	Methylome Profiling Reveals Distinct Alterations in Phenotypic and Mutational Subgroups of Myeloproliferative Neoplasms. <i>Cancer Research</i> , 2013, 73, 1076-1085.	0.4	50
9417	The BEN domain is a novel sequence-specific DNA-binding domain conserved in neural transcriptional repressors. <i>Genes and Development</i> , 2013, 27, 602-614.	2.7	70
9418	Toxygates: interactive toxicity analysis on a hybrid microarray and linked data platform. <i>Bioinformatics</i> , 2013, 29, 3080-3086.	1.8	30
9419	The Eimeria Transcript DB: an integrated resource for annotated transcripts of protozoan parasites of the genus Eimeria. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat006.	1.4	5
9420	A graphical model method for integrating multiple sources of genome-scale data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 469-87.	0.2	5
9421	Genome-Wide Analysis of miRNA Signature Differentially Expressed in Doxorubicin-Resistant and Parental Human Hepatocellular Carcinoma Cell Lines. <i>PLoS ONE</i> , 2013, 8, e54111.	1.1	32
9422	Genetic circuitry of <i>Survival motor neuron</i> , the gene underlying spinal muscular atrophy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2371-80.	3.3	37
9423	Gene-set analysis is severely biased when applied to genome-wide methylation data. <i>Bioinformatics</i> , 2013, 29, 1851-1857.	1.8	124
9424	A combined omics study on activated macrophages' enhanced role of STATs in apoptosis, immunity and lipid metabolism. <i>Bioinformatics</i> , 2013, 29, 2735-2743.	1.8	28
9425	A modular framework for gene set analysis integrating multilevel omics data. <i>Nucleic Acids Research</i> , 2013, 41, 9622-9633.	6.5	32

#	ARTICLE	IF	CITATIONS
9426	RhesusBase: a knowledgebase for the monkey research community. <i>Nucleic Acids Research</i> , 2013, 41, D892-D905.	6.5	27
9427	dbWFA: a web-based database for functional annotation of <i>Triticum aestivum</i> transcripts. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat014.	1.4	9
9428	miRNA-100 Inhibits Human Bladder Urothelial Carcinogenesis by Directly Targeting mTOR. <i>Molecular Cancer Therapeutics</i> , 2013, 12, 207-219.	1.9	89
9429	Genomic and Secretomic Analyses Reveal Unique Features of the Lignocellulolytic Enzyme System of <i>Penicillium decumbens</i> . <i>PLoS ONE</i> , 2013, 8, e55185.	1.1	159
9430	JiffyNet: a web-based instant protein network modeler for newly sequenced species. <i>Nucleic Acids Research</i> , 2013, 41, W192-W197.	6.5	31
9431	Global microRNA elevation by inducible Exportin 5 regulates cell cycle entry. <i>Rna</i> , 2013, 19, 490-497.	1.6	56
9432	Cross-Species Protein Interactome Mapping Reveals Species-Specific Wiring of Stress Response Pathways. <i>Science Signaling</i> , 2013, 6, ra38.	1.6	47
9433	The Presence of Methylation Quantitative Trait Loci Indicates a Direct Genetic Influence on the Level of DNA Methylation in Adipose Tissue. <i>PLoS ONE</i> , 2013, 8, e55923.	1.1	83
9435	Complete genome sequence of <i>Arthrobacter</i> sp. strain FB24. <i>Standards in Genomic Sciences</i> , 2013, 9, 106-116.	1.5	17
9436	Integrative Modeling of eQTLs and Cis-Regulatory Elements Suggests Mechanisms Underlying Cell Type Specificity of eQTLs. <i>PLoS Genetics</i> , 2013, 9, e1003649.	1.5	151
9437	Cataloging the biomedical world of pain through semi-automated curation of molecular interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat033.	1.4	14
9438	From manual curation to visualization of gene families and networks across <i>Solanaceae</i> plant species. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat028.	1.4	8
9439	Fragment recruitment on metabolic pathways: comparative metabolic profiling of metagenomes and metatranscriptomes. <i>Bioinformatics</i> , 2013, 29, 790-791.	1.8	8
9440	yApoptosis: yeast apoptosis database. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat068.	1.4	7
9441	Physical and genetic-interaction density reveals functional organization and informs significance cutoffs in genome-wide screens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7389-7394.	3.3	16
9442	Evolutionary Rate Covariation in Meiotic Proteins Results from Fluctuating Evolutionary Pressure in Yeasts and Mammals. <i>Genetics</i> , 2013, 193, 529-538.	1.2	34
9443	Variants in exons and in transcription factors affect gene expression in trans. <i>Genome Biology</i> , 2013, 14, R71.	13.9	8
9444	The mutational landscape of chromatin regulatory factors across 4,623 tumor samples. <i>Genome Biology</i> , 2013, 14, r106.	13.9	102

#	ARTICLE	IF	CITATIONS
9445	Analysis of Differentiation Potentials and Gene Expression Profiles of Mesenchymal Stem Cells Derived from Periodontal Ligament and Wharton's Jelly of the Umbilical Cord. <i>Cells Tissues Organs</i> , 2013, 197, 209-223.	1.3	39
9446	Microarray Profiling of Human Renal Cell Carcinoma: Identification for Potential Biomarkers and Critical Pathways. <i>Kidney and Blood Pressure Research</i> , 2013, 37, 506-513.	0.9	6
9447	Revealing the Underlying Mechanism of Ischemia Reperfusion Injury Using Bioinformatics Approach. <i>Kidney and Blood Pressure Research</i> , 2013, 38, 99-108.	0.9	13
9448	Along signal paths: an empirical gene set approach exploiting pathway topology. <i>Nucleic Acids Research</i> , 2013, 41, e19-e19.	6.5	105
9449	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
9450	PlantGSEA: a gene set enrichment analysis toolkit for plant community. <i>Nucleic Acids Research</i> , 2013, 41, W98-W103.	6.5	267
9451	Translational Bioinformatics Approaches to Drug Development. <i>Advances in Wound Care</i> , 2013, 2, 470-489.	2.6	26
9452	FYPO: the fission yeast phenotype ontology. <i>Bioinformatics</i> , 2013, 29, 1671-1678.	1.8	53
9453	The human gene connectome as a map of short cuts for morbid allele discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5558-5563.	3.3	79
9454	Monosodium Urate Activates Src/Pyk2/PI3 Kinase and Cathepsin Dependent Unconventional Protein Secretion From Human Primary Macrophages. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 749-763.	2.5	36
9455	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
9456	Distinct Signaling Roles of Ceramide Species in Yeast Revealed Through Systematic Perturbation and Systems Biology Analyses. <i>Science Signaling</i> , 2013, 6, rs14.	1.6	33
9457	Cytotoxic Necrotizing Factor 1 and Hemolysin from Uropathogenic <i>Escherichia coli</i> Elicit Different Host Responses in the Murine Bladder. <i>Infection and Immunity</i> , 2013, 81, 99-109.	1.0	66
9458	The twilight zone of cis element alignments. <i>Nucleic Acids Research</i> , 2013, 41, 1438-1449.	6.5	11
9459	Expression profiling based on graph-clustering approach to determine colon cancer pathway. <i>Journal of Cancer Research and Therapeutics</i> , 2013, 9, 467.	0.3	4
9460	SUS-BAR: a database of pig proteins with statistically validated structural and functional annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat065-bat065.	1.4	4
9461	Developing a system for advanced monitoring and intelligent drug administration in critical care units using ontologies. <i>International Journal of Knowledge-Based and Intelligent Engineering Systems</i> , 2013, 17, 45-53.	0.7	1
9462	Ontology model: Towards bridging the gap between African traditional medicine and conventional medicine. <i>International Journal of Knowledge-Based and Intelligent Engineering Systems</i> , 2013, 17, 37-43.	0.7	2

#	ARTICLE	IF	CITATIONS
9463	Systems Biology as an Integrated Platform for Bioinformatics, Systems Synthetic Biology, and Systems Metabolic Engineering. <i>Cells</i> , 2013, 2, 635-688.	1.8	30
9464	On Crowd-verification of Biological Networks. <i>Bioinformatics and Biology Insights</i> , 2013, 7, BBI.S12932.	1.0	25
9465	An Integrative Genomics Approach for Associating GWAS Information with Triple-Negative Breast Cancer. <i>Cancer Informatics</i> , 2013, 12, CIN.S10413.	0.9	29
9466	Genomics Insights: Inter-Laboratory Variability in Array-Based RNA Quantification Methods. <i>Genomics Insights</i> , 2013, 6, GEI.S11909.	3.0	0
9467	Patterns of methylation heritability in a genome-wide analysis of four brain regions. <i>Nucleic Acids Research</i> , 2013, 41, 2095-2104.	6.5	44
9468	Intratumoral regulatory <scp>T</scp> cells with higher prevalence and more suppressive activity in hepatocellular carcinoma patients. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2013, 28, 1555-1564.	1.4	25
9469	Construction of a cDNA Library from the Ephemeral Plant <i>Olimarabidopsis pumila</i> and Preliminary Analysis of Expressed Sequence Tags. <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , 2013, 68, 499-508.	0.6	3
9470	Target Gene and Function Prediction of Differentially Expressed MicroRNAs in Lactating Mammary Glands of Dairy Goats. <i>International Journal of Genomics</i> , 2013, 2013, 1-13.	0.8	24
9471	Sequential Binary Gene Ratio Tests Define a Novel Molecular Diagnostic Strategy for Malignant Pleural Mesothelioma. <i>Clinical Cancer Research</i> , 2013, 19, 2493-2502.	3.2	27
9472	BioModels Database: A Repository of Mathematical Models of Biological Processes. , 2013, , 134-138.		2
9473	SPINAL: scalable protein interaction network alignment. <i>Bioinformatics</i> , 2013, 29, 917-924.	1.8	113
9474	A graph kernel approach for alignment-free domain-peptide interaction prediction with an application to human SH3 domains. <i>Bioinformatics</i> , 2013, 29, i335-i343.	1.8	15
9475	Activation of the Wnt/ β -catenin pathway and tissue inhibitor of metalloprotease 1 during tertiary dentinogenesis. <i>Journal of Biochemistry</i> , 2013, 153, 43-50.	0.9	25
9476	TriPal v1.1: a standards-based toolkit for construction of online genetic and genomic databases. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat075.	1.4	52
9477	Punctuated Emergences of Genetic and Phenotypic Innovations in Eumetazoan, Bilaterian, Euteleostome, and Hominidae Ancestors. <i>Genome Biology and Evolution</i> , 2013, 5, 1949-1968.	1.1	24
9478	Review of Biological Network Data and Its Applications. <i>Genomics and Informatics</i> , 2013, 11, 200.	0.4	79
9479	A Novel Approach to the Problem of Non-uniqueness of the Solution in Hierarchical Clustering. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2013, 24, 1166-1173.	7.2	42
9480	Molecular function prediction for a family exhibiting evolutionary tendencies toward substrate specificity swapping: Recurrence of tyrosine aminotransferase activity in the β subfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1593-1609.	1.5	6

#	ARTICLE	IF	CITATIONS
9481	Network analysis of endogenous gene expression profiles after polyethyleneimine-mediated DNA delivery. <i>Journal of Gene Medicine</i> , 2013, 15, 142-154.	1.4	15
9482	CoDNAS: a database of conformational diversity in the native state of proteins. <i>Bioinformatics</i> , 2013, 29, 2512-2514.	1.8	31
9483	Differential gene expression in notochord and nerve cord fate segregation in the <i>Ciona intestinalis</i> embryo. <i>Genesis</i> , 2013, 51, 647-659.	0.8	4
9484	Characterization of transcriptomes from sexual and asexual lineages of a New Zealand snail (<i>Tj ETQq1 1 0.784314 rsgBT /Overlock 10 T</i>)	2.2	14
9485	What is an anatomy ontology?. <i>Anatomical Record</i> , 2013, 296, 1797-1799.	0.8	1
9486	Genetic analysis of the toxic effect of Tachyplesin I on the embryonic development of zebrafish. , 2013, , .		0
9487	Actin knock-out mouse embryonic fibroblasts show increased expression of LIM, CH, EF domain containing proteins with predicted common upstream regulators. <i>Cytoskeleton</i> , 2013, 70, 766-774.	1.0	3
9488	How to discriminate between potentially novel and considered biomarkers within molecular signature?. , 2013, , .		1
9489	Human disease locus discovery and mapping to molecular pathways through phylogenetic profiling. <i>Molecular Systems Biology</i> , 2013, 9, 692.	3.2	54
9490	Optimize Querying of LOINC with an Ontology: Give Me the Chlamydia Tests the Epidemiologists Want Me to Use!. , 2013, , .		2
9491	ECOH: An Enzyme Commission number predictor using mutual information and a support vector machine. <i>Bioinformatics</i> , 2013, 29, 365-372.	1.8	28
9492	Promoters maintain their relative activity levels under different growth conditions. <i>Molecular Systems Biology</i> , 2013, 9, 701.	3.2	181
9493	Transcriptome sequencing as a platform to elucidate molecular components of the diapause response in the Asian tiger mosquito <i>Aedes albopictus</i> . <i>Physiological Entomology</i> , 2013, 38, 173-181.	0.6	26
9494	Mass flowering of the tropical tree <i>Schorea beccariana</i> was preceded by expression changes in flowering and drought-responsive genes. <i>Molecular Ecology</i> , 2013, 22, 4767-4782.	2.0	71
9495	A comparison of multi-label techniques based on problem transformation for protein functional prediction. , 2013, 2013, 2688-91.		2
9496	Burkholderia cenocepacia conditional growth mutant library created by random promoter replacement of essential genes. <i>MicrobiologyOpen</i> , 2013, 2, 243-258.	1.2	22
9497	Biocatalytic Production of Chemical Building Blocks in Technical Scale with Ketoglutarate-Dependent Dioxygenases. <i>Chemie-Ingenieur-Technik</i> , 2013, 85, 809-817.	0.4	21
9498	Inferring semantic similarity through correlating information contents of gene ontology terms. , 2013, , .		0

#	ARTICLE	IF	CITATIONS
9499	An Ontology for Clinical Trial Data Integration. , 2013, , .		4
9500	Restoration of the gut microbial habitat as a disease therapy. Nature Biotechnology, 2013, 31, 35-37.	9.4	9
9501	PRIMOS: An Integrated Database of Reassessed Protein-Protein Interactions Providing Web-Based Access to In Silico Validation of Experimentally Derived Data. Assay and Drug Development Technologies, 2013, 11, 333-346.	0.6	10
9502	Blood-based gene expression predictors of PTSD risk and resilience among deployed marines: A pilot study. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 313-326.	1.1	63
9503	Epilepsy informatics and an ontology-driven infrastructure for large database research and patient care in epilepsy. Epilepsia, 2013, 54, 1335-1341.	2.6	12
9504	Widespread splicing changes in human brain development and aging. Molecular Systems Biology, 2013, 9, 633.	3.2	183
9505	DIFFERENCES IN THE REGULATION OF GROWTH AND BIOMINERALIZATION GENES REVEALED THROUGH LONG-TERM COMMON-GARDEN ACCLIMATION AND EXPERIMENTAL GENOMICS IN THE PURPLE SEA URCHIN. Evolution; International Journal of Organic Evolution, 2013, 67, 1901-1914.	1.1	58
9506	<i>Sca1</i> expression defines developmental stages of mouse pDCs that show functional heterogeneity in the endosomal but not lysosomal TLR9 response. European Journal of Immunology, 2013, 43, 2993-3005.	1.6	19
9507	Disturbed protein-protein interaction networks in metastatic melanoma are associated with worse prognosis and increased functional mutation burden. Pigment Cell and Melanoma Research, 2013, 26, 708-722.	1.5	12
9508	Mass Informatics: From Mass Spectrometry Peaks to Biological Pathways. Israel Journal of Chemistry, 2013, 53, 157-165.	1.0	1
9510	Apocynin, an NADPH oxidase inhibitor, suppresses rat prostate carcinogenesis. Cancer Science, 2013, 104, 1711-1717.	1.7	31
9512	AAPL: assessing association between <i>p</i> -value lists. Statistical Analysis and Data Mining, 2013, 6, 144-155.	1.4	1
9513	Comparative meta-analysis between human and mouse cancer microarray data reveals critical pathways. International Journal of Data Mining and Bioinformatics, 2013, 8, 349.	0.1	3
9514	In Silico Approaches and the Role of Ontologies in Aging Research. Rejuvenation Research, 2013, 16, 540-546.	0.9	2
9515	Practice and Challenges of Building a Semantic Framework for Chemogenomics Research. Molecular Informatics, 2013, 32, 1000-1008.	1.4	1
9516	Evaluating topology-based metrics for GO term similarity measures. , 2013, , .		3
9517	OrtholugeDB: a bacterial and archaeal orthology resource for improved comparative genomic analysis. Nucleic Acids Research, 2013, 41, D366-D376.	6.5	73
9518	Sesame: A new bioinformatics semantic workflow design system. , 2013, , .		3

#	ARTICLE	IF	CITATIONS
9519	Analysis of the genomic response of human prostate cancer cells to histone deacetylase inhibitors. <i>Epigenetics</i> , 2013, 8, 907-920.	1.3	32
9520	Evidence for multiple roles for grainyhead-like 2 in the establishment and maintenance of human mucociliary airway epithelium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9356-9361.	3.3	76
9521	UniVIO: A Multiple Omics Database with Hormonome and Transcriptome Data from Rice. <i>Plant and Cell Physiology</i> , 2013, 54, e9-e9.	1.5	42
9522	Number Variation of High Stability Regions Is Correlated with Gene Functions. <i>Genome Biology and Evolution</i> , 2013, 5, 484-493.	1.1	9
9523	Evolutionary Survey of Druggable Protein Targets with Respect to Their Subcellular Localizations. <i>Genome Biology and Evolution</i> , 2013, 5, 1291-1297.	1.1	18
9524	All or Nothing: Protein Complexes Flip Essentiality between Distantly Related Eukaryotes. <i>Genome Biology and Evolution</i> , 2013, 5, 1049-1059.	1.1	38
9525	Evolution of Coding Microsatellites in Primate Genomes. <i>Genome Biology and Evolution</i> , 2013, 5, 283-295.	1.1	22
9526	The C-terminal domain of Brd2 is important for chromatin interaction and regulation of transcription and alternative splicing. <i>Molecular Biology of the Cell</i> , 2013, 24, 3557-3568.	0.9	48
9527	RECONN: A CYTOSCAPE PLUG-IN FOR EXPLORING AND VISUALIZING REACTOME. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1350004.	0.3	5
9528	WEB-based GEne SeT Analysis Toolkit (WebGestalt): update 2013. <i>Nucleic Acids Research</i> , 2013, 41, W77-W83.	6.5	1,458
9529	BRES: EXTRACTING MULTICLASS BIOMEDICAL RELATIONS WITH SEMANTIC NETWORK. <i>Biomedical Engineering - Applications, Basis and Communications</i> , 2013, 25, 1350009.	0.3	1
9530	Genome evolution during progression to breast cancer. <i>Genome Research</i> , 2013, 23, 1097-1108.	2.4	98
9531	Gene expression is highly correlated on the chromosome level in urinary bladder cancer. <i>Cell Cycle</i> , 2013, 12, 1544-1559.	1.3	9
9532	The impact of collapsing data on microarray analysis and DILI prediction. <i>Systems Biomedicine (Austin)</i> Tj ETQq1 10.784314rgBT /O	0.7	4
9533	Tissue specificity in the nuclear envelope supports its functional complexity. <i>Nucleus</i> , 2013, 4, 460-477.	0.6	77
9534	Gene expression in archived newborn blood spots distinguishes infants who will later develop cerebral palsy from matched controls. <i>Pediatric Research</i> , 2013, 73, 450-456.	1.1	22
9535	The mutational landscape of phosphorylation signaling in cancer. <i>Scientific Reports</i> , 2013, 3, 2651.	1.6	149
9536	<i>Glycyrrhiza uralensis</i> Transcriptome Landscape and Study of Phytochemicals. <i>Plant and Cell Physiology</i> , 2013, 54, 697-710.	1.5	80

#	ARTICLE	IF	CITATIONS
9545	A Network Approach to Wound Healing. <i>Advances in Wound Care</i> , 2013, 2, 499-509.	2.6	17
9546	Increased Expression of Endoplasmic Reticulum Stress and Unfolded Protein Response Genes in Peripheral Blood Mononuclear Cells From Patients With Limited Cutaneous Systemic Sclerosis and Pulmonary Arterial Hypertension. <i>Arthritis and Rheumatism</i> , 2013, 65, 1357-1366.	6.7	54
9547	Inhibition of TGF- β 2 and EGF pathway gene expression and migration of oral carcinoma cells by mucosa-associated lymphoid tissue 1. <i>British Journal of Cancer</i> , 2013, 109, 207-214.	2.9	9
9548	Protooncogene TCL1b functions as an Akt kinase co-activator that exhibits oncogenic potency in vivo. <i>Oncogenesis</i> , 2013, 2, e70-e70.	2.1	13
9549	THE NEXT GENERATION OF SIMILARITY MEASURES THAT FULLY EXPLORE THE SEMANTICS IN BIOMEDICAL ONTOLOGIES. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1371001.	0.3	29
9550	A survey of intelligent assistants for data analysis. <i>ACM Computing Surveys</i> , 2013, 45, 1-35.	16.1	65
9551	Alphacoronavirus Protein 7 Modulates Host Innate Immune Response. <i>Journal of Virology</i> , 2013, 87, 9754-9767.	1.5	41
9552	The Evolutionary Genetics of the Genes Underlying Phenotypic Associations for Loblolly Pine (<i>Pinus taeda</i> , Pinaceae). <i>Genetics</i> , 2013, 195, 1353-1372.	1.2	41
9553	Reconstruction of novel transcription factor regulons through inference of their binding sites. , 2013, , .		0
9554	A genome-wide study shows a limited contribution of rare copy number variants to Alzheimer's disease risk. <i>Human Molecular Genetics</i> , 2013, 22, 816-824.	1.4	33
9555	Transcriptome Analysis to Identify Putative Floral-Specific Genes and Flowering Regulatory-Related Genes of Sweet Potato. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 2169-2174.	0.6	33
9556	RNA-Seq reveals early distinctions and late convergence of gene expression between diapause and quiescence in the Asian tiger mosquito, <i>Aedes albopictus</i> . <i>Journal of Experimental Biology</i> , 2013, 216, 4082-90.	0.8	68
9557	Potential for sexual conflict assessed via testosterone-mediated transcriptional changes in liver and muscle of a songbird. <i>Journal of Experimental Biology</i> , 2014, 217, 507-17.	0.8	28
9558	Computational detection of abundant long-range nucleotide covariation in <i>Drosophila</i> genomes. <i>Rna</i> , 2013, 19, 1171-1182.	1.6	6
9559	dcGO: database of domain-centric ontologies on functions, phenotypes, diseases and more. <i>Nucleic Acids Research</i> , 2013, 41, D536-D544.	6.5	98
9560	Missense mutation in the MEN1 gene discovered through whole exome sequencing co-segregates with familial hyperparathyroidism. <i>Genetical Research</i> , 2013, 95, 114-120.	0.3	11
9561	Expression of the Placental Transcriptome in Maternal Nutrient Reduction in Baboons Is Dependent on Fetal Sex. <i>Journal of Nutrition</i> , 2013, 143, 1698-1708.	1.3	37
9562	Adaptive responses by mouse fetus to a maternal HLE diet by downregulating SREBP1: a microarray- and bio-analytic-based study. <i>Journal of Lipid Research</i> , 2013, 54, 3269-3280.	2.0	9

#	ARTICLE	IF	CITATIONS
9563	CluePedia Cytoscape plugin: pathway insights using integrated experimental and <i>in silico</i> data. <i>Bioinformatics</i> , 2013, 29, 661-663.	1.8	958
9564	Being <i>Aquifex aeolicus</i> : Untangling a Hyperthermophile's Checkered Past. <i>Genome Biology and Evolution</i> , 2013, 5, 2478-2497.	1.1	22
9565	PosMed: ranking genes and bioresources based on Semantic Web Association Study. <i>Nucleic Acids Research</i> , 2013, 41, W109-W114.	6.5	15
9566	Genetic heterogeneity of diffuse large B-cell lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1398-1403.	3.3	494
9567	miR-23b regulates cytoskeletal remodeling, motility and metastasis by directly targeting multiple transcripts. <i>Nucleic Acids Research</i> , 2013, 41, 5400-5412.	6.5	111
9568	Portraying the expression landscapes of cancer subtypes. <i>Systems Biomedicine (Austin, Tex)</i> , 2013, 1, 99-121.	0.7	43
9569	Inferring gene correlation networks from transcription factor binding sites. <i>Genes and Genetic Systems</i> , 2013, 88, 301-309.	0.2	6
9570	Multi-way blockmodels for analyzing coordinated high-dimensional responses. <i>Annals of Applied Statistics</i> , 2013, 7, 2431-2457.	0.5	9
9571	Clear cell renal cell carcinoma associated microRNA expression signatures identified by an integrated bioinformatics analysis. <i>Journal of Translational Medicine</i> , 2013, 11, 169.	1.8	52
9572	The environment ontology: contextualising biological and biomedical entities. <i>Journal of Biomedical Semantics</i> , 2013, 4, 43.	0.9	244
9573	BREEDING AND GENETICS SYMPOSIUM: Networks and pathways to guide genomic selection ¹ . <i>Journal of Animal Science</i> , 2013, 91, 537-552.	0.2	57
9574	Grouped False-Discovery Rate for Removing the Gene-set-Level Bias of RNA-seq. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S13099.	0.6	3
9575	BacillOndex: An Integrated Data Resource for Systems and Synthetic Biology. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 103-116.	1.0	12
9576	A Pathway-Based Analysis on the Effects of Obstructive Sleep Apnea in Modulating Visceral Fat Transcriptome. <i>Sleep</i> , 2013, 36, 23-30.	0.6	38
9577	Automatically transforming pre- to post-composed phenotypes: EQ-lising HPO and MP. <i>Journal of Biomedical Semantics</i> , 2013, 4, 29.	0.9	5
9578	Representing annotation compositionality and provenance for the Semantic Web. <i>Journal of Biomedical Semantics</i> , 2013, 4, 38.	0.9	10
9579	Genomic characterization of remission in juvenile idiopathic arthritis. <i>Arthritis Research and Therapy</i> , 2013, 15, R100.	1.6	33
9580	Integrative DNA methylation and gene expression analysis in high-grade soft tissue sarcomas. <i>Genome Biology</i> , 2013, 14, r137.	13.9	78

#	ARTICLE	IF	CITATIONS
9581	Genomic analyses with biofilter 2.0: knowledge driven filtering, annotation, and model development. <i>BioData Mining</i> , 2013, 6, 25.	2.2	50
9582	Sequence signatures extracted from proximal promoters can be used to predict distal enhancers. <i>Genome Biology</i> , 2013, 14, R117.	13.9	32
9583	Genome sequence of the moderately halophilic bacterium <i>Salinicoccus carniancri</i> type strain CrmT (= DSM 23852T). <i>Standards in Genomic Sciences</i> , 2013, 8, 255-263.	1.5	11
9584	A distinct group of CpG islands shows differential DNA methylation between replicas of the same cell line in vitro. <i>BMC Genomics</i> , 2013, 14, 692.	1.2	6
9585	De novo assembly and characterization of leaf transcriptome for the development of functional molecular markers of the extremophile multipurpose tree species <i>Prosopis alba</i> . <i>BMC Genomics</i> , 2013, 14, 705.	1.2	45
9586	Transcriptome analysis of <i>Pinus monticola</i> primary needles by RNA-seq provides novel insight into host resistance to <i>Cronartium ribicola</i> . <i>BMC Genomics</i> , 2013, 14, 884.	1.2	63
9588	ENNET: inferring large gene regulatory networks from expression data using gradient boosting. <i>BMC Systems Biology</i> , 2013, 7, 106.	3.0	41
9589	Insulin-Like Growth Factor 2 mRNA Binding Protein 3 Expression Is an Independent Prognostic Factor in Pediatric Pilocytic and Pilocytic Astrocytoma. <i>Journal of Neuropathology and Experimental Neurology</i> , 2013, 72, 442-449.	0.9	20
9590	Comprehensive analysis of correlation coefficients estimated from pooling heterogeneous microarray data. <i>BMC Bioinformatics</i> , 2013, 14, 214.	1.2	14
9591	Metabolite and transcriptome analysis during fasting suggest a role for the p53-Ddit4 axis in major metabolic tissues. <i>BMC Genomics</i> , 2013, 14, 758.	1.2	65
9592	Automated design of bacterial genome sequences. <i>BMC Systems Biology</i> , 2013, 7, 108.	3.0	1
9593	The Complete Genome Sequence of <i>Methanobrevibacter</i> sp. AbM4. <i>Standards in Genomic Sciences</i> , 2013, 8, 215-227.	1.5	42
9594	Non-contiguous finished genome sequence and description of <i>Clostridium dakarensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 9, 14-27.	1.5	45
9595	Complete genome sequence of <i>Granulicella mallensis</i> type strain MP5ACTX8T, an acidobacterium from tundra soil. <i>Standards in Genomic Sciences</i> , 2013, 9, 71-82.	1.5	20
9596	Non-contiguous finished genome sequence and description of <i>Nosocomiicoccus massiliensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 9, 205-219.	1.5	18
9597	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain SRDI943.. <i>Standards in Genomic Sciences</i> , 2013, 9, 232-242.	1.5	3
9598	Genome sequence of the <i>Trifolium rueppellianum</i> -nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM2012.. <i>Standards in Genomic Sciences</i> , 2013, 9, 283-293.	1.5	3
9599	Genome sequence of the <i>Listia angolensis</i> microsymbiont <i>Microvirga lotononidis</i> strain WSM3557T. <i>Standards in Genomic Sciences</i> , 2013, 9, 540-550.	1.5	7

#	ARTICLE	IF	CITATIONS
9600	Non-contiguous finished genome sequence and description of <i>Holdemania massiliensis</i> sp. nov.. Standards in Genomic Sciences, 2013, 9, 395-409.	1.5	25
9601	Genome sequence of <i>Ensifer medicae</i> strain WSM1369; an effective microsymbiont of the annual legume <i>Medicago sphaerocarpos</i> . Standards in Genomic Sciences, 2013, 9, 420-430.	1.5	1
9602	Genome sequence of <i>Burkholderia mimosarum</i> strain LMG 23256T, a <i>Mimosa pigra</i> microsymbiont from Anso, Taiwan. Standards in Genomic Sciences, 2013, 9, 484-494.	1.5	6
9603	Genome sequence of <i>Ensifer medicae</i> strain WSM1115; an acid-tolerant <i>Medicago-nodulating</i> microsymbiont from Samothraki, Greece. Standards in Genomic Sciences, 2013, 9, 514-526.	1.5	2
9604	Accessing Cancer Metabolic Pathways by the Use of Microarray Technology. Current Pharmaceutical Design, 2013, 19, 790-805.	0.9	5
9605	Cellular Relationships of Testicular Germ Cell Tumors Determined by Partial Canonical Correlation Analysis of Gene Expression Signatures. Current Bioinformatics, 2013, 8, 72-79.	0.7	2
9606	Fluorescentâ€Ligandâ€Mediated Screening of Câ€Quadruplex Structures Using a DNA Microarray. Angewandte Chemie - International Edition, 2013, 52, 12052-12055.	7.2	45
9607	Fluorescentâ€Ligandâ€Mediated Screening of Câ€Quadruplex Structures Using a DNA Microarray. Angewandte Chemie, 2013, 125, 12274-12277.	1.6	2
9608	Comparative analysis of saltâ€responsive phosphoproteins in maize leaves using <sc>T</sc>i⁴⁺â€<sc>IMAC</sc> enrichment and <sc>ESI</sc>â€<sc>Q</sc>â€<sc>TOF</sc> <sc>MS</sc>. Electrophoresis, 2013, 34, 485-492.	1.3	26
9609	Non contiguous-finished genome sequence and description of <i>Peptoniphilus grossensis</i> sp. nov.. Standards in Genomic Sciences, 2012, 7, 320-330.	1.5	34
9610	Non contiguous-finished genome sequence and description of <i>Peptoniphilus obesi</i> sp. nov.. Standards in Genomic Sciences, 2013, 7, 357-369.	1.5	31
9611	Non contiguous-finished genome sequence and description of <i>Alistipes obesi</i> sp. nov. Standards in Genomic Sciences, 2013, 7, 427-439.	1.5	54
9612	Non contiguous-finished genome sequence and description of <i>Peptoniphilus senegalensis</i> sp. nov.. Standards in Genomic Sciences, 2013, 7, 370-381.	1.5	38
9613	Non contiguous-finished genome sequence and description of <i>Enterobacter massiliensis</i> sp. nov.. Standards in Genomic Sciences, 2013, 7, 399-412.	1.5	66
9614	Non contiguous-finished genome sequence and description of <i>Enorma massiliensis</i> gen. nov., sp. nov., a new member of the Family Coriobacteriaceae. Standards in Genomic Sciences, 2013, 8, 290-305.	1.5	37
9615	Non-contiguous finished genome sequence and description of <i>Brevibacillus massiliensis</i> sp. nov.. Standards in Genomic Sciences, 2013, 8, 1-14.	1.5	47
9616	Genome of the marine alphaproteobacterium <i>Hoeflea phototrophica</i> type strain (DFL-43T). Standards in Genomic Sciences, 2013, 7, 440-448.	1.5	8
9617	Non contiguous-finished genome sequence and description of <i>Bacillus massilosenegalensis</i> sp. nov.. Standards in Genomic Sciences, 2013, 8, 264-278.	1.5	33

#	ARTICLE	IF	CITATIONS
9618	Complete genome sequence of <i>Coriobacterium glomerans</i> type strain (PW2T) from the midgut of <i>Pyrhocoris apterus</i> L. (red soldier bug). <i>Standards in Genomic Sciences</i> , 2013, 8, 15-25.	1.5	8
9619	Complete genome sequence of the bile-resistant pigment-producing anaerobe <i>Alistipes finegoldii</i> type strain (AHN2437T). <i>Standards in Genomic Sciences</i> , 2013, 8, 26-36.	1.5	12
9620	High-quality-draft genome sequence of the yellow-pigmented flavobacterium <i>Joostella marina</i> type strain (En5T). <i>Standards in Genomic Sciences</i> , 2013, 8, 37-46.	1.5	11
9621	Complete genome sequence of the moderate thermophile <i>Anaerobaculum mobile</i> type strain (NGAT). <i>Standards in Genomic Sciences</i> , 2013, 8, 47-57.	1.5	11
9622	Non contiguous-finished genome sequence and description of <i>Dielma fastidiosa</i> gen. nov., sp. nov., a new member of the Family <i>Erysipelotrichaceae</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 336-351.	1.5	52
9623	Genome sequence of the free-living aerobic spirochete <i>Turneriella parva</i> type strain (HT), and emendation of the species <i>Turneriella parva</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 228-238.	1.5	11
9624	Genome analysis of <i>Desulfotomaculum kuznetsovii</i> strain 17T reveals a physiological similarity with <i>Pelotomaculum thermopropionicum</i> strain SIT.. <i>Standards in Genomic Sciences</i> , 2013, 8, 69-87.	1.5	42
9625	<i>Thermus oshimai</i> JL-2 and <i>T. thermophilus</i> JL-18 genome analysis illuminates pathways for carbon, nitrogen, and sulfur cycling. <i>Standards in Genomic Sciences</i> , 2013, 7, 449-468.	1.5	31
9626	Complete genome sequence of <i>Halorhodospira halophila</i> SL1. <i>Standards in Genomic Sciences</i> , 2013, 8, 206-214.	1.5	26
9627	Complete genome sequence of <i>Streptococcus agalactiae</i> strain SA20-06, a fish pathogen associated to meningoencephalitis outbreaks. <i>Standards in Genomic Sciences</i> , 2013, 8, 188-197.	1.5	33
9628	<i>Staphylococcus aureus</i> subsp. <i>anaerobius</i> strain ST1464 genome sequence. <i>Standards in Genomic Sciences</i> , 2013, 9, 1-11.	1.5	8
9629	Non-contiguous finished genome sequence and description of <i>Salmonella enterica</i> subsp. <i>houtenae</i> str. RKS3027. <i>Standards in Genomic Sciences</i> , 2013, 8, 198-205.	1.5	2
9630	Complete genome sequence of <i>Dehalobacter restrictus</i> PER-K23T. <i>Standards in Genomic Sciences</i> , 2013, 8, 375-388.	1.5	44
9631	Permanent draft genome sequences of the symbiotic nitrogen fixing <i>Ensifer meliloti</i> strains BO21CC and AK58. <i>Standards in Genomic Sciences</i> , 2013, 9, 352-333.	1.5	7
9632	Non-contiguous finished genome sequence and description of <i>Bartonella senegalensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 8, 279-289.	1.5	20
9633	Genome sequence of the phage-gene rich marine <i>Phaeobacter arcticus</i> type strain DSM 23566T. <i>Standards in Genomic Sciences</i> , 2013, 8, 450-464.	1.5	9
9634	Genome sequence of the <i>Leisingera aquimarina</i> type strain (DSM 24565T), a member of the marine <i>Roseobacter</i> clade rich in extrachromosomal elements. <i>Standards in Genomic Sciences</i> , 2013, 8, 389-402.	1.5	17
9635	Genome sequence of <i>Phaeobacter caeruleus</i> type strain (DSM 24564T), a surface-associated member of the marine <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013, 8, 403-419.	1.5	12

#	ARTICLE	IF	CITATIONS
9636	Non contiguous-finished genome sequence of <i>Pseudomonas syringae</i> pathovar <i>syringae</i> strain B64 isolated from wheat. <i>Standards in Genomic Sciences</i> , 2013, 8, 420-429.	1.5	10
9637	Complete genome sequence of <i>Ilumatobacter coccineum</i> YM16-304T. <i>Standards in Genomic Sciences</i> , 2013, 8, 430-440.	1.5	10
9638	Non-contiguous finished genome sequence of plant-growth promoting <i>Serratia proteamaculans</i> S4. <i>Standards in Genomic Sciences</i> , 2013, 8, 441-449.	1.5	26
9639	Non-contiguous finished genome sequence and description of <i>Kallipyga massiliensis</i> gen. nov., sp. nov., a new member of the family <i>Clostridiales</i> Incertae Sedis XI. <i>Standards in Genomic Sciences</i> , 2013, 8, 500-515.	1.5	23
9640	Genome sequence of the marine bacterium <i>Corynebacterium maris</i> type strain <i>Coryn-1T</i> (= DSM 45190T). <i>Standards in Genomic Sciences</i> , 2013, 8, 516-524.	1.5	2
9641	Non-contiguous finished genome sequence and description of <i>Megasphaera massiliensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 8, 525-538.	1.5	28
9642	Draft Genome Sequence of <i>Amphibacillus jilinesis</i> Y1T, a Facultatively Anaerobic, Alkaliphilic and Halotolerant Bacterium. <i>Standards in Genomic Sciences</i> , 2013, 8, 491-499.	1.5	1
9643	Non-contiguous finished genome sequence and description of <i>Anaerococcus pacaensis</i> sp. nov., a new species of anaerobic bacterium. <i>Standards in Genomic Sciences</i> , 2013, 8, 548-560.	1.5	9
9644	Genome sequence of the chemoheterotrophic soil bacterium <i>Saccharomonospora cyanea</i> type strain (NA-134T). <i>Standards in Genomic Sciences</i> , 2013, 9, 28-41.	1.5	4
9645	Genome sequence and description of the heavy metal tolerant bacterium <i>Lysinibacillus sphaericus</i> strain OT4b.31. <i>Standards in Genomic Sciences</i> , 2013, 9, 42-56.	1.5	35
9646	Genome sequence of the moderately thermophilic sulfur-reducing bacterium <i>Thermanaerovibrio velox</i> type strain (Z-9701T) and emended description of the genus <i>Thermanaerovibrio</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 57-70.	1.5	8
9647	Genome sequence of the <i>Litoreibacter arenae</i> type strain (DSM 19593T), a member of the <i>Roseobacter</i> clade isolated from sea sand. <i>Standards in Genomic Sciences</i> , 2013, 9, 117-127.	1.5	8
9648	Non-contiguous finished genome sequence and description of <i>Oceanobacillus massiliensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 9, 370-384.	1.5	23
9649	Genome sequence of <i>Frateuria aurantia</i> type strain (KondÃ´ 67T), a xanthomonade isolated from <i>Lilium auratum</i> Lindl.. <i>Standards in Genomic Sciences</i> , 2013, 9, 83-92.	1.5	3
9650	Non-contiguous finished genome sequence and description of <i>Bartonella florenciae</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 9, 185-196.	1.5	26
9651	Non-contiguous finished genome sequence and description of <i>Bacillus massiliogorillae</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 9, 93-105.	1.5	32
9652	Draft genome sequence of <i>Rubidibacter lacunae</i> strain KORDI 51-2T, a cyanobacterium isolated from seawater of Chuuk lagoon. <i>Standards in Genomic Sciences</i> , 2013, 9, 197-204.	1.5	4
9653	Non-contiguous finished genome sequence of <i>Phocaeicola abscessus</i> type strain 7401987T. <i>Standards in Genomic Sciences</i> , 2013, 9, 351-358.	1.5	2

#	ARTICLE	IF	CITATIONS
9654	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain SRDI565.. Standards in Genomic Sciences, 2013, 9, 220-231.	1.5	4
9655	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain TA1. Standards in Genomic Sciences, 2013, 9, 243-253.	1.5	10
9656	Genome sequence of the <i>Ornithopus/Lupinus</i> -nodulating <i>Bradyrhizobium</i> sp. strain WSM471. Standards in Genomic Sciences, 2013, 9, 254-263.	1.5	0
9657	Genome sequence of the South American clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM597. Standards in Genomic Sciences, 2013, 9, 264-272.	1.5	4
9658	Genome sequence of the lupin-nodulating <i>Bradyrhizobium</i> sp. strain WSM1417. Standards in Genomic Sciences, 2013, 9, 273-282.	1.5	3
9659	Complete genome sequence of <i>Mesorhizobium opportunistum</i> type strain WSM2075T. Standards in Genomic Sciences, 2013, 9, 294-303.	1.5	12
9660	Non-contiguous finished genome sequence and description of <i>Halopiger djelfamassiliensis</i> sp. nov.. Standards in Genomic Sciences, 2013, 9, 160-174.	1.5	14
9661	Genome sequence of <i>Ensifer</i> sp. TW10; a <i>Tephrosia wallichii</i> (Biyani) microsymbiont native to the Indian Thar Desert. Standards in Genomic Sciences, 2013, 9, 304-314.	1.5	12
9662	Genome sequence of <i>Ensifer meliloti</i> strain WSM1022; a highly effective microsymbiont of the model legume <i>Medicago truncatula</i> A17. Standards in Genomic Sciences, 2013, 9, 315-324.	1.5	13
9663	Non-contiguous finished genome sequence and description of <i>Halopiger goleamassiliensis</i> sp. nov.. Standards in Genomic Sciences, 2013, 9, 956-959.	1.5	10
9664	Complete genome sequence of <i>Granulicella tundricola</i> type strain MP5ACTX9T, an Acidobacteria from tundra soil. Standards in Genomic Sciences, 2013, 9, 449-461.	1.5	17
9665	Genome sequence of the chromate-resistant bacterium <i>Leucobacter salsicius</i> type strain M1-8T. Standards in Genomic Sciences, 2013, 9, 495-504.	1.5	9
9666	Genome sequence of <i>Ensifer arboris</i> strain LMG 14919T; a microsymbiont of the legume <i>Prosopis chilensis</i> growing in Kosti, Sudan. Standards in Genomic Sciences, 2013, 9, 473-483.	1.5	6
9667	Genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM1689, the microsymbiont of the one flowered clover <i>Trifolium uniflorum</i> . Standards in Genomic Sciences, 2013, 9, 527-539.	1.5	27
9668	Genome sequence of the acid-tolerant <i>Burkholderia</i> sp. strain WSM2230 from Karijini National Park, Australia. Standards in Genomic Sciences, 2013, 9, 551-561.	1.5	3
9669	Genome sequence of the acid-tolerant <i>Burkholderia</i> sp. strain WSM2232 from Karijini National Park, Australia. Standards in Genomic Sciences, 2013, 9, 1168-1180.	1.5	2
9670	Genome of the R-body producing marine alphaproteobacterium <i>Labrenzia alexandrii</i> type strain (DFL-11T). Standards in Genomic Sciences, 2013, 7, 413-426.	1.5	10
9671	Genome sequence and description of <i>Timonella senegalensis</i> gen. nov., sp. nov., a new member of the suborder Micrococccinae. Standards in Genomic Sciences, 2013, 8, 318-335.	1.5	32

#	ARTICLE	IF	CITATIONS
9672	Permanent draft genome sequence of <i>Comamonas testosteroni</i> KF-1. <i>Standards in Genomic Sciences</i> , 2013, 8, 239-254.	1.5	14
9673	Non-contiguous finished genome sequence and description of <i>Bacillus massilioanorexius</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2013, 8, 465-479.	1.5	24
9674	Complete genome sequence of <i>Mesorhizobium australicum</i> type strain (WSM2073T). <i>Standards in Genomic Sciences</i> , 2013, 9, 410-419.	1.5	11
9675	Genome sequence of the squalene-degrading bacterium <i>Corynebacterium terpenotabidum</i> type strain Y-11T (= DSM 44721T). <i>Standards in Genomic Sciences</i> , 2013, 9, 505-513.	1.5	7
9676	Virus-ECC-mPloc: A Multi-Label Predictor for Predicting the Subcellular Localization of Virus Proteins with Both Single and Multiple Sites Based on a General Form of Chou's Pseudo Amino Acid Composition. <i>Protein and Peptide Letters</i> , 2013, 20, 309-317.	0.4	16
9677	Genome-scale cold stress response regulatory networks in ten <i>Arabidopsis thaliana</i> ecotypes. <i>BMC Genomics</i> , 2013, 14, 722.	1.2	73
9678	Genome sequence of the thermophilic fresh-water bacterium <i>Spirochaeta caldaria</i> type strain (H1T), reclassification of <i>Spirochaeta caldaria</i> , <i>Spirochaeta stenostrepta</i> , and <i>Spirochaeta zuelzeriae</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov., and <i>Treponema zuelzeriae</i> comb. nov., and emendation of the genus <i>Treponema</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 88-105.	1.5	44
9679	The Genomic Blueprint of <i>Salmonella enterica</i> subspecies <i>enterica</i> serovar Typhi P-stx-12. <i>Standards in Genomic Sciences</i> , 2013, 7, 483-496.	1.5	6
9680	Complete genome sequence of the halophilic bacterium <i>Spirochaeta africana</i> type strain (Z-7692T) from the alkaline Lake Magadi in the East African Rift. <i>Standards in Genomic Sciences</i> , 2013, 8, 165-176.	1.5	3
9681	Genome sequence of the phylogenetically isolated spirochete <i>Leptonema illini</i> type strain (3055T). <i>Standards in Genomic Sciences</i> , 2013, 8, 177-187.	1.5	5
9682	Non-contiguous genome sequence of <i>Mycobacterium simiae</i> strain DSM 44165T. <i>Standards in Genomic Sciences</i> , 2013, 8, 306-317.	1.5	5
9683	Genome sequence of the reddish-pigmented <i>Rubellimicrobium thermophilum</i> type strain (DSM 16684T), a member of the <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013, 8, 480-490.	1.5	6
9684	Genome sequence of <i>Phaeobacter daeponensis</i> type strain (DSM 23529T), a facultatively anaerobic bacterium isolated from marine sediment, and emendation of <i>Phaeobacter daeponensis</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 142-159.	1.5	12
9685	Complete genome sequence of the marine methyl-halide oxidizing <i>Leisingera methylohalidivorans</i> type strain (DSM 14336T), a representative of the <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013, 9, 128-141.	1.5	15
9686	Complete genome sequence of <i>Enterobacter</i> sp. IIT-BT 08: A potential microbial strain for high rate hydrogen production. <i>Standards in Genomic Sciences</i> , 2013, 9, 359-369.	1.5	16
9687	Genome sequence of <i>Phaeobacter inhibens</i> type strain (T5T), a secondary metabolite producing representative of the marine <i>Roseobacter</i> clade, and emendation of the species description of <i>Phaeobacter inhibens</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 334-350.	1.5	26
9688	Complete genome sequence of <i>Mesorhizobium ciceri</i> bv. <i>biserrulae</i> type strain (WSM1271T). <i>Standards in Genomic Sciences</i> , 2013, 9, 462-472.	1.5	17
9689	Genome sequence of the <i>Lebeckia ambigua</i> -nodulating <i>Burkholderia sprentiae</i> strain WSM5005T. <i>Standards in Genomic Sciences</i> , 2013, 9, 385-394.	1.5	9

#	ARTICLE	IF	CITATIONS
9690	Use of data mining to determine changes in the gene expression profiles of rat embryos following prenatal exposure to inflammatory stimulants. <i>Molecular Medicine Reports</i> , 2013, 8, 95-102.	1.1	3
9691	Screening of Key Genes Associated with Ischemic Stroke via Microarray Data. <i>Canadian Journal of Neurological Sciences</i> , 2013, 40, 864-869.	0.3	2
9692	The switches.ELM Resource: A Compendium of Conditional Regulatory Interaction Interfaces. <i>Science Signaling</i> , 2013, 6, rs7.	1.6	101
9693	BigYAP: Exo-compilation meets UDI. <i>Theory and Practice of Logic Programming</i> , 2013, 13, 799-813.	1.1	2
9694	B 6 Ontologien. , 2013, , 207-218.		3
9695	miRNA Profiling Discriminates Types of Rejection and Injury in Human Renal Allografts. <i>Transplantation</i> , 2013, 95, 835-841.	0.5	80
9696	Stealthy annotation of experimental biology by spreadsheets. <i>Concurrency Computation Practice and Experience</i> , 2013, 25, 467-480.	1.4	3
9697	<i>Solute carrier family 2 member 1</i> is involved in the development of nonalcoholic fatty liver disease. <i>Hepatology</i> , 2013, 57, 505-514.	3.6	25
9698	Transcriptomic and proteomic analysis of human hepatic stellate cells treated with natural taurine. <i>Molecular Medicine Reports</i> , 2013, 7, 1442-1452.	1.1	8
9699	Draft Genome Sequence of <i>Lactobacillus pobuzihii</i> E100301 T. <i>Genome Announcements</i> , 2013, 1, .	0.8	1
9700	"Mining events from the literature for bioinformatics applications" by S. Ananiadou, P. Thompson, and R. Nawaz; with Martin Vesely as coordinator. <i>SIGWEB Newsletter: the Newsletter of ACM's Special Interest Group on Hypertext and Hypermedia</i> , 2013, , 1-12.	0.5	1
9701	Global regulation of alternative splicing by adenosine deaminase acting on RNA (ADAR). <i>Rna</i> , 2013, 19, 591-604.	1.6	125
9702	Parkinson's disease: dopaminergic nerve cell model is consistent with experimental finding of increased extracellular transport of α -synuclein. <i>BMC Neuroscience</i> , 2013, 14, 136.	0.8	16
9703	Transcription Factor β Plays an Important Role in the Production of Extracellular Membrane-Derived Vesicles in <i>Listeria monocytogenes</i> . <i>PLoS ONE</i> , 2013, 8, e73196.	1.1	89
9704	Network Characteristic Analysis of ADR-related Proteins and Identification of ADR-ADR Associations. <i>Scientific Reports</i> , 2013, 3, 1744.	1.6	15
9705	InterMOD: integrated data and tools for the unification of model organism research. <i>Scientific Reports</i> , 2013, 3, 1802.	1.6	25
9706	Network Analysis Reveals Functional Cross-links between Disease and Inflammation Genes. <i>Scientific Reports</i> , 2013, 3, 3426.	1.6	22
9707	Identifying potential cancer driver genes by genomic data integration. <i>Scientific Reports</i> , 2013, 3, 3538.	1.6	60

#	ARTICLE	IF	CITATIONS
9708	Identifying overlapping communities as well as hubs and outliers via nonnegative matrix factorization. <i>Scientific Reports</i> , 2013, 3, 2993.	1.6	67
9709	A Review of Protein Function Prediction Under Machine Learning Perspective. <i>Recent Patents on Biotechnology</i> , 2013, 7, 122-141.	0.4	43
9710	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
9711	Comparison of Computational Tools for Protein-Protein Interaction (PPI) Mapping and Analysis. <i>Jurnal Teknologi (Sciences and Engineering)</i> , 2013, 63, .	0.3	1
9713	From Concept Representations to Ontologies: A Paradigm Shift in Health Informatics?. <i>Healthcare Informatics Research</i> , 2013, 19, 235.	1.0	23
9714	Influence of Aromatase Absence on the Gene Expression and Histology of the Mouse Meibomian Gland. , 2013, 54, 987.		18
9715	Formal Ontologies in Biomedical Knowledge Representation. <i>Yearbook of Medical Informatics</i> , 2013, 22, 132-146.	0.8	20
9716	Comprehensive Assessment and Network Analysis of the Emerging Genetic Susceptibility Landscape of Prostate Cancer. <i>Cancer Informatics</i> , 2013, 12, CIN.S12128.	0.9	10
9717	Comparison of Modules of Wild Type and Mutant Huntingtin and TP53 Protein Interaction Networks: Implications in Biological Processes and Functions. <i>PLoS ONE</i> , 2013, 8, e64838.	1.1	8
9718	A Conserved Mammalian Protein Interaction Network. <i>PLoS ONE</i> , 2013, 8, e52581.	1.1	10
9719	Wrangling Phosphoproteomic Data to Elucidate Cancer Signaling Pathways. <i>PLoS ONE</i> , 2013, 8, e52884.	1.1	22
9720	Effects of Warm Ischemic Time on Gene Expression Profiling in Colorectal Cancer Tissues and Normal Mucosa. <i>PLoS ONE</i> , 2013, 8, e53406.	1.1	44
9721	From QTL to QTN: Candidate Gene Set Approach and a Case Study in Porcine IGF1-FoxO Pathway. <i>PLoS ONE</i> , 2013, 8, e53452.	1.1	7
9722	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
9723	De Novo Transcriptome Sequencing and Analysis for <i>Venturia inaequalis</i> , the Devastating Apple Scab Pathogen. <i>PLoS ONE</i> , 2013, 8, e53937.	1.1	32
9724	Increasing Sequence Search Sensitivity with Transitive Alignments. <i>PLoS ONE</i> , 2013, 8, e54422.	1.1	3
9725	Relevance of TNBS-Colitis in Rats: A Methodological Study with Endoscopic, Histologic and Transcriptomic Characterization and Correlation to IBD. <i>PLoS ONE</i> , 2013, 8, e54543.	1.1	59
9726	Statistical Assessment of Crosstalk Enrichment between Gene Groups in Biological Networks. <i>PLoS ONE</i> , 2013, 8, e54945.	1.1	34

#	ARTICLE	IF	CITATIONS
9727	TGF- β 2/Smad2/3 Signaling Directly Regulates Several miRNAs in Mouse ES Cells and Early Embryos. PLoS ONE, 2013, 8, e55186.	1.1	17
9728	Post-Embryonic Transcriptomes of the Prawn <i>Macrobrachium rosenbergii</i> : Multigenic Succession through Metamorphosis. PLoS ONE, 2013, 8, e55322.	1.1	39
9729	miR-221/222 Compensates for Skp2-Mediated p27 Degradation and Is a Primary Target of Cell Cycle Regulation by Prostacyclin and cAMP. PLoS ONE, 2013, 8, e56140.	1.1	18
9730	Improved Detection of Remote Homologues Using Cascade PSI-BLAST: Influence of Neighbouring Protein Families on Sequence Coverage. PLoS ONE, 2013, 8, e56449.	1.1	10
9731	Primary Analysis of the Expressed Sequence Tags in a Pentastomid Nymph cDNA Library. PLoS ONE, 2013, 8, e56511.	1.1	1
9732	Insights on the Functional Impact of MicroRNAs Present in Autism-Associated Copy Number Variants. PLoS ONE, 2013, 8, e56781.	1.1	67
9733	Seasonal and Regional Differences in Gene Expression in the Brain of a Hibernating Mammal. PLoS ONE, 2013, 8, e58427.	1.1	109
9734	Digital Gene Expression Tag Profiling Analysis of the Gene Expression Patterns Regulating the Early Stage of Mouse Spermatogenesis. PLoS ONE, 2013, 8, e58680.	1.1	18
9735	Comparative GO: A Web Application for Comparative Gene Ontology and Gene Ontology-Based Gene Selection in Bacteria. PLoS ONE, 2013, 8, e58759.	1.1	97
9736	Identifying Gene Set Association Enrichment Using the Coefficient of Intrinsic Dependence. PLoS ONE, 2013, 8, e58851.	1.1	5
9737	Diversity of Natural Self-Derived Ligands Presented by Different HLA Class I Molecules in Transporter Antigen Processing-Deficient Cells. PLoS ONE, 2013, 8, e59118.	1.1	8
9738	Systematic Analysis of Experimental Phenotype Data Reveals Gene Functions. PLoS ONE, 2013, 8, e60847.	1.1	19
9739	Microarray and Pathway Analysis Reveal Distinct Mechanisms Underlying Cannabinoid-Mediated Modulation of LPS-Induced Activation of BV-2 Microglial Cells. PLoS ONE, 2013, 8, e61462.	1.1	94
9740	When Is Hub Gene Selection Better than Standard Meta-Analysis?. PLoS ONE, 2013, 8, e61505.	1.1	243
9741	Testosterone Affects Neural Gene Expression Differently in Male and Female Juncos: A Role for Hormones in Mediating Sexual Dimorphism and Conflict. PLoS ONE, 2013, 8, e61784.	1.1	52
9742	Rapid Catalytic Template Searching as an Enzyme Function Prediction Procedure. PLoS ONE, 2013, 8, e62535.	1.1	28
9743	Modular Biological Function Is Most Effectively Captured by Combining Molecular Interaction Data Types. PLoS ONE, 2013, 8, e62670.	1.1	16
9744	Transcriptome Analysis of Buds and Leaves Using 454 Pyrosequencing to Discover Genes Associated with the Biosynthesis of Active Ingredients in <i>Lonicera japonica</i> Thunb.. PLoS ONE, 2013, 8, e62922.	1.1	47

#	ARTICLE	IF	CITATIONS
9745	Comparative Genomic and Transcriptomic Analysis of Tandemly and Segmentally Duplicated Genes in Rice. PLoS ONE, 2013, 8, e63551.	1.1	36
9746	FFPred 2.0: Improved Homology-Independent Prediction of Gene Ontology Terms for Eukaryotic Protein Sequences. PLoS ONE, 2013, 8, e63754.	1.1	40
9747	Transcriptome Sequencing of Zhikong Scallop (<i>Chlamys farreri</i>) and Comparative Transcriptomic Analysis with Yesso Scallop (<i>Patinopecten yessoensis</i>). PLoS ONE, 2013, 8, e63927.	1.1	45
9748	Transcriptomic Analysis of a Tertiary Relict Plant, Extreme Xerophyte <i>Reaumuria soongorica</i> to Identify Genes Related to Drought Adaptation. PLoS ONE, 2013, 8, e63993.	1.1	55
9749	Reverse Engineering of Modified Genes by Bayesian Network Analysis Defines Molecular Determinants Critical to the Development of Glioblastoma. PLoS ONE, 2013, 8, e64140.	1.1	41
9750	A Rapid Transcriptome Response Is Associated with Desiccation Resistance in Aerially-Exposed Killifish Embryos. PLoS ONE, 2013, 8, e64410.	1.1	17
9751	Profiling and Quantifying Differential Gene Transcription Provide Insights into Ganoderic Acid Biosynthesis in <i>Ganoderma lucidum</i> in Response to Methyl Jasmonate. PLoS ONE, 2013, 8, e65027.	1.1	41
9752	Comparative Transcriptome Analysis Using High Papaverine Mutant of <i>Papaver somniferum</i> Reveals Pathway and Uncharacterized Steps of Papaverine Biosynthesis. PLoS ONE, 2013, 8, e65622.	1.1	48
9753	Centromere Binding and a Conserved Role in Chromosome Stability for SUMO-Dependent Ubiquitin Ligases. PLoS ONE, 2013, 8, e65628.	1.1	29
9754	Revealing the Hidden Relationship by Sparse Modules in Complex Networks with a Large-Scale Analysis. PLoS ONE, 2013, 8, e66020.	1.1	3
9755	Normalizing RNA-Sequencing Data by Modeling Hidden Covariates with Prior Knowledge. PLoS ONE, 2013, 8, e68141.	1.1	68
9756	Distinct Contributions of TNF Receptor 1 and 2 to TNF-Induced Glomerular Inflammation in Mice. PLoS ONE, 2013, 8, e68167.	1.1	24
9757	Cross-Amplification and Validation of SNPs Conserved over 44 Million Years between Seals and Dogs. PLoS ONE, 2013, 8, e68365.	1.1	24
9758	A Systems-Genetics Approach and Data Mining Tool to Assist in the Discovery of Genes Underlying Complex Traits in <i>Oryza sativa</i> . PLoS ONE, 2013, 8, e68551.	1.1	26
9759	Genotypic and Phenotypic Versatility of <i>Aspergillus flavus</i> during Maize Exploitation. PLoS ONE, 2013, 8, e68735.	1.1	35
9760	HSC-Explorer: A Curated Database for Hematopoietic Stem Cells. PLoS ONE, 2013, 8, e70348.	1.1	17
9761	Bovine Mammary Gene Expression Profiling during the Onset of Lactation. PLoS ONE, 2013, 8, e70393.	1.1	60
9762	Voting-Based Cancer Module Identification by Combining Topological and Data-Driven Properties. PLoS ONE, 2013, 8, e70498.	1.1	9

#	ARTICLE	IF	CITATIONS
9763	Identification of Potential Plk1 Targets in a Cell-Cycle Specific Proteome through Structural Dynamics of Kinase and Polo Box-Mediated Interactions. PLoS ONE, 2013, 8, e70843.	1.1	20
9764	Transcription Factor TFAP2C Regulates Major Programs Required for Murine Fetal Germ Cell Maintenance and Haploinsufficiency Predisposes to Teratomas in Male Mice. PLoS ONE, 2013, 8, e71113.	1.1	41
9765	Genome-Wide Survey and Comparative Analysis of LTR Retrotransposons and Their Captured Genes in Rice and Sorghum. PLoS ONE, 2013, 8, e71118.	1.1	33
9766	Identification and Characterization of Long Non-Coding RNAs Related to Mouse Embryonic Brain Development from Available Transcriptomic Data. PLoS ONE, 2013, 8, e71152.	1.1	55
9767	Prioritizing Disease Candidate Proteins in Cardiomyopathy-Specific Protein-Protein Interaction Networks Based on <i>GWAS</i> by Association Analysis. PLoS ONE, 2013, 8, e71191.	1.1	14
9768	Network Topology Reveals Key Cardiovascular Disease Genes. PLoS ONE, 2013, 8, e71537.	1.1	44
9769	Molecular Phenotypes in Triple Negative Breast Cancer from African American Patients Suggest Targets for Therapy. PLoS ONE, 2013, 8, e71915.	1.1	67
9770	Association Signals Unveiled by a Comprehensive Gene Set Enrichment Analysis of Dental Caries Genome-Wide Association Studies. PLoS ONE, 2013, 8, e72653.	1.1	15
9771	A Minimal Set of Tissue-Specific Hypomethylated CpGs Constitute Epigenetic Signatures of Developmental Programming. PLoS ONE, 2013, 8, e72670.	1.1	18
9772	Learning to Recognize Phenotype Candidates in the Auto-Immune Literature Using SVM Re-Ranking. PLoS ONE, 2013, 8, e72965.	1.1	10
9773	Genome Wide Transcriptome Analysis of Dendritic Cells Identifies Genes with Altered Expression in Psoriasis. PLoS ONE, 2013, 8, e73435.	1.1	9
9774	Adhesion to Carbon Nanotube Conductive Scaffolds Forces Action-Potential Appearance in Immature Rat Spinal Neurons. PLoS ONE, 2013, 8, e73621.	1.1	53
9775	Identification of Genes Involved in Wild Crucifer <i>Rorippa indica</i> Resistance Response on Mustard Aphid <i>Lipaphis erysimi</i> Challenge. PLoS ONE, 2013, 8, e73632.	1.1	21
9776	Metagenomic Profiling Reveals Lignocellulose Degrading System in a Microbial Community Associated with a Wood-Feeding Beetle. PLoS ONE, 2013, 8, e73827.	1.1	125
9777	Genome-Wide Discovery and Information Resource Development of DNA Polymorphisms in Cassava. PLoS ONE, 2013, 8, e74056.	1.1	12
9778	Alterations in Energy Metabolism, Neuroprotection and Visual Signal Transduction in the Retina of Parkinsonian, MPTP-Treated Monkeys. PLoS ONE, 2013, 8, e74439.	1.1	30
9779	Analysis of Nonlinear Gene Expression Progression Reveals Extensive Pathway and Age-Specific Transitions in Aging Human Brains. PLoS ONE, 2013, 8, e74578.	1.1	2
9780	Microarray Analyses and Comparisons of Upper or Lower Flanks of Rice Shoot Base Preceding Gravitropic Bending. PLoS ONE, 2013, 8, e74646.	1.1	16

#	ARTICLE	IF	CITATIONS
9781	The Genome-Wide Early Temporal Response of <i>Saccharomyces cerevisiae</i> to Oxidative Stress Induced by Cumene Hydroperoxide. PLoS ONE, 2013, 8, e74939.	1.1	29
9782	Comparative Genomics Reveals Insight into Virulence Strategies of Plant Pathogenic Oomycetes. PLoS ONE, 2013, 8, e75072.	1.1	164
9783	Evaluation and Cross-Comparison of Lexical Entities of Biological Interest (LexEBI). PLoS ONE, 2013, 8, e75185.	1.1	9
9784	Analysis of the Host Transcriptome from Demyelinating Spinal Cord of Murine Coronavirus-Infected Mice. PLoS ONE, 2013, 8, e75346.	1.1	34
9785	Automatic Identification of Highly Conserved Family Regions and Relationships in Genome Wide Datasets Including Remote Protein Sequences. PLoS ONE, 2013, 8, e75458.	1.1	7
9786	Measuring the Evolution of Ontology Complexity: The Gene Ontology Case Study. PLoS ONE, 2013, 8, e75993.	1.1	9
9787	Going the Distance for Protein Function Prediction: A New Distance Metric for Protein Interaction Networks. PLoS ONE, 2013, 8, e76339.	1.1	94
9788	GRAPES: A Software for Parallel Searching on Biological Graphs Targeting Multi-Core Architectures. PLoS ONE, 2013, 8, e76911.	1.1	33
9789	Comparative Proteomic Analysis of the Hepatic Response to Heat Stress in Muscovy and Pekin Ducks: Insight into Thermal Tolerance Related to Energy Metabolism. PLoS ONE, 2013, 8, e76917.	1.1	37
9790	A DNA-Based Semantic Fusion Model for Remote Sensing Data. PLoS ONE, 2013, 8, e77090.	1.1	2
9791	Non-Specific dsRNA-Mediated Antiviral Response in the Honey Bee. PLoS ONE, 2013, 8, e77263.	1.1	115
9792	Using a Search Engine-Based Mutually Reinforcing Approach to Assess the Semantic Relatedness of Biomedical Terms. PLoS ONE, 2013, 8, e77868.	1.1	2
9793	Integrative Pathway-Based Approach for Genome-Wide Association Studies: Identification of New Pathways for Rheumatoid Arthritis and Type 1 Diabetes. PLoS ONE, 2013, 8, e78577.	1.1	9
9794	Profiling of Parkin-Binding Partners Using Tandem Affinity Purification. PLoS ONE, 2013, 8, e78648.	1.1	38
9795	Functional Networking of Human Divergently Paired Genes (DPGs). PLoS ONE, 2013, 8, e78896.	1.1	3
9796	A Comparison of Gene Set Analysis Methods in Terms of Sensitivity, Prioritization and Specificity. PLoS ONE, 2013, 8, e79217.	1.1	164
9797	An Algorithm for Network-Based Gene Prioritization That Encodes Knowledge Both in Nodes and in Links. PLoS ONE, 2013, 8, e79564.	1.1	9
9798	Insight into the Genetic Components of Community Genetics: QTL Mapping of Insect Association in a Fast-Growing Forest Tree. PLoS ONE, 2013, 8, e79925.	1.1	18

#	ARTICLE	IF	CITATIONS
9799	De Novo Assembly, Gene Annotation, and Marker Discovery in Stored-Product Pest <i>Liposcelis entomophila</i> (Enderlein) Using Transcriptome Sequences. <i>PLoS ONE</i> , 2013, 8, e80046.	1.1	38
9800	Functional Categorization of Transcriptome in the Species <i>Symphysodon aequifasciatus</i> Pellegrin 1904 (Perciformes: Cichlidae) Exposed to Benzo[a]pyrene and Phenanthrene. <i>PLoS ONE</i> , 2013, 8, e81083.	1.1	10
9801	De novo Assembly and Characterization of the Global Transcriptome for <i>Rhyacionia leptotubula</i> Using Illumina Paired-End Sequencing. <i>PLoS ONE</i> , 2013, 8, e81096.	1.1	13
9802	Profiling mRNAs of Two <i>Cuscuta</i> Species Reveals Possible Candidate Transcripts Shared by Parasitic Plants. <i>PLoS ONE</i> , 2013, 8, e81389.	1.1	22
9803	Caste-Specific Expression Patterns of Immune Response and Chemosensory Related Genes in the Leaf-Cutting Ant, <i>Atta vollenweideri</i> . <i>PLoS ONE</i> , 2013, 8, e81518.	1.1	30
9804	Floral Transcriptome Sequencing for SSR Marker Development and Linkage Map Construction in the Tea Plant (<i>Camellia sinensis</i>). <i>PLoS ONE</i> , 2013, 8, e81611.	1.1	80
9805	De novo Sequencing, Characterization, and Comparison of Inflorescence Transcriptomes of <i>Cornus canadensis</i> and <i>C. florida</i> (Cornaceae). <i>PLoS ONE</i> , 2013, 8, e82674.	1.1	12
9806	Identification and Functional Analysis of Flowering Related microRNAs in Common Wild Rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overbo	1.1	31
9807	Long-Term Effects of Subacute Ruminal Acidosis (SARA) on Milk Quality and Hepatic Gene Expression in Lactating Goats Fed a High-Concentrate Diet. <i>PLoS ONE</i> , 2013, 8, e82850.	1.1	67
9808	Partitioning the Human Transcriptome Using HKera, a Novel Classifier of Housekeeping and Tissue-Specific Genes. <i>PLoS ONE</i> , 2013, 8, e83040.	1.1	3
9809	Protein Complex Identification by Integrating Protein-Protein Interaction Evidence from Multiple Sources. <i>PLoS ONE</i> , 2013, 8, e83841.	1.1	11
9810	Transcriptomic Analysis of Brown Adipose Tissue across the Physiological Extremes of Natural Hibernation. <i>PLoS ONE</i> , 2013, 8, e85157.	1.1	69
9811	RNA-Seq Differentiates Tumour and Host mRNA Expression Changes Induced by Treatment of Human Tumour Xenografts with the VEGFR Tyrosine Kinase Inhibitor Cediranib. <i>PLoS ONE</i> , 2013, 8, e66003.	1.1	29
9812	Distinct MicroRNAs Expression Profile in Primary Biliary Cirrhosis and Evaluation of miR 505-3p and miR197-3p as Novel Biomarkers. <i>PLoS ONE</i> , 2013, 8, e66086.	1.1	77
9813	Infection with a Virulent Strain of <i>Wolbachia</i> Disrupts Genome Wide-Patterns of Cytosine Methylation in the Mosquito <i>Aedes aegypti</i> . <i>PLoS ONE</i> , 2013, 8, e66482.	1.1	57
9814	Improving the Measurement of Semantic Similarity between Gene Ontology Terms and Gene Products: Insights from an Edge- and IC-Based Hybrid Method. <i>PLoS ONE</i> , 2013, 8, e66745.	1.1	61
9815	Accelerating the Original Profile Kernel. <i>PLoS ONE</i> , 2013, 8, e68459.	1.1	11
9816	Effective use of latent semantic indexing and computational linguistics in biological and biomedical applications. <i>Frontiers in Physiology</i> , 2013, 4, 8.	1.3	32

#	ARTICLE	IF	CITATIONS
9817	From Protein-Protein Interactions to Rational Drug Design: Are Computational Methods Up to the Challenge?. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 602-618.	1.0	23
9818	Inferring Quantitative Trait Pathways Associated with Bull Fertility from a Genome-Wide Association Study. <i>Frontiers in Genetics</i> , 2012, 3, 307.	1.1	45
9819	Use of the Protein Ontology for Multi-Faceted Analysis of Biological Processes: A Case Study of the Spindle Checkpoint. <i>Frontiers in Genetics</i> , 2013, 4, 62.	1.1	7
9820	Annotation extension through protein family annotation coherence metrics. <i>Frontiers in Genetics</i> , 2013, 4, 201.	1.1	5
9821	Small RNA sequencing-microarray analyses in Parkinson leukocytes reveal deep brain stimulation-induced splicing changes that classify brain region transcriptomes. <i>Frontiers in Molecular Neuroscience</i> , 2013, 6, 10.	1.4	114
9822	Changes in RNA Splicing in Developing Soybean (<i>Glycine max</i>) Embryos. <i>Biology</i> , 2013, 2, 1311-1337.	1.3	18
9823	Portraying the Expression Landscapes of B-CellLymphoma-Intuitive Detection of Outlier Samples and of Molecular Subtypes. <i>Biology</i> , 2013, 2, 1411-1437.	1.3	17
9824	A Robust Hybrid Approach Based on Estimation of Distribution Algorithm and Support Vector Machine for Hunting Candidate Disease Genes. <i>Scientific World Journal, The</i> , 2013, 2013, 1-7.	0.8	5
9825	Molecular Signatures in <i>Arabidopsis thaliana</i> in Response to Insect Attack and Bacterial Infection. <i>PLoS ONE</i> , 2013, 8, e58987.	1.1	67
9826	HomoKinase: A Curated Database of Human Protein Kinases. <i>ISRN Computational Biology</i> , 2013, 2013, 1-5.	0.3	18
9827	Comparative Analysis of Proteomes and Functionomes Provides Insights into Origins of Cellular Diversification. <i>Archaea</i> , 2013, 2013, 1-13.	2.3	17
9828	From Ontology to Semantic Similarity: Calculation of Ontology-Based Semantic Similarity. <i>Scientific World Journal, The</i> , 2013, 2013, 1-11.	0.8	70
9829	Bioinformatics analysis of the gene expression profile in Bladder carcinoma. <i>Genetics and Molecular Biology</i> , 2013, 36, 287-291.	0.6	7
9831	PathAct: a novel method for pathway analysis using gene expression profiles. <i>Bioinformation</i> , 2013, 9, 394-400.	0.2	5
9832	Virus-ECC-mPLOC: A Multi-Label Predictor for Predicting the Subcellular Localization of Virus Proteins with Both Single and Multiple Sites Based on a General Form of Chou's Pseudo Amino Acid Composition. <i>Protein and Peptide Letters</i> , 2013, 20, 309-317.	0.4	36
9833	Peptidase V. , 2013, , 1586-1592.		0
9834	Comparison between Pearson Correlation Coefficient and Mutual Information as a Similarity Measure of Gene Expression Profiles. <i>Japanese Journal of Biometrics</i> , 2013, 33, 125-143.	0.0	7
9835	Using the relation ontology Metarel for modelling Linked Data as multi-digraphs. <i>Semantic Web</i> , 2014, 5, 115-126.	1.1	3

#	ARTICLE	IF	CITATIONS
9836	Comparison of Potato and Asian Citrus Psyllid Adult and Nymph Transcriptomes Identified Vector Transcripts with Potential Involvement in Circulative, Propagative Liberibacter Transmission. <i>Pathogens</i> , 2014, 3, 875-907.	1.2	37
9837	Genome-Wide Analysis of miRNA Signature in the APP ^{swe} /PS1 ^{E9} Mouse Model of Alzheimer's Disease. <i>PLoS ONE</i> , 2014, 9, e101725.	1.1	23
9838	Microarray Profiling and Co-Expression Network Analysis of Circulating lncRNAs and mRNAs Associated with Major Depressive Disorder. <i>PLoS ONE</i> , 2014, 9, e93388.	1.1	103
9839	Whole Genome and Global Gene Expression Analyses of the Model Mushroom <i>Flammulina velutipes</i> Reveal a High Capacity for Lignocellulose Degradation. <i>PLoS ONE</i> , 2014, 9, e93560.	1.1	107
9840	Investigation of Key Genes associated with Prostate Cancer using RNA-Seq Data. <i>International Journal of Biological Markers</i> , 2014, 29, e86-e92.	0.7	1
9841	BiNA: A Visual Analytics Tool for Biological Network Data. <i>PLoS ONE</i> , 2014, 9, e87397.	1.1	31
9842	Functional Annotation of Rheumatoid Arthritis and Osteoarthritis Associated Genes by Integrative Genome-Wide Gene Expression Profiling Analysis. <i>PLoS ONE</i> , 2014, 9, e85784.	1.1	25
9843	Functional Module Connectivity Map (FMCM): A Framework for Searching Repurposed Drug Compounds for Systems Treatment of Cancer and an Application to Colorectal Adenocarcinoma. <i>PLoS ONE</i> , 2014, 9, e86299.	1.1	34
9844	Genome and Transcriptome Analysis of the Basidiomycetous Yeast <i>Pseudozyma antarctica</i> Producing Extracellular Glycolipids, Mannosylerythritol Lipids. <i>PLoS ONE</i> , 2014, 9, e86490.	1.1	45
9845	Transcriptomic Meta-Analysis of Multiple Sclerosis and Its Experimental Models. <i>PLoS ONE</i> , 2014, 9, e86643.	1.1	27
9846	Link Community Detection Using Generative Model and Nonnegative Matrix Factorization. <i>PLoS ONE</i> , 2014, 9, e86899.	1.1	26
9847	The Role of Viral and Host MicroRNAs in the Aujeszky's Disease Virus during the Infection Process. <i>PLoS ONE</i> , 2014, 9, e86965.	1.1	21
9848	Transcriptomic Analysis of Flower Development in Wintersweet (<i>Chimonanthus praecox</i>). <i>PLoS ONE</i> , 2014, 9, e86976.	1.1	40
9849	Expression of Signaling Components in Embryonic Eyelid Epithelium. <i>PLoS ONE</i> , 2014, 9, e87038.	1.1	5
9850	Differential Induction of TLR3-Dependent Innate Immune Signaling by Closely Related Parasite Species. <i>PLoS ONE</i> , 2014, 9, e88398.	1.1	57
9851	RNA-Seq Analysis of Transcriptome and Glucosinolate Metabolism in Seeds and Sprouts of Broccoli (<i>Brassica oleracea</i> var. <i>italica</i>). <i>PLoS ONE</i> , 2014, 9, e88804.	1.1	63
9852	A Vanillin Derivative Causes Mitochondrial Dysfunction and Triggers Oxidative Stress in <i>Cryptococcus neoformans</i> . <i>PLoS ONE</i> , 2014, 9, e89122.	1.1	42
9853	Meta-Analysis of Pathway Enrichment: Combining Independent and Dependent Omics Data Sets. <i>PLoS ONE</i> , 2014, 9, e89297.	1.1	44

#	ARTICLE	IF	CITATIONS
9854	Revealing Missing Parts of the Interactome via Link Prediction. PLoS ONE, 2014, 9, e90073.	1.1	42
9855	Functional Abstraction as a Method to Discover Knowledge in Gene Ontologies. PLoS ONE, 2014, 9, e90191.	1.1	19
9856	Long Non-Coding RNA Expression Profiles in Hereditary Haemorrhagic Telangiectasia. PLoS ONE, 2014, 9, e90272.	1.1	21
9857	Hierarchical Partitioning of Metazoan Protein Conservation Profiles Provides New Functional Insights. PLoS ONE, 2014, 9, e90282.	1.1	1
9858	Biclustering Methods: Biological Relevance and Application in Gene Expression Analysis. PLoS ONE, 2014, 9, e90801.	1.1	72
9859	A Systematic In Silico Mining of the Mechanistic Implications and Therapeutic Potentials of Estrogen Receptor (ER)- α in Breast Cancer. PLoS ONE, 2014, 9, e91894.	1.1	5
9860	Cancer-Risk Module Identification and Module-Based Disease Risk Evaluation: A Case Study on Lung Cancer. PLoS ONE, 2014, 9, e92395.	1.1	7
9861	Micro-Environment Causes Reversible Changes in DNA Methylation and mRNA Expression Profiles in Patient-Derived Glioma Stem Cells. PLoS ONE, 2014, 9, e94045.	1.1	33
9862	Alteration of Protein Levels during Influenza Virus H1N1 Infection in Host Cells: A Proteomic Survey of Host and Virus Reveals Differential Dynamics. PLoS ONE, 2014, 9, e94257.	1.1	38
9863	The Immune Strategy and Stress Response of the Mediterranean Species of the Bemisia tabaci Complex to an Orally Delivered Bacterial Pathogen. PLoS ONE, 2014, 9, e94477.	1.1	24
9864	Prediction and Experimental Characterization of nsSNPs Altering Human PDZ-Binding Motifs. PLoS ONE, 2014, 9, e94507.	1.1	10
9865	Identification of Logic Relationships between Genes and Subtypes of Non-Small Cell Lung Cancer. PLoS ONE, 2014, 9, e94644.	1.1	9
9866	Characterization of Withania somnifera Leaf Transcriptome and Expression Analysis of Pathogenesis Related Genes during Salicylic Acid Signaling. PLoS ONE, 2014, 9, e94803.	1.1	26
9867	Unraveling Patterns of Site-to-Site Synonymous Rates Variation and Associated Gene Properties of Protein Domains and Families. PLoS ONE, 2014, 9, e95034.	1.1	17
9868	Transcriptional Changes in Canine Distemper Virus-Induced Demyelinating Leukoencephalitis Favor a Biphasic Mode of Demyelination. PLoS ONE, 2014, 9, e95917.	1.1	26
9869	An Integrated Map of HIV-Human Protein Complexes that Facilitate Viral Infection. PLoS ONE, 2014, 9, e96687.	1.1	13
9870	Predicting DNA-Binding Proteins and Binding Residues by Complex Structure Prediction and Application to Human Proteome. PLoS ONE, 2014, 9, e96694.	1.1	32
9871	Ovary Transcriptome Profiling via Artificial Intelligence Reveals a Transcriptomic Fingerprint Predicting Egg Quality in Striped Bass, Morone saxatilis. PLoS ONE, 2014, 9, e96818.	1.1	73

#	ARTICLE	IF	CITATIONS
9872	Protein-Protein Interface Detection Using the Energy Centrality Relationship (ECR) Characteristic of Proteins. PLoS ONE, 2014, 9, e97115.	1.1	2
9873	Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. PLoS ONE, 2014, 9, e98076.	1.1	128
9874	The Reference Transcriptome of the Adult Female Biting Midge (<i>Culicoides sonorensis</i>) and Differential Gene Expression Profiling during Teneral, Blood, and Sucrose Feeding Conditions. PLoS ONE, 2014, 9, e98123.	1.1	20
9875	Integrated Pathway Clusters with Coherent Biological Themes for Target Prioritisation. PLoS ONE, 2014, 9, e99030.	1.1	38
9876	SemFunSim: A New Method for Measuring Disease Similarity by Integrating Semantic and Gene Functional Association. PLoS ONE, 2014, 9, e99415.	1.1	117
9877	Responses of the Insulin Signaling Pathways in the Brown Adipose Tissue of Rats following Cold Exposure. PLoS ONE, 2014, 9, e99772.	1.1	32
9878	dbCerEx: A Web-Based Database for the Analysis of Cervical Cancer Transcriptomes. PLoS ONE, 2014, 9, e99834.	1.1	2
9879	Fed State Prior to Hemorrhagic Shock and Polytrauma in a Porcine Model Results in Altered Liver Transcriptomic Response. PLoS ONE, 2014, 9, e100088.	1.1	14
9880	IIS – Integrated Interactome System: A Web-Based Platform for the Annotation, Analysis and Visualization of Protein-Metabolite-Gene-Drug Interactions by Integrating a Variety of Data Sources and Tools. PLoS ONE, 2014, 9, e100385.	1.1	58
9881	Proteomics Analysis of the Non-Muscle Myosin Heavy Chain IIA-Enriched Actin-Myosin Complex Reveals Multiple Functions within the Podocyte. PLoS ONE, 2014, 9, e100660.	1.1	14
9882	Toxin Diversity Revealed by a Transcriptomic Study of <i>Ornithoctonus huwena</i> . PLoS ONE, 2014, 9, e100682.	1.1	15
9883	Novel Insights into the Regulatory Architecture of CD4+ T Cells in Rheumatoid Arthritis. PLoS ONE, 2014, 9, e100690.	1.1	22
9884	OMIT: Dynamic, Semi-Automated Ontology Development for the microRNA Domain. PLoS ONE, 2014, 9, e100855.	1.1	18
9885	Differentially Expressed Plasma MicroRNAs and the Potential Regulatory Function of Let-7b in Chronic Thromboembolic Pulmonary Hypertension. PLoS ONE, 2014, 9, e101055.	1.1	50
9886	Characterization of Transcriptional Complexity during Adipose Tissue Development in Bovines of Different Ages and Sexes. PLoS ONE, 2014, 9, e101261.	1.1	32
9887	Fumaric Acid Esters Can Block Pro-Inflammatory Actions of Human CRP and Ameliorate Metabolic Disturbances in Transgenic Spontaneously Hypertensive Rats. PLoS ONE, 2014, 9, e101906.	1.1	22
9888	Discovery and Comparative Profiling of microRNAs in Representative Monopodial Bamboo (<i>Phyllostachys edulis</i>) and Sympodial Bamboo (<i>Dendrocalamus latiflorus</i>). PLoS ONE, 2014, 9, e102375.	1.1	11
9889	Fast and Sensitive Alignment of Microbial Whole Genome Sequencing Reads to Large Sequence Datasets on a Desktop PC: Application to Metagenomic Datasets and Pathogen Identification. PLoS ONE, 2014, 9, e103441.	1.1	9

#	ARTICLE	IF	CITATIONS
9890	Genome-Wide Association Studies Identify the Loci for 5 Exterior Traits in a Large White \times Minzhu Pig Population. PLoS ONE, 2014, 9, e103766.	1.1	32
9891	Phosphorylation Site Dynamics of Early T-cell Receptor Signaling. PLoS ONE, 2014, 9, e104240.	1.1	54
9892	A Set of Structural Features Defines the Cis-Regulatory Modules of Antenna-Expressed Genes in <i>Drosophila melanogaster</i> . PLoS ONE, 2014, 9, e104342.	1.1	2
9893	Grouping Annotations on the Subcellular Layered Interactome Demonstrates Enhanced Autophagy Activity in a Recurrent Experimental Autoimmune Uveitis T Cell Line. PLoS ONE, 2014, 9, e104404.	1.1	5
9894	Evaluating the Good Ontology Design Guideline (GoodOD) with the Ontology Quality Requirements and Evaluation Method and Metrics (OQuARE). PLoS ONE, 2014, 9, e104463.	1.1	25
9895	SNP Identification by Transcriptome Sequencing and Candidate Gene-Based Association Analysis for Heat Tolerance in the Bay Scallop <i>Argopecten irradians</i> . PLoS ONE, 2014, 9, e104960.	1.1	20
9896	A Class-Information-Based Penalized Matrix Decomposition for Identifying Plants Core Genes Responding to Abiotic Stresses. PLoS ONE, 2014, 9, e106097.	1.1	11
9897	Discovering Study-Specific Gene Regulatory Networks. PLoS ONE, 2014, 9, e106524.	1.1	8
9898	Full-Length Enriched cDNA Libraries and ORFeome Analysis of Sugarcane Hybrid and Ancestor Genotypes. PLoS ONE, 2014, 9, e107351.	1.1	26
9899	Angiogenesis Interactome and Time Course Microarray Data Reveal the Distinct Activation Patterns in Endothelial Cells. PLoS ONE, 2014, 9, e110871.	1.1	17
9900	Transcriptional Network Analysis Reveals that AT1 and AT2 Angiotensin II Receptors Are Both Involved in the Regulation of Genes Essential for Glioma Progression. PLoS ONE, 2014, 9, e110934.	1.1	13
9901	Comparative Transcriptome Analysis of Two Oysters, <i>Crassostrea gigas</i> and <i>Crassostrea hongkongensis</i> Provides Insights into Adaptation to Hypo-Osmotic Conditions. PLoS ONE, 2014, 9, e111915.	1.1	46
9902	The Genome of the Generalist Plant Pathogen <i>Fusarium avenaceum</i> Is Enriched with Genes Involved in Redox, Signaling and Secondary Metabolism. PLoS ONE, 2014, 9, e112703.	1.1	78
9903	Community Structure Detection for Overlapping Modules through Mathematical Programming in Protein Interaction Networks. PLoS ONE, 2014, 9, e112821.	1.1	18
9904	RNA-Seq Reveals Leaf Cuticular Wax-Related Genes in Welsh Onion. PLoS ONE, 2014, 9, e113290.	1.1	24
9905	Roles of Intragenic and Intergenic L1s in Mouse and Human. PLoS ONE, 2014, 9, e113434.	1.1	12
9906	De novo Sequencing, Assembly and Characterization of Antennal Transcriptome of <i>Anomala corpulenta</i> Motschulsky (Coleoptera: Rutelidae). PLoS ONE, 2014, 9, e114238.	1.1	22
9907	Transcriptional Profiling of Adult Neural Stem-Like Cells from the Human Brain. PLoS ONE, 2014, 9, e114739.	1.1	15

#	ARTICLE	IF	CITATIONS
9908	The Human Pancreas Proteome Defined by Transcriptomics and Antibody-Based Profiling. PLoS ONE, 2014, 9, e115421.	1.1	35
9909	Div-BLAST: Diversification of Sequence Search Results. PLoS ONE, 2014, 9, e115445.	1.1	1
9910	The Application of the Open Pharmacological Concepts Triple Store (Open PHACTS) to Support Drug Discovery Research. PLoS ONE, 2014, 9, e115460.	1.1	31
9911	The Kidney Transcriptome and Proteome Defined by Transcriptomics and Antibody-Based Profiling. PLoS ONE, 2014, 9, e116125.	1.1	49
9912	Using neuron specific RNAi in Drosophila for understanding the molecular and neuronal basis of behavior. , 0, , 202-216.		2
9913	Mining 3D Patterns from Gene Expression Temporal Data: A New Tricuster Evaluation Measure. Scientific World Journal, The, 2014, 2014, 1-16.	0.8	15
9914	RRHGE: A Novel Approach to Classify the Estrogen Receptor Based Breast Cancer Subtypes. Scientific World Journal, The, 2014, 2014, 1-13.	0.8	3
9915	Breast Cancer Prognosis Risk Estimation Using Integrated Gene Expression and Clinical Data. BioMed Research International, 2014, 2014, 1-15.	0.9	5
9916	Archaea: The First Domain of Diversified Life. Archaea, 2014, 2014, 1-26.	2.3	27
9917	Gene Expression Profile Analysis in Epilepsy by Using the Partial Least Squares Method. Scientific World Journal, The, 2014, 2014, 1-5.	0.8	5
9918	Ratsnake: A Versatile Image Annotation Tool with Application to Computer-Aided Diagnosis. Scientific World Journal, The, 2014, 2014, 1-12.	0.8	41
9919	A Phylogenomic Census of Molecular Functions Identifies Modern Thermophilic Archaea as the Most Ancient Form of Cellular Life. Archaea, 2014, 2014, 1-15.	2.3	21
9920	Health Information Technology in Oncology Practice: A Literature Review. Cancer Informatics, 2014, 13, CIN.S12417.	0.9	15
9921	A Novel Method for Functional Annotation Prediction Based on Combination of Classification Methods. Scientific World Journal, The, 2014, 2014, 1-9.	0.8	0
9922	Differential Evolutionary Constraints in the Evolution of Chemoreceptors: A Murine and Human Case Study. Scientific World Journal, The, 2014, 2014, 1-9.	0.8	3
9923	Transcriptome Analysis of Self- and Cross-pollinated Pistils of Japanese Apricot (<i>Prunus mume</i> Sieb. et Tj ETQq1 1 0,784314 rgBT /Over	0.8	14
9924	Impact of Amorphous SiO ₂ Nanoparticles on a Living Organism: Morphological, Behavioral, and Molecular Biology Implications. Frontiers in Bioengineering and Biotechnology, 2014, 2, 37.	2.0	43
9925	Improving Collaboration by Standardization Efforts in Systems Biology. Frontiers in Bioengineering and Biotechnology, 2014, 2, 61.	2.0	52

#	ARTICLE	IF	CITATIONS
9926	Myeloid decidual dendritic cells and immunoregulation of pregnancy: defective responsiveness to <i>Coxiella burnetii</i> and <i>Brucella abortus</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2014, 4, 179.	1.8	17
9927	Neighbor Preferences of Amino Acids and Context-Dependent Effects of Amino Acid Substitutions in Human, Mouse, and Dog. <i>International Journal of Molecular Sciences</i> , 2014, 15, 15963-15980.	1.8	4
9928	Multi-omic network signatures of disease. <i>Frontiers in Genetics</i> , 2014, 4, 309.	1.1	21
9929	The gene regulatory network for breast cancer: integrated regulatory landscape of cancer hallmarks. <i>Frontiers in Genetics</i> , 2014, 5, 15.	1.1	74
9930	Editorial: biological ontologies and semantic biology. <i>Frontiers in Genetics</i> , 2014, 5, 18.	1.1	5
9931	Interactive exploration of integrated biological datasets using context-sensitive workflows. <i>Frontiers in Genetics</i> , 2014, 5, 21.	1.1	4
9932	categoryCompare, an analytical tool based on feature annotations. <i>Frontiers in Genetics</i> , 2014, 5, 98.	1.1	29
9933	Analysis pipeline for the epistasis search – statistical versus biological filtering. <i>Frontiers in Genetics</i> , 2014, 5, 106.	1.1	57
9934	Mining a database of single amplified genomes from Red Sea brine pool extremophiles – improving reliability of gene function prediction using a profile and pattern matching algorithm (PPMA). <i>Frontiers in Microbiology</i> , 2014, 5, 134.	1.5	15
9935	Deciphering the Molecular Profile of Plaques, Memory Decline and Neuron Loss in Two Mouse Models for Alzheimer’s Disease by Deep Sequencing. <i>Frontiers in Aging Neuroscience</i> , 2014, 6, 75.	1.7	78
9936	Interdisciplinary perspectives on the development, integration, and application of cognitive ontologies. <i>Frontiers in Neuroinformatics</i> , 2014, 8, 62.	1.3	51
9937	The hermit crab's nose – antennal transcriptomics. <i>Frontiers in Neuroscience</i> , 2013, 7, 266.	1.4	26
9939	POEAS: Automated Plant Phenomic Analysis Using Plant Ontology. <i>Bioinformatics and Biology Insights</i> , 2014, 8, BBI.S19057.	1.0	6
9940	High-Throughput Sequencing and De Novo Assembly of <i>Brassica oleracea</i> var. <i>Capitata</i> L. for Transcriptome Analysis. <i>PLoS ONE</i> , 2014, 9, e92087.	1.1	38
9941	Custom Microarray Analysis for Transcript Profiling of Dormant Vegetative Buds of Japanese Apricot during Prolonged Chilling Exposure. <i>Japanese Society for Horticultural Science</i> , 2014, 83, 1-16.	0.8	16
9942	Analysis of intervertebral disc-related genes. <i>Genetics and Molecular Research</i> , 2014, 13, 2032-2038.	0.3	3
9943	Modelos cognitivos del desarrollo de las funciones ejecutivas. Limitaciones metodológicas y desafíos teóricos. <i>Anales De Psicología</i> , 2014, 30, .	0.3	3
9944	Transcriptomics of the human endometrium. <i>International Journal of Developmental Biology</i> , 2014, 58, 127-137.	0.3	52

#	ARTICLE	IF	CITATIONS
9945	Sequence Features and Subset Selection Technique for the Prediction of Protein Trafficking Phenomenon in Eukaryotic Non Membrane Proteins. International Journal of Biomedical Data Mining, 2014, 03, .	0.1	0
9946	Proteomics-Based Identification of Differentially Abundant Proteins from Human Keratinocytes Exposed to Arsenic Trioxide. Journal of Proteomics and Bioinformatics, 2014, 07, 166-178.	0.4	17
9947	Identification of genes in HepG2 cells that respond to DNA methylation and histone deacetylation inhibitor treatment. Experimental and Therapeutic Medicine, 2014, 8, 813-817.	0.8	3
9948	Dictionary and Gene Ontology Based Similarity for Named Entity Relationship Protein-protein Interaction Prediction from Biotext Corpus. Research Journal of Applied Sciences, Engineering and Technology, 2014, 8, 2282-2289.	0.1	0
9949	Expression analysis of miRNA and target mRNAs in esophageal cancer. Brazilian Journal of Medical and Biological Research, 2014, 47, 811-817.	0.7	22
9950	Plasma proteomic changes during hypothermic and normothermic cardiopulmonary bypass in aortic surgeries. International Journal of Molecular Medicine, 2014, 34, 947-56.	1.8	9
9951	Serum-Induced Differentiation of Human Meibomian Gland Epithelial Cells. , 2014, 55, 3866.		50
9952	Semantically Linking in Silico Cancer Models. Cancer Informatics, 2014, 13s1, CIN.S13895.	0.9	9
9954	Domain-Based Approaches to Prediction and Analysis of Protein-Protein Interactions. International Journal of Knowledge Discovery in Bioinformatics, 2014, 4, 24-41.	0.8	2
9955	Symbolic Biomedical Knowledge. , 2014, , 179-341.		0
9956	Translational research combining orthologous genes and human diseases with the OGOLOD dataset. Semantic Web, 2014, 5, 145-149.	1.1	5
9957	IDENTIFYING MUTATION SPECIFIC CANCER PATHWAYS USING A STRUCTURALLY RESOLVED PROTEIN INTERACTION NETWORK. , 2014, , .		3
9958	Text Mining. , 2014, , 51-66.		3
9961	Structure Based Functional Annotation of Putative Conserved Proteins from Treponema pallidum: Search for a Potential Drug Target. Letters in Drug Design and Discovery, 2014, 12, 46-59.	0.4	13
9962	Data Management Challenges in Paediatric Information Systems. , 2014, , 211-232.		0
9964	Deep autoencoder neural networks for gene ontology annotation predictions. , 2014, , .		105
9965	Defining the human gallbladder proteome by transcriptomics and affinity proteomics. Proteomics, 2014, 14, 2498-2507.	1.3	19
9966	Neanderthal Introgression at Chromosome 3p21.31 Was Under Positive Natural Selection in East Asians. Molecular Biology and Evolution, 2014, 31, 683-695.	3.5	63

#	ARTICLE	IF	CITATIONS
9967	Dissection of thousands of cell type-specific enhancers identifies dinucleotide repeat motifs as general enhancer features. <i>Genome Research</i> , 2014, 24, 1147-1156.	2.4	129
9968	PBNA: An improved probabilistic biological network alignment method. <i>Tsinghua Science and Technology</i> , 2014, 19, 658-667.	4.1	0
9969	The NHGRI GWAS Catalog, a curated resource of SNP-trait associations. <i>Nucleic Acids Research</i> , 2014, 42, D1001-D1006.	6.5	2,608
9970	GENETIC MUTATIONS ARE CHARACTERIZED BY INCREASE IN ENTROPY AT THE TRANSCRIPTIONAL LEVEL. <i>Journal of Biological Systems</i> , 2014, 22, 377-391.	0.5	2
9971	The Conditional-Potts Clustering Model. <i>Journal of Computational and Graphical Statistics</i> , 2014, 23, 717-739.	0.9	9
9972	Temporal separation of replication and transcription during S-phase progression. <i>Cell Cycle</i> , 2014, 13, 3241-3248.	1.3	39
9973	Altered Retinal MicroRNA Expression Profiles in Early Diabetic Retinopathy: An <i>In Silico</i> Analysis. <i>Current Eye Research</i> , 2014, 39, 720-729.	0.7	32
9974	Epstein-Barr virus encoded microRNA's target SUMO-regulated cellular functions. <i>FEBS Journal</i> , 2014, 281, 4935-4950.	2.2	15
9975	Biological process annotation of proteins across the plant kingdom. <i>Current Plant Biology</i> , 2014, 1, 73-82.	2.3	7
9976	CpG island-mediated global gene regulatory modes in mouse embryonic stem cells. <i>Nature Communications</i> , 2014, 5, 5490.	5.8	26
9977	PREDICTION OF ESSENTIAL PROTEINS BASED ON EDGE CLUSTERING COEFFICIENT AND GENE ONTOLOGY INFORMATION. <i>Journal of Biological Systems</i> , 2014, 22, 339-351.	0.5	4
9978	Bone Signaling in Middle Ear Development: A Genome-Wide Differential Expression Analysis. <i>Anatomical Record</i> , 2014, 297, 2349-2355.	0.8	4
9979	Ensembl 2014. <i>Nucleic Acids Research</i> , 2014, 42, D749-D755.	6.5	1,211
9980	Genetic algorithm based detection of general linear biclusters. , 2014, , .		4
9981	ReSAPP: Predicting overlapping protein complexes by merging multiple-sampled partitions of proteins. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1442004.	0.3	5
9982	BEAMS: backbone extraction and merge strategy for the global many-to-many alignment of multiple PPI networks. <i>Bioinformatics</i> , 2014, 30, 531-539.	1.8	63
9983	Nemertean Toxin Genes Revealed through Transcriptome Sequencing. <i>Genome Biology and Evolution</i> , 2014, 6, 3314-3325.	1.1	22
9984	Fungal Genomics. <i>Advances in Botanical Research</i> , 2014, , 1-52.	0.5	25

#	ARTICLE	IF	CITATIONS
9986	The Membrane Proteome of Sensory Cilia to the Depth of Olfactory Receptors. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1828-1843.	2.5	45
9987	PIERO ontology for analysis of biochemical transformations: Effective implementation of reaction information in the IUBMB enzyme list. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1442001.	0.3	7
9988	Mouse model phenotypes provide information about human drug targets. <i>Bioinformatics</i> , 2014, 30, 719-725.	1.8	38
9989	miR-499 protects cardiomyocytes from H ₂ O ₂ -induced apoptosis via its effects on <i>Pdcd4</i> and <i>Pacs2</i> . <i>RNA Biology</i> , 2014, 11, 339-350.	1.5	103
9990	Combining bioinformatics and MS-based proteomics: clinical implications. <i>Expert Review of Proteomics</i> , 2014, 11, 269-284.	1.3	7
9991	ASeCS: Assistive Self-Care Software Architectures for Delivering Service in Care Homes. , 2014, , .		5
9992	Global gene expression profiling of <i>Homarus americanus</i> (Crustacea) larval stages during development and metamorphosis. <i>Invertebrate Reproduction and Development</i> , 2014, 58, 97-107.	0.3	11
9993	A Functional Cancer Genomics Screen Identifies a Druggable Synthetic Lethal Interaction between <i>MSH3</i> and <i>PRKDC</i> . <i>Cancer Discovery</i> , 2014, 4, 592-605.	7.7	60
9994	Pleiotropic Mutations Are Subject to Strong Stabilizing Selection. <i>Genetics</i> , 2014, 197, 1051-1062.	1.2	38
9995	Knowledge-driven genomic interactions: an application in ovarian cancer. <i>BioData Mining</i> , 2014, 7, 20.	2.2	21
9996	Identification of miRNAs involved in pear fruit development and quality. <i>BMC Genomics</i> , 2014, 15, 953.	1.2	102
9997	Transcriptional profiling of the spleen in progressive visceral leishmaniasis reveals mixed expression of type 1 and type 2 cytokine-responsive genes. <i>BMC Immunology</i> , 2014, 15, 38.	0.9	16
9998	<i>Pichia pastoris</i> Aft1 - a novel transcription factor, enhancing recombinant protein secretion. <i>Microbial Cell Factories</i> , 2014, 13, 120.	1.9	33
9999	A-WINGS: an integrated genome database for <i>Pleurocybella porrigens</i> (Angel's wing oyster mushroom,) Tj ETQq1.1 0.784314 rgB / 0.6 7		7
10000	PPDB – A tool for investigation of plants physiology based on gene ontology. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2014, 7, 295.	2.2	0
10001	The genome of <i>Eimeria falciformis</i> - reduction and specialization in a single host apicomplexan parasite. <i>BMC Genomics</i> , 2014, 15, 696.	1.2	44
10002	Anatomo-proteomic characterization of human basal ganglia: focus on striatum and globus pallidus. <i>Molecular Brain</i> , 2014, 7, 83.	1.3	9
10003	PROGeneV2: enhancements on the existing database. <i>BMC Cancer</i> , 2014, 14, 970.	1.1	417

#	ARTICLE	IF	CITATIONS
10004	De-novo assembly of mango fruit peel transcriptome reveals mechanisms of mango response to hot water treatment. BMC Genomics, 2014, 15, 957.	1.2	58
10005	Transcriptomic dissection of the rice <i>Burkholderia glumae</i> interaction. BMC Genomics, 2014, 15, 755.	1.2	21
10006	Predicting the Dynamics of Protein Abundance. Molecular and Cellular Proteomics, 2014, 13, 1330-1340.	2.5	21
10007	Analysis and integration of microarray data of Arabidopsis mutants. Canadian Journal of Plant Science, 2014, 94, 235-243.	0.3	0
10008	Pathway clusters of aging genes using data mining techniques. , 2014, , .		1
10009	An effective measure corresponding to biological significance. Network Modeling Analysis in Health Informatics and Bioinformatics, 2014, 3, 1.	1.2	1
10010	Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. BMC Plant Biology, 2014, 14, 329.	1.6	42
10011	Structuring research methods and data with the research object model: genomics workflows as a case study. Journal of Biomedical Semantics, 2014, 5, 41.	0.9	26
10012	A deep transcriptomic analysis of pod development in the vanilla orchid (<i>Vanilla planifolia</i>). BMC Genomics, 2014, 15, 964.	1.2	42
10013	Understanding disease mechanisms with models of signaling pathway activities. BMC Systems Biology, 2014, 8, 121.	3.0	42
10014	Prioritization of candidate genes in QTL regions based on associations between traits and biological processes. BMC Plant Biology, 2014, 14, 330.	1.6	40
10015	Abundance, arrangement, and function of sequence motifs in the chicken promoters. BMC Genomics, 2014, 15, 900.	1.2	19
10016	Functional genomics and microbiome profiling of the Asian longhorned beetle (<i>Anoplophora</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 beetles. BMC Genomics, 2014, 15, 1096.	1.2	93
10017	Finding gene regulatory network candidates using the gene expression knowledge base. BMC Bioinformatics, 2014, 15, 386.	1.2	8
10018	Systematic identification of transcriptional and post-transcriptional regulations in human respiratory epithelial cells during influenza A virus infection. BMC Bioinformatics, 2014, 15, 336.	1.2	35
10019	Multi-tissue transcriptomics of the black widow spider reveals expansions, co-options, and functional processes of the silk gland gene toolkit. BMC Genomics, 2014, 15, 365.	1.2	70
10020	VariantDB: a flexible annotation and filtering portal for next generation sequencing data. Genome Medicine, 2014, 6, 74.	3.6	60
10021	Metagenomics reveals that detoxification systems are underrepresented in marine bacterial communities. BMC Genomics, 2014, 15, 749.	1.2	35

#	ARTICLE	IF	CITATIONS
10022	Evolution of the miR199-214 cluster and vertebrate skeletal development. <i>RNA Biology</i> , 2014, 11, 281-294.	1.5	54
10023	Application of high-throughput sequencing for studying genomic variations in congenital heart disease. <i>Briefings in Functional Genomics</i> , 2014, 13, 51-65.	1.3	16
10024	TGF β 2 Receptor 1: An Immune Susceptibility Gene in HPV-Associated Cancer. <i>Cancer Research</i> , 2014, 74, 6833-6844.	0.4	42
10025	Methodology for the inference of gene function from phenotype data. <i>BMC Bioinformatics</i> , 2014, 15, 405.	1.2	5
10026	Identification and functional characterization of copy number variations in diverse chicken breeds. <i>BMC Genomics</i> , 2014, 15, 934.	1.2	29
10027	Comprehensive characterization and RNA-Seq profiling of the HD-Zip transcription factor family in soybean (<i>Glycine max</i>) during dehydration and salt stress. <i>BMC Genomics</i> , 2014, 15, 950.	1.2	120
10028	Identification and molecular characterization of tissue-preferred rice genes and their upstream regularly sequences on a genome-wide level. <i>BMC Plant Biology</i> , 2014, 14, 331.	1.6	4
10029	In silico analysis of autoimmune diseases and genetic relationships to vaccination against infectious diseases. <i>BMC Immunology</i> , 2014, 15, 61.	0.9	21
10030	Global population-specific variation in miRNA associated with cancer risk and clinical biomarkers. <i>BMC Medical Genomics</i> , 2014, 7, 53.	0.7	90
10031	Cortical Spreading Depression Increases the Phosphorylation of AMP-Activated Protein Kinase in the Cerebral Cortex. <i>Neurochemical Research</i> , 2014, 39, 2431-2439.	1.6	15
10032	Joint genetic analysis of hippocampal size in mouse and human identifies a novel gene linked to neurodegenerative disease. <i>BMC Genomics</i> , 2014, 15, 850.	1.2	59
10033	Identification of genomic regions associated with feed efficiency in Nelore cattle. <i>BMC Genetics</i> , 2014, 15, 100.	2.7	87
10034	FOAM (Functional Ontology Assignments for Metagenomes): a Hidden Markov Model (HMM) database with environmental focus. <i>Nucleic Acids Research</i> , 2014, 42, e145-e145.	6.5	90
10035	Profiles of the auditory epithelia related microRNA expression in neonatal and adult rats. <i>European Journal of Medical Research</i> , 2014, 19, 48.	0.9	4
10036	Genomes of the rice pest brown planthopper and its endosymbionts reveal complex complementary contributions for host adaptation. <i>Genome Biology</i> , 2014, 15, 521.	3.8	404
10037	Genome-wide analysis of gene expression in human embryonic tooth germ. <i>Journal of Molecular Histology</i> , 2014, 45, 609-617.	1.0	11
10038	Impact of analytic provenance in genome analysis. <i>BMC Genomics</i> , 2014, 15, S1.	1.2	13
10039	New Tricks for Old Domains: How Novel Architectures and Promiscuous Hubs Contributed to the Organization and Evolution of the ECM. <i>Genome Biology and Evolution</i> , 2014, 6, 2897-2917.	1.1	14

#	ARTICLE	IF	CITATIONS
10040	The Porifera Ontology (PORO): enhancing sponge systematics with an anatomy ontology. <i>Journal of Biomedical Semantics</i> , 2014, 5, 39.	0.9	12
10041	A genome-wide association study on thyroid function and anti-thyroid peroxidase antibodies in Koreans. <i>Human Molecular Genetics</i> , 2014, 23, 4433-4442.	1.4	30
10042	Integrative genomics of chronic obstructive pulmonary disease. <i>Biochemical and Biophysical Research Communications</i> , 2014, 452, 276-286.	1.0	41
10043	Integration of molecular network data reconstructs Gene Ontology. <i>Bioinformatics</i> , 2014, 30, i594-i600.	1.8	30
10044	Optimization of Cost Sensitive Models to Improve Prediction of Molecular Functions. <i>Communications in Computer and Information Science</i> , 2014, , 207-222.	0.4	1
10045	Molecular interplay between Δ^5/Δ^6 desaturases and long-chain fatty acids in the pathogenesis of non-alcoholic steatohepatitis. <i>Gut</i> , 2014, 63, 344-355.	6.1	107
10046	The CF-modifying gene EHF promotes p.Phe508del-CFTR residual function by altering protein glycosylation and trafficking in epithelial cells. <i>European Journal of Human Genetics</i> , 2014, 22, 660-666.	1.4	26
10047	Keratin 17 in premalignant and malignant squamous lesions of the cervix: proteomic discovery and immunohistochemical validation as a diagnostic and prognostic biomarker. <i>Modern Pathology</i> , 2014, 27, 621-630.	2.9	85
10048	Deorphanizing the human transmembrane genome: A landscape of uncharacterized membrane proteins. <i>Acta Pharmacologica Sinica</i> , 2014, 35, 11-23.	2.8	34
10049	Ontology-supported research on vaccine efficacy, safety and integrative biological networks. <i>Expert Review of Vaccines</i> , 2014, 13, 825-841.	2.0	12
10050	Nitric oxide production and scavenging in waterlogged roots of rape seedlings. <i>Genes and Genomics</i> , 2014, 36, 691-699.	0.5	11
10051	MOPED 2.5 – An Integrated Multi-Omics Resource: Multi-Omics Profiling Expression Database Now Includes Transcriptomics Data. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 335-343.	1.0	42
10052	Bioinformatic Tools in Arabidopsis Research. <i>Methods in Molecular Biology</i> , 2014, 1062, 97-136.	0.4	6
10053	Shifting-and-Scaling Correlation Based Biclustering Algorithm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 1239-1252.	1.9	29
10054	Foodomics. <i>Comprehensive Analytical Chemistry</i> , 2014, , 395-440.	0.7	9
10055	Extending <i>in silico</i> mechanism-of-action analysis by annotating targets with pathways: application to cellular cytotoxicity readouts. <i>Future Medicinal Chemistry</i> , 2014, 6, 2029-2056.	1.1	19
10056	De novo transcriptome of the desert beetle <i>Microdera punctipennis</i> (Coleoptera: Tenebrionidae) using illumina RNA-seq technology. <i>Molecular Biology Reports</i> , 2014, 41, 7293-7303.	1.0	16
10057	Mutation spectrum and differential gene expression in cystic and solid vestibular schwannoma. <i>Genetics in Medicine</i> , 2014, 16, 264-270.	1.1	17

#	ARTICLE	IF	CITATIONS
10058	Kidney Cancer Is Characterized by Aberrant Methylation of Tissue-Specific Enhancers That Are Prognostic for Overall Survival. <i>Clinical Cancer Research</i> , 2014, 20, 4349-4360.	3.2	60
10059	Increased expression of c-Jun in nonalcoholic fatty liver disease. <i>Laboratory Investigation</i> , 2014, 94, 394-408.	1.7	73
10060	PATHOME: an algorithm for accurately detecting differentially expressed subpathways. <i>Oncogene</i> , 2014, 33, 4941-4951.	2.6	70
10061	MYCN repression of Lifeguard/FAIM2 enhances neuroblastoma aggressiveness. <i>Cell Death and Disease</i> , 2014, 5, e1401-e1401.	2.7	15
10062	Polygenic inheritance of paclitaxel-induced sensory peripheral neuropathy driven by axon outgrowth gene sets in CALGB 40101 (Alliance). <i>Pharmacogenomics Journal</i> , 2014, 14, 336-342.	0.9	33
10063	Premorbid risk factors for major depressive disorder: Are they associated with early onset and recurrent course?. <i>Development and Psychopathology</i> , 2014, 26, 1477-1493.	1.4	54
10064	A Combined Transgenic Proteomic Analysis and Regulated Trafficking of Neuroligin-2. <i>Journal of Biological Chemistry</i> , 2014, 289, 29350-29364.	1.6	37
10065	A high-resolution network model for global gene regulation in <i>Mycobacterium tuberculosis</i> . <i>Nucleic Acids Research</i> , 2014, 42, 11291-11303.	6.5	61
10066	Using Fisher's Method to Identify Enriched Gene Sets. <i>Statistics in Biopharmaceutical Research</i> , 2014, 6, 154-162.	0.6	4
10067	Using data fusion for scoring reliability of protein-protein interactions. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1450014.	0.3	2
10068	Phycoremediation Coupled with Generation of Value-Added Products. , 2014, , 341-387.		3
10069	Transcriptome analysis of the salivary glands of <i>Nephotettix cincticeps</i> (Uhler). <i>Journal of Insect Physiology</i> , 2014, 71, 170-176.	0.9	44
10070	Contributions of Genomic and Informatic Approaches to Understanding Alcohol Dependence. , 2014, , 523-537.		0
10071	RNA-sequencing reveals early, dynamic transcriptome changes in the corollas of pollinated petunias. <i>BMC Plant Biology</i> , 2014, 14, 307.	1.6	41
10072	Unbiased Functional Clustering of Gene Variants with a Phenotypic-Linkage Network. <i>PLoS Computational Biology</i> , 2014, 10, e1003815.	1.5	48
10073	Antimicrobial targets localize to the extracellular vesicle-associated proteome of <i>Pseudomonas aeruginosa</i> grown in a biofilm. <i>Frontiers in Microbiology</i> , 2014, 5, 464.	1.5	33
10074	Disease-Gene Association Using a Genetic Algorithm. , 2014, , .		6
10075	Finding Novel Molecular Connections between Developmental Processes and Disease. <i>PLoS Computational Biology</i> , 2014, 10, e1003578.	1.5	10

#	ARTICLE	IF	CITATIONS
10076	A set-based association test identifies sex-specific gene sets associated with type 2 diabetes. <i>Frontiers in Genetics</i> , 2014, 5, 395.	1.1	9
10077	Proteomics of a fuzzy organelle: interphase chromatin. <i>EMBO Journal</i> , 2014, 33, 648-664.	3.5	58
10078	Large-Scale Determination of Sequence, Structure, and Function Relationships in Cytosolic Glutathione Transferases across the Biosphere. <i>PLoS Biology</i> , 2014, 12, e1001843.	2.6	79
10079	VarWalker: Personalized Mutation Network Analysis of Putative Cancer Genes from Next-Generation Sequencing Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003460.	1.5	96
10080	Hypoxia Adaptations in the Grey Wolf (<i>Canis lupus chanco</i>) from Qinghai-Tibet Plateau. <i>PLoS Genetics</i> , 2014, 10, e1004466.	1.5	169
10081	5.2 Functional -Omics for Cell Lines and Processes: The -Omics Technologies on the Example of CHO Cells. , 2014, , 326-367.		0
10082	Genes Involved in the Endoplasmic Reticulum N-Glycosylation Pathway of the Red Microalga <i>Porphyridium</i> sp.: A Bioinformatic Study. <i>International Journal of Molecular Sciences</i> , 2014, 15, 2305-2326.	1.8	30
10083	Research on Ontology Structure Characteristics Analysis and Matching Application. <i>Applied Mechanics and Materials</i> , 0, 556-562, 4396-4399.	0.2	0
10084	Optimization of gene set annotations via entropy minimization over variable clusters (EMVC). <i>Bioinformatics</i> , 2014, 30, 1698-1706.	1.8	65
10085	GoMapMan: integration, consolidation and visualization of plant gene annotations within the MapMan ontology. <i>Nucleic Acids Research</i> , 2014, 42, D1167-D1175.	6.5	108
10086	Integration of Two Ancestral Chaperone Systems into One: The Evolution of Eukaryotic Molecular Chaperones in Light of Eukaryogenesis. <i>Molecular Biology and Evolution</i> , 2014, 31, 410-418.	3.5	17
10087	Egas: a collaborative and interactive document curation platform. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau048-bau048.	1.4	20
10088	Quantitative Protein Localization Signatures Reveal an Association between Spatial and Functional Divergences of Proteins. <i>PLoS Computational Biology</i> , 2014, 10, e1003504.	1.5	23
10089	iRegulon: From a Gene List to a Gene Regulatory Network Using Large Motif and Track Collections. <i>PLoS Computational Biology</i> , 2014, 10, e1003731.	1.5	787
10090	Co-regulated Transcripts Associated to Cooperating eSNPs Define Bi-fan Motifs in Human Gene Networks. <i>PLoS Genetics</i> , 2014, 10, e1004587.	1.5	0
10091	Harnessing Natural Sequence Variation to Dissect Posttranscriptional Regulatory Networks in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1539-1553.	0.8	9
10092	The Ontogeny and Evolution of Sex-Biased Gene Expression in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 1206-1219.	3.5	108
10093	Wigwags: identifying gene modules co-regulated across multiple biological conditions. <i>Bioinformatics</i> , 2014, 30, 962-970.	1.8	36

#	ARTICLE	IF	CITATIONS
10094	Unsupervised gene function extraction using semantic vectors. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau084-bau084.	1.4	2
10095	Patterns of Positive Selection in Seven Ant Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 1661-1685.	3.5	138
10096	Profiling Dose-Dependent Activation of p53-Mediated Signaling Pathways by Chemicals with Distinct Mechanisms of DNA Damage. <i>Toxicological Sciences</i> , 2014, 142, 56-73.	1.4	43
10097	The ATXN2-SH2B3 locus is associated with peripheral arterial disease: an electronic medical record-based genome-wide association study. <i>Frontiers in Genetics</i> , 2014, 5, 166.	1.1	40
10098	Systems biology and brain activity in neuronal pathways by smart device and advanced signal processing. <i>Frontiers in Genetics</i> , 2014, 5, 253.	1.1	13
10099	Locus heterogeneity disease genes encode proteins with high interconnectivity in the human protein interaction network. <i>Frontiers in Genetics</i> , 2014, 5, 434.	1.1	8
10100	New insights into the targeting of a subset of tail-anchored proteins to the outer mitochondrial membrane. <i>Frontiers in Plant Science</i> , 2014, 5, 426.	1.7	29
10101	Molecular effects of resistance elicitors from biological origin and their potential for crop protection. <i>Frontiers in Plant Science</i> , 2014, 5, 655.	1.7	138
10102	Computational and Experimental Approaches to Reveal the Effects of Single Nucleotide Polymorphisms with Respect to Disease Diagnostics. <i>International Journal of Molecular Sciences</i> , 2014, 15, 9670-9717.	1.8	31
10103	Transcriptome Sequencing and Developmental Regulation of Gene Expression in <i>Anopheles aquasalis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3005.	1.3	9
10104	Clues From the Cloud. <i>American Journal of Psychiatry</i> , 2014, 171, 705-708.	4.0	0
10105	Probabilistic Approach to Predicting Substrate Specificity of Methyltransferases. <i>PLoS Computational Biology</i> , 2014, 10, e1003514.	1.5	19
10106	dcGOR: An R Package for Analysing Ontologies and Protein Domain Annotations. <i>PLoS Computational Biology</i> , 2014, 10, e1003929.	1.5	18
10107	RNA-Seq Reveals Infection-Induced Gene Expression Changes in the Snail Intermediate Host of the Carcinogenic Liver Fluke, <i>Opisthorchis viverrini</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2765.	1.3	14
10108	Comparative transcriptomic analysis of male and female flowers of monoecious <i>Quercus suber</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 599.	1.7	59
10109	Differential Transcriptome Analysis between <i>Paulownia fortunei</i> and Its Synthesized Autopolyploid. <i>International Journal of Molecular Sciences</i> , 2014, 15, 5079-5093.	1.8	35
10110	The Transcriptomes of the Crucian Carp Complex (<i>Carassius auratus</i>) Provide Insights into the Distinction between Unisexual Triploids and Sexual Diploids. <i>International Journal of Molecular Sciences</i> , 2014, 15, 9386-9406.	1.8	12
10111	STITCH 4: integration of protein-chemical interactions with user data. <i>Nucleic Acids Research</i> , 2014, 42, D401-D407.	6.5	388

#	ARTICLE	IF	CITATIONS
10112	Genetic resources for advanced biofuel production described with the Gene Ontology. <i>Frontiers in Microbiology</i> , 2014, 5, 528.	1.5	18
10113	The impact of incomplete knowledge on the evaluation of protein function prediction: a structured-output learning perspective. <i>Bioinformatics</i> , 2014, 30, i609-i616.	1.8	43
10114	PLIC: protein-ligand interaction clusters. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau029.	1.4	37
10115	Genetic Analysis of <i>DEFFECTIVE KERNEL1</i> Loop Function in Three-Dimensional Body Patterning in <i>Physcomitrella patens</i> . <i>Plant Physiology</i> , 2014, 166, 903-919.	2.3	40
10116	Network Analyses Reveal Pervasive Functional Regulation Between Proteases in the Human Protease Web. <i>PLoS Biology</i> , 2014, 12, e1001869.	2.6	137
10117	Manually curated database of rice proteins. <i>Nucleic Acids Research</i> , 2014, 42, D1214-D1221.	6.5	19
10118	Imatinib Treatment Causes Substantial Transcriptional Changes in Adult <i>Schistosoma mansoni</i> In Vitro Exhibiting Pleiotropic Effects. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2923.	1.3	34
10119	Global Patterns of Protein Domain Gain and Loss in Superkingdoms. <i>PLoS Computational Biology</i> , 2014, 10, e1003452.	1.5	65
10120	Regression Analysis of Combined Gene Expression Regulation in Acute Myeloid Leukemia. <i>PLoS Computational Biology</i> , 2014, 10, e1003908.	1.5	62
10121	Genomic Insights into Processes Driving the Infection of <i>Alexandrium tamarense</i> by the Parasitoid <i>Amoebophrya</i> sp. <i>Eukaryotic Cell</i> , 2014, 13, 1439-1449.	3.4	42
10122	Differential Protein Network Analysis of the Immune Cell Lineage. <i>BioMed Research International</i> , 2014, 2014, 1-11.	0.9	5
10123	Identification of Modules Related to Programmed Cell Death in CHD Based on EHEN. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	2
10124	Gene Expression Profiling of Biological Pathway Alterations by Radiation Exposure. <i>BioMed Research International</i> , 2014, 2014, 1-9.	0.9	18
10125	Hierarchical Ensemble Methods for Protein Function Prediction. , 2014, 2014, 1-34.		32
10126	Pinpointing a hotspot in adrenal Cushing syndrome. <i>Nature Reviews Endocrinology</i> , 2014, 10, 447-448.	4.3	6
10127	Molecular mechanisms of system responses to novel stimuli are predictable from public data. <i>Nucleic Acids Research</i> , 2014, 42, 1442-1460.	6.5	28
10128	Transcriptome Profiles of the Protoscolecids of <i>Echinococcus granulosus</i> Reveal that Excretory-Secretory Products Are Essential to Metabolic Adaptation. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3392.	1.3	28
10129	Clustering of gene ontology terms in genomes. <i>Gene</i> , 2014, 550, 155-164.	1.0	27

#	ARTICLE	IF	CITATIONS
10130	Transcriptome Analysis of Salt Tolerant Common Bean (<i>Phaseolus vulgaris</i> L.) under Saline Conditions. <i>PLoS ONE</i> , 2014, 9, e92598.	1.1	107
10131	Phenotype Ontologies and Cross-Species Analysis for Translational Research. <i>PLoS Genetics</i> , 2014, 10, e1004268.	1.5	63
10132	Allele-Specific Network Reveals Combinatorial Interaction That Transcends Small Effects in Psoriasis GWAS. <i>PLoS Computational Biology</i> , 2014, 10, e1003766.	1.5	25
10133	FSim: A Novel Functional Similarity Search Algorithm and Tool for Discovering Functionally Related Gene Products. <i>BioMed Research International</i> , 2014, 2014, 1-9.	0.9	2
10134	Detection of Pleiotropy through a Phenome-Wide Association Study (PheWAS) of Epidemiologic Data as Part of the Environmental Architecture for Genes Linked to Environment (EAGLE) Study. <i>PLoS Genetics</i> , 2014, 10, e1004678.	1.5	64
10135	A Virulent Strain of Deformed Wing Virus (DWV) of Honeybees (<i>Apis mellifera</i>) Prevails after <i>Varroa destructor</i> -Mediated, or In Vitro, Transmission. <i>PLoS Pathogens</i> , 2014, 10, e1004230.	2.1	294
10136	Phenotypic profiling of ABC transporter coding genes in <i>Myxococcus xanthus</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 352.	1.5	8
10137	Ontological realism, concepts and classification in molecular biology. <i>Journal of Documentation</i> , 2014, 70, 173-193.	0.9	13
10138	Proteomic landscape of bronchoalveolar lavage fluid in human immunodeficiency virus infection. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2014, 306, L35-L42.	1.3	10
10139	Genome-Wide Tissue-Specific Gene Expression, Co-expression and Regulation of Co-expressed Genes in Adult Nematode <i>Ascaris suum</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2678.	1.3	50
10140	SANTA: Quantifying the Functional Content of Molecular Networks. <i>PLoS Computational Biology</i> , 2014, 10, e1003808.	1.5	66
10141	Coiled-Coil Proteins Facilitated the Functional Expansion of the Centrosome. <i>PLoS Computational Biology</i> , 2014, 10, e1003657.	1.5	32
10142	Long Non-Coding RNA and Alternative Splicing Modulations in Parkinson's Leukocytes Identified by RNA Sequencing. <i>PLoS Computational Biology</i> , 2014, 10, e1003517.	1.5	167
10143	Inferring Host Gene Subnetworks Involved in Viral Replication. <i>PLoS Computational Biology</i> , 2014, 10, e1003626.	1.5	6
10144	Negative Example Selection for Protein Function Prediction: The NoGO Database. <i>PLoS Computational Biology</i> , 2014, 10, e1003644.	1.5	32
10145	Linear Motif-Mediated Interactions Have Contributed to the Evolution of Modularity in Complex Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2014, 10, e1003881.	1.5	16
10146	Evidence for Mito-Nuclear and Sex-Linked Reproductive Barriers between the Hybrid Italian Sparrow and Its Parent Species. <i>PLoS Genetics</i> , 2014, 10, e1004075.	1.5	124
10147	The Functional Consequences of Variation in Transcription Factor Binding. <i>PLoS Genetics</i> , 2014, 10, e1004226.	1.5	187

#	ARTICLE	IF	CITATIONS
10148	Integrated Pathway-Based Approach Identifies Association between Genomic Regions at CTCF and CACNB2 and Schizophrenia. <i>PLoS Genetics</i> , 2014, 10, e1004345.	1.5	44
10149	Comparative Analysis of Salivary Gland Transcriptomes of <i>Phlebotomus orientalis</i> Sand Flies from Endemic and Non-endemic Foci of Visceral Leishmaniasis. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2709.	1.3	53
10150	Systems Biology Studies of Adult <i>Paragonimus</i> Lung Flukes Facilitate the Identification of Immunodominant Parasite Antigens. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3242.	1.3	24
10151	Pathophysiologic and Transcriptomic Analyses of Viscerotropic Yellow Fever in a Rhesus Macaque Model. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3295.	1.3	54
10152	Post-Translational Regulation via Clp Protease Is Critical for Survival of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2014, 10, e1003994.	2.1	69
10153	Insilico analysis of hypothetical proteins unveils putative metabolic pathways and essential genes in <i>Leishmania donovani</i> . <i>Frontiers in Genetics</i> , 2014, 5, 291.	1.1	31
10154	Type I Interferon Regulates the Expression of Long Non-Coding RNAs. <i>Frontiers in Immunology</i> , 2014, 5, 548.	2.2	54
10155	Elucidating gene function and function evolution through comparison of co-expression networks of plants. <i>Frontiers in Plant Science</i> , 2014, 5, 394.	1.7	77
10156	A Novel Highly Divergent Protein Family Identified from a Viviparous Insect by RNA-seq Analysis: A Potential Target for Tsetse Fly-Specific Abortifacients. <i>PLoS Genetics</i> , 2014, 10, e1003874.	1.5	46
10157	Community detection for networks with unipartite and bipartite structure. <i>New Journal of Physics</i> , 2014, 16, 093001.	1.2	9
10159	Survey of Network-Based Approaches to Research of Cardiovascular Diseases. <i>BioMed Research International</i> , 2014, 2014, 1-10.	0.9	8
10160	Overview of the gene ontology task at BioCreative IV. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau086-bau086.	1.4	45
10161	COMPARTMENTS: unification and visualization of protein subcellular localization evidence. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau012-bau012.	1.4	483
10162	CCAT: Combinatorial Code Analysis Tool for transcriptional regulation. <i>Nucleic Acids Research</i> , 2014, 42, 2833-2847.	6.5	22
10163	Genome-wide Analysis of <i>Drosophila</i> Circular RNAs Reveals Their Structural and Sequence Properties and Age-Dependent Neural Accumulation. <i>Cell Reports</i> , 2014, 9, 1966-1980.	2.9	866
10164	microPIR2: a comprehensive database for human-mouse comparative study of microRNA-promoter interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau115-bau115.	1.4	15
10165	Applied Graph-Mining Algorithms to Study Biomolecular Interaction Networks. <i>BioMed Research International</i> , 2014, 2014, 1-11.	0.9	6
10166	De Novo Transcriptome Sequence Assembly and Identification of AP2/ERF Transcription Factor Related to Abiotic Stress in Parsley (<i>Petroselinum crispum</i>). <i>PLoS ONE</i> , 2014, 9, e108977.	1.1	21

#	ARTICLE	IF	CITATIONS
10167	The Domain Landscape of Virus-Host Interactomes. <i>BioMed Research International</i> , 2014, 2014, 1-13.	0.9	30
10168	Integrative omics analysis. A study based on <i>Plasmodium falciparum</i> mRNA and protein data. <i>BMC Systems Biology</i> , 2014, 8, S4.	3.0	13
10169	Genetic resources for methane production from biomass described with the Gene Ontology. <i>Frontiers in Microbiology</i> , 2014, 5, 634.	1.5	16
10170	Comparison of Long Noncoding RNA and mRNA Expression Profiles in Mesenchymal Stem Cells Derived from Human Periodontal Ligament and Bone Marrow. <i>BioMed Research International</i> , 2014, 2014, 1-12.	0.9	21
10171	Shotgun metagenomics reveals a wide array of antibiotic resistance genes and mobile elements in a polluted lake in India. <i>Frontiers in Microbiology</i> , 2014, 5, 648.	1.5	193
10172	Network Assessor: An automated method for quantitative assessment of a network's potential for gene function prediction. <i>Frontiers in Genetics</i> , 2014, 5, 123.	1.1	10
10173	High atomic weight, high-energy radiation (HZE) induces transcriptional responses shared with conventional stresses in addition to a core DSB response specific to clastogenic treatments. <i>Frontiers in Plant Science</i> , 2014, 5, 364.	1.7	19
10174	Identification of Simple Sequence Repeat Biomarkers through Cross-Species Comparison in a Tag Cloud Representation. <i>BioMed Research International</i> , 2014, 2014, 1-11.	0.9	3
10175	Transcriptome profiling of malignant transformed rat hepatic stem-like cells by aflatoxin B1. <i>Neoplasma</i> , 2014, 61, 193-204.	0.7	9
10176	MicroRNA Dysregulation, Gene Networks, and Risk for Schizophrenia in 22q11.2 Deletion Syndrome. <i>Frontiers in Neurology</i> , 2014, 5, 238.	1.1	42
10177	MoDPeplnt: an interactive web server for prediction of modular domain-peptide interactions. <i>Bioinformatics</i> , 2014, 30, 2668-2669.	1.8	37
10178	Leveraging additional knowledge to support coherent bicluster discovery in gene expression data. <i>Intelligent Data Analysis</i> , 2014, 18, 837-855.	0.4	8
10179	A biologist, a statistician, and a bioinformatician walk into a conference room and walk out with a great metagenomics project plan. <i>Frontiers in Plant Science</i> , 2014, 5, 250.	1.7	1
10180	Genome sequence of a crustacean iridovirus, IIV31, isolated from the pill bug, <i>Armadillidium vulgare</i> . <i>Journal of General Virology</i> , 2014, 95, 1585-1590.	1.3	24
10181	Field-omics understanding large-scale molecular data from field crops. <i>Frontiers in Plant Science</i> , 2014, 5, 286.	1.7	53
10182	An Unsupervised Approach to Predict Functional Relations between Genes Based on Expression Data. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	5
10183	Integrating Multiple Genomic Data to Predict Disease-Causing Nonsynonymous Single Nucleotide Variants in Exome Sequencing Studies. <i>PLoS Genetics</i> , 2014, 10, e1004237.	1.5	50
10184	Co-ordination and divergence of cell-specific transcription and translation of genes in arabidopsis root cells. <i>Annals of Botany</i> , 2014, 114, 1109-1123.	1.4	10

#	ARTICLE	IF	CITATIONS
10185	Draft Genome Sequence of the Novel Exopolysaccharide-Producing Bacterium <i>Altibacter lentus</i> Strain JLT2010T, Isolated from Deep Seawater of the South China Sea. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
10186	Childhood abuse is associated with methylation of multiple loci in adult DNA. <i>BMC Medical Genomics</i> , 2014, 7, 13.	0.7	149
10187	Regulatory interplay between soybean root and soybean cyst nematode during a resistant and susceptible reaction. <i>BMC Plant Biology</i> , 2014, 14, 300.	1.6	30
10188	Yeast Systems Biology: Our Best Shot at Modeling a Cell. <i>Genetics</i> , 2014, 198, 435-437.	1.2	23
10189	Optimization and Analysis of Seriation Algorithm for Ordering Protein Networks. , 2014, , .		3
10190	Matrix factorization-based data fusion for drug-induced liver injury prediction. <i>Systems Biomedicine (Austin, Tex)</i> , 2014, 2, 16-22.	0.7	13
10191	Development of a parallel program to perform a permutation test with the use of GPU. , 2014, , .		4
10192	Prediction of gene expression in human using rat in vivo gene expression in Japanese Toxicogenomics Project. <i>Systems Biomedicine (Austin, Tex)</i> , 2014, 2, 8-15.	0.7	5
10193	A two-stage geometric method for detecting unreliable links in protein-protein networks. , 2014, , .		1
10194	Essential protein identification based on essential protein-protein interaction prediction by integrated edge weights. , 2014, , .		1
10195	A hybrid measure for the semantic similarity of gene ontology terms. , 2014, , .		1
10196	LSL: A new measure to evaluate triclusters. , 2014, , .		7
10197	Transcriptome profiling of gene expression in fall dormant and nondormant alfalfa. <i>Genomics Data</i> , 2014, 2, 282-284.	1.3	2
10198	Complete genome sequence of the lignin-degrading bacterium <i>Klebsiella</i> sp. strain BRL6-2. <i>Standards in Genomic Sciences</i> , 2014, 9, 19.	1.5	40
10199	ReShare: An Operational Ontology Framework for Research Modeling, Combining and Sharing. , 2014, , .		0
10200	A new hybrid semantic similarity computation method based on gene ontology. , 2014, , .		4
10201	Prediction of protein function by combining phylogenetic tree and mathematical inference. , 2014, , .		0
10202	High-Resolution Profiling of Novel Transcribed Regions During Rat Spermatogenesis1. <i>Biology of Reproduction</i> , 2014, 91, 5.	1.2	50

#	ARTICLE	IF	CITATIONS
10203	LateBiclustering: Efficient Heuristic Algorithm for Time-Lagged Bicluster Identification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 801-813.	1.9	15
10204	Improving identification of key players in aging via network de-noising. , 2014, , .		3
10205	Inference of Disease E3s from Integrated Functional Relation Network. , 2014, , .		1
10206	Environmentally Selected Aphid Variants in Clonality Context Display Differential Patterns of Methylation in the Genome. PLoS ONE, 2014, 9, e115022.	1.1	15
10207	Nucleotide excision repair/transcription gene defects in the fetus and impaired TFIIH-mediated function in transcription in placenta leading to preeclampsia. BMC Genomics, 2014, 15, 373.	1.2	10
10208	Genome sequencing of four Aureobasidium pullulans varieties: biotechnological potential, stress tolerance, and description of new species. BMC Genomics, 2014, 15, 549.	1.2	262
10209	Sex- and tissue-specific profiles of chemosensory gene expression in a herbivorous gall-inducing fly (Diptera: Cecidomyiidae). BMC Genomics, 2014, 15, 501.	1.2	81
10210	Addressing the Increasing Volume and Variety of Digital Evidence Using an Ontology. , 2014, , .		7
10211	Comparison of gene expression of Paramecium bursaria with and without Chlorella variabilissymbionts. BMC Genomics, 2014, 15, 183.	1.2	57
10212	Genome Sequence of the Aerobic Arsenate-Reducing Bacterium <i>Pantoea</i> sp. Strain IMH. Genome Announcements, 2014, 2, .	0.8	11
10213	Systematic permutation testing in GWAS pathway analyses: identification of genetic networks in dilated cardiomyopathy and ulcerative colitis. BMC Genomics, 2014, 15, 622.	1.2	23
10214	Beyond genomic variation - comparison and functional annotation of three Brassica rapagenomes: a turnip, a rapid cycling and a Chinese cabbage. BMC Genomics, 2014, 15, 250.	1.2	87
10215	Variation Ontology for annotation of variation effects and mechanisms. Genome Research, 2014, 24, 356-364.	2.4	52
10216	Human Tra2 proteins jointly control a CHEK1 splicing switch among alternative and constitutive target exons. Nature Communications, 2014, 5, 4760.	5.8	47
10217	Digital expression profiling of the compartmentalized translome of Purkinje neurons. Genome Research, 2014, 24, 1396-1410.	2.4	49
10218	Literature-Based Gene Curation and Proposed Genetic Nomenclature for Cryptococcus. Eukaryotic Cell, 2014, 13, 878-883.	3.4	18
10219	Using biological networks to improve our understanding of infectious diseases. Computational and Structural Biotechnology Journal, 2014, 11, 1-10.	1.9	43
10220	Inactivation of the budding yeast cohesin loader Scc2 alters gene expression both globally and in response to a single DNA double strand break. Cell Cycle, 2014, 13, 3645-3658.	1.3	11

#	ARTICLE	IF	CITATIONS
10221	Failure mode databases and their knowledge-based management. , 2014, , .		0
10222	Bioinformatics: Hypothesis Freeâ€”Or Hypotheses Freed?. <i>BioScience</i> , 2014, 64, 844-845.	2.2	0
10223	Evolving relational hierarchical classification rules for predicting gene ontology-based protein functions. , 2014, , .		5
10224	Unveiling new biological relationships using shared hits of chemical screening assay pairs. <i>Bioinformatics</i> , 2014, 30, i579-i586.	1.8	7
10225	Draft Genome Sequence of Eggplant (<i>Solanum melongena</i> L.): the Representative <i>Solanum</i> Species Indigenous to the Old World. <i>DNA Research</i> , 2014, 21, 649-660.	1.5	254
10226	The first eNanoMapper prototype: A substance database to support safe-by-design. , 2014, , .		5
10227	Network-based analysis of time series RNA-seq gene expression data by integrating the interactome and gene ontology information. , 2014, , .		0
10228	Three-dimensional eukaryotic genomic organization is strongly correlated with codon usage expression and function. <i>Nature Communications</i> , 2014, 5, 5876.	5.8	24
10229	Integrative Quantitative Proteomics Unveils Proteostasis Imbalance in Human Hepatocellular Carcinoma Developed on Nonfibrotic Livers. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3473-3483.	2.5	15
10230	A Comprehensive Proteomic View of Responses of A549 Type II Alveolar Epithelial Cells to Human Respiratory Syncytial Virus Infection. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3250-3269.	2.5	28
10231	Short-Term and Continuing Stresses Differentially Interplay with Multiple Hormones to Regulate Plant Survival and Growth. <i>Molecular Plant</i> , 2014, 7, 841-855.	3.9	55
10232	Genomeâ€”wide microarray analysis identifies a potential role for striatal retrograde endocannabinoid signaling in the pathogenesis of experimental <scp>l</scp>â€”DOPAâ€”induced dyskinesia. <i>Synapse</i> , 2014, 68, 332-343.	0.6	13
10233	Analysis of biological networks and biological pathways associated with residual feed intake in beef cattle. <i>Animal Science Journal</i> , 2014, 85, 374-387.	0.6	67
10234	Covering complete proteomes with X-ray structures: a current snapshot. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2781-2793.	2.5	30
10235	The complex jujube genome provides insights into fruit tree biology. <i>Nature Communications</i> , 2014, 5, 5315.	5.8	251
10236	Enabling scientific collaboration and discovery through the use of data standardization. , 2014, , .		0
10237	Semantic Breakthrough in Drug Discovery. <i>Synthesis Lectures on the Semantic Web: Theory and Technology</i> , 2014, 4, 1-142.	5.0	4
10238	Hydrophobic Triarylâ€”Substituted Î²â€”Lactams as Activityâ€”Based Probes for Profiling Eukaryotic Enzymes and Hostâ€”Pathogen Interactions. <i>ChemBioChem</i> , 2014, 15, 2195-2200.	1.3	12

#	ARTICLE	IF	CITATIONS
10239	Simultaneous analysis of the gene expression profiles of cancer and stromal cells in endometrial cancer. <i>Genes Chromosomes and Cancer</i> , 2014, 53, 725-737.	1.5	4
10240	Multi-label learning: a review of the state of the art and ongoing research. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2014, 4, 411-444.	4.6	130
10241	Decelerated genome evolution in modern vertebrates revealed by analysis of multiple lancelet genomes. <i>Nature Communications</i> , 2014, 5, 5896.	5.8	136
10242	Caries: Review of Human Genetics Research. <i>Caries Research</i> , 2014, 48, 491-506.	0.9	127
10243	The Lotus japonicus Genome. <i>Compendium of Plant Genomes</i> , 2014, , .	0.3	7
10244	Conceptual Modeling. <i>Lecture Notes in Computer Science</i> , 2014, , .	1.0	31
10245	Rapid neurogenesis through transcriptional activation in human stem cells. <i>Molecular Systems Biology</i> , 2014, 10, 760.	3.2	187
10246	An R-based tool for miRNA data analysis and correlation with clinical ontologies. , 2014, , .		0
10247	Modeling transcriptional networks regulating secondary growth and wood formation in forest trees. <i>Physiologia Plantarum</i> , 2014, 151, 156-163.	2.6	16
10248	Identification of gene ontologies linked to prefrontal hippocampal functional coupling in the human brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9657-9662.	3.3	9
10249	Challenges for an enzymatic reaction kinetics database. <i>FEBS Journal</i> , 2014, 281, 572-582.	2.2	22
10250	No large-effect low-frequency coding variation found for myocardial infarction. <i>Human Molecular Genetics</i> , 2014, 23, 4721-4728.	1.4	16
10251	A New Protein Structure Representation for Efficient Protein Function Prediction. <i>Journal of Computational Biology</i> , 2014, 21, 936-946.	0.8	7
10252	Genome-scale prediction of proteins with long intrinsically disordered regions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 145-158.	1.5	104
10253	Single nucleotide variations: Biological impact and theoretical interpretation. <i>Protein Science</i> , 2014, 23, 1650-1666.	3.1	94
10255	Interatrial differences of basal molecular set-up and changes in tachycardia-induced heart failure—a proteomic profiling study. <i>European Journal of Heart Failure</i> , 2014, 16, 835-845.	2.9	9
10256	Deconstructing transcriptional heterogeneity in pluripotent stem cells. <i>Nature</i> , 2014, 516, 56-61.	13.7	343
10257	Global molecular changes in rat livers treated with RXR agonists: a comparison using transcriptomics and proteomics. <i>Pharmacology Research and Perspectives</i> , 2014, 2, e00074.	1.1	5

#	ARTICLE	IF	CITATIONS
10258	Ontological realism and classification: Structures and concepts in the <i>Gene Ontology</i> . <i>Journal of the Association for Information Science and Technology</i> , 2014, 65, 686-697.	1.5	3
10259	Deep Proteomic Evaluation of Primary and Cell Line Motoneuron Disease Models Delineates Major Differences in Neuronal Characteristics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3410-3420.	2.5	51
10260	Extracellular vesicles shed from gefitinib-resistant nonsmall cell lung cancer regulate the tumor microenvironment. <i>Proteomics</i> , 2014, 14, 1845-1856.	1.3	44
10261	The unfolded protein response affects readthrough of premature termination codons. <i>EMBO Molecular Medicine</i> , 2014, 6, 685-701.	3.3	31
10262	Heme-related gene expression signatures of meat intakes in lung cancer tissues. <i>Molecular Carcinogenesis</i> , 2014, 53, 548-556.	1.3	13
10263	miXGENE Tool for Learning from Heterogeneous Gene Expression Data Using Prior Knowledge. , 2014, ,		2
10264	Measurement and genetics of human subcortical and hippocampal asymmetries in large datasets. <i>Human Brain Mapping</i> , 2014, 35, 3277-3289.	1.9	43
10265	Cancer stem cells and cisplatin-resistant cells isolated from non-small cell lung cancer cell lines constitute related cell populations. <i>Cancer Medicine</i> , 2014, 3, 1099-1111.	1.3	66
10266	A rare sequence variant in intron 1 of <i>THAP1</i> is associated with primary dystonia. <i>Molecular Genetics & Genomic Medicine</i> , 2014, 2, 261-272.	0.6	24
10267	Differential expression of synaptic proteins in unilateral 6-OHDA lesioned rat model: A comparative proteomics approach. <i>Proteomics</i> , 2014, 14, 1808-1819.	1.3	20
10268	<i>De novo</i> assembly and characterization of the skeletal muscle and electric organ transcriptomes of the African weakly electric fish <i>Campylomormyrus compressirostris</i> (Mormyridae, Teleostei). <i>Molecular Ecology Resources</i> , 2014, 14, 1222-1230.	2.2	31
10269	Chromatin regulators in neurodevelopment and disease: Analysis of fly neural circuits provides insights. <i>BioEssays</i> , 2014, 36, 872-883.	1.2	11
10270	PredictProtein: an open resource for online prediction of protein structural and functional features. <i>Nucleic Acids Research</i> , 2014, 42, W337-W343.	6.5	589
10271	Pathway Analysis Approaches for Rare and Common Variants: Insights From Genetic Analysis Workshop 18. <i>Genetic Epidemiology</i> , 2014, 38, S86-91.	0.6	19
10272	Molecular Aspects of Adipoepithelial Transdifferentiation in Mouse Mammary Gland. <i>Stem Cells</i> , 2014, 32, 2756-2766.	1.4	47
10273	RNA Sequencing of Creatine Transporter (SLC6A8) Deficient Fibroblasts Reveals Impairment of the Extracellular Matrix. <i>Human Mutation</i> , 2014, 35, 1128-1135.	1.1	8
10274	<i>De novo</i> characterization of the <i>Drosophila</i> <i>citri</i> transcriptome: mining genes involved in stress resistance and simple sequence repeats (SSRs) discovery. <i>Insect Molecular Biology</i> , 2014, 23, 52-66.	1.0	32
10275	Transcriptional profiling predicts overwhelming homology of schwann cells, olfactory ensheathing cells, and schwann cell-like glia. <i>Glia</i> , 2014, 62, 1559-1581.	2.5	32

#	ARTICLE	IF	CITATIONS
10276	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
10277	Shared signatures of social stress and aging in peripheral blood mononuclear cell gene expression profiles. <i>Aging Cell</i> , 2014, 13, 954-957.	3.0	18
10278	miR-429 Identified by Dynamic Transcriptome Analysis Is a New Candidate Biomarker for Colorectal Cancer Prognosis. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 54-64.	1.0	36
10280	Finding Alignments of Conserved Graphlets in Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2014, 21, 234-246.	0.8	8
10281	Proteome reference maps of the <i>Lotus japonicus</i> nodule and root. <i>Proteomics</i> , 2014, 14, 230-240.	1.3	21
10282	Computational characterization of moonlighting proteins. <i>Biochemical Society Transactions</i> , 2014, 42, 1780-1785.	1.6	26
10283	Conformational changes in DNA-binding proteins: Relationships with precomplex features and contributions to specificity and stability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 841-857.	1.5	32
10284	Fuelling genetic and metabolic exploration of <i>C₃</i> bioenergy crops through the first reference transcriptome of <i>Azadirachta indica</i> . <i>Plant Biotechnology Journal</i> , 2014, 12, 554-567.	4.1	37
10285	Interdisciplinary Collaboration in Philosophy. <i>Metaphilosophy</i> , 2014, 45, 372-398.	0.2	6
10286	Comparing different knowledge sources for the automatic summarization of biomedical literature. <i>Journal of Biomedical Informatics</i> , 2014, 52, 319-328.	2.5	14
10287	GC-made protein disorder sheds new light on vertebrate evolution. <i>Genomics</i> , 2014, 104, 530-537.	1.3	7
10288	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	6.0	895
10289	New Frontiers in Mining Complex Patterns. <i>Lecture Notes in Computer Science</i> , 2014, , .	1.0	2
10290	Genome-Wide Protein Function Prediction through Multi-Instance Multi-Label Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 891-902.	1.9	67
10291	Cascleave 2.0, a new approach for predicting caspase and granzyme cleavage targets. <i>Bioinformatics</i> , 2014, 30, 71-80.	1.8	63
10292	CellMiner ^{HCC} : a microarray-based expression database for hepatocellular carcinoma cell lines. <i>Liver International</i> , 2014, 34, 621-631.	1.9	15
10293	A distinct set of long non-coding RNAs in childhood MLL-rearranged acute lymphoblastic leukemia: biology and epigenetic target. <i>Human Molecular Genetics</i> , 2014, 23, 3278-3288.	1.4	49
10294	From the era of genome analysis to the era of genomic drug discovery: a pioneering example of rheumatoid arthritis. <i>Clinical Genetics</i> , 2014, 86, 432-440.	1.0	16

#	ARTICLE	IF	CITATIONS
10295	Spotlite: Web Application and Augmented Algorithms for Predicting Co-Complexed Proteins from Affinity Purification " Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2014, 13, 5944-5955.	1.8	18
10296	Identifying progression related disease risk modules based on the human subcellular signaling networks. <i>Molecular BioSystems</i> , 2014, 10, 3298-3309.	2.9	2
10297	Exacerbated oxidative stress in the fasting liver according to fuel partitioning. <i>Proteomics</i> , 2014, 14, 1905-1921.	1.3	27
10298	<i>Tetrahymena thermophila</i> : A divergent perspective on membrane traffic. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2014, 322, 500-516.	0.6	15
10299	Separate enrichment analysis of pathways for up- and downregulated genes. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20130950.	1.5	159
10300	Comparison of the transcriptional landscapes between human and mouse tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17224-17229.	3.3	337
10301	A computational bioinformatics analysis of gene expression identifies candidate agents for prostate cancer. <i>Andrologia</i> , 2014, 46, 625-632.	1.0	9
10302	Biological Network Module-Based Model for the Analysis of Differential Expression in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2014, 13, 5743-5750.	1.8	5
10303	Genetic interaction analysis of point mutations enables interrogation of gene function at a residue-level resolution. <i>BioEssays</i> , 2014, 36, 706-713.	1.2	9
10304	Minimal metabolic pathway structure is consistent with associated biomolecular interactions. <i>Molecular Systems Biology</i> , 2014, 10, 737.	3.2	41
10305	Prioritization of orphan disease-causing genes using topological feature and GO similarity between proteins in interaction networks. <i>Science China Life Sciences</i> , 2014, 57, 1064-1071.	2.3	20
10306	Improvement of a sample preparation method assisted by sodium deoxycholate for mass-spectrometry-based shotgun membrane proteomics. <i>Journal of Separation Science</i> , 2014, 37, 3321-3329.	1.3	20
10307	Molecular Determinants of Head and Neck Cancer. , 2014, , .		2
10308	Neurogenomics of Behavioral Plasticity. <i>Advances in Experimental Medicine and Biology</i> , 2014, 781, 149-168.	0.8	41
10309	Distinguishing between driver and passenger mutations in individual cancer genomes by network enrichment analysis. <i>BMC Bioinformatics</i> , 2014, 15, 308.	1.2	68
10310	Genome-Wide Analysis of Functional and Evolutionary Features of <i>Tele</i> -Enhancers. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 579-593.	0.8	3
10311	High-Sensitivity Low-Noise Miniature Fluxgate Magnetometers Using a Flip Chip Conceptual Design. <i>Sensors</i> , 2014, 14, 13815-13829.	2.1	39
10312	Extensive Differences in Gene Expression Between Symbiotic and Aposymbiotic Cnidarians. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 277-295.	0.8	150

#	ARTICLE	IF	CITATIONS
10313	Whole Genome Sequence Analysis Suggests Intratumoral Heterogeneity in Dissemination of Breast Cancer to Lymph Nodes. PLoS ONE, 2014, 9, e115346.	1.1	15
10314	MMP28 promotes macrophage polarization toward M2 cells and augments pulmonary fibrosis. Journal of Leukocyte Biology, 2013, 95, 9-18.	1.5	115
10315	3PFDB+: improved search protocol and update for the identification of representatives of protein sequence domain families. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau026.	1.4	5
10316	DIVE: a data intensive visualization engine. Bioinformatics, 2014, 30, 593-595.	1.8	12
10317	Draft Sequences of the Radish (<i>Raphanus sativus</i> L.) Genome. DNA Research, 2014, 21, 481-490.	1.5	165
10318	Interaction-based discovery of functionally important genes in cancers. Nucleic Acids Research, 2014, 42, e18-e18.	6.5	25
10319	Random Forest and Gene Ontology for functional analysis of microarray data. , 2014, , .		2
10320	Compartment-specific transcriptomics in a reef-building coral exposed to elevated temperatures. Molecular Ecology, 2014, 23, 5816-5830.	2.0	73
10321	Anatomical entity mention recognition at literature scale. Bioinformatics, 2014, 30, 868-875.	1.8	49
10322	The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of Pathway/Genome Databases. Nucleic Acids Research, 2014, 42, D459-D471.	6.5	1,023
10323	Proteomic Analysis of Solid Pseudopapillary Tumor of the Pancreas Reveals Dysfunction of the Endoplasmic Reticulum Protein Processing Pathway. Molecular and Cellular Proteomics, 2014, 13, 2593-2603.	2.5	87
10324	What Makes Biology Tick?. BioScience, 2014, 64, 845-847.	2.2	0
10325	Two novel pathway analysis methods based on a hierarchical model. Bioinformatics, 2014, 30, 690-697.	1.8	11
10326	P3DB 3.0: From plant phosphorylation sites to protein networks. Nucleic Acids Research, 2014, 42, D1206-D1213.	6.5	75
10327	New directions for diffusion-based network prediction of protein function: incorporating pathways with confidence. Bioinformatics, 2014, 30, i219-i227.	1.8	108
10328	The palmitoyl acyltransferase HIP14 shares a high proportion of interactors with huntingtin: implications for a role in the pathogenesis of Huntington's disease. Human Molecular Genetics, 2014, 23, 4142-4160.	1.4	58
10329	Large-scale modeling of condition-specific gene regulatory networks by information integration and inference. Nucleic Acids Research, 2014, 42, e166-e166.	6.5	12
10330	A Tree of Cellular Life Inferred from a Genomic Census of Molecular Functions. Journal of Molecular Evolution, 2014, 79, 240-262.	0.8	25

#	ARTICLE	IF	CITATIONS
10331	Architecture for interoperable software in biology. <i>Briefings in Bioinformatics</i> , 2014, 15, 626-636.	3.2	4
10332	The functional therapeutic chemical classification system. <i>Bioinformatics</i> , 2014, 30, 876-883.	1.8	6
10333	Predicting disease associations via biological network analysis. <i>BMC Bioinformatics</i> , 2014, 15, 304.	1.2	86
10334	Key regulators in prostate cancer identified by co-expression module analysis. <i>BMC Genomics</i> , 2014, 15, 1015.	1.2	28
10335	Genomic characterisation of an endometrial pathogenic <i>Escherichia coli</i> strain reveals the acquisition of genetic elements associated with extra-intestinal pathogenicity. <i>BMC Genomics</i> , 2014, 15, 1075.	1.2	13
10336	The genetics of colony form and function in Caribbean <i>Acropora</i> corals. <i>BMC Genomics</i> , 2014, 15, 1133.	1.2	46
10337	Sequence search and analysis of gene products containing RNA recognition motifs in the human genome. <i>BMC Genomics</i> , 2014, 15, 1159.	1.2	10
10338	Systematic exploration of autonomous modules in noisy microRNA-target networks for testing the generality of the ceRNA hypothesis. <i>BMC Genomics</i> , 2014, 15, 1178.	1.2	10
10339	Maize and millet transcription factors annotated using comparative genomic and transcriptomic data. <i>BMC Genomics</i> , 2014, 15, 818.	1.2	18
10340	Genes and signaling networks regulated during zebrafish optic vesicle morphogenesis. <i>BMC Genomics</i> , 2014, 15, 825.	1.2	24
10341	Transcriptome sequencing of rhizome tissue of <i>Sinopodophyllum hexandrum</i> at two temperatures. <i>BMC Genomics</i> , 2014, 15, 871.	1.2	35
10342	Comparative genome analysis of <i>Wolbachia</i> strain wAu. <i>BMC Genomics</i> , 2014, 15, 928.	1.2	50
10343	What do all the (human) micro-RNAs do?. <i>BMC Genomics</i> , 2014, 15, 976.	1.2	5
10344	Distance-based assessment of the localization of functional annotations in 3D genome reconstructions. <i>BMC Genomics</i> , 2014, 15, 992.	1.2	14
10345	Partial least squares based gene expression analysis in renal failure. <i>Diagnostic Pathology</i> , 2014, 9, 137.	0.9	3
10346	Two-layer modular analysis of gene and protein networks in breast cancer. <i>BMC Systems Biology</i> , 2014, 8, 81.	3.0	9
10347	RNA sequencing and de novo assembly of the digestive gland transcriptome in <i>Mytilus galloprovincialis</i> fed with toxinogenic and non-toxic strains of <i>Alexandrium minutum</i> . <i>BMC Research Notes</i> , 2014, 7, 722.	0.6	47
10348	Predicting expression: the complementary power of histone modification and transcription factor binding data. <i>Epigenetics and Chromatin</i> , 2014, 7, 36.	1.8	32

#	ARTICLE	IF	CITATIONS
10349	Semi-automated literature mining to identify putative biomarkers of disease from multiple biofluids. <i>Journal of Clinical Bioinformatics</i> , 2014, 4, 13.	1.2	6
10350	A comparative study of improvements Pre-filter methods bring on feature selection using microarray data. <i>Health Information Science and Systems</i> , 2014, 2, 7.	3.4	5
10351	A shortcut for multiple testing on the directed acyclic graph of gene ontology. <i>BMC Bioinformatics</i> , 2014, 15, 349.	1.2	5
10352	Pathway activity inference for multiclass disease classification through a mathematical programming optimisation framework. <i>BMC Bioinformatics</i> , 2014, 15, 390.	1.2	6
10353	Kiwi: a tool for integration and visualization of network topology and gene-set analysis. <i>BMC Bioinformatics</i> , 2014, 15, 408.	1.2	12
10354	chromoWIZ: a web tool to query and visualize chromosome-anchored genes from cereal and model genomes. <i>BMC Plant Biology</i> , 2014, 14, 348.	1.6	7
10355	Insights from systems pharmacology into cardiovascular drug discovery and therapy. <i>BMC Systems Biology</i> , 2014, 8, 141.	3.0	27
10356	<i>Neisseria meningitidis</i> elicits a pro-inflammatory response involving $\text{IL-1}\beta$ in a human blood-cerebrospinal fluid barrier model. <i>Journal of Neuroinflammation</i> , 2014, 11, 163.	3.1	36
10357	Shift in GATA3 functions, and GATA3 mutations, control progression and clinical presentation in breast cancer. <i>Breast Cancer Research</i> , 2014, 16, 464.	2.2	40
10358	The small RNA diversity from <i>Medicago truncatula</i> roots under biotic interactions evidences the environmental plasticity of the miRNAome. <i>Genome Biology</i> , 2014, 15, 457.	3.8	78
10359	Sequence specificity incompletely defines the genome-wide occupancy of Myc. <i>Genome Biology</i> , 2014, 15, 482.	3.8	63
10360	Genome-scale identification and characterization of moonlighting proteins. <i>Biology Direct</i> , 2014, 9, 30.	1.9	37
10361	High-resolution functional annotation of human transcriptome: predicting isoform functions by a novel multiple instance-based label propagation method. <i>Nucleic Acids Research</i> , 2014, 42, e39-e39.	6.5	45
10362	The long non-coding RNA Paupar regulates the expression of both local and distal genes. <i>EMBO Journal</i> , 2014, 33, 296-311.	3.5	195
10363	NeXO Web: the NeXO ontology database and visualization platform. <i>Nucleic Acids Research</i> , 2014, 42, D1269-D1274.	6.5	13
10364	CellFinder: a cell data repository. <i>Nucleic Acids Research</i> , 2014, 42, D950-D958.	6.5	26
10365	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2765-2775.	2.5	130
10366	Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. <i>Genes and Development</i> , 2014, 28, 1957-1975.	2.7	86

#	ARTICLE	IF	CITATIONS
10367	Approaches to uncovering cancer diagnostic and prognostic molecular signatures. <i>Molecular and Cellular Oncology</i> , 2014, 1, e957981.	0.3	1
10369	UniHI 7: an enhanced database for retrieval and interactive analysis of human molecular interaction networks. <i>Nucleic Acids Research</i> , 2014, 42, D408-D414.	6.5	91
10370	Visual account of protein investment in cellular functions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8488-8493.	3.3	304
10371	Applying Differentially Expressed Genes From Rodent Models of Chronic Stress to Research of Stress-Related Disease. <i>Psychosomatic Medicine</i> , 2014, 76, 644-649.	1.3	1
10372	Hippo Signaling Influences HNF4A and FOXA2 Enhancer Switching during Hepatocyte Differentiation. <i>Cell Reports</i> , 2014, 9, 261-271.	2.9	89
10373	miR-21 is a negative modulator of T-cell activation. <i>Biochimie</i> , 2014, 107, 319-326.	1.3	50
10374	Functional Network Pipeline Reveals Genetic Determinants Associated with in Situ Lymphocyte Proliferation and Survival of Cancer Patients. <i>Science Translational Medicine</i> , 2014, 6, 228ra37.	5.8	181
10375	SNPsea: an algorithm to identify cell types, tissues and pathways affected by risk loci. <i>Bioinformatics</i> , 2014, 30, 2496-2497.	1.8	60
10376	Global Regulation of a Differentiation MAPK Pathway in Yeast. <i>Genetics</i> , 2014, 198, 1309-1328.	1.2	33
10377	Detection of Alternative Splice and Gene Duplication by RNA Sequencing in Japanese Flounder, <i><i>Paralichthys olivaceus</i></i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2419-2424.	0.8	27
10378	Population- and Sex-Biased Gene Expression in the Excretion Organs of <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2307-2315.	0.8	35
10379	Networks' characteristics are important for systems biology. <i>Network Science</i> , 2014, 2, 139-161.	0.8	5
10380	The Natural Diyne-Furan Fatty Acid EV-086 Is an Inhibitor of Fungal Delta-9 Fatty Acid Desaturation with Efficacy in a Model of Skin Dermatophytosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 455-466.	1.4	12
10381	Gene Family Level Comparative Analysis of Gene Expression in Mammals Validates the Ortholog Conjecture. <i>Genome Biology and Evolution</i> , 2014, 6, 754-762.	1.1	51
10382	Mitochondrial Dysfunction and Decrease in Body Weight of a Transgenic Knock-in Mouse Model for TDP-43. <i>Journal of Biological Chemistry</i> , 2014, 289, 10769-10784.	1.6	100
10383	Evolutionary Algorithm Based on New Crossover for the Biclustering of Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2014, , 48-59.	1.0	7
10384	Semantic Particularity Measure for Functional Characterization of Gene Sets Using Gene Ontology. <i>PLoS ONE</i> , 2014, 9, e86525.	1.1	12
10385	Inferring gene ontologies from pairwise similarity data. <i>Bioinformatics</i> , 2014, 30, i34-i42.	1.8	78

#	ARTICLE	IF	CITATIONS
10386	Identification of functional miRNA regulatory modules and their associations via dynamic miRNA regulatory function. , 2014, , .		2
10387	The evolution of the ribosome biogenesis pathway from a yeast perspective. <i>Nucleic Acids Research</i> , 2014, 42, 1509-1523.	6.5	87
10388	MORPHIN: a web tool for human disease research by projecting model organism biology onto a human integrated gene network. <i>Nucleic Acids Research</i> , 2014, 42, W147-W153.	6.5	16
10389	Twist1-induced dissemination preserves epithelial identity and requires E-cadherin. <i>Journal of Cell Biology</i> , 2014, 204, 839-856.	2.3	178
10390	Mining the <i>Pseudomonas</i> Genome. <i>Methods in Molecular Biology</i> , 2014, 1149, 417-432.	0.4	4
10391	Chromosomal Instability Selects Gene Copy-Number Variants Encoding Core Regulators of Proliferation in ER+ Breast Cancer. <i>Cancer Research</i> , 2014, 74, 4853-4863.	0.4	66
10392	Dynamic Clustering of Gene Expression Data Using a Fuzzy Approach. , 2014, , .		2
10393	Identification by high-throughput imaging of the histone methyltransferase EHMT2 as an epigenetic regulator of VEGFA alternative splicing. <i>Nucleic Acids Research</i> , 2014, 42, 13662-13673.	6.5	44
10394	SIMAPâ€™the database of all-against-all protein sequence similarities and annotations with new interfaces and increased coverage. <i>Nucleic Acids Research</i> , 2014, 42, D279-D284.	6.5	24
10395	LipidGO: database for lipid-related GO terms and applications. <i>Bioinformatics</i> , 2014, 30, 1043-1044.	1.8	2
10396	Complete genome sequence of the Radiation-Resistant bacterium <i>Rubrobacter radiotolerans</i> RSPS-4. <i>Standards in Genomic Sciences</i> , 2014, 9, 1062-1075.	1.5	43
10397	Network-based detection of disease modules and potential drug targets in intractable epilepsy. , 2014, , .		2
10398	Positive correlation between ADAR expression and its targets suggests a complex regulation mediated by RNA editing in the human brain. <i>RNA Biology</i> , 2014, 11, 1447-1456.	1.5	14
10399	Studies on Periodontal Disease. <i>Oxidative Stress in Applied Basic Research and Clinical Practice</i> , 2014, , .	0.4	0
10400	Domain Ontology As Conceptual Model for Big Data Management: Application in Biomedical Informatics. <i>Lecture Notes in Computer Science</i> , 2014, , 144-157.	1.0	12
10401	Bioprospecting in the Genomic Age. <i>Advances in Applied Microbiology</i> , 2014, 87, 111-146.	1.3	10
10404	Exploiting Cell-To-Cell Variability To Detect Cellular Perturbations. <i>PLoS ONE</i> , 2014, 9, e90540.	1.1	12
10405	BioMet Toolbox 2.0: genome-wide analysis of metabolism and omics data. <i>Nucleic Acids Research</i> , 2014, 42, W175-W181.	6.5	40

#	ARTICLE	IF	CITATIONS
10406	Identification of Genes Related to the Early Stage of Angiotensin II-induced Acute Renal Injury by Microarray and Integrated Gene Network Analysis. <i>Cellular Physiology and Biochemistry</i> , 2014, 34, 1137-1151.	1.1	21
10407	Heterosis in Early Maize Ear Inflorescence Development: A Genome-Wide Transcription Analysis for Two Maize Inbred Lines and Their Hybrid. <i>International Journal of Molecular Sciences</i> , 2014, 15, 13892-13915.	1.8	25
10408	A robust data-driven approach for gene ontology annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau113-bau113.	1.4	4
10409	Evolutionary Conservation and Expression of Human RNA-Binding Proteins and Their Role in Human Genetic Disease. <i>Advances in Experimental Medicine and Biology</i> , 2014, 825, 1-55.	0.8	119
10410	<i>Translational Bioinformatics</i> . , 2014, , 721-754.		1
10411	RUNX1 positively regulates a cell adhesion and migration program in murine hemogenic endothelium prior to blood emergence. <i>Blood</i> , 2014, 124, e11-e20.	0.6	61
10412	Comparative analysis of knowledge representation and reasoning requirements across a range of life sciences textbooks. <i>Journal of Biomedical Semantics</i> , 2014, 5, 51.	0.9	4
10413	Motif Enrichment Tool. <i>Nucleic Acids Research</i> , 2014, 42, W20-W25.	6.5	7
10414	HubAlign: an accurate and efficient method for global alignment of protein-protein interaction networks. <i>Bioinformatics</i> , 2014, 30, i438-i444.	1.8	94
10415	Differential proteomic analysis of synovial fluid from rheumatoid arthritis and osteoarthritis patients. <i>Clinical Proteomics</i> , 2014, 11, 1.	1.1	113
10416	The top skin-associated genes: a comparative analysis of human and mouse skin transcriptomes. <i>Biological Chemistry</i> , 2014, 395, 577-591.	1.2	82
10417	Identifying transcription factor complexes and their roles. <i>Bioinformatics</i> , 2014, 30, i415-i421.	1.8	25
10418	RNA-Seq Analysis and De Novo Transcriptome Assembly of Jerusalem Artichoke (<i>Helianthus tuberosus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.1	31
10419	Characterization of the rainbow trout spleen transcriptome and identification of immune-related genes. <i>Frontiers in Genetics</i> , 2014, 5, 348.	1.1	41
10420	Causal inference of gene regulation with subnetwork assembly from genetical genomics data. <i>Nucleic Acids Research</i> , 2014, 42, 2803-2819.	6.5	15
10421	BC4GO: a full-text corpus for the BioCreative IV GO task. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau074-bau074.	1.4	36
10422	The integrated disease network. <i>Integrative Biology (United Kingdom)</i> , 2014, 6, 1069-1079.	0.6	28
10423	(Non-)Succinctness of uniform interpolants of general terminologies in the description logic <mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si1.gif" overflow="scroll"><mml:mi mathvariant="script">EL</mml:mi></mml:math>. <i>Artificial Intelligence</i> , 2014, 215, 120-140.	3.9	18

#	ARTICLE	IF	CITATIONS
10424	The cell behavior ontology: describing the intrinsic biological behaviors of real and model cells seen as active agents. <i>Bioinformatics</i> , 2014, 30, 2367-2374.	1.8	35
10425	Genome-wide association study identifies new disease loci for isolated clubfoot. <i>Journal of Medical Genetics</i> , 2014, 51, 334-339.	1.5	23
10426	CarrotDB: a genomic and transcriptomic database for carrot. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau096-bau096.	1.4	87
10427	Exploring the application of gene ontology semantic similarity measure for identifying protein complexes. , 2014, , .		1
10428	Genomic and Functional Analysis of the Toxic Effect of Tachyplesin I on the Embryonic Development of Zebrafish. <i>Computational and Mathematical Methods in Medicine</i> , 2014, 2014, 1-6.	0.7	3
10429	Complexity of Gene Expression Evolution after Duplication: Protein Dosage Rebalancing. <i>Genetics Research International</i> , 2014, 2014, 1-8.	2.0	25
10430	Update on Abdominal Aortic Aneurysm Research: From Clinical to Genetic Studies. <i>Scientifica</i> , 2014, 2014, 1-14.	0.6	32
10431	Systematic Analysis of Time-Series Gene Expression Data on Tumor Cell-Selective Apoptotic Responses to HDAC Inhibitors. <i>Computational and Mathematical Methods in Medicine</i> , 2014, 2014, 1-15.	0.7	4
10432	Correlating Information Contents of Gene Ontology Terms to Infer Semantic Similarity of Gene Products. <i>Computational and Mathematical Methods in Medicine</i> , 2014, 2014, 1-9.	0.7	10
10433	Genome-wide identification and analysis of growth regulating factor genes in <i>Brachypodium distachyon</i> : in silico approaches. <i>Turkish Journal of Biology</i> , 2014, 38, 296-306.	2.1	34
10434	A Pan-Cancer Modular Regulatory Network Analysis to Identify Common and Cancer-Specific Network Components. <i>Cancer Informatics</i> , 2014, 13s5, CIN.S14058.	0.9	18
10435	Innate Immunity Interactome Dynamics. <i>Gene Regulation and Systems Biology</i> , 2014, 8, GRSB.S12850.	2.3	1
10436	Gene Expression and Gene Ontology Enrichment Analysis for H3K4me3 and H3K4me1 in Mouse Liver and Mouse Embryonic Stem Cell Using ChIP-Seq and RNA-Seq. <i>Gene Regulation and Systems Biology</i> , 2014, 8, GRSB.S13612.	2.3	3
10437	The Potential Role of Sexual Conflict and Sexual Selection in Shaping the Genomic Distribution of Mito-nuclear Genes. <i>Genome Biology and Evolution</i> , 2014, 6, 1096-1104.	1.1	34
10438	An Integrative Analysis of Meningioma Tumors Reveals the Determinant Genes and Pathways of Malignant Transformation. <i>Frontiers in Oncology</i> , 2014, 4, 147.	1.3	8
10439	Integration of partial least squares and Monte Carlo gene expression analysis in coronary artery disease. <i>Experimental and Therapeutic Medicine</i> , 2014, 7, 1151-1154.	0.8	2
10440	Alzheimer disease: An interactome of many diseases. <i>Annals of Indian Academy of Neurology</i> , 2014, 17, 48.	0.2	5
10441	GOssTo: a stand-alone application and a web tool for calculating semantic similarities on the Gene Ontology. <i>Bioinformatics</i> , 2014, 30, 2235-2236.	1.8	44

#	ARTICLE	IF	CITATIONS
10443	PortEco: a resource for exploring bacterial biology through high-throughput data and analysis tools. <i>Nucleic Acids Research</i> , 2014, 42, D677-D684.	6.5	25
10444	Functional signature for the recognition of specific target mRNAs by human Staufen1 protein. <i>Nucleic Acids Research</i> , 2014, 42, 4516-4526.	6.5	36
10445	Time-resolved dissection of early phosphoproteome and ensuing proteome changes in response to TGF- β 2. <i>Science Signaling</i> , 2014, 7, rs5.	1.6	39
10446	Protein Domains of Unknown Function Are Essential in Bacteria. <i>MBio</i> , 2014, 5, e00744-13.	1.8	112
10447	Rapid Evolution of Phenotypic Plasticity and Shifting Thresholds of Genetic Assimilation in the Nematode <i>Caenorhabditis remanei</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1103-1112.	0.8	66
10448	Reproducibility enhancement and differential expression of non predefined functional gene sets in human genome. <i>BMC Genomics</i> , 2014, 15, 1181.	1.2	13
10449	Begin at the beginning: A BAC-end view of the passion fruit (<i>Passiflora</i>) genome. <i>BMC Genomics</i> , 2014, 15, 816.	1.2	34
10450	A vascular biology network model focused on inflammatory processes to investigate atherogenesis and plaque instability. <i>Journal of Translational Medicine</i> , 2014, 12, 185.	1.8	26
10451	Transcriptome sequencing and analysis of the zoonotic parasite <i>Spirometra erinacei</i> spargana (plerocercoids). <i>Parasites and Vectors</i> , 2014, 7, 368.	1.0	15
10452	The sialotranscriptome of <i>Amblyomma triste</i> , <i>Amblyomma parvum</i> and <i>Amblyomma cajennense</i> ticks, uncovered by 454-based RNA-seq. <i>Parasites and Vectors</i> , 2014, 7, 430.	1.0	75
10453	DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. <i>Molecular Autism</i> , 2014, 5, 22.	2.6	111
10454	Thematic series on biomedical ontologies in JBMS: challenges and new directions. <i>Journal of Biomedical Semantics</i> , 2014, 5, 15.	0.9	8
10455	Evaluating the Emotion Ontology through use in the self-reporting of emotional responses at an academic conference. <i>Journal of Biomedical Semantics</i> , 2014, 5, 38.	0.9	14
10456	Automatically exposing OpenLifeData via SADI semantic Web Services. <i>Journal of Biomedical Semantics</i> , 2014, 5, 46.	0.9	10
10457	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. <i>Journal of Biomedical Semantics</i> , 2014, 5, 5.	0.9	47
10458	Accounting for cellular heterogeneity is critical in epigenome-wide association studies. <i>Genome Biology</i> , 2014, 15, R31.	13.9	880
10459	Broad metabolic sensitivity profiling of a prototrophic yeast deletion collection. <i>Genome Biology</i> , 2014, 15, R64.	13.9	57
10460	Integrated genomic and prospective clinical studies show the importance of modular pleiotropy for disease susceptibility, diagnosis and treatment. <i>Genome Medicine</i> , 2014, 6, 17.	3.6	27

#	ARTICLE	IF	CITATIONS
10461	Predicting targeted drug combinations based on Pareto optimal patterns of coexpression network connectivity. <i>Genome Medicine</i> , 2014, 6, 33.	3.6	10
10462	Novel cardiovascular gene functions revealed via systematic phenotype prediction in zebrafish. <i>Development (Cambridge)</i> , 2014, 141, 224-235.	1.2	22
10463	Fluctuation of Rac1 activity is associated with the phenotypic and transcriptional heterogeneity of glioma cells. <i>Journal of Cell Science</i> , 2014, 127, 1805-1815.	1.2	21
10464	Characterization of Serum MicroRNAs Profile of PCOS and Identification of Novel Non-Invasive Biomarkers. <i>Cellular Physiology and Biochemistry</i> , 2014, 33, 1304-1315.	1.1	115
10465	Network portal: a database for storage, analysis and visualization of biological networks. <i>Nucleic Acids Research</i> , 2014, 42, D184-D190.	6.5	20
10466	Genetic robustness and functional evolution of gene duplicates. <i>Nucleic Acids Research</i> , 2014, 42, 2405-2414.	6.5	41
10467	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014, 42, D231-D239.	6.5	526
10468	Epstein-Barr virus-mediated transformation of B cells induces global chromatin changes independent to the acquisition of proliferation. <i>Nucleic Acids Research</i> , 2014, 42, 249-263.	6.5	34
10469	PubServer: literature searches by homology. <i>Nucleic Acids Research</i> , 2014, 42, W430-W435.	6.5	13
10470	Effect of pharmacologic resuscitation on the brain gene expression profiles in a swine model of traumatic brain injury and hemorrhage. <i>Journal of Trauma and Acute Care Surgery</i> , 2014, 77, 906-912.	1.1	32
10471	Robust clinical outcome prediction based on Bayesian analysis of transcriptional profiles and prior causal networks. <i>Bioinformatics</i> , 2014, 30, i69-i77.	1.8	21
10472	Linking tissues to phenotypes using gene expression profiles. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau017-bau017.	1.4	15
10473	RADB: a database of rheumatoid arthritis-related polymorphisms. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau090-bau090.	1.4	7
10474	iPathCons and iPathDB: an improved insect pathway construction tool and the database. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	1.4	14
10475	Increased Substitution Rates Surrounding Low-Complexity Regions within Primate Proteins. <i>Genome Biology and Evolution</i> , 2014, 6, 655-665.	1.1	21
10476	Developmental Cell Fate and Virulence Are Linked to Trehalose Homeostasis in <i>Cryptococcus neoformans</i> . <i>Eukaryotic Cell</i> , 2014, 13, 1158-1168.	3.4	18
10477	Aggregation of Ontology Matchers in Lieu of a Reference Ontology. , 2014, , .		1
10478	Curbing false discovery rates in interpretation of genome-wide expression profiles. <i>Journal of Biomedical Informatics</i> , 2014, 47, 58-61.	2.5	10

#	ARTICLE	IF	CITATIONS
10479	Spatial and Temporal Effects in Protein Post-translational Modification Distributions in the Developing Mouse Brain. <i>Journal of Proteome Research</i> , 2014, 13, 260-267.	1.8	21
10480	Systems Analysis of Chromatin-Related Protein Complexes in Cancer. , 2014, , .		0
10481	Long non-coding RNA NR_045623 and NR_028291 involved in benzene hematotoxicity in occupationally benzene-exposed workers. <i>Experimental and Molecular Pathology</i> , 2014, 96, 354-360.	0.9	30
10482	Proteinâ€“protein interaction network analysis and gene set enrichment analysis in epilepsy patients with brain cancer. <i>Journal of Clinical Neuroscience</i> , 2014, 21, 316-319.	0.8	14
10483	White matter as a transport system. <i>Neuroscience</i> , 2014, 276, 117-125.	1.1	55
10484	Unraveling molecular mechanistic differences in liver metabolism between lean and fat lines of Pekin duck (<i>Anas platyrhynchos domestica</i>): A proteomic study. <i>Journal of Proteomics</i> , 2014, 98, 271-288.	1.2	23
10485	The Dinoflagellate <i>Lingulodinium</i> has Predicted Casein Kinase 2 Sites in Many RNA Binding Proteins. <i>Protist</i> , 2014, 165, 330-342.	0.6	6
10486	Differential gene expression profiling analysis in workers occupationally exposed to benzene. <i>Science of the Total Environment</i> , 2014, 472, 872-879.	3.9	22
10487	Induction of apoptosis through ER stress and TP53 in MCF-7 cells by the nanoparticle [Gd@C82(OH)22]n: A systems biology study. <i>Methods</i> , 2014, 67, 394-406.	1.9	15
10488	Landscape of the relationship between type 2 diabetes and coronary heart disease through an integrated gene network analysis. <i>Gene</i> , 2014, 539, 30-36.	1.0	14
10489	Comparative proteomic analysis of <i>Saccharomyces cerevisiae</i> under different nitrogen sources. <i>Journal of Proteomics</i> , 2014, 101, 102-112.	1.2	27
10490	Arsenic exposure triggers a shift in microRNA expression. <i>Science of the Total Environment</i> , 2014, 472, 672-680.	3.9	41
10491	Global analysis of induced transcription factors and cofactors identifies Tfdp2 as an essential coregulator during terminal erythropoiesis. <i>Experimental Hematology</i> , 2014, 42, 464-476.e5.	0.2	15
10492	Structural network analysis of biological networks for assessment of potential disease model organisms. <i>Journal of Biomedical Informatics</i> , 2014, 47, 178-191.	2.5	5
10493	Transcriptional and proteomic analysis reveal recombinant galectins of <i>Haemonchus contortus</i> down-regulated functions of goat PBMC and modulation of several signaling cascades in vitro. <i>Journal of Proteomics</i> , 2014, 98, 123-137.	1.2	41
10494	Robust gene signatures from microarray data using genetic algorithms enriched with biological pathway keywords. <i>Journal of Biomedical Informatics</i> , 2014, 49, 32-44.	2.5	24
10495	Flor Revisited (Again): eQTL and Mutational Analysis of NB-LRR Mediated Immunity to Powdery Mildew in Barley. <i>Journal of Integrative Agriculture</i> , 2014, 13, 237-243.	1.7	1
10496	MSLoc-DT: A new method for predicting the protein subcellular location of multispecies based on decision templates. <i>Analytical Biochemistry</i> , 2014, 449, 164-171.	1.1	21

#	ARTICLE	IF	CITATIONS
10497	MicroRNAs Cooperatively Inhibit a Network of Tumor Suppressor Genes to Promote Pancreatic Tumor Growth and Progression. <i>Gastroenterology</i> , 2014, 146, 268-277.e18.	0.6	141
10498	Transcription Factor/microRNA Axis Blocks Melanoma Invasion Program by miR-211 Targeting NUA1. <i>Journal of Investigative Dermatology</i> , 2014, 134, 441-451.	0.3	95
10499	Likelihood-Based Approach to Gene Set Enrichment Analysis with a Finite Mixture Model. <i>Statistics in Biosciences</i> , 2014, 6, 38-54.	0.6	1
10500	N-hexane inhalation during pregnancy alters DNA promoter methylation in the ovarian granulosa cells of rat offspring. <i>Journal of Applied Toxicology</i> , 2014, 34, 841-856.	1.4	11
10501	Prediction of pathological mutations in proteins: the challenge of integrating sequence conservation and structure stability principles. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2014, 4, 249-268.	6.2	19
10502	In search of genome annotation consistency: solid gene clusters and how to use them. <i>3 Biotech</i> , 2014, 4, 331-335.	1.1	5
10503	The Human Interactome Knowledge Base (HINT-KB): an integrative human protein interaction database enriched with predicted protein-protein interaction scores using a novel hybrid technique. <i>Artificial Intelligence Review</i> , 2014, 42, 427-443.	9.7	5
10504	Computational SNP Analysis: Current Approaches and Future Prospects. <i>Cell Biochemistry and Biophysics</i> , 2014, 68, 233-239.	0.9	42
10505	Integrating Pathways of Parkinson's Disease in a Molecular Interaction Map. <i>Molecular Neurobiology</i> , 2014, 49, 88-102.	1.9	231
10506	Shared and distinct functions of two <i>G</i> protein-coupled receptor family proteins in growth, morphogenesis and pathogenicity of <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2014, 16, 788-801.	1.8	36
10507	Chromatin Biology and Cancer Linked Through Protein-Protein Interactions. , 2014, , 49-63.		0
10508	Guidelines for managing data and processes in bone and cartilage tissue engineering. <i>BMC Bioinformatics</i> , 2014, 15, S14.	1.2	8
10509	CorrelGenes: a new tool for the interpretation of the human transcriptome. <i>BMC Bioinformatics</i> , 2014, 15, S6.	1.2	4
10510	Network-assisted analysis to prioritize GWAS results: principles, methods and perspectives. <i>Human Genetics</i> , 2014, 133, 125-138.	1.8	86
10511	Proximal methods for the latent group lasso penalty. <i>Computational Optimization and Applications</i> , 2014, 58, 381-407.	0.9	19
10512	Analysis of expressed sequence tags from <i>Centella asiatica</i> (L.) Urban hairy roots elicited by methyl jasmonate to discover genes related to cytochrome P450s and glucosyltransferases. <i>Plant Biotechnology Reports</i> , 2014, 8, 211-220.	0.9	19
10513	Comparative Gene Expression Signature of Pig, Human and Mouse Induced Pluripotent Stem Cell Lines Reveals Insight into Pig Pluripotency Gene Networks. <i>Stem Cell Reviews and Reports</i> , 2014, 10, 162-176.	5.6	35
10514	Age distribution patterns of human gene families: divergent for Gene Ontology categories and concordant between different subcellular localizations. <i>Molecular Genetics and Genomics</i> , 2014, 289, 137-147.	1.0	3

#	ARTICLE	IF	CITATIONS
10515	De novo transcriptome analysis of an imminent biofuel crop, <i>Camelina sativa</i> L. using Illumina GAII-X sequencing platform and identification of SSR markers. <i>Plant Molecular Biology</i> , 2014, 84, 159-171.	2.0	84
10516	Screening drug target proteins based on sequence information. <i>Journal of Biomedical Informatics</i> , 2014, 49, 269-274.	2.5	7
10517	Paternal high-fat diet consumption induces common changes in the transcriptomes of retroperitoneal adipose and pancreatic islet tissues in female rat offspring. <i>FASEB Journal</i> , 2014, 28, 1830-1841.	0.2	122
10518	Exploring the Occurrence of Classic Selective Sweeps in Humans Using Whole-Genome Sequencing Data Sets. <i>Molecular Biology and Evolution</i> , 2014, 31, 1850-1868.	3.5	72
10519	Herpes Simplex Virus. <i>Methods in Molecular Biology</i> , 2014, , .	0.4	1
10520	Using VisANT to Analyze Networks. <i>Current Protocols in Bioinformatics</i> , 2014, 45, 8.8.1-39.	25.8	13
10521	An Introduction to RNA Databases. <i>Methods in Molecular Biology</i> , 2014, 1097, 107-123.	0.4	7
10522	Comparative analysis of two phenologically divergent populations of the pine processionary moth (<i>Thaumetopoea pityocampa</i>) by de novo transcriptome sequencing. <i>Insect Biochemistry and Molecular Biology</i> , 2014, 46, 31-42.	1.2	10
10523	cDNA-Microarray Analysis as a New Tool to Predict Lymph Node Metastasis in Gastric Cancer. <i>World Journal of Surgery</i> , 2014, 38, 2058-2064.	0.8	10
10524	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , 2014, 46, 261-269.	9.4	166
10525	Genomics: moving behavioural ecology beyond the phenotypic gambit. <i>Animal Behaviour</i> , 2014, 92, 263-270.	0.8	47
10526	Heterosis profile of sunflower leaves: A label free proteomics approach. <i>Journal of Proteomics</i> , 2014, 99, 101-110.	1.2	31
10527	Gene co-expression network analysis reveals common system-level properties of prognostic genes across cancer types. <i>Nature Communications</i> , 2014, 5, 3231.	5.8	385
10528	Extracting data from the muck: deriving biological insight from complex microbial communities and non-model organisms with next generation sequencing. <i>Current Opinion in Biotechnology</i> , 2014, 28, 103-110.	3.3	31
10529	Identifying functions of protein complexes based on topology similarity with random forest. <i>Molecular BioSystems</i> , 2014, 10, 514.	2.9	5
10530	Genome-wide pathway analysis in neuroblastoma. <i>Tumor Biology</i> , 2014, 35, 3471-3485.	0.8	12
10531	An HIV-Encoded Antisense Long Noncoding RNA Epigenetically Regulates Viral Transcription. <i>Molecular Therapy</i> , 2014, 22, 1164-1175.	3.7	162
10532	Dual RNA-seq of the plant pathogen <i>Phytophthora ramorum</i> and its tanoak host. <i>Tree Genetics and Genomes</i> , 2014, 10, 489-502.	0.6	45

#	ARTICLE	IF	CITATIONS
10533	Data extraction for the reaction kinetics database SABIO-RK. <i>Perspectives in Science</i> , 2014, 1, 33-40.	0.6	14
10534	Fungal Genomics. , 2014, , .		2
10535	Gene expression changes in aging Zebrafish (<i>Danio rerio</i>) brains are sexually dimorphic. <i>BMC Neuroscience</i> , 2014, 15, 29.	0.8	54
10536	Patchwork sequencing of tomato San Marzano and Vesuviano varieties highlights genome-wide variations. <i>BMC Genomics</i> , 2014, 15, 138.	1.2	32
10537	Dormancy within <i>Staphylococcus epidermidis</i> biofilms: a transcriptomic analysis by RNA-seq. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 2585-2596.	1.7	25
10538	DanQi Pill protects against heart failure through the arachidonic acid metabolism pathway by attenuating different cyclooxygenases and leukotrienes B4. <i>BMC Complementary and Alternative Medicine</i> , 2014, 14, 67.	3.7	32
10539	Gene expression analysis of familial hypercholesterolemia. <i>Molecular Biology</i> , 2014, 48, 158-164.	0.4	0
10540	Virus-independent and common transcriptome responses of leafhopper vectors feeding on maize infected with semi-persistently and persistent propagatively transmitted viruses. <i>BMC Genomics</i> , 2014, 15, 133.	1.2	33
10541	DFLAT: functional annotation for human development. <i>BMC Bioinformatics</i> , 2014, 15, 45.	1.2	27
10542	ComPlex: conservation and divergence of co-expression networks in <i>A. thaliana</i> , <i>Populus</i> and <i>O. sativa</i> . <i>BMC Genomics</i> , 2014, 15, 106.	1.2	69
10543	Computational Identification and Comparative Analysis of miRNAs in Wheat Group 7 Chromosomes. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 487-500.	1.0	10
10544	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014, 15, 86.	1.2	375
10545	Genotype-environment interactions for quantitative traits in Korea Associated Resource (KARE) cohorts. <i>BMC Genetics</i> , 2014, 15, 18.	2.7	6
10546	Computational developments in microRNA-regulated protein-protein interactions. <i>BMC Systems Biology</i> , 2014, 8, 14.	3.0	10
10547	Genome-wide transcriptome analysis of Chinese pollination-constant nonastringent persimmon fruit treated with ethanol. <i>BMC Genomics</i> , 2014, 15, 112.	1.2	38
10548	PrionScan: an online database of predicted prion domains in complete proteomes. <i>BMC Genomics</i> , 2014, 15, 102.	1.2	42
10549	De novo sequencing and comparative analysis of three red algal species of Family Solieriaceae to discover putative genes associated with carrageenan biosynthesis. <i>Acta Oceanologica Sinica</i> , 2014, 33, 45-53.	0.4	7
10550	Genome-wide identification and functional annotation of <i>Plasmodium falciparum</i> long noncoding RNAs from RNA-seq data. <i>Parasitology Research</i> , 2014, 113, 1269-1281.	0.6	41

#	ARTICLE	IF	CITATIONS
10551	Analyzing gene expression data in mice with the Neuro Behavior Ontology. <i>Mammalian Genome</i> , 2014, 25, 32-40.	1.0	19
10552	The BRANCHING ENZYME1 gene, encoding a glycoside hydrolase family 13 protein, is required for in vitro plant regeneration in Arabidopsis. <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 117, 279-291.	1.2	8
10553	Potential of Bioinformatics as functional genomics tool: an overview. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2014, 3, 1.	1.2	3
10554	MicroRNA miR-378 promotes BMP2-induced osteogenic differentiation of mesenchymal progenitor cells. <i>BMC Molecular Biology</i> , 2014, 15, 1.	3.0	67
10555	Sex differences in the human peripheral blood transcriptome. <i>BMC Genomics</i> , 2014, 15, 33.	1.2	131
10556	Constitutive patterns of gene expression regulated by RNA-binding proteins. <i>Genome Biology</i> , 2014, 15, R13.	13.9	35
10557	Cluster based prediction of PDZ-peptide interactions. <i>BMC Genomics</i> , 2014, 15, S5.	1.2	16
10558	Towards integrative gene functional similarity measurement. <i>BMC Bioinformatics</i> , 2014, 15, S5.	1.2	26
10559	On the selection of appropriate distances for gene expression data clustering. <i>BMC Bioinformatics</i> , 2014, 15, S2.	1.2	113
10560	Application of microRNA and mRNA expression profiling on prognostic biomarker discovery for hepatocellular carcinoma. <i>BMC Genomics</i> , 2014, 15, S13.	1.2	54
10561	Genome sequencing of high-penicillin producing industrial strain of <i>Penicillium chrysogenum</i> . <i>BMC Genomics</i> , 2014, 15, S11.	1.2	41
10562	Transcriptome profiling of granulosa cells from bovine ovarian follicles during atresia. <i>BMC Genomics</i> , 2014, 15, 40.	1.2	101
10563	TrigNER: automatically optimized biomedical event trigger recognition on scientific documents. <i>Source Code for Biology and Medicine</i> , 2014, 9, 1.	1.7	31
10564	Genome characteristics reveal the impact of lichenization on lichen-forming fungus <i>Endocarpon pusillum</i> Hedwig (Verrucariales, Ascomycota). <i>BMC Genomics</i> , 2014, 15, 34.	1.2	79
10565	ISAAC - InterSpecies Analysing Application using Containers. <i>BMC Bioinformatics</i> , 2014, 15, 18.	1.2	5
10566	Transcriptome profiling of granulosa cells of bovine ovarian follicles during growth from small to large antral sizes. <i>BMC Genomics</i> , 2014, 15, 24.	1.2	124
10567	Mitochondrial-related proteomic changes during obesity and fasting in mice are greater in the liver than skeletal muscles. <i>Functional and Integrative Genomics</i> , 2014, 14, 245-259.	1.4	25
10568	Functional genomics suggest neurogenesis in the adult human olfactory bulb. <i>Brain Structure and Function</i> , 2014, 219, 1991-2000.	1.2	45

#	ARTICLE	IF	CITATIONS
10569	Molecular sub-group-specific immunophenotypic changes are associated with outcome in recurrent posterior fossa ependymoma. <i>Acta Neuropathologica</i> , 2014, 127, 731-745.	3.9	73
10570	The transcription factor BATF operates as an essential differentiation checkpoint in early effector CD8+ T cells. <i>Nature Immunology</i> , 2014, 15, 373-383.	7.0	289
10571	Software platforms to facilitate reconstructing genome-scale metabolic networks. <i>Environmental Microbiology</i> , 2014, 16, 49-59.	1.8	69
10572	cis-Regulatory Requirements for Tissue-Specific Programs of the Circadian Clock. <i>Current Biology</i> , 2014, 24, 1-10.	1.8	376
10573	RNA Sequence, Structure, and Function: Computational and Bioinformatic Methods. <i>Methods in Molecular Biology</i> , 2014, , .	0.4	14
10574	Gene-disease association with literature based enrichment. <i>Journal of Biomedical Informatics</i> , 2014, 49, 221-226.	2.5	3
10575	Time-series RNA-seq analysis package (TRAP) and its application to the analysis of rice, <i>Oryza sativa</i> L. ssp. <i>Japonica</i> , upon drought stress. <i>Methods</i> , 2014, 67, 364-372.	1.9	31
10576	Impact of gestational chronodisruption on fetal cardiac genomics. <i>Journal of Molecular and Cellular Cardiology</i> , 2014, 66, 1-11.	0.9	23
10577	BLAST output visualization in the new sequencing era. <i>Briefings in Bioinformatics</i> , 2014, 15, 484-503.	3.2	25
10578	Metaproteomics of our microbiome - Developing insight in function and activity in man and model systems. <i>Journal of Proteomics</i> , 2014, 97, 3-16.	1.2	97
10579	A Draft Genome Sequence Reveals the <i>Helminthosporium solani</i> Arsenal for Cell Wall Degradation. <i>American Journal of Potato Research</i> , 2014, 91, 517-524.	0.5	6
10580	Fuzzy clustering with biological knowledge for gene selection. <i>Applied Soft Computing Journal</i> , 2014, 16, 102-111.	4.1	18
10581	Origins and functional evolution of Y chromosomes across mammals. <i>Nature</i> , 2014, 508, 488-493.	13.7	448
10582	Calculating structural complexity in phylogenies using ancestral ontologies. <i>Cladistics</i> , 2014, 30, 635-649.	1.5	30
10584	VEGF-binding aptides and the inhibition of choroidal and retinal neovascularization. <i>Biomaterials</i> , 2014, 35, 3052-3059.	5.7	16
10585	Modeling disease progression using dynamics of pathway connectivity. <i>Bioinformatics</i> , 2014, 30, 2343-2350.	1.8	56
10586	Exhaustive exercise modifies different gene expression profiles and pathways in LPS-stimulated and un-stimulated whole blood cultures. <i>Brain, Behavior, and Immunity</i> , 2014, 39, 130-141.	2.0	47
10587	RNA-seq Analysis of Antibiotic-Producing <i>Bacillus subtilis</i> SC-8 in Response to Signal Peptide PapR of <i>Bacillus cereus</i> . <i>Applied Biochemistry and Biotechnology</i> , 2014, 172, 580-594.	1.4	3

#	ARTICLE	IF	CITATIONS
10588	Genetic Predisposition, Humans. , 2014, , 341-364.		3
10589	Antimicrobial Mechanism Analysis of an Oil in Water Microemulsion by <i>DNA</i> Microarray-Mediated Transcriptional Profiling of <i>Escherichia Coli</i> . Journal of Food Safety, 2014, 34, 176-183.	1.1	3
10590	Gene expression in closely related species mirrors local adaptation: consequences for responses to a warming world. Molecular Ecology, 2014, 23, 2686-2698.	2.0	23
10591	Comparative genomics analysis of Lactobacillus species associated with weight gain or weight protection. Nutrition and Diabetes, 2014, 4, e109-e109.	1.5	95
10592	A novel ant colony optimization based single path hierarchical classification algorithm for predicting gene ontology. Applied Soft Computing Journal, 2014, 16, 34-49.	4.1	21
10593	Quantitative Real-Time PCR. Methods in Molecular Biology, 2014, , .	0.4	27
10594	Integrative Literature and Data Mining to Rank Disease Candidate Genes. Methods in Molecular Biology, 2014, 1159, 207-226.	0.4	1
10595	Global transcriptome analyses of human and murine terminal erythroid differentiation. Blood, 2014, 123, 3466-3477.	0.6	292
10596	A comparison of algorithms for the pairwise alignment of biological networks. Bioinformatics, 2014, 30, 2351-2359.	1.8	100
10597	FlyBase 102â€”advanced approaches to interrogating FlyBase. Nucleic Acids Research, 2014, 42, D780-D788.	6.5	287
10598	A <i>de novo</i> transcriptome of <i>E</i> uropean pollen beetle populations and its analysis, with special reference to insecticide action and resistance. Insect Molecular Biology, 2014, 23, 511-526.	1.0	29
10599	Converging Genetic and Functional Brain Imaging Evidence Links Neuronal Excitability to Working Memory, Psychiatric Disease, and Brain Activity. Neuron, 2014, 81, 1203-1213.	3.8	86
10600	Characterization of the canine urinary proteome. Veterinary Clinical Pathology, 2014, 43, 193-205.	0.3	24
10601	Glycolytic genes are targets of the nuclear receptor Ad4BP/SF-1. Nature Communications, 2014, 5, 3634.	5.8	57
10602	ISMARA: automated modeling of genomic signals as a democracy of regulatory motifs. Genome Research, 2014, 24, 869-884.	2.4	278
10603	The ctenophore genome and the evolutionary origins of neural systems. Nature, 2014, 510, 109-114.	13.7	606
10604	Global identification of <i>O</i> -GlcNAc transferase (OGT) interactors by a human proteome microarray and the construction of an OGT interactome. Proteomics, 2014, 14, 1020-1030.	1.3	35
10605	System-level multi-target drug discovery from natural products with applications to cardiovascular diseases. Molecular Diversity, 2014, 18, 621-635.	2.1	37

#	ARTICLE	IF	CITATIONS
10606	Microarray gene expression analysis of <i>Monochamus alternatus</i> (Coleoptera: Cerambycidae) after treatment with a sublethal dose of chloramine phosphorus. <i>Applied Entomology and Zoology</i> , 2014, 49, 223-230.	0.6	5
10607	Meta-Analysis of Retrograde Signaling in <i>Arabidopsis thaliana</i> Reveals a Core Module of Genes Embedded in Complex Cellular Signaling Networks. <i>Molecular Plant</i> , 2014, 7, 1167-1190.	3.9	69
10608	Neanderthal ancestry drives evolution of lipid catabolism in contemporary Europeans. <i>Nature Communications</i> , 2014, 5, 3584.	5.8	70
10609	Computational Identification of Pathogenic Associated nsSNPs and its Structural Impact in UROD Gene: A Molecular Dynamics Approach. <i>Cell Biochemistry and Biophysics</i> , 2014, 70, 735-746.	0.9	3
10611	Transcriptome profile of human neuroblastoma cells in the hypomagnetic field. <i>Science China Life Sciences</i> , 2014, 57, 448-461.	2.3	33
10612	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794.	13.5	363
10613	Bioinformatics analysis of time-series genes profiling to explore key genes affected by age in fracture healing. <i>Molecular Biology Reports</i> , 2014, 41, 3881-3889.	1.0	5
10614	GeneProf data: a resource of curated, integrated and reusable high-throughput genomics experiments. <i>Nucleic Acids Research</i> , 2014, 42, D851-D858.	6.5	18
10615	Evidence for Selection on Gene Expression in Cultivated Rice (<i>Oryza sativa</i>). <i>Molecular Biology and Evolution</i> , 2014, 31, 1514-1525.	3.5	29
10616	Systems genetics: From GWAS to disease pathways. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2014, 1842, 1903-1909.	1.8	67
10617	Anti-angiogenic effect of bare titanium dioxide nanoparticles on pathologic neovascularization without unbearable toxicity. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2014, 10, e1109-e1117.	1.7	48
10618	Global proteomic analysis of <i>Chelidonium majus</i> and <i>Corydalis cava</i> (Papaveraceae) extracts revealed similar defense-related protein compositions. <i>FÄ-toterapÄ-Äc</i> , 2014, 94, 77-87.	1.1	19
10619	Network Modeling to Understand Plant Immunity. <i>Annual Review of Phytopathology</i> , 2014, 52, 93-111.	3.5	38
10620	The role of carbon starvation in the induction of enzymes that degrade plant-derived carbohydrates in <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2014, 72, 34-47.	0.9	95
10621	The role of de novo mutations in the genetics of autism spectrum disorders. <i>Nature Reviews Genetics</i> , 2014, 15, 133-141.	7.7	339
10622	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2014, 42, D7-D17.	6.5	349
10623	Advances in Artificial Intelligence. <i>Lecture Notes in Computer Science</i> , 2014, , .	1.0	0
10624	A MicroRNA Cluster at 14q32 Drives Aggressive Lung Adenocarcinoma. <i>Clinical Cancer Research</i> , 2014, 20, 3107-3117.	3.2	92

#	ARTICLE	IF	CITATIONS
10625	Integrative gene set analysis of multi-platform data with sample heterogeneity. <i>Bioinformatics</i> , 2014, 30, 1501-1507.	1.8	10
10626	Comparison of gene expression profiles and related pathways in chronic thromboembolic pulmonary hypertension. <i>International Journal of Molecular Medicine</i> , 2014, 33, 277-300.	1.8	20
10627	Multiteric Regulation by Structural Disorder in Modular Signaling Proteins: An Extension of the Concept of Allostery. <i>Chemical Reviews</i> , 2014, 114, 6715-6732.	23.0	96
10628	A review of genomic data warehousing systems. <i>Briefings in Bioinformatics</i> , 2014, 15, 471-483.	3.2	22
10629	Coexpression network analysis associated with call of rice seedlings for encountering heat stress. <i>Plant Molecular Biology</i> , 2014, 84, 125-143.	2.0	90
10630	Similarity-based machine learning methods for predicting drug-target interactions: a brief review. <i>Briefings in Bioinformatics</i> , 2014, 15, 734-747.	3.2	321
10632	Functional combination strategy for prioritization of human miRNA target. <i>Gene</i> , 2014, 533, 132-141.	1.0	10
10633	<i>Biomedical Data.</i> , 2014, , 1-177.		1
10634	<i>Biomedical Information Access.</i> , 2014, , 397-478.		1
10635	Methylation of the DNA/RNA-binding protein Kin17 by METTL22 affects its association with chromatin. <i>Journal of Proteomics</i> , 2014, 100, 115-124.	1.2	36
10636	An Overview of the Challenges in Designing, Integrating, and Delivering BARD: A Public Chemical-Biology Resource and Query Portal for Multiple Organizations, Locations, and Disciplines. <i>Journal of Biomolecular Screening</i> , 2014, 19, 614-627.	2.6	22
10637	Complete genome sequence of invertebrate iridovirus IIV30 isolated from the corn earworm, <i>Helicoverpa zea</i> . <i>Journal of Invertebrate Pathology</i> , 2014, 116, 43-47.	1.5	11
10638	Extensive Oscillatory Gene Expression during <i>C.Âlegans</i> Larval Development. <i>Molecular Cell</i> , 2014, 53, 380-392.	4.5	188
10639	Algorithms and tools for protein-protein interaction networks clustering, with a special focus on population-based stochastic methods. <i>Bioinformatics</i> , 2014, 30, 1343-1352.	1.8	91
10640	De novo mutations in schizophrenia implicate synaptic networks. <i>Nature</i> , 2014, 506, 179-184.	13.7	1,510
10641	Identifying protein complexes and functional modules—from static PPI networks to dynamic PPI networks. <i>Briefings in Bioinformatics</i> , 2014, 15, 177-194.	3.2	149
10642	Molecular and biochemical responses to wounding in mesocarp of ripe peach (<i>Prunus persica</i> L.) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 1	2.9	16
10643	Transcriptome Analysis of Psoriasis in a Large Case-Control Sample: RNA-Seq Provides Insights into Disease Mechanisms. <i>Journal of Investigative Dermatology</i> , 2014, 134, 1828-1838.	0.3	318

#	ARTICLE	IF	CITATIONS
10644	The genomic landscape of Neanderthal ancestry in present-day humans. <i>Nature</i> , 2014, 507, 354-357.	13.7	877
10645	Secretome Analysis of Testicular Peritubular Cells: A Window into the Human Testicular Microenvironment and the Spermatogonial Stem Cell Niche in Man. <i>Journal of Proteome Research</i> , 2014, 13, 1259-1269.	1.8	47
10646	Approaches in Integrative Bioinformatics. , 2014, , .		4
10647	Network orientation via shortest paths. <i>Bioinformatics</i> , 2014, 30, 1449-1455.	1.8	27
10648	Global gene expression responses to waterlogging in leaves of rape seedlings. <i>Plant Cell Reports</i> , 2014, 33, 289-299.	2.8	56
10649	A hybrid method for prediction and repositioning of drug Anatomical Therapeutic Chemical classes. <i>Molecular BioSystems</i> , 2014, 10, 868.	2.9	70
10650	Pathway Analysis for Drug Repositioning Based on Public Database Mining. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 407-418.	2.5	40
10651	Changes in gene expression within the extended amygdala following binge-like alcohol drinking by adolescent alcohol-preferring (P) rats. <i>Pharmacology Biochemistry and Behavior</i> , 2014, 117, 52-60.	1.3	23
10652	Long Noncoding RNAs Expression Profile of the Developing Mouse Heart. <i>Journal of Cellular Biochemistry</i> , 2014, 115, 910-918.	1.2	34
10653	Towards revealing the functions of all genes in plants. <i>Trends in Plant Science</i> , 2014, 19, 212-221.	4.3	221
10654	Transgenic: An evolutionary algorithm operator. <i>Neurocomputing</i> , 2014, 127, 104-113.	3.5	7
10655	The semantic measures library and toolkit: fast computation of semantic similarity and relatedness using biomedical ontologies. <i>Bioinformatics</i> , 2014, 30, 740-742.	1.8	103
10656	Serotonergic neuron regulation informed by in vivo single-cell transcriptomics. <i>FASEB Journal</i> , 2014, 28, 771-780.	0.2	55
10657	Ontodog: a web-based ontology community view generation tool. <i>Bioinformatics</i> , 2014, 30, 1340-1342.	1.8	13
10658	PIP ₃ Induces the Recycling of Receptor Tyrosine Kinases. <i>Science Signaling</i> , 2014, 7, ra5.	1.6	39
10659	The WAVE Regulatory Complex Links Diverse Receptors to the Actin Cytoskeleton. <i>Cell</i> , 2014, 156, 195-207.	13.5	260
10660	Intelligent Strategies for Pathway Mining. <i>Lecture Notes in Computer Science</i> , 2014, , .	1.0	0
10661	Bioinformatic analysis to find small molecules related to rheumatoid arthritis. <i>International Journal of Rheumatic Diseases</i> , 2014, 17, 71-77.	0.9	2

#	ARTICLE	IF	CITATIONS
10662	<scp>M</scp>ercator: a fast and simple web server for genome scale functional annotation of plant sequence data. <i>Plant, Cell and Environment</i> , 2014, 37, 1250-1258.	2.8	575
10663	Minke whale genome and aquatic adaptation in cetaceans. <i>Nature Genetics</i> , 2014, 46, 88-92.	9.4	227
10664	In vivo genome-wide profiling of RNA secondary structure reveals novel regulatory features. <i>Nature</i> , 2014, 505, 696-700.	13.7	710
10665	Non-coding RNAs and Cancer. , 2014, , .		6
10666	Hypoxia induces a HIF-1 \pm dependent signaling cascade to make a complex metabolic switch in SGBS-adipocytes. <i>Molecular and Cellular Endocrinology</i> , 2014, 383, 21-31.	1.6	29
10667	Celiac Disease as a Model for the Evolution of Multifactorial Disease in Humans. <i>Human Biology</i> , 2014, 86, 19-36.	0.4	8
10668	The ENCODE Project and Perspectives on Pathways. <i>Genetic Epidemiology</i> , 2014, 38, 275-280.	0.6	47
10669	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	6.0	2,096
10670	Exploiting open data: a new era in pharmacoinformatics. <i>Future Medicinal Chemistry</i> , 2014, 6, 503-514.	1.1	18
10671	Genomic and transcriptomic analyses of the medicinal fungus <i>Antrodia cinnamomea</i> for its metabolite biosynthesis and sexual development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4743-52.	3.3	79
10672	A systems biology analysis for the whole genome sequencing data. , 2014, , .		0
10673	A Spaetzle-like role for nerve growth factor $\hat{1}^2$ in vertebrate immunity to <i>Staphylococcus aureus</i> . <i>Science</i> , 2014, 346, 641-646.	6.0	68
10674	High-throughput Sequencing Technology and Its Application. <i>The Journal of Northeast Agricultural University</i> , 2014, 21, 84-96.	0.1	16
10675	Adaptation to abiotic stress in the oyster <i>Crassostrea angulata</i> relays on genetic polymorphisms. <i>Fish and Shellfish Immunology</i> , 2014, 41, 618-624.	1.6	8
10676	Determining Microbial Products and Identifying Molecular Targets in the Human Microbiome. <i>Cell Metabolism</i> , 2014, 20, 731-741.	7.2	82
10677	Regulation of gene expression by the BLM helicase correlates with the presence of G-quadruplex DNA motifs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9905-9910.	3.3	108
10678	Using association rule mining to determine promising secondary phenotyping hypotheses. <i>Bioinformatics</i> , 2014, 30, i52-i59.	1.8	9
10679	miR-125b-1-3p inhibits trophoblast cell invasion by targeting sphingosine-1-phosphate receptor 1 in preeclampsia. <i>Biochemical and Biophysical Research Communications</i> , 2014, 453, 57-63.	1.0	57

#	ARTICLE	IF	CITATIONS
10680	Identification of four novel serum protein biomarkers in sepsis patients encoded by target genes of sepsis-related miRNAs. <i>Clinical Science</i> , 2014, 126, 857-867.	1.8	18
10681	tRanslatome: an R/Bioconductor package to portray translational control. <i>Bioinformatics</i> , 2014, 30, 289-291.	1.8	20
10682	Data management strategies for multinational large-scale systems biology projects. <i>Briefings in Bioinformatics</i> , 2014, 15, 65-78.	3.2	28
10683	Functional module identification in protein interaction networks by interaction patterns. <i>Bioinformatics</i> , 2014, 30, 81-93.	1.8	48
10684	EBI metagenomics—a new resource for the analysis and archiving of metagenomic data. <i>Nucleic Acids Research</i> , 2014, 42, D600-D606.	6.5	127
10685	MEGANTE: A Web-Based System for Integrated Plant Genome Annotation. <i>Plant and Cell Physiology</i> , 2014, 55, e2-e2.	1.5	27
10686	BEReX: Biomedical Entity-Relationship eXplorer. <i>Bioinformatics</i> , 2014, 30, 135-136.	1.8	7
10687	The nutritionally responsive transcriptome of the polyphenic beetle <i>Onthophagus taurus</i> and the importance of sexual dimorphism and body region. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20142084.	1.2	29
10688	starBase v2.0: decoding miRNA-ceRNA, miRNA-ncRNA and protein-miRNA interaction networks from large-scale CLIP-Seq data. <i>Nucleic Acids Research</i> , 2014, 42, D92-D97.	6.5	4,113
10689	Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17230-17235.	3.3	281
10690	InterProScan 5: genome-scale protein function classification. <i>Bioinformatics</i> , 2014, 30, 1236-1240.	1.8	6,553
10691	Natural Language Processing and Information Systems. <i>Lecture Notes in Computer Science</i> , 2014, , .	1.0	1
10692	A relative shift in cloacal location repositions external genitalia in amniote evolution. <i>Nature</i> , 2014, 516, 391-394.	13.7	70
10693	Auditing the multiply-related concepts within the UMLS. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2014, 21, e185-e193.	2.2	11
10694	Poster: Context-sensitive use of bioinformatics tools with complementary functionalities for hypothesis generation. , 2014, , .		0
10695	Average oxidation state of carbon in proteins. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20131095.	1.5	33
10696	A candidate gene approach for virally induced cancer with application to HIV-related Kaposi's sarcoma. <i>International Journal of Cancer</i> , 2014, 134, 397-404.	2.3	5
10697	Cell-Type-Specific Repression by Methyl-CpG-Binding Protein 2 Is Biased toward Long Genes. <i>Journal of Neuroscience</i> , 2014, 34, 12877-12883.	1.7	119

#	ARTICLE	IF	CITATIONS
10698	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
10699	Macrophages: Biology and Role in the Pathology of Diseases. , 2014, , .		13
10700	Biological Cluster Evaluation for Gene Function Prediction. <i>Journal of Computational Biology</i> , 2014, 21, 428-445.	0.8	13
10701	A Bayesian extension of the hypergeometric test for functional enrichment analysis. <i>Biometrics</i> , 2014, 70, 84-94.	0.8	50
10702	Endometrial gene expression reveals compromised progesterone signaling in women refractory to embryo implantation. <i>Reproductive Biology and Endocrinology</i> , 2014, 12, 92.	1.4	34
10703	Fine-scale population epigenetic structure in relation to gastrointestinal parasite load in red grouse (<i>Lagopus lagopus scoticus</i>). <i>Molecular Ecology</i> , 2014, 23, 4256-4273.	2.0	51
10704	Shotgun MS proteomic analysis of bronchoalveolar lavage fluid in normal subjects. <i>Proteomics - Clinical Applications</i> , 2014, 8, 737-747.	0.8	17
10705	BioTextQuest + : a knowledge integration platform for literature mining and concept discovery. <i>Bioinformatics</i> , 2014, 30, 3249-3256.	1.8	23
10706	Quantitative proteomics reveals novel therapeutic and diagnostic markers in hypertension. <i>BBA Clinical</i> , 2014, 2, 79-87.	4.1	26
10707	Copy Number Variants in Short Children Born Small for Gestational Age. <i>Hormone Research in Paediatrics</i> , 2014, 82, 310-318.	0.8	25
10708	Characterization of wound-induced serine protease inhibitor (wip1) genes and proteins in Turkish maize varieties. <i>Biochemistry (Moscow)</i> , 2014, 79, 836-844.	0.7	3
10709	E2F1 induces miR-224/452 expression to drive EMT through TXNIP downregulation. <i>EMBO Reports</i> , 2014, 15, 1315-1329.	2.0	78
10710	Learning regulatory programs by threshold SVD regression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15675-15680.	3.3	21
10711	Identification of <i>Cdca7</i> as a novel Notch transcriptional target involved in hematopoietic stem cell emergence. <i>Journal of Experimental Medicine</i> , 2014, 211, 2411-2423.	4.2	46
10712	Fuzzy ontologies: The state of the art. , 2014, , .		8
10713	Analysis of the Human Tissue-specific Expression by Genome-wide Integration of Transcriptomics and Antibody-based Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 397-406.	2.5	2,819
10714	A census of human RNA-binding proteins. <i>Nature Reviews Genetics</i> , 2014, 15, 829-845.	7.7	1,671
10715	Epigenomic profiling of men exposed to early-life stress reveals DNA methylation differences in association with current mental state. <i>Translational Psychiatry</i> , 2014, 4, e448-e448.	2.4	54

#	ARTICLE	IF	CITATIONS
10716	Autosomal dominant immune dysregulation syndrome in humans with CTLA4 mutations. <i>Nature Medicine</i> , 2014, 20, 1410-1416.	15.2	723
10717	A Functional and Evolutionary Perspective on Transcription Factor Binding in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2014, 26, 3894-3910.	3.1	102
10718	TRAQ-based proteomic analysis of dioscin on human HCT116 colon cancer cells. <i>Proteomics</i> , 2014, 14, 51-73.	1.3	43
10719	The human liver-specific proteome defined by transcriptomics and antibody-based profiling. <i>FASEB Journal</i> , 2014, 28, 2901-2914.	0.2	73
10720	Drug-pathway interaction prediction via multiple feature fusion. <i>Molecular BioSystems</i> , 2014, 10, 2907-2913.	2.9	15
10721	Complementarity between distance- and probability-based methods of gene neighbourhood identification for pathway reconstruction. <i>Molecular BioSystems</i> , 2014, 10, 24-29.	2.9	25
10722	Analysis of clock-regulated genes in <i>Neurospora</i> reveals widespread posttranscriptional control of metabolic potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16995-17002.	3.3	131
10723	Genome-wide identification of aberrantly methylated promoters in ovarian tissue of prenatally androgenized rats. <i>Fertility and Sterility</i> , 2014, 102, 1458-1467.	0.5	24
10724	Comparative analysis of deep-sea bacterioplankton OMICS revealed the occurrence of habitat-specific genomic attributes. <i>Marine Genomics</i> , 2014, 17, 1-8.	0.4	11
10725	Coordinated regulation of photosynthesis in rice increases yield and tolerance to environmental stress. <i>Nature Communications</i> , 2014, 5, 5302.	5.8	254
10726	PSEA-Quant: A Protein Set Enrichment Analysis on Label-Free and Label-Based Protein Quantification Data. <i>Journal of Proteome Research</i> , 2014, 13, 5496-5509.	1.8	57
10727	The Global Phosphoproteome of <i>Chlamydomonas reinhardtii</i> Reveals Complex Organellar Phosphorylation in the Flagella and Thylakoid Membrane. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2337-2353.	2.5	100
10728	The relationship between classification of multi-domain proteins using an alignment-free approach and their functions: a case study with immunoglobulins. <i>Molecular BioSystems</i> , 2014, 10, 1082.	2.9	8
10729	A Weighted Multipath Measurement Based on Gene Ontology for Estimating Gene Products Similarity. <i>Journal of Computational Biology</i> , 2014, 21, 964-974.	0.8	1
10730	Comprehensive Comparative and Semiquantitative Proteome of a Very Low Number of Native and Matched Epstein-Barr-Virus-Transformed B Lymphocytes Infiltrating Human Melanoma. <i>Journal of Proteome Research</i> , 2014, 13, 2830-2845.	1.8	15
10732	Shedding light on black boxes in protein identification. <i>Proteomics</i> , 2014, 14, 1001-1005.	1.3	20
10733	Affinity purification-mass spectrometry and network analysis to understand protein-protein interactions. <i>Nature Protocols</i> , 2014, 9, 2539-2554.	5.5	169
10734	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

#	ARTICLE	IF	CITATIONS
10735	Ensemble learning prediction of protein-protein interactions using proteins functional annotations. <i>Molecular BioSystems</i> , 2014, 10, 820.	2.9	47
10736	Semantic Web, Ontologies, and Linked Data. , 2014, , 67-76.		1
10737	Co-expression and co-localization of hub proteins and their partners are encoded in protein sequence. <i>Molecular BioSystems</i> , 2014, 10, 787.	2.9	1
10738	A Root-Expressed <i>scp</i> -Phenylalanine:4-Hydroxyphenylpyruvate Aminotransferase Is Required for Tropane Alkaloid Biosynthesis in <i>Atropa belladonna</i> . <i>Plant Cell</i> , 2014, 26, 3745-3762.	3.1	69
10739	Genomic Analysis of the Pacific Oyster (<i>Crassostrea gigas</i>) Reveals Possible Conservation of Vertebrate Sex Determination in a Mollusc. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2207-2217.	0.8	81
10740	MetalPrint: an information repository of mammalian imprinted genes. <i>Development (Cambridge)</i> , 2014, 141, 2516-2523.	1.2	68
10741	Organizing knowledge to enable personalization of medicine in cancer. <i>Genome Biology</i> , 2014, 15, 438.	3.8	81
10742	Microarray gene expression profiling and bioinformatics analysis of premature ovarian failure in a rat model. <i>Experimental and Molecular Pathology</i> , 2014, 97, 535-541.	0.9	12
10743	Evaluating the Significance of Protein Functional Similarity Based on Gene Ontology. <i>Journal of Computational Biology</i> , 2014, 21, 809-822.	0.8	3
10744	A Newtonian Framework for Community Detection in Undirected Biological Networks. <i>IEEE Transactions on Biomedical Circuits and Systems</i> , 2014, 8, 65-73.	2.7	9
10746	Proteomic Investigation of Signatures for Geniposide-Induced Hepatotoxicity. <i>Journal of Proteome Research</i> , 2014, 13, 5724-5733.	1.8	29
10747	Human Adult White Matter Progenitor Cells Are Multipotent Neuroprogenitors Similar to Adult Hippocampal Progenitors. <i>Stem Cells Translational Medicine</i> , 2014, 3, 458-469.	1.6	26
10748	Energy metabolism analysis reveals the mechanism of inhibition of breast cancer cell metastasis by PEG-modified graphene oxide nanosheets. <i>Biomaterials</i> , 2014, 35, 9833-9843.	5.7	99
10750	Analysis and identification of essential genes in humans using topological properties and biological information. <i>Gene</i> , 2014, 551, 138-151.	1.0	22
10751	Classification of Hepatotoxicants Using HepG2 Cells: A Proof of Principle Study. <i>Chemical Research in Toxicology</i> , 2014, 27, 433-442.	1.7	59
10752	DIVE: A Graph-Based Visual-Analytics Framework for Big Data. <i>IEEE Computer Graphics and Applications</i> , 2014, 34, 26-37.	1.0	34
10753	Elucidating Influenza Inhibition Pathways via Network Reconstruction. <i>Journal of Computational Biology</i> , 2014, 21, 394-404.	0.8	1
10754	Glycaemia and insulin after acute myocardial infarction. <i>Nature Reviews Endocrinology</i> , 2014, 10, 448-450.	4.3	3

#	ARTICLE	IF	CITATIONS
10755	Transcriptomic Responses of Cancerous and Noncancerous Human Colon Cells to Sulforaphane and Selenium. <i>Chemical Research in Toxicology</i> , 2014, 27, 377-386.	1.7	10
10757	Role of Blimp-1 in programming Th effector cells into IL-10 producers. <i>Journal of Experimental Medicine</i> , 2014, 211, 1807-1819.	4.2	161
10758	Changes in proteome of the <i>P</i> strain derived from <i>Francisella tularensis</i> LVS correspond with its attenuated phenotype. <i>Proteomics</i> , 2014, 14, 2400-2409.	1.3	6
10759	T cell transcripts and T cell activities in the gills of the teleost fish sea bass (<i>Dicentrarchus labrax</i>). <i>Developmental and Comparative Immunology</i> , 2014, 47, 309-318.	1.0	58
10760	Structural, Syntactic, and Statistical Pattern Recognition. <i>Lecture Notes in Computer Science</i> , 2014, , .	1.0	3
10761	Discovery of Spatially Cohesive Itemsets in Three-Dimensional Protein Structures. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 814-825.	1.9	5
10762	Global identification of CobB interactors by an <i>Escherichia coli</i> proteome microarray. <i>Acta Biochimica Et Biophysica Sinica</i> , 2014, 46, 548-555.	0.9	33
10763	HSF-1-mediated cytoskeletal integrity determines thermotolerance and life span. <i>Science</i> , 2014, 346, 360-363.	6.0	174
10764	Current advances in systems and integrative biology. <i>Computational and Structural Biotechnology Journal</i> , 2014, 11, 35-46.	1.9	29
10765	Using Pseudogene Database to Identify Lineage-Specific Genes and Pseudogenes in Humans and Chimpanzees. <i>Journal of Heredity</i> , 2014, 105, 436-443.	1.0	4
10766	Brain Proteome Changes Induced by Olfactory Learning in <i>Drosophila</i> . <i>Journal of Proteome Research</i> , 2014, 13, 3763-3770.	1.8	7
10767	Exosomes from docetaxel-resistant breast cancer cells alter chemosensitivity by delivering microRNAs. <i>Tumor Biology</i> , 2014, 35, 9649-9659.	0.8	126
10768	Phen-Gen: combining phenotype and genotype to analyze rare disorders. <i>Nature Methods</i> , 2014, 11, 935-937.	9.0	130
10769	Metatranscriptomic analysis of ectomycorrhizal roots reveals genes associated with <i>loderma</i> symbiosis: improved methodologies for assessing gene expression <i>in situ</i> . <i>Environmental Microbiology</i> , 2014, 16, 3730-3742.	1.8	71
10770	Genome-wide identification of housekeeping genes in maize. <i>Plant Molecular Biology</i> , 2014, 86, 543-554.	2.0	68
10771	Mass Spectrometry and Imaging Analysis of Nanoparticle-Containing Vesicles Provide a Mechanistic Insight into Cellular Trafficking. <i>ACS Nano</i> , 2014, 8, 10077-10088.	7.3	84
10773	De novo assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits. <i>Nature Biotechnology</i> , 2014, 32, 1045-1052.	9.4	535
10774	Compartment Proteomics Analysis of White Perch (<i>Morone americana</i>) Ovary Using Support Vector Machines. <i>Journal of Proteome Research</i> , 2014, 13, 1515-1526.	1.8	20

#	ARTICLE	IF	CITATIONS
10775	Computational Methods to Predict Long Noncoding RNA Functions Based on Co-expression Network. <i>Methods in Molecular Biology</i> , 2014, 1182, 209-218.	0.4	11
10776	Widespread intron retention in mammals functionally tunes transcriptomes. <i>Genome Research</i> , 2014, 24, 1774-1786.	2.4	554
10777	Bioinformatics for Cancer Genomics. , 2014, , 133-152.		1
10778	Adaptive, convergent origins of the pygmy phenotype in African rainforest hunter-gatherers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3596-603.	3.3	91
10779	Lean Big Data integration in systems biology and systems pharmacology. <i>Trends in Pharmacological Sciences</i> , 2014, 35, 450-460.	4.0	85
10780	Exploring differentially expressed genes in the ovaries of uniparous and multiparous goats using the RNA-Seq (Quantification) method. <i>Gene</i> , 2014, 550, 148-153.	1.0	28
10781	Sma3s: A Three-Step Modular Annotator for Large Sequence Datasets. <i>DNA Research</i> , 2014, 21, 341-353.	1.5	80
10782	Bioinformatics: Concepts, Methods, and Data. , 2014, , 259-287.		9
10783	Extracellular Matrix Remodeling by Bone Marrow Fibroblast-like Cells Correlates with Disease Progression in Multiple Myeloma. <i>Journal of Proteome Research</i> , 2014, 13, 844-854.	1.8	46
10784	Functional and genomic context in pathway analysis of GWAS data. <i>Trends in Genetics</i> , 2014, 30, 390-400.	2.9	95
10785	Hemicellulase production by <i>Aspergillus niger</i> DSM 26641 in hydrothermal palm oil empty fruit bunch hydrolysate and transcriptome analysis. <i>Journal of Bioscience and Bioengineering</i> , 2014, 118, 696-701.	1.1	15
10786	A Dual Program for Translation Regulation in Cellular Proliferation and Differentiation. <i>Cell</i> , 2014, 158, 1281-1292.	13.5	414
10787	Inhibition of Cancer Cell Migration by Gold Nanorods: Molecular Mechanisms and Implications for Cancer Therapy. <i>Advanced Functional Materials</i> , 2014, 24, 6922-6932.	7.8	69
10788	Evolution of the mir-181 microRNA family. <i>Computers in Biology and Medicine</i> , 2014, 52, 82-87.	3.9	31
10789	Adolescent Mouse Takes on An Active Transcriptomic Expression During Postnatal Cerebral Development. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 111-119.	3.0	4
10790	Statistical stage transition detection method for small sample gene expression time series data. <i>Mathematical Biosciences</i> , 2014, 254, 58-63.	0.9	0
10791	Global Protein-Protein Interaction Network of Rice Sheath Blight Pathogen. <i>Journal of Proteome Research</i> , 2014, 13, 3277-3293.	1.8	25
10793	DNA-damage-induced differentiation of leukaemic cells as an anti-cancer barrier. <i>Nature</i> , 2014, 514, 107-111.	13.7	174

#	ARTICLE	IF	CITATIONS
10794	Identification and Evolution of Structurally Dominant Nodes in Protein-Protein Interaction Networks. <i>IEEE Transactions on Biomedical Circuits and Systems</i> , 2014, 8, 87-97.	2.7	57
10795	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	13.7	725
10796	Proteomic analysis of zoxamide-induced changes in <i>Phytophthora cactorum</i> . <i>Pesticide Biochemistry and Physiology</i> , 2014, 113, 31-39.	1.6	18
10797	Differential DNA methylation status between breast carcinomatous and normal tissues. <i>Biomedicine and Pharmacotherapy</i> , 2014, 68, 699-707.	2.5	21
10798	Automated hypothesis generation based on mining scientific literature. , 2014, , .		82
10799	A Foundation for Reliable Spatial Proteomics Data Analysis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1937-1952.	2.5	49
10800	Comparative Genomics of Flatworms (Platyhelminthes) Reveals Shared Genomic Features of Ecto- and Endoparasitic Neodermata. <i>Genome Biology and Evolution</i> , 2014, 6, 1105-1117.	1.1	73
10801	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
10802	Does estrogen deficiency cause lacrimal gland inflammation and aqueous-deficient dry eye in mice?. <i>Experimental Eye Research</i> , 2014, 127, 153-160.	1.2	23
10803	Characterizing the transcriptome of yellow-cheek carp (<i>Elopichthys bambusa</i>) enables evolutionary analyses within endemic East Asian Cyprinidae. <i>Gene</i> , 2014, 547, 267-272.	1.0	9
10804	Improving functional annotation for industrial microbes: a case study with <i>Pichia pastoris</i> . <i>Trends in Biotechnology</i> , 2014, 32, 396-399.	4.9	23
10805	Bioinformatics analysis of plant orthologous introns: identification of an intronic tRNA-like sequence. <i>Gene</i> , 2014, 548, 81-90.	1.0	4
10806	Computational integration of genomic traits into 16S rDNA microbiota sequencing studies. <i>Gene</i> , 2014, 549, 186-191.	1.0	19
10807	Genome-wide association analyses identify variants in developmental genes associated with hypospadias. <i>Nature Genetics</i> , 2014, 46, 957-963.	9.4	97
10808	Interactive transcriptome analysis of malaria patients and infecting <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2014, 24, 1433-1444.	2.4	76
10809	RNA Mapping. <i>Methods in Molecular Biology</i> , 2014, , .	0.4	4
10810	The Role of Historical Bioactivity Data in the Deconvolution of Phenotypic Screens. <i>Journal of Biomolecular Screening</i> , 2014, 19, 696-706.	2.6	12
10811	Antennal transcriptome analysis and comparison of olfactory genes in two sympatric defoliators, <i>Dendrolimus houi</i> and <i>Dendrolimus kikuchii</i> (Lepidoptera: Lasiocampidae). <i>Insect Biochemistry and Molecular Biology</i> , 2014, 52, 69-81.	1.2	74

#	ARTICLE	IF	CITATIONS
10812	Drugâ€‘target interaction prediction via chemogenomic space: learning-based methods. Expert Opinion on Drug Metabolism and Toxicology, 2014, 10, 1273-1287.	1.5	83
10813	CpG island methylator phenotype of myelodysplastic syndrome identified through genomeâ€‘wide profiling of <scp>DNA</scp> methylation and gene expression. British Journal of Haematology, 2014, 165, 649-658.	1.2	24
10814	From commonsense to science, and back: The use of cognitive concepts in neuroscience. Consciousness and Cognition, 2014, 29, 248-258.	0.8	24
10815	â€‘N-of-1<i> pathways</i>â€™ unveils personal deregulated mechanisms from a single pair of RNA-Seq samples: towards precision medicine. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 1015-1025.	2.2	42
10816	Concept mapping One-Carbon Metabolism to model future ontologies for nutrientâ€‘geneâ€‘phenotype interactions. Genes and Nutrition, 2014, 9, 419.	1.2	2
10817	Algorithms for global proteinâ€‘protein interaction network alignment. Network Modeling Analysis in Health Informatics and Bioinformatics, 2014, 3, 1.	1.2	3
10818	A novel method for gathering and prioritizing disease candidate genes based on construction of a set of disease-related MeSHâ® terms. BMC Bioinformatics, 2014, 15, 179.	1.2	8
10819	Detecting overlapping protein complexes based on a generative model with functional and topological properties. BMC Bioinformatics, 2014, 15, 186.	1.2	39
10820	eXamine: Exploring annotated modules in networks. BMC Bioinformatics, 2014, 15, 201.	1.2	16
10821	Homology-based prediction of interactions between proteins using Averaged One-Dependence Estimators. BMC Bioinformatics, 2014, 15, 213.	1.2	77
10822	DBSecSys: a database of Burkholderia malleisecretion systems. BMC Bioinformatics, 2014, 15, 244.	1.2	9
10823	Gene set enrichment analysis for multiple continuous phenotypes. BMC Bioinformatics, 2014, 15, 260.	1.2	9
10824	A comprehensive assessment of the transcriptome of cork oak (Quercus suber) through EST sequencing. BMC Genomics, 2014, 15, 371.	1.2	53
10825	Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds. BMC Genomics, 2014, 15, 442.	1.2	191
10826	Sequencing and characterization of the transcriptome of half-smooth tongue sole (Cynoglossus) Tj ETQq0 0 0 rgBT //Overlock 10 Tf 50 1	1.2	24
10827	Comparative genomics of Riemerella anatipestifer reveals genetic diversity. BMC Genomics, 2014, 15, 479.	1.2	60
10828	The genome of the white-rot fungus Pycnoporus cinnabarinus: a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. BMC Genomics, 2014, 15, 486.	1.2	91
10829	Characterizing a collective and dynamic component of chromatin immunoprecipitation enrichment profiles in yeast. BMC Genomics, 2014, 15, 494.	1.2	2

#	ARTICLE	IF	CITATIONS
10830	Gene Set Enrichment Analysis (GSEA) of <i>Toxoplasma gondii</i> expression datasets links cell cycle progression and the bradyzoite developmental program. <i>BMC Genomics</i> , 2014, 15, 515.	1.2	58
10831	Detection of genome-wide copy number variations in two chicken lines divergently selected for abdominal fat content. <i>BMC Genomics</i> , 2014, 15, 517.	1.2	37
10832	ChIPseek, a web-based analysis tool for ChIP data. <i>BMC Genomics</i> , 2014, 15, 539.	1.2	57
10833	Elucidation of the evolutionary expansion of phosphorylation signaling networks using comparative phosphomotif analysis. <i>BMC Genomics</i> , 2014, 15, 546.	1.2	8
10834	Comparing reference-based RNA-Seq mapping methods for non-human primate data. <i>BMC Genomics</i> , 2014, 15, 570.	1.2	35
10835	RNA-Seq for gene identification and transcript profiling of three <i>Stevia rebaudiana</i> genotypes. <i>BMC Genomics</i> , 2014, 15, 571.	1.2	55
10836	Oil accumulation mechanisms of the oleaginous microalga <i>Chlorella protothecoides</i> revealed through its genome, transcriptomes, and proteomes. <i>BMC Genomics</i> , 2014, 15, 582.	1.2	134
10837	Transcriptome analysis of the differences in gene expression between testis and ovary in green mud crab (<i>Scylla paramamosain</i>). <i>BMC Genomics</i> , 2014, 15, 585.	1.2	96
10838	De novo sequencing and comparative analysis of holy and sweet basil transcriptomes. <i>BMC Genomics</i> , 2014, 15, 588.	1.2	113
10839	The genome of the Tiger Milk mushroom, <i>Lignosus rhinocerotis</i> , provides insights into the genetic basis of its medicinal properties. <i>BMC Genomics</i> , 2014, 15, 635.	1.2	65
10840	A network-based approach to dissect the cilia/centrosome complex interactome. <i>BMC Genomics</i> , 2014, 15, 658.	1.2	19
10841	Transcriptome instability as a molecular pan-cancer characteristic of carcinomas. <i>BMC Genomics</i> , 2014, 15, 672.	1.2	15
10842	Ranking non-synonymous single nucleotide polymorphisms based on disease concepts. <i>Human Genomics</i> , 2014, 8, 11.	1.4	163
10843	Descending Controls Modulate Inflammatory Joint Pain and Regulate CXC Chemokine and iNOS Expression in the Dorsal Horn. <i>Molecular Pain</i> , 2014, 10, 1744-8069-10-39.	1.0	20
10844	Annokey: an annotation tool based on key term search of the NCBI Entrez Gene database. <i>Source Code for Biology and Medicine</i> , 2014, 9, 15.	1.7	6
10845	A dedicated database system for handling multi-level data in systems biology. <i>Source Code for Biology and Medicine</i> , 2014, 9, 17.	1.7	2
10846	Pedigree-based random effect tests to screen gene pathways. <i>BMC Proceedings</i> , 2014, 8, S100.	1.8	7
10847	Placental gene-expression profiles of intrahepatic cholestasis of pregnancy reveal involvement of multiple molecular pathways in blood vessel formation and inflammation. <i>BMC Medical Genomics</i> , 2014, 7, 42.	0.7	42

#	ARTICLE	IF	CITATIONS
10848	Global transcriptome-wide analysis of CIK cells identify distinct roles of IL-2 and IL-15 in acquisition of cytotoxic capacity against tumor. <i>BMC Medical Genomics</i> , 2014, 7, 49.	0.7	29
10849	Computational prediction of disease microRNAs in domestic animals. <i>BMC Research Notes</i> , 2014, 7, 403.	0.6	18
10850	Integrative proteomic analysis of the NMDA NR1 knockdown mouse model reveals effects on central and peripheral pathways associated with schizophrenia and autism spectrum disorders. <i>Molecular Autism</i> , 2014, 5, 38.	2.6	33
10851	The Software Ontology (SWO): a resource for reproducibility in biomedical data analysis, curation and digital preservation. <i>Journal of Biomedical Semantics</i> , 2014, 5, 25.	0.9	56
10852	Generalising semantic category disambiguation with large lexical resources for fun and profit. <i>Journal of Biomedical Semantics</i> , 2014, 5, 26.	0.9	2
10853	Why functions are not special dispositions: an improved classification of realizable for top-level ontologies. <i>Journal of Biomedical Semantics</i> , 2014, 5, 27.	0.9	15
10854	CSEO – the Cigarette Smoke Exposure Ontology. <i>Journal of Biomedical Semantics</i> , 2014, 5, 31.	0.9	7
10855	Differentially-expressed genes in rice infected by <i>Xanthomonas oryzae pv. oryzae</i> relative to a flagellin-deficient mutant reveal potential functions of flagellin in host-pathogen interactions. <i>Rice</i> , 2014, 7, 20.	1.7	18
10856	BioModels linked dataset. <i>BMC Systems Biology</i> , 2014, 8, 91.	3.0	11
10857	Integration of proteomic and transcriptomic profiles identifies a novel PDGF-MYC network in human smooth muscle cells. <i>Cell Communication and Signaling</i> , 2014, 12, 44.	2.7	24
10858	Overexpression of the soybean transcription factor GmDof4 significantly enhances the lipid content of <i>Chlorella ellipsoidea</i> . <i>Biotechnology for Biofuels</i> , 2014, 7, 128.	6.2	47
10859	Synergistic effects of combined DNA methyltransferase inhibition and MBD2 depletion on breast cancer cells; MBD2 depletion blocks 5-aza-2'-deoxycytidine-triggered invasiveness. <i>Carcinogenesis</i> , 2014, 35, 2436-2446.	1.3	16
10860	Epilepsy and seizure ontology: towards an epilepsy informatics infrastructure for clinical research and patient care. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2014, 21, 82-89.	2.2	70
10861	Modeling dynamic functional relationship networks and application to <i>ex vivo</i> human erythroid differentiation. <i>Bioinformatics</i> , 2014, 30, 3325-3333.	1.8	10
10862	Genome-wide screening and co-expression network analysis identify recurrence-specific biomarkers of esophageal squamous cell carcinoma. <i>Tumor Biology</i> , 2014, 35, 10959-10968.	0.8	8
10863	Deciphering the proteomic signature of human endometrial receptivity. <i>Human Reproduction</i> , 2014, 29, 1957-1967.	0.4	49
10864	Comparison of good- and bad-quality cork: application of high-throughput sequencing of phellogenetic tissue. <i>Journal of Experimental Botany</i> , 2014, 65, 4887-4905.	2.4	42
10865	A sentinel protein assay for simultaneously quantifying cellular processes. <i>Nature Methods</i> , 2014, 11, 1045-1048.	9.0	70

#	ARTICLE	IF	CITATIONS
10866	Predicting protein-protein interactions between human and hepatitis C virus via an ensemble learning method. <i>Molecular BioSystems</i> , 2014, 10, 3147-3154.	2.9	46
10867	Dimensionality reduction and topographic mapping of binary tensors. <i>Pattern Analysis and Applications</i> , 2014, 17, 497-515.	3.1	6
10869	WISP 1 is an important survival factor in human mesenchymal stromal cells. <i>Gene</i> , 2014, 551, 243-254.	1.0	18
10870	Hypoxia-mediated retinal neovascularization and vascular leakage in diabetic retina is suppressed by HIF-1 β destabilization by SH-1242 and SH-1280, novel hsp90 inhibitors. <i>Journal of Molecular Medicine</i> , 2014, 92, 1083-1092.	1.7	36
10871	Evidence for contribution of epigenetic mechanisms in the pathogenesis of systemic mast cell activation disease. <i>Immunogenetics</i> , 2014, 66, 287-297.	1.2	15
10872	The inhibitory effect of <i>Bacillus megaterium</i> on aflatoxin and cyclopiazonic acid biosynthetic pathway gene expression in <i>Aspergillus flavus</i> . <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 5161-5172.	1.7	50
10873	Precise genetic mapping and integrative bioinformatics in Diversity Outbred mice reveals Hydin as a novel pain gene. <i>Mammalian Genome</i> , 2014, 25, 211-222.	1.0	54
10874	Molecular pathology of acute kidney injury in a choline-deficient model and fish oil protective effect. <i>European Journal of Nutrition</i> , 2014, 53, 897-906.	1.8	3
10875	Co-expression network analysis identifies transcriptional modules in the mouse liver. <i>Molecular Genetics and Genomics</i> , 2014, 289, 847-853.	1.0	17
10876	Complete genome sequence of invertebrate iridovirus IIV-25 isolated from a blackfly larva. <i>Archives of Virology</i> , 2014, 159, 1181-1185.	0.9	12
10877	Finding maximal homogeneous clique sets. <i>Knowledge and Information Systems</i> , 2014, 39, 579-608.	2.1	4
10878	Transcriptional Assessment by Microarray Analysis and Large-Scale Meta-analysis of the Metabolic Capacity of Cardiac and Skeletal Muscle Tissues to Cope With Reduced Nutrient Availability in Gilthead Sea Bream (<i>Sparus aurata</i> L.). <i>Marine Biotechnology</i> , 2014, 16, 423-435.	1.1	48
10879	Leaf-, panel- and latex-expressed sequenced tags from the rubber tree (<i>Hevea brasiliensis</i>) under cold-stressed and suboptimal growing conditions: the development of gene-targeted functional markers for stress response. <i>Molecular Breeding</i> , 2014, 34, 1035-1053.	1.0	32
10880	MAGNA: Maximizing Accuracy in Global Network Alignment. <i>Bioinformatics</i> , 2014, 30, 2931-2940.	1.8	154
10881	Secretome of the Biocontrol Agent <i>Metarhizium anisopliae</i> Induced by the Cuticle of the Cotton Pest <i>Dysdercus peruvianus</i> Reveals New Insights into Infection. <i>Journal of Proteome Research</i> , 2014, 13, 2282-2296.	1.8	32
10882	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014, 345, 1250091.	6.0	318
10883	Measure the Semantic Similarity of GO Terms Using Aggregate Information Content. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 468-476.	1.9	44
10884	Benchmarking infrastructure for mutation text mining. <i>Journal of Biomedical Semantics</i> , 2014, 5, 11.	0.9	4

#	ARTICLE	IF	CITATIONS
10885	The zebrafish anatomy and stage ontologies: representing the anatomy and development of <i>Danio rerio</i> . <i>Journal of Biomedical Semantics</i> , 2014, 5, 12.	0.9	53
10886	Semantic interestingness measures for discovering association rules in the skeletal dysplasia domain. <i>Journal of Biomedical Semantics</i> , 2014, 5, 8.	0.9	17
10887	Understanding how and why the Gene Ontology and its annotations evolve: the GO within UniProt. <i>GigaScience</i> , 2014, 3, 4.	3.3	70
10888	Think globally and solve locally: secondary memory-based network learning for automated multi-species function prediction. <i>GigaScience</i> , 2014, 3, 5.	3.3	12
10889	Search for overrepresented characteristics of genes: Implementation of permutation tests using GPUs. <i>Optoelectronics, Instrumentation and Data Processing</i> , 2014, 50, 102-107.	0.2	3
10890	FLOPPIES: A Framework for Large-Scale Ontology Population of Product Information from Tabular Data in E-commerce Stores. <i>Decision Support Systems</i> , 2014, 59, 296-311.	3.5	28
10891	Ontologies in Biological Data Visualization. <i>IEEE Computer Graphics and Applications</i> , 2014, 34, 8-15.	1.0	19
10892	An extensive analysis of disease-gene associations using network integration and fast kernel-based gene prioritization methods. <i>Artificial Intelligence in Medicine</i> , 2014, 61, 63-78.	3.8	49
10893	Classification of Intrinsically Disordered Regions and Proteins. <i>Chemical Reviews</i> , 2014, 114, 6589-6631.	23.0	1,618
10894	In Silico Prediction and Characterization of MicroRNAs from <i>Aphis gossypii</i> (Hemiptera: Tj ETQq1 1 0.784314 _{1.3} rgBT /Oylock 10		
10895	Long noncoding RNA are aberrantly expressed in vivo in the cystic fibrosis bronchial epithelium. <i>International Journal of Biochemistry and Cell Biology</i> , 2014, 52, 184-191.	1.2	51
10896	Biomedical Literature Mining. <i>Methods in Molecular Biology</i> , 2014, , .	0.4	6
10897	Profiling post-transcriptionally networked mRNA subsets using RIP-Chip and RIP-Seq. <i>Methods</i> , 2014, 67, 13-19.	1.9	29
10898	Genome sequence of the cultivated cotton <i>Gossypium arboreum</i> . <i>Nature Genetics</i> , 2014, 46, 567-572.	9.4	883
10899	Peripheral nerve morphogenesis induced by scaffold micropatterning. <i>Biomaterials</i> , 2014, 35, 4035-4045.	5.7	39
10900	Integrative Gene Set Analysis: Application to Platinum Pharmacogenomics. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 34-41.	1.0	18
10901	Expanding the computational toolbox for mining cancer genomes. <i>Nature Reviews Genetics</i> , 2014, 15, 556-570.	7.7	166
10902	Proteomic Mapping of the Human Mitochondrial Intermembrane Space in Live Cells via Ratiometric APEX Tagging. <i>Molecular Cell</i> , 2014, 55, 332-341.	4.5	414

#	ARTICLE	IF	CITATIONS
10903	Expansion of Biological Pathways Based on Evolutionary Inference. <i>Cell</i> , 2014, 158, 213-225.	13.5	107
10904	Genome-wide analysis reveals DNA methylation markers that vary with both age and obesity. <i>Gene</i> , 2014, 548, 61-67.	1.0	83
10905	Genome-wide pathway analysis of breast cancer. <i>Tumor Biology</i> , 2014, 35, 7699-7705.	0.8	13
10906	Alternating decision tree algorithm for assessing protein interaction reliability. <i>Vietnam Journal of Computer Science</i> , 2014, 1, 169-178.	1.0	9
10907	Improving clustering with metabolic pathway data. <i>BMC Bioinformatics</i> , 2014, 15, 101.	1.2	7
10908	Identifying pathogenic processes by integrating microarray data with prior knowledge. <i>BMC Bioinformatics</i> , 2014, 15, 115.	1.2	2
10909	GO2MSIG, an automated GO based multi-species gene set generator for gene set enrichment analysis. <i>BMC Bioinformatics</i> , 2014, 15, 146.	1.2	49
10910	Large-scale biomedical concept recognition: an evaluation of current automatic annotators and their parameters. <i>BMC Bioinformatics</i> , 2014, 15, 59.	1.2	94
10911	The characteristic direction: a geometrical approach to identify differentially expressed genes. <i>BMC Bioinformatics</i> , 2014, 15, 79.	1.2	148
10912	Functional and genetic analysis of the colon cancer network. <i>BMC Bioinformatics</i> , 2014, 15, S6.	1.2	33
10913	A multicopy Y-chromosomal SGNH hydrolase gene expressed in the testis of the platyfish has been captured and mobilized by a Helitron transposon. <i>BMC Genetics</i> , 2014, 15, 44.	2.7	13
10914	A gain-of-function screen to identify genes that reduce lifespan in the adult of <i>Drosophila melanogaster</i> . <i>BMC Genetics</i> , 2014, 15, 46.	2.7	8
10915	Transcriptome sequencing of Atlantic salmon (<i>Salmo salar</i> L.) notochord prior to development of the vertebrae provides clues to regulation of positional fate, chordoblast lineage and mineralisation. <i>BMC Genomics</i> , 2014, 15, 141.	1.2	44
10916	Identification of mycoparasitism-related genes against the phytopathogen <i>Sclerotinia sclerotiorum</i> through transcriptome and expression profile analysis in <i>Trichoderma harzianum</i> . <i>BMC Genomics</i> , 2014, 15, 204.	1.2	99
10917	Hen uterine gene expression profiling during eggshell formation reveals putative proteins involved in the supply of minerals or in the shell mineralization process. <i>BMC Genomics</i> , 2014, 15, 220.	1.2	85
10918	An overlapping set of genes is regulated by both NFIB and the glucocorticoid receptor during lung maturation. <i>BMC Genomics</i> , 2014, 15, 231.	1.2	15
10919	High throughput sequencing of two celery varieties small RNAs identifies microRNAs involved in temperature stress response. <i>BMC Genomics</i> , 2014, 15, 242.	1.2	56
10920	Gene expression profile analysis of Manila clam (<i>Ruditapes philippinarum</i>) hemocytes after a <i>Vibrio alginolyticus</i> challenge using an immune-enriched oligo-microarray. <i>BMC Genomics</i> , 2014, 15, 267.	1.2	41

#	ARTICLE	IF	CITATIONS
10921	A house finch (<i>Haemorhous mexicanus</i>) spleen transcriptome reveals intra- and interspecific patterns of gene expression, alternative splicing and genetic diversity in passerines. <i>BMC Genomics</i> , 2014, 15, 305.	1.2	12
10922	Applying genome-wide gene-based expression quantitative trait locus mapping to study population ancestry and pharmacogenetics. <i>BMC Genomics</i> , 2014, 15, 319.	1.2	7
10923	Comparative transcriptome analysis of eggplant (<i>Solanum melongena</i> L.) and turkey berry (<i>Solanum</i>) Tj ETQq0 0 0 1gBT /Overlock 10 Tf	1.2	66
10924	Expression-based network biology identifies immune-related functional modules involved in plant defense. <i>BMC Genomics</i> , 2014, 15, 421.	1.2	36
10925	Gene co-expression network analysis identifies porcine genes associated with variation in <i>Salmonella</i> shedding. <i>BMC Genomics</i> , 2014, 15, 452.	1.2	65
10926	Transcriptomic and metabolomic analysis of copper stress acclimation in <i>Ectocarpus siliculosus</i> highlights signaling and tolerance mechanisms in brown algae. <i>BMC Plant Biology</i> , 2014, 14, 116.	1.6	98
10927	Identification of boron-deficiency-responsive microRNAs in <i>Citrus sinensis</i> roots by Illumina sequencing. <i>BMC Plant Biology</i> , 2014, 14, 123.	1.6	57
10928	Genes associated with agronomic traits in non-heading Chinese cabbage identified by expression profiling. <i>BMC Plant Biology</i> , 2014, 14, 71.	1.6	21
10929	Proteomic analysis of human osteoarthritis synovial fluid. <i>Clinical Proteomics</i> , 2014, 11, 6.	1.1	122
10930	Predicting gene ontology annotations of orphan GWAS genes using protein-protein interactions. <i>Algorithms for Molecular Biology</i> , 2014, 9, 10.	0.3	3
10931	Improving protein function prediction using domain and protein complexes in PPI networks. <i>BMC Systems Biology</i> , 2014, 8, 35.	3.0	43
10932	Transcriptional override: a regulatory network model of indirect responses to modulations in microRNA expression. <i>BMC Systems Biology</i> , 2014, 8, 36.	3.0	19
10933	The protein-protein interaction network of eyestalk, Y-organ and hepatopancreas in Chinese mitten crab <i>Eriocheir sinensis</i> . <i>BMC Systems Biology</i> , 2014, 8, 39.	3.0	18
10934	EndoNet: an information resource about the intercellular signaling network. <i>BMC Systems Biology</i> , 2014, 8, 49.	3.0	10
10935	TGF- β 2 stimulation in human and murine cells reveals commonly affected biological processes and pathways at transcription level. <i>BMC Systems Biology</i> , 2014, 8, 55.	3.0	33
10936	Identifying aging-related genes in mouse hippocampus using gateway nodes. <i>BMC Systems Biology</i> , 2014, 8, 62.	3.0	12
10937	Data integration in the era of omics: current and future challenges. <i>BMC Systems Biology</i> , 2014, 8, 11.	3.0	300
10938	The common ground of genomics and systems biology. <i>BMC Systems Biology</i> , 2014, 8, S1.	3.0	22

#	ARTICLE	IF	CITATIONS
10939	Bioinformatic analysis of proteomics data. BMC Systems Biology, 2014, 8, S3.	3.0	131
10940	The global landscape of intron retentions in lung adenocarcinoma. BMC Medical Genomics, 2014, 7, 15.	0.7	32
10941	Concordance of deregulated mechanisms unveiled in underpowered experiments: PTBP1 knockdown case study. BMC Medical Genomics, 2014, 7, S1.	0.7	16
10942	Comparative analysis of the gonadal transcriptomes of the all-female species <i>Poecilia formosa</i> and its maternal ancestor <i>Poecilia mexicana</i> . BMC Research Notes, 2014, 7, 249.	0.6	6
10943	Integration, visualization and analysis of human interactome. Biochemical and Biophysical Research Communications, 2014, 445, 757-773.	1.0	37
10944	The human testis-specific proteome defined by transcriptomics and antibody-based profiling. Molecular Human Reproduction, 2014, 20, 476-488.	1.3	189
10945	Evaluation of metatranscriptomic protocols and application to the study of freshwater microbial communities. Environmental Microbiology Reports, 2014, 6, 640-655.	1.0	36
10946	Proteomic Profile of <i>Cryptococcus neoformans</i> Biofilm Reveals Changes in Metabolic Processes. Journal of Proteome Research, 2014, 13, 1545-1559.	1.8	58
10947	Abnormalities in human pluripotent cells due to reprogramming mechanisms. Nature, 2014, 511, 177-183.	13.7	307
10948	Inference of Transcriptional Networks in <i>Arabidopsis</i> through Conserved Noncoding Sequence Analysis. Plant Cell, 2014, 26, 2729-2745.	3.1	57
10949	Text mining of cancer-related information: Review of current status and future directions. International Journal of Medical Informatics, 2014, 83, 605-623.	1.6	171
10950	Sequential transcriptional changes dictate safe and effective antigen-specific immunotherapy. Nature Communications, 2014, 5, 4741.	5.8	147
10951	Annexin V Incorporated into Influenza Virus Particles Inhibits Gamma Interferon Signaling and Promotes Viral Replication. Journal of Virology, 2014, 88, 11215-11228.	1.5	26
10952	Biomedical Big Data for Clinical Research and Patient Care: Role of Semantic Computing. , 2014, , .		2
10953	Defining the Human Adipose Tissue Proteome To Reveal Metabolic Alterations in Obesity. Journal of Proteome Research, 2014, 13, 5106-5119.	1.8	55
10954	SNP2GO: Functional Analysis of Genome-Wide Association Studies. Genetics, 2014, 197, 285-289.	1.2	30
10955	Genome-based vaccine design: the promise for malaria and other infectious diseases. International Journal for Parasitology, 2014, 44, 901-913.	1.3	39
10956	The lung-specific proteome defined by integration of transcriptomics and antibody-based profiling. FASEB Journal, 2014, 28, 5184-5196.	0.2	54

#	ARTICLE	IF	CITATIONS
10957	Active learning for protein function prediction in protein-protein interaction networks. <i>Neurocomputing</i> , 2014, 145, 44-52.	3.5	18
10958	Widespread Signals of Convergent Adaptation to High Altitude in Asia and America. <i>American Journal of Human Genetics</i> , 2014, 95, 394-407.	2.6	131
10959	Viral proteins that bridge unconnected proteins and components in the human PPI network. <i>Molecular BioSystems</i> , 2014, 10, 2448-2458.	2.9	11
10960	The Mouse Genome Database: integration of and access to knowledge about the laboratory mouse. <i>Nucleic Acids Research</i> , 2014, 42, D810-D817.	6.5	196
10961	Broad-Enrich: functional interpretation of large sets of broad genomic regions. <i>Bioinformatics</i> , 2014, 30, i393-i400.	1.8	21
10962	In-silico identification and characterization of organic and inorganic chemical stress responding genes in yeast (<i>Saccharomyces cerevisiae</i>). <i>Gene</i> , 2014, 550, 74-80.	1.0	1
10963	ReliefF for Hierarchical Multi-label Classification. <i>Lecture Notes in Computer Science</i> , 2014, , 148-161.	1.0	8
10964	The importance of using realistic evolutionary models for retrodicting proteomes. <i>Biochimie</i> , 2014, 99, 129-137.	1.3	17
10965	BRIC-seq: A genome-wide approach for determining RNA stability in mammalian cells. <i>Methods</i> , 2014, 67, 55-63.	1.9	64
10966	Phevor Combines Multiple Biomedical Ontologies for Accurate Identification of Disease-Causing Alleles in Single Individuals and Small Nuclear Families. <i>American Journal of Human Genetics</i> , 2014, 94, 599-610.	2.6	175
10967	Protein Function Prediction with Incomplete Annotations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 579-591.	1.9	25
10968	Identifying Beneficial Qualities of <i>Trichoderma parareesei</i> for Plants. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1864-1873.	1.4	124
10969	rClca2 is associated with epidermal differentiation and is strongly downregulated by ultraviolet radiation. <i>British Journal of Dermatology</i> , 2014, 171, 376-387.	1.4	12
10970	Lipids in health and disease. <i>Nature</i> , 2014, 510, 47-47.	13.7	24
10971	Heparin-protein interactions: From affinity and kinetics to biological roles. Application to an interaction network regulating angiogenesis. <i>Matrix Biology</i> , 2014, 35, 73-81.	1.5	103
10972	Gene expression studies in human abdominal aortic aneurysm. <i>Reviews in Vascular Medicine</i> , 2014, 2, 77-82.	0.4	10
10973	Identification and characterization of lysine-methylated sites on histones and non-histone proteins. <i>Computational Biology and Chemistry</i> , 2014, 50, 11-18.	1.1	24
10974	The Niche Component Periostin Is Produced by Cancer-Associated Fibroblasts, Supporting Growth of Gastric Cancer through ERK Activation. <i>American Journal of Pathology</i> , 2014, 184, 859-870.	1.9	100

#	ARTICLE	IF	CITATIONS
10975	Deep transcriptome sequencing of <i>Pecten maximus</i> hemocytes: A genomic resource for bivalve immunology. <i>Fish and Shellfish Immunology</i> , 2014, 37, 154-165.	1.6	72
10976	ADO: A disease ontology representing the domain knowledge specific to Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2014, 10, 238-246.	0.4	77
10977	Assessing mechanisms of toxicant response in the amphipod <i>Melita plumulosa</i> through transcriptomic profiling. <i>Aquatic Toxicology</i> , 2014, 146, 247-257.	1.9	32
10978	Aberrant miRNA profiles associated with chronic benzene poisoning. <i>Experimental and Molecular Pathology</i> , 2014, 96, 426-430.	0.9	46
10979	Use of toxicogenomics to predict the potential toxic effect of Benzo(a)pyrene on zebrafish embryos: Ocular developmental toxicity. <i>Chemosphere</i> , 2014, 108, 55-61.	4.2	51
10980	Autoimmune profiling with protein microarrays in clinical applications. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 977-987.	1.1	19
10981	Building and exploring an integrated human kinase network: Global organization and medical entry points. <i>Journal of Proteomics</i> , 2014, 107, 113-127.	1.2	16
10982	A case study: semantic integration of gene-disease associations for type 2 diabetes mellitus from literature and biomedical data resources. <i>Drug Discovery Today</i> , 2014, 19, 882-889.	3.2	10
10983	Aberrant hypomethylated STAT3 was identified as a biomarker of chronic benzene poisoning through integrating DNA methylation and mRNA expression data. <i>Experimental and Molecular Pathology</i> , 2014, 96, 346-353.	0.9	28
10984	Predicting essential genes for identifying potential drug targets in <i>Aspergillus fumigatus</i> . <i>Computational Biology and Chemistry</i> , 2014, 50, 29-40.	1.1	50
10985	Gene expression profiling of bovine mammary gland epithelial cells stimulated with lipoteichoic acid plus peptidoglycan from <i>Staphylococcus aureus</i> . <i>International Immunopharmacology</i> , 2014, 21, 231-240.	1.7	19
10986	Entropic Biological Score: a cell cycle investigation for GRNs inference. <i>Gene</i> , 2014, 541, 129-137.	1.0	17
10987	Pentachlorophenol exposure causes Warburg-like effects in zebrafish embryos at gastrulation stage. <i>Toxicology and Applied Pharmacology</i> , 2014, 277, 183-191.	1.3	29
10988	Bias tradeoffs in the creation and analysis of protein-protein interaction networks. <i>Journal of Proteomics</i> , 2014, 100, 44-54.	1.2	60
10989	Completion-based generalization inferences for the Description Logic $\langle \text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si1.gif" overflow="scroll"} \rangle \langle \text{mml:mi mathvariant="script"} \rangle \text{ELOR} \langle \text{mml:mi} \rangle \langle \text{mml:math} \rangle$ with subjective probabilities. <i>International Journal of Approximate Reasoning</i> , 2014, 55, 1939-1970.	1.9	2
10990	Incorporation of gene exchangeabilities improves the reproducibility of gene set rankings. <i>Computational Statistics and Data Analysis</i> , 2014, 71, 588-598.	0.7	0
10991	A bioinformatics-based update on microRNAs and their targets in rainbow trout (<i>Oncorhynchus</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 1	1.0	12
10992	Siri of the Cell: What Biology Could Learn from the iPhone. <i>Cell</i> , 2014, 157, 534-538.	13.5	31

#	ARTICLE	IF	CITATIONS
10993	Transcriptional profiling reveals differential expression of a neuropeptide-like protein and pseudogenes in aryl hydrocarbon receptor-1 mutant <i>Caenorhabditis elegans</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2014, 9, 40-48.	0.4	5
10994	Age-related vascular gene expression profiling in mice. <i>Mechanisms of Ageing and Development</i> , 2014, 135, 15-23.	2.2	31
10995	Studying <i>Culicoides</i> vectors of BTV in the post-genomic era: Resources, bottlenecks to progress and future directions. <i>Virus Research</i> , 2014, 182, 43-49.	1.1	49
10996	The emerging era of genomic data integration for analyzing splice isoform function. <i>Trends in Genetics</i> , 2014, 30, 340-347.	2.9	82
10997	Gene set analysis: limitations in popular existing methods and proposed improvements. <i>Bioinformatics</i> , 2014, 30, 2747-2756.	1.8	15
10998	Cross-talk between the circadian clock and the cell cycle in cancer. <i>Annals of Medicine</i> , 2014, 46, 221-232.	1.5	114
10999	Meta-analysis of the differentially expressed breast cancer-related microRNA expression profiles. <i>Journal of Obstetrics and Gynaecology</i> , 2014, 34, 630-633.	0.4	4
11000	Gene Expression Profiles of Entorhinal Cortex in Alzheimer's Disease. <i>American Journal of Alzheimer's Disease and Other Dementias</i> , 2014, 29, 526-532.	0.9	28
11001	Dynamic networks reveal key players in aging. <i>Bioinformatics</i> , 2014, 30, 1721-1729.	1.8	80
11002	Quantitative Temporal Viromics: An Approach to Investigate Host-Pathogen Interaction. <i>Cell</i> , 2014, 157, 1460-1472.	13.5	409
11003	PITPs as targets for selectively interfering with phosphoinositide signaling in cells. <i>Nature Chemical Biology</i> , 2014, 10, 76-84.	3.9	39
11004	Modern bioinformatics meets traditional Chinese medicine. <i>Briefings in Bioinformatics</i> , 2014, 15, 984-1003.	3.2	95
11006	Informatics in Radiology: Radiology Gamuts Ontology: Differential Diagnosis for the Semantic Web. <i>Radiographics</i> , 2014, 34, 254-264.	1.4	24
11007	Time-resolved characterization of cAMP/PKA-dependent signaling reveals that platelet inhibition is a concerted process involving multiple signaling pathways. <i>Blood</i> , 2014, 123, e1-e10.	0.6	80
11008	Advanced Computing, Networking and Informatics- Volume 1. <i>Smart Innovation, Systems and Technologies</i> , 2014, , .	0.5	8
11009	Advances in Practical Applications of Heterogeneous Multi-Agent Systems. <i>The PAAMS Collection. Lecture Notes in Computer Science</i> , 2014, , .	1.0	1
11010	Inhibitory activity of gold and silica nanospheres to vascular endothelial growth factor (VEGF)-mediated angiogenesis is determined by their sizes. <i>Nano Research</i> , 2014, 7, 844-852.	5.8	22
11011	Cold-Induced Cysts of the Photosynthetic Dinoflagellate <i>Lingulodinium polyedrum</i> Have an Arrested Circadian Bioluminescence Rhythm and Lower Levels of Protein Phosphorylation. <i>Plant Physiology</i> , 2014, 164, 966-977.	2.3	43

#	ARTICLE	IF	CITATIONS
11012	Pseudomonas Methods and Protocols. <i>Methods in Molecular Biology</i> , 2014, 1149, v.	0.4	78
11013	Transporter taxonomy – a comparison of different transport protein classification schemes. <i>Drug Discovery Today: Technologies</i> , 2014, 12, e37-e46.	4.0	7
11014	Exogenous expression of WT1 gene influences U937 cell biological behaviors and activates MAPK and JAK-STAT signaling pathways. <i>Leukemia Research</i> , 2014, 38, 931-939.	0.4	12
11015	Signaling hypergraphs. <i>Trends in Biotechnology</i> , 2014, 32, 356-362.	4.9	39
11016	Human Dopamine Receptors Interaction Network (DRIN): A systems biology perspective on topology, stability and functionality of the network. <i>Journal of Theoretical Biology</i> , 2014, 357, 169-183.	0.8	7
11017	Collaborative error reduction for hierarchical classification. <i>Computer Vision and Image Understanding</i> , 2014, 124, 79-90.	3.0	6
11018	Omics and the Future of Sustainable Biomaterials. <i>ACS Symposium Series</i> , 2014, , 59-79.	0.5	3
11019	Transporter assays and assay ontologies: useful tools for drug discovery. <i>Drug Discovery Today: Technologies</i> , 2014, 12, e47-e54.	4.0	4
11020	Human proteins characterization with subcellular localizations. <i>Journal of Theoretical Biology</i> , 2014, 358, 61-73.	0.8	11
11021	Proteome analysis of the HIV-1 Gag interactome. <i>Virology</i> , 2014, 460-461, 194-206.	1.1	46
11022	Genetics of the human metabolome, what is next?. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2014, 1842, 1923-1931.	1.8	28
11023	Congenital taurine deficiency in mice is associated with reduced sensitivity to nociceptive chemical stimulation. <i>Neuroscience</i> , 2014, 259, 63-70.	1.1	17
11024	Integrative analysis of many RNA-seq datasets to study alternative splicing. <i>Methods</i> , 2014, 67, 313-324.	1.9	18
11025	An ontology for unifying behavior-change literature. <i>CIRP Annals - Manufacturing Technology</i> , 2014, 63, 173-176.	1.7	5
11026	Integrative analysis of the connectivity and gene expression atlases in the mouse brain. <i>NeuroImage</i> , 2014, 84, 245-253.	2.1	41
11027	Comparative transcriptome analysis of sex pheromone glands of two sympatric lepidopteran congener species. <i>Genomics</i> , 2014, 103, 308-315.	1.3	22
11028	ProfileDB: A resource for proteomics and cross-omics biomarker discovery. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 960-966.	1.1	2
11029	Identification of four genes required for mammalian blastocyst formation. <i>Zygote</i> , 2014, 22, 331-339.	0.5	11

#	ARTICLE	IF	CITATIONS
11030	Using R and Bioconductor for proteomics data analysis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 42-51.	1.1	60
11031	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 98-107.	1.1	36
11032	Messenger RNAs in metaphase II oocytes correlate with successful embryo development to the blastocyst stage. <i>Zygote</i> , 2014, 22, 69-79.	0.5	21
11033	Genetics of diabetes – Are we missing the genes or the disease?. <i>Molecular and Cellular Endocrinology</i> , 2014, 382, 726-739.	1.6	127
11034	Applying mass spectrometry-based qualitative proteomics to human amygdaloid complex. <i>Frontiers in Cellular Neuroscience</i> , 2014, 8, 80.	1.8	13
11035	ENZYMAP: Exploiting Protein Annotation for Modeling and Predicting EC Number Changes in UniProt/Swiss-Prot. <i>PLoS ONE</i> , 2014, 9, e89162.	1.1	5
11036	Non-contiguous finished genome sequence and description of <i>Clostridium saudii</i> sp. nov. <i>Standards in Genomic Sciences</i> , 2014, 9, 8.	1.5	15
11037	Contemporary Network Proteomics and Its Requirements. <i>Biology</i> , 2014, 3, 22-38.	1.3	8
11038	A collaborative methodology for developing a semantic model for interlinking Cancer Chemoprevention linked-data sources. <i>Semantic Web</i> , 2014, 5, 127-142.	1.1	21
11039	A mutation in POLE predisposing to a multi-tumour phenotype. <i>International Journal of Oncology</i> , 2014, 45, 77-81.	1.4	61
11040	The EcoCyc Database. <i>EcoSal Plus</i> , 2014, 6, .	2.1	101
11041	A Semantic Framework to Integrate Healthcare and Clinical Knowledge in Medical Device Innovation and Design. , 2014, , .		0
11042	Genome sequence of <i>Coxiella burnetii</i> strain Namibia. <i>Standards in Genomic Sciences</i> , 2014, 9, 22.	1.5	12
11044	Structural Annotation of the <i>Mycobacterium tuberculosis</i> Proteome. <i>Microbiology Spectrum</i> , 2014, 2, .	1.2	2
11045	Râ€¦flurbiprofen attenuates experimental autoimmune encephalomyelitis in mice. <i>EMBO Molecular Medicine</i> , 2014, 6, 1398-1422.	3.3	47
11046	Pathway Composite Variables: A Useful Tool for the Interpretation of Biological Pathways in the Analysis of Gene Expression Data. , 2014, , 141-150.		1
11047	Complete genome sequence of <i>Ornithobacterium rhinotracheale</i> strain ORT-UMN 88. <i>Standards in Genomic Sciences</i> , 2014, 9, 16.	1.5	10
11048	Draft genome sequence of <i>Bacillus azotoformans</i> MEV2011, a (Co-) denitrifying strain unable to grow with oxygen. <i>Standards in Genomic Sciences</i> , 2014, 9, 23.	1.5	4

#	ARTICLE	IF	CITATIONS
11049	Complete genome sequence of Roseophage vB_DshP-R1, which infects <i>Dinoroseobacter shibae</i> DFL12. <i>Standards in Genomic Sciences</i> , 2014, 9, 31.	1.5	4
11050	Gene expression signature in adipose tissue of acromegaly patients. <i>BMC Bioinformatics</i> , 2014, 15, .	1.2	0
11051	Context-sensitive use of bioinformatics tools with complementary functionalities for generation of relevant hypothesis. <i>BMC Bioinformatics</i> , 2014, 15, .	1.2	0
11052	The ins and outs of metal homeostasis by the root nodule actinobacterium <i>Frankia</i> . <i>BMC Genomics</i> , 2014, 15, 1092.	1.2	26
11053	The COPD Knowledge Base: enabling data analysis and computational simulation in translational COPD research. <i>Journal of Translational Medicine</i> , 2014, 12, S6.	1.8	26
11054	Complete genome sequence of <i>Planctomyces brasiliensis</i> type strain (DSM 5305T), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of <i>Gimesia</i> gen. nov., <i>Planctopirus</i> gen. nov. and <i>Rubinisphaera</i> gen. nov. and emended descriptions of the order Planctomycetales and the family Planctomycetaceae. <i>Standards in Genomic Sciences</i> , 2014, 9, 10.	1.5	76
11055	Non-contiguous finished genome sequence of <i>Ornithobacterium rhinotracheale</i> strain H06-030791. <i>Standards in Genomic Sciences</i> , 2014, 9, 14.	1.5	2
11056	Complete genome sequence of DSM 30083T, the type strain (U5/41T) of <i>Escherichia coli</i> , and a proposal for delineating subspecies in microbial taxonomy. <i>Standards in Genomic Sciences</i> , 2014, 9, 2.	1.5	454
11057	Genome sequence of the <i>Lotus corniculatus</i> microsymbiont <i>Mesorhizobium loti</i> strain R88B. <i>Standards in Genomic Sciences</i> , 2014, 9, 3.	1.5	12
11058	High quality draft genome sequence of the heavy metal resistant bacterium <i>Halomonas zincidurans</i> type strain B6T. <i>Standards in Genomic Sciences</i> , 2014, 9, 30.	1.5	17
11059	Non-contiguous finished genome sequence and description of the gliding bacterium <i>Flavobacterium seoulense</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2014, 9, 34.	1.5	9
11060	Genome sequence of <i>Ensifer medicae</i> Di28; an effective N ₂ -fixing microsymbiont of <i>Medicago murex</i> and <i>M. polymorpha</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 4.	1.5	0
11061	Genome sequence of the dark pink pigmented <i>Listia bainesii</i> microsymbiont <i>Methylobacterium</i> sp. WSM2598. <i>Standards in Genomic Sciences</i> , 2014, 9, 5.	1.5	3
11062	Genome sequence of the <i>Lotus</i> spp. microsymbiont <i>Mesorhizobium loti</i> strain NZP2037. <i>Standards in Genomic Sciences</i> , 2014, 9, 7.	1.5	5
11063	High quality draft genome sequence and description of <i>Occidentia massiliensis</i> gen. nov., sp. nov., a new member of the family Rickettsiaceae. <i>Standards in Genomic Sciences</i> , 2014, 9, 9.	1.5	34
11064	Genome sequence of the <i>Lotus</i> spp. microsymbiont <i>Mesorhizobium loti</i> strain R7A. <i>Standards in Genomic Sciences</i> , 2014, 9, 6.	1.5	22
11065	eQTL Networks Reveal Complex Genetic Architecture in the Immature Soybean Seed. <i>Plant Genome</i> , 2014, 7, plantgenome2013.08.0027.	1.6	15
11066	A Bayesian nonparametric mixture model for selecting genes and gene subnetworks. <i>Annals of Applied Statistics</i> , 2014, 8, 999-1021.	0.5	10

#	ARTICLE	IF	CITATIONS
11067	A proteomics study of hyperhomocysteinemia injury of the hippocampal neurons using iTRAQ. <i>Molecular Medicine Reports</i> , 2014, 10, 2511-2516.	1.1	6
11068	Celiac Disease as a Model for the Evolution of Multifactorial Disease in Humans. <i>Human Biology</i> , 2014, 86, 19.	0.4	0
11069	Deep sequencing reveals complex mechanisms of microRNA deregulation in colorectal cancer. <i>International Journal of Oncology</i> , 2014, 45, 603-610.	1.4	16
11070	Identifying significant associations of orthologous simple sequence repeats with gene ontologies. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 9, 37.	0.1	0
11071	A novel strategy for molecular signature discovery based on independent component analysis. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 9, 277.	0.1	6
11072	Improving named entity recognition accuracy for gene and protein in biomedical text literature. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 10, 239.	0.1	1
11073	Identification of SSRs and differentially expressed genes in two cultivars of celery (<i>Apium graveolens</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 29 116	0.2	1
11074	The complete genome sequence of the rumen methanogen <i>Methanobacterium formicicum</i> BRM9. <i>Standards in Genomic Sciences</i> , 2014, 9, 15.	1.5	27
11075	Quantitative phosphoproteomics unveils temporal dynamics of thrombin signaling in human endothelial cells. <i>Blood</i> , 2014, 123, e22-e36.	0.6	36
11076	MicroRNA expression profiles in supraglottic carcinoma. <i>Oncology Reports</i> , 2014, 31, 2029-2034.	1.2	11
11078	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
11079	Integrative Genomic Analysis for the Discovery of Biomarkers in Prostate Cancer. <i>Biomarker Insights</i> , 2014, 9, BMI.S13729.	1.0	7
11080	Text Mining in Cancer Gene and Pathway Prioritization. <i>Cancer Informatics</i> , 2014, 13s1, CIN.S13874.	0.9	32
11081	The Comparative Genomics and Phylogenomics of <i>Leishmania Amazonensis</i> Parasite. <i>Evolutionary Bioinformatics</i> , 2014, 10, EBO.S13759.	0.6	23
11082	Genome-Wide Transcriptional Analysis of <i>Drosophila</i> Larvae Infected by Entomopathogenic Nematodes Shows Involvement of Complement, Recognition and Extracellular Matrix Proteins. <i>Journal of Innate Immunity</i> , 2014, 6, 192-204.	1.8	102
11083	Next Generation Distributed Computing for Cancer Research. <i>Cancer Informatics</i> , 2014, 13s7, CIN.S16344.	0.9	7
11084	Probabilistic Latent Semantic Analysis Applied to Whole Bacterial Genomes Identifies Common Genomic Features. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 93-105.	1.0	2
11085	A joint framework for missing values estimation and biclusters detection in gene expression data. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 574.	0.1	1

#	ARTICLE	IF	CITATIONS
11086	Bioinformatic Analysis of Msx1 and Msx2 Involved in Craniofacial Development. Journal of Craniofacial Surgery, 2014, 25, 129-134.	0.3	13
11087	Genome sequence and emended description of <i>Leisingera nanhaiensis</i> strain DSM 24252T isolated from marine sediment. Standards in Genomic Sciences, 2014, 9, 585-601.	1.5	8
11088	Genomic analysis of <i>Agrobacterium radiobacter</i> DSM 30147T and emended description of <i>A. radiobacter</i> (Beijerinck and van Delden 1902) Conn 1942 (Approved Lists 1980) emend. Sawada et al. 1993. Standards in Genomic Sciences, 2014, 9, 574-584.	1.5	12
11089	Draft genome sequence of <i>Gluconobacter thailandicus</i> NBRC 3257. Standards in Genomic Sciences, 2014, 9, 614-623.	1.5	12
11090	Draft genome sequence of <i>Bacillus amyloliquefaciens</i> HB-26. Standards in Genomic Sciences, 2014, 9, 775-782.	1.5	4
11091	Complete genome sequence of the <i>Phaeobacter gallaeciensis</i> type strain CIP 105210T (= DSM 26640T =) Tj ETQq1_1_0.784314 rgBT	1.5	21
11092	Non-contiguous finished genome sequence and description of <i>Gorillibacterium massiliense</i> gen. nov, sp. nov., a new member of the family Paenibacillaceae. Standards in Genomic Sciences, 2014, 9, 807-820.	1.5	17
11093	Non-contiguous finished genome sequence and description of <i>Collinsella massiliensis</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 1144-1158.	1.5	13
11094	Non-contiguous finished genome sequence and description of <i>Bacillus massilioalgeriensis</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 1046-1061.	1.5	8
11095	Non-contiguous finished genome sequence and description of <i>Corynebacterium jeddahense</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 987-1002.	1.5	11
11096	Non-contiguous finished genome sequence and description of <i>Paucisalibacillus algeriensis</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 1352-1365.	1.5	6
11097	Genome sequence and description of <i>Nesterenkonia massiliensis</i> sp. nov. strain NP1T. Standards in Genomic Sciences, 2014, 9, 866-882.	1.5	18
11098	Non-contiguous finished genome sequence and description of <i>Anaerococcus provenciensis</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 1198-1210.	1.5	15
11099	Draft genome sequence of <i>Dyadobacter tibetensis</i> type strain (Y620-1) isolated from glacial ice. Standards in Genomic Sciences, 2014, 9, 883-892.	1.5	4
11100	Genome sequence of the <i>Thermotoga thermarum</i> type strain (LA3T) from an African solfataric spring. Standards in Genomic Sciences, 2014, 9, 1105-1117.	1.5	7
11101	Genome sequence of the anaerobic bacterium <i>Bacillus</i> sp. strain ZYK, a selenite and nitrate reducer from paddy soil. Standards in Genomic Sciences, 2014, 9, 646-654.	1.5	6
11102	The Genome Sequence of a Type ST239 Methicillin-Resistant <i>Staphylococcus aureus</i> Isolate from a Malaysian Hospital. Standards in Genomic Sciences, 2014, 9, 933-939.	1.5	2
11103	Non-contiguous finished genome sequence and description of <i>Fenollaria massiliensis</i> gen. nov., sp. nov., a new genus of anaerobic bacterium. Standards in Genomic Sciences, 2014, 9, 704-717.	1.5	21

#	ARTICLE	IF	CITATIONS
11104	Non-contiguous finished genome sequence of <i>Corynebacterium timonense</i> type strain 5401744T. Standards in Genomic Sciences, 2014, 9, 948-955.	1.5	1
11105	Non-contiguous finished genome sequence and description of <i>Alistipes ihumii</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 1221-1235.	1.5	48
11106	Genome analyses of the carboxydrotrophic sulfate-reducers <i>Desulfotomaculum nigrificans</i> and <i>Desulfotomaculum carboxydivorans</i> and reclassification of <i>Desulfotomaculum caboxydivorans</i> as a later synonym of <i>Desulfotomaculum nigrificans</i> . Standards in Genomic Sciences, 2014, 9, 655-675.	1.5	25
11107	High-quality draft genome sequence of nematocidal <i>Bacillus thuringiensis</i> Sbt003. Standards in Genomic Sciences, 2014, 9, 1-10.	1.5	3
11108	Complete genome sequence of a plant associated bacterium <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> UCMB5033. Standards in Genomic Sciences, 2014, 9, 718-725.	1.5	21
11109	Complete genome of the switchgrass endophyte <i>Enterobacter cloacae</i> P101. Standards in Genomic Sciences, 2014, 9, 726-734.	1.5	8
11110	Non contiguous-finished genome sequence and description of <i>Enorma timonensis</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 970-986.	1.5	10
11111	Genome sequence of the exopolysaccharide-producing <i>Salipiger mucosus</i> type strain (DSM 16094T), a moderately halophilic member of the <i>Roseobacter</i> clade. Standards in Genomic Sciences, 2014, 9, 1333-1345.	1.5	11
11112	Genome sequence of the <i>Medicago</i> -nodulating <i>Ensifer meliloti</i> commercial inoculant strain RRI128. Standards in Genomic Sciences, 2014, 9, 602-613.	1.5	3
11113	Non-contiguous finished genome sequence and description of <i>Sulfurimonas hongkongensis</i> sp. nov., a strictly anaerobic denitrifying, hydrogen- and sulfur-oxidizing chemolithoautotroph isolated from marine sediment. Standards in Genomic Sciences, 2014, 9, 1302-1310.	1.5	30
11114	Non-contiguous finished genome sequence of <i>Anoxybacillus flavithermus</i> subsp. <i>yunnanensis</i> type strain (E13T), a strictly thermophilic and organic solvent-tolerant bacterium. Standards in Genomic Sciences, 2014, 9, 735-743.	1.5	7
11115	Draft genome sequence of marine alphaproteobacterial strain HIMB11, the first cultivated representative of a unique lineage within the <i>Roseobacter</i> clade possessing an unusually small genome. Standards in Genomic Sciences, 2014, 9, 632-645.	1.5	40
11116	Metagenomic analysis of microbial consortium from natural crude oil that seeps into the marine ecosystem offshore Southern California. Standards in Genomic Sciences, 2014, 9, 1259-1274.	1.5	31
11117	High quality draft genome sequence of <i>Streptomyces</i> sp. strain AW19M42 isolated from a sea squirt in Northern Norway. Standards in Genomic Sciences, 2014, 9, 676-686.	1.5	5
11118	Draft genome sequences and description of <i>Lactobacillus rhamnosus</i> strains L31, L34, and L35. Standards in Genomic Sciences, 2014, 9, 744-754.	1.5	5
11119	Complete genome sequence of invertebrate iridovirus IIV22A, a variant of IIV22, isolated originally from a blackfly larva. Standards in Genomic Sciences, 2014, 9, 940-947.	1.5	7
11120	Non-contiguous finished genome sequence and description of <i>Kurthia senegalensis</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 1321-1332.	1.5	13
11121	High quality draft genome sequence of <i>Olivibacter sitiensis</i> type strain (AW-6T), a diphenol degrader with genes involved in the catechol pathway. Standards in Genomic Sciences, 2014, 9, 783-793.	1.5	18

#	ARTICLE	IF	CITATIONS
11122	Non-contiguous finished genome sequence of <i>Prevotella timonensis</i> type strain 4401737T. Standards in Genomic Sciences, 2014, 9, 1346-1353.	1.5	2
11123	Genome sequence of the mud-dwelling archaeon <i>Methanoplanus limicola</i> type strain (DSM 2279T), reclassification of <i>Methanoplanus petrolearius</i> as <i>Methanolacinia petrolearia</i> and emended descriptions of the genera <i>Methanoplanus</i> and <i>Methanolacinia</i> . Standards in Genomic Sciences, 2014, 9, 1076-1088.	1.5	22
11124	Genome sequence and description of <i>Corynebacterium ihumii</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 1128-1143.	1.5	10
11125	Non-contiguous finished genome sequence and description of <i>Bacteroides neonati</i> sp. nov., a new species of anaerobic bacterium. Standards in Genomic Sciences, 2014, 9, 794-806.	1.5	8
11126	Genome analysis of <i>Desulfotomaculum gibsoniae</i> strain GrollT a highly versatile Gram-positive sulfate-reducing bacterium. Standards in Genomic Sciences, 2014, 9, 821-839.	1.5	27
11127	Complete genome sequence of <i>Thalassolituus oleivorans</i> R6-15, an obligate hydrocarbonoclastic marine bacterium from the Arctic Ocean. Standards in Genomic Sciences, 2014, 9, 893-901.	1.5	8
11128	The complete genome sequence of <i>Clostridium indolis</i> DSM 755T. Standards in Genomic Sciences, 2014, 9, 1089-1104.	1.5	23
11129	Genome sequence and description of <i>Bacteroides timonensis</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 1181-1197.	1.5	10
11130	High quality draft genome sequence of <i>Staphylococcus cohnii</i> subsp. <i>cohnii</i> strain hu-01. Standards in Genomic Sciences, 2014, 9, 755-762.	1.5	8
11131	High quality draft genome sequence of the slightly halophilic bacterium <i>Halomonas zhanjiangensis</i> type strain JSM 078169T (DSM 21076T) from a sea urchin in southern China. Standards in Genomic Sciences, 2014, 9, 1020-1030.	1.5	9
11132	Non-contiguous finished genome sequence of <i>Staphylococcus capitis</i> CR01 (pulsetype NRCS-A). Standards in Genomic Sciences, 2014, 9, 1118-1127.	1.5	11
11133	Complete genome sequence of the bacteriochlorophyll a-containing <i>Roseobacterium elongatum</i> type strain (DSM 19469T), a representative of the <i>Roseobacter</i> group isolated from Australian coast sand. Standards in Genomic Sciences, 2014, 9, 840-854.	1.5	4
11134	Non contiguous-finished genome sequence and description of <i>Clostridium jeddahense</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 1003-1019.	1.5	26
11135	Genome sequence of the <i>Wenxinia marina</i> type strain (DSM 24838T), a representative of the <i>Roseobacter</i> group isolated from oilfield sediments. Standards in Genomic Sciences, 2014, 9, 855-865.	1.5	3
11136	Genomic analysis of <i>Skermanella stibiirensistens</i> type strain SB22T. Standards in Genomic Sciences, 2014, 9, 1211-1220.	1.5	14
11137	Furby: fuzzy force-directed bicluster visualization. BMC Bioinformatics, 2014, 15, S4.	1.2	38
11138	Complete genome sequence of <i>Anabaena variabilis</i> ATCC 29413. Standards in Genomic Sciences, 2014, 9, 562-573.	1.5	43
11139	Complete Genome sequence of <i>Burkholderia phymatum</i> STM815T, a broad host range and efficient nitrogen-fixing symbiont of <i>Mimosa</i> species. Standards in Genomic Sciences, 2014, 9, 763-774.	1.5	71

#	ARTICLE	IF	CITATIONS
11140	Non-contiguous finished genome sequence and description of <i>Paenibacillus gorillae</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 1031-1045.	1.5	7
11141	Genome sequence of <i>Microvirga lupini</i> strain LUT6T, a novel <i>Lupinus</i> alphaproteobacterial microsymbiont from Texas. Standards in Genomic Sciences, 2014, 9, 1159-1167.	1.5	6
11142	Genome sequence of the pink to light reddish-pigmented <i>Rubellimicrobium mesophilum</i> type strain (DSM 19309T), a representative of the <i>Roseobacter</i> group isolated from soil, and emended description of the species. Standards in Genomic Sciences, 2014, 9, 902-913.	1.5	12
11143	A modified cutoff scanning matrix protein representation for enhancing protein function prediction. , 2014, , .		3
11144	Network-based modular latent structure analysis. BMC Bioinformatics, 2014, 15, S6.	1.2	2
11145	Identification of genes and pathways involved in kidney renal clear cell carcinoma. BMC Bioinformatics, 2014, 15, S2.	1.2	45
11146	Orthology and paralogy constraints: satisfiability and consistency. BMC Genomics, 2014, 15, S12.	1.2	35
11147	A meta-approach for improving the prediction and the functional annotation of ortholog groups. BMC Genomics, 2014, 15, S16.	1.2	20
11148	Gene expression and fractionation resistance. BMC Genomics, 2014, 15, S19.	1.2	5
11149	Joint clustering of protein interaction networks through Markov random walk. BMC Systems Biology, 2014, 8, S9.	3.0	6
11150	Discovery of small protein complexes from PPI networks with size-specific supervised weighting. BMC Systems Biology, 2014, 8, S3.	3.0	34
11151	Robustness analysis on interspecies interaction network for iron and glucose competition between <i>Candida albicans</i> and zebrafish during infection. BMC Systems Biology, 2014, 8, S6.	3.0	10
11152	Pituitary transcriptome profile of liver cancer mice with different syndromes reveals the relevance of pituitary to the cancer and syndromes. Journal of Traditional Chinese Medicine = Chung I Tsa Chih Ying Wen Pan / Sponsored By All-China Association of Traditional Chinese Medicine, Academy of Traditional Chinese Medicine, 2014, 34, 691-698.	0.4	2
11153	BCL2DB: database of BCL-2 family members and BH3-only proteins. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau013-bau013.	1.4	17
11154	PlantCAZyme: a database for plant carbohydrate-active enzymes. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	1.4	38
11155	RCMDE-GMD: Predicting gene ontology terms using differential evolution. , 2014, , .		1
11156	SysPTM 2.0: an updated systematic resource for post-translational modification. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau025-bau025.	1.4	58
11157	A semi-automated methodology for finding lipid-related GO terms. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	1.4	1

#	ARTICLE	IF	CITATIONS
11158	A study of lightweight ontology for herb domain. , 2014, , .		0
11159	A Large Number of Nuclear Genes in the Human Parasite Blastocystis Require mRNA Polyadenylation to Create Functional Termination Codons. <i>Genome Biology and Evolution</i> , 2014, 6, 1956-1961.	1.1	11
11160	Soft Approach to Identification of Cohesive Clusters in Two Gene Representations. <i>Procedia Computer Science</i> , 2014, 35, 281-289.	1.2	4
11161	Whole Genome Sequence of the Probiotic Strain <i>Lactobacillus paracasei</i> N1115, Isolated from Traditional Chinese Fermented Milk. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
11162	Operon prediction by Markov clustering. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 9, 424.	0.1	3
11163	Whole transcriptome analysis of the poultry red mite <i>Dermanyssus gallinae</i> (De Geer, 1778). <i>Parasitology</i> , 2014, 141, 336-346.	0.7	40
11164	Noncontiguous finished genome sequence and description of <i>Paenibacillus antibiotrophicus</i> sp. nov. GD11T, the type strain of <i>Paenibacillus antibiotrophicus</i> . <i>New Microbes and New Infections</i> , 2015, 8, 137-147.	0.8	5
11165	Sex-related gene expression profiles in the adrenal cortex in the mature rat: Microarray analysis with emphasis on genes involved in steroidogenesis. <i>International Journal of Molecular Medicine</i> , 2015, 35, 702-714.	1.8	34
11166	PADPIN: protein-protein interaction networks of angiogenesis, arteriogenesis, and inflammation in peripheral arterial disease. <i>Physiological Genomics</i> , 2015, 47, 331-343.	1.0	12
11167	Noncontiguous finished genome sequence and description of <i>Weeksellia massiliensis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2015, 8, 89-98.	0.8	12
11168	Graded gene expression changes determine phenotype severity in mouse models of CRX-associated retinopathies. <i>Genome Biology</i> , 2015, 16, 171.	3.8	37
11169	Complete genome sequence of <i>Geobacillus thermoglucosidasius</i> C56-YS93, a novel biomass degrader isolated from obsidian hot spring in Yellowstone National Park. <i>Standards in Genomic Sciences</i> , 2015, 10, 73.	1.5	21
11170	Multiple sources of bias confound functional enrichment analysis of global -omics data. <i>Genome Biology</i> , 2015, 16, 186.	3.8	131
11171	Integrated analysis of differentially expressed genes in breast cancer pathogenesis. <i>Oncology Letters</i> , 2015, 9, 2560-2566.	0.8	15
11172	Association between DNA methylation and multidrug resistance in human glioma SHG-44 cells. <i>Molecular Medicine Reports</i> , 2015, 11, 43-52.	1.1	6
11173	Putative synaptic genes defined from a <i>Drosophila</i> whole body developmental transcriptome by a machine learning approach. <i>BMC Genomics</i> , 2015, 16, 694.	1.2	16
11174	Complete genome sequence of <i>Novosphingobium pentaromativorans</i> US6-1T. <i>Standards in Genomic Sciences</i> , 2015, 10, 107.	1.5	24
11175	A visual spreadsheet using HTML5 for whole genome display. , 2015, , .		1

#	ARTICLE	IF	CITATIONS
11176	Jasmonate signalling drives time-of-day differences in susceptibility of Arabidopsis to the fungal pathogen <i>Botrytis cinerea</i> . <i>Plant Journal</i> , 2015, 84, 937-948.	2.8	81
11177	PhenomeCentral: A Portal for Phenotypic and Genotypic Matchmaking of Patients with Rare Genetic Diseases. <i>Human Mutation</i> , 2015, 36, 931-940.	1.1	107
11178	Association rule mining of gene ontology annotation terms for SGD. , 2015, , .		1
11179	Hierarchical classification of Gene Ontology-based protein functions with neural networks. , 2015, , .		21
11180	A Semantically Adaptable Integrated Visualization and Natural Exploration of Multi-scale Biomedical Data. , 2015, , .		1
11181	Gene expression profiling during adventitious root formation in carnation stem cuttings. <i>BMC Genomics</i> , 2015, 16, 789.	1.2	67
11183	Biocuration at the <i>Saccharomyces</i> genome database. <i>Genesis</i> , 2015, 53, 450-457.	0.8	16
11184	<i>ZFIN</i> , The zebrafish model organism database: Updates and new directions. <i>Genesis</i> , 2015, 53, 498-509.	0.8	68
11185	Biology-Driven Gene-Gene Interaction Analysis of Age-Related Cataract in the eMERGE Network. <i>Genetic Epidemiology</i> , 2015, 39, 376-384.	0.6	20
11186	A systems biology strategy to identify molecular mechanisms of action and protein indicators of traumatic brain injury. <i>Journal of Neuroscience Research</i> , 2015, 93, 199-214.	1.3	14
11187	Integration of "omics" data in aging research: from biomarkers to systems biology. <i>Aging Cell</i> , 2015, 14, 933-944.	3.0	103
11188	An application of MeSH enrichment analysis in livestock. <i>Animal Genetics</i> , 2015, 46, 381-387.	0.6	26
11189	E2F1 controls germ cell apoptosis during the first wave of spermatogenesis. <i>Andrology</i> , 2015, 3, 1000-1014.	1.9	24
11190	Does FACS perturb gene expression?. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2015, 87, 166-175.	1.1	59
11191	Mouse Genome Database: From sequence to phenotypes and disease models. <i>Genesis</i> , 2015, 53, 458-473.	0.8	13
11192	Identification of therapeutic targets for breast cancer using biological informatics methods. <i>Molecular Medicine Reports</i> , 2015, 12, 1789-1795.	1.1	14
11193	Gene expression changes in human mesenchymal stem cells from patients with osteoporosis. <i>Molecular Medicine Reports</i> , 2015, 12, 981-987.	1.1	18
11194	Identification of key genes associated with the human abdominal aortic aneurysm based on the gene expression profile. <i>Molecular Medicine Reports</i> , 2015, 12, 7891-7898.	1.1	4

#	ARTICLE	IF	CITATIONS
11195	The proportion of genes in a functional category is linked to mass-specific metabolic rate and lifespan. <i>Scientific Reports</i> , 2015, 5, 10008.	1.6	7
11196	Integrative analysis of human protein, function and disease networks. <i>Scientific Reports</i> , 2015, 5, 14344.	1.6	32
11197	Transcriptome Analysis of Nine Tissues to Discover Genes Involved in the Biosynthesis of Active Ingredients in <i>Sophora flavescens</i> . <i>Biological and Pharmaceutical Bulletin</i> , 2015, 38, 876-883.	0.6	22
11198	Effects of a Tricaprylin Emulsion on Anti-glomerular Basement Membrane Glomerulonephritis in Rats: <i>In Vivo</i> and <i>In Silico</i> Studies. <i>Biological and Pharmaceutical Bulletin</i> , 2015, 38, 1175-1184.	0.6	6
11199	Improving biological significance of gene expression biclusters with key missing genes. , 2015, , .		0
11200	Methods for biological data integration: perspectives and challenges. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150571.	1.5	196
11201	High Concentrations of Uric Acid Inhibit Angiogenesis via Regulation of the KrÄ¼ppel-Like Factor 2-Vascular Endothelial Growth Factor-A Axis by miR-92a. <i>Circulation Journal</i> , 2015, 79, 2487-2498.	0.7	31
11202	Does the Rewarmed Heart Restore the Myocardial Proteome to That of the Pre-Cooled State?â€”A Proteomic Analysis of Surgical Samples â€”. <i>Circulation Journal</i> , 2015, 79, 2648-2658.	0.7	7
11203	Deregulated microRNA species in the plasma and placenta of patients with preeclampsia. <i>Molecular Medicine Reports</i> , 2015, 12, 527-534.	1.1	92
11204	The complete genome sequence of the rumen methanogen <i>Methanosarcina barkeri</i> CM1. <i>Standards in Genomic Sciences</i> , 2015, 10, 57.	1.5	42
11206	Functional analysis of the nasopharyngeal carcinoma primary tumor-associated gene interaction network. <i>Molecular Medicine Reports</i> , 2015, 12, 4975-4980.	1.1	9
11207	Managing changes in distributed biomedical ontologies using hierarchical distributed graph transformation. <i>International Journal of Data Mining and Bioinformatics</i> , 2015, 11, 53.	0.1	9
11208	MicroRNA profiling of CD3+CD56+ cytokine-induced killer cells. <i>Scientific Reports</i> , 2015, 5, 9571.	1.6	8
11209	Two methods for constructing a gene ontology-based feature network for a Bayesian network classifier and applications to datasets of aging-related genes. , 2015, , .		13
11210	Regulatory network of differentially expressed genes in metastatic osteosarcoma. <i>Molecular Medicine Reports</i> , 2015, 11, 2104-2110.	1.1	7
11211	Developmental genes significantly afflicted by aberrant promoter methylation and somatic mutation predict overall survival of late-stage colorectal cancer. <i>Scientific Reports</i> , 2015, 5, 18616.	1.6	13
11212	PALM-IST: Pathway Assembly from Literature Mining - an Information Search Tool. <i>Scientific Reports</i> , 2015, 5, 10021.	1.6	21
11213	Revealing crosstalk of plant and fungi in the symbiotic roots of sewage-cleaning <i>Eichhornia crassipes</i> using direct de novo metatranscriptomic analysis. <i>Scientific Reports</i> , 2015, 5, 15407.	1.6	15

#	ARTICLE	IF	CITATIONS
11214	Moyamoya disease susceptibility gene RNF213 links inflammatory and angiogenic signals in endothelial cells. <i>Scientific Reports</i> , 2015, 5, 13191.	1.6	105
11215	Type of in vitro cultivation influences cytoadhesion, knob structure, protein localization and transcriptome profile of <i>Plasmodium falciparum</i> . <i>Scientific Reports</i> , 2015, 5, 16766.	1.6	15
11216	The Gibbs-plaid biclustering model. <i>Annals of Applied Statistics</i> , 2015, 9, .	0.5	7
11217	Novel drug target identification for the treatment of dementia using multi-relational association mining. <i>Scientific Reports</i> , 2015, 5, 11104.	1.6	11
11218	A comprehensive analysis of differentially expressed genes and pathways in abdominal aortic aneurysm. <i>Molecular Medicine Reports</i> , 2015, 12, 2707-2714.	1.1	13
11219	Prediction of high- and low-risk multiple myeloma based on gene expression and the International Staging System. <i>Blood</i> , 2015, 126, 1996-2004.	0.6	106
11221	Identification and comparative expression analysis of odorant binding protein genes in the tobacco cutworm <i>Spodoptera litura</i> . <i>Scientific Reports</i> , 2015, 5, 13800.	1.6	75
11222	Quantitative assessment of gene expression network module-validation methods. <i>Scientific Reports</i> , 2015, 5, 15258.	1.6	20
11223	Pathogenic mechanisms of lung adenocarcinoma in smokers and non-smokers determined by gene expression interrogation. <i>Oncology Letters</i> , 2015, 10, 1350-1370.	0.8	16
11224	TRRUST: a reference database of human transcriptional regulatory interactions. <i>Scientific Reports</i> , 2015, 5, 11432.	1.6	339
11225	Copy number variation-based genome wide association study reveals additional variants contributing to meat quality in Swine. <i>Scientific Reports</i> , 2015, 5, 12535.	1.6	26
11226	Gene Expression Profiling in the APP/PS1KI Mouse Model of Familial Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2016, 50, 397-409.	1.2	12
11227	High-throughput transcriptome sequencing of the cold seep mussel <i>Bathymodiolus platifrons</i> . <i>Scientific Reports</i> , 2015, 5, 16597.	1.6	78
11228	Protein Localization Analysis of Essential Genes in Prokaryotes. <i>Scientific Reports</i> , 2014, 4, 6001.	1.6	27
11229	LENS: web-based lens for enrichment and network studies of human proteins. <i>BMC Medical Genomics</i> , 2015, 8, S2.	0.7	27
11230	Converting neXtProt into Linked Data and nanopublications. <i>Semantic Web</i> , 2015, 6, 147-153.	1.1	13
11231	Characterization of the Transcriptional Complexity of the Receptive and Pre-receptive Endometria of Dairy Goats. <i>Scientific Reports</i> , 2015, 5, 14244.	1.6	28
11232	Gene Expression Changes Associated With the Developmental Plasticity of Sea Urchin Larvae in Response to Food Availability. <i>Biological Bulletin</i> , 2015, 228, 171-180.	0.7	38

#	ARTICLE	IF	CITATIONS
11233	Indexing Method for Hierarchical Graphs based on Relation among Interlacing Sequences of Eigenvalues. <i>Journal of Information Processing</i> , 2015, 23, 210-220.	0.3	2
11234	Combining computational models, semantic annotations and simulation experiments in a graph database. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	42
11236	TRANSCRIPTIONAL PROFILE ANALYSIS OF YOUNG AND MATURE LEAVES OF CITRUS TREES ACCLIMATED TO SALINITY. <i>Acta Horticulturae</i> , 2015, , 1359-1369.	0.1	0
11237	Ecological transcriptomics – a non-lethal sampling approach for endangered fire salamanders. <i>Methods in Ecology and Evolution</i> , 2015, 6, 1417-1425.	2.2	16
11239	Insights into the Transcriptional Architecture of Behavioral Plasticity in the Honey Bee <i>Apis mellifera</i> . <i>Scientific Reports</i> , 2015, 5, 11136.	1.6	59
11242	Joining the dots: network analysis of gene perturbation data. , 0, , 83-107.		0
11243	Computational paradigms for analyzing genetic interaction networks. , 0, , 12-35.		0
11244	A novel analysis strategy for integrating methylation and expression data reveals core pathways for thyroid cancer aetiology. <i>BMC Genomics</i> , 2015, 16, S7.	1.2	3
11245	Identification of genes associated with osteoarthritis by microarray analysis. <i>Molecular Medicine Reports</i> , 2015, 12, 5211-5216.	1.1	14
11246	MicroRNA 19a replacement partially rescues fin and cardiac defects in zebrafish model of Holt Oram syndrome. <i>Scientific Reports</i> , 2015, 5, 18240.	1.6	21
11247	Detection of Composite Communities in Multiplex Biological Networks. <i>Scientific Reports</i> , 2015, 5, 10345.	1.6	37
11248	Transcriptome changes in apple peel tissues during CO ₂ injury – symptom development under controlled atmosphere storage regimens. <i>Horticulture Research</i> , 2015, 2, 15061.	2.9	9
11249	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
11250	An acorn squash (<i>Cucurbita pepo</i> ssp. <i>ovifera</i>) fruit and seed transcriptome as a resource for the study of fruit traits in <i>Cucurbita</i> . <i>Horticulture Research</i> , 2015, 2, 14070.	2.9	32
11251	Parallel molecular routes to cold adaptation in eight genera of New Zealand stick insects. <i>Scientific Reports</i> , 2015, 5, 13965.	1.6	45
11253	<i>De Novo</i> Assembly and Characterization of Four Anthozoan (Phylum Cnidaria) Transcriptomes. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2441-2452.	0.8	74
11254	Importance of collection in gene set enrichment analysis of drug response in cancer cell lines. <i>Scientific Reports</i> , 2014, 4, 4092.	1.6	21
11255	Integration of extracellular RNA profiling data using metadata, biomedical ontologies and Linked Data technologies. <i>Journal of Extracellular Vesicles</i> , 2015, 4, 27497.	5.5	48

#	ARTICLE	IF	CITATIONS
11256	Genetic variation in insulin-induced kinase signaling. <i>Molecular Systems Biology</i> , 2015, 11, 820.	3.2	14
11257	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
11258	Mechanosensitive Kinases Regulate Stiffness-Induced Cardiomyocyte Maturation. <i>Scientific Reports</i> , 2014, 4, 6425.	1.6	56
11259	Primary sequence contribution to the optical function of the eye lens. <i>Scientific Reports</i> , 2014, 4, 5195.	1.6	28
11260	WaspAtlas: a <i>Nasonia vitripennis</i> gene database and analysis platform. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav103.	1.4	18
11261	Advanced Applications of RNA Sequencing and Challenges. <i>Bioinformatics and Biology Insights</i> , 2015, 9s1, BBI.S28991.	1.0	178
11263	Prioritization Of Nonsynonymous Single Nucleotide Variants For Exome Sequencing Studies Via Integrative Learning On Multiple Genomic Data. <i>Scientific Reports</i> , 2015, 5, 14955.	1.6	10
11264	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
11265	NET-GE: a novel NETWORK-based Gene Enrichment for detecting biological processes associated to Mendelian diseases. <i>BMC Genomics</i> , 2015, 16, S6.	1.2	15
11266	A computational framework for the prioritization of disease-gene candidates. <i>BMC Genomics</i> , 2015, 16, S2.	1.2	20
11267	Overview of the Cancer Genetics and Pathway Curation tasks of BioNLP Shared Task 2013. <i>BMC Bioinformatics</i> , 2015, 16, S2.	1.2	44
11268	Protein complex detection in PPI networks based on data integration and supervised learning method. <i>BMC Bioinformatics</i> , 2015, 16, S3.	1.2	11
11269	Sieve-based relation extraction of gene regulatory networks from biological literature. <i>BMC Bioinformatics</i> , 2015, 16, S1.	1.2	10
11270	Signal reachability facilitates characterization of probabilistic signaling networks. <i>BMC Bioinformatics</i> , 2015, 16, S6.	1.2	2
11271	Mining the human proteome for conserved mechanisms. <i>BMC Bioinformatics</i> , 2015, 16, .	1.2	1
11272	Functional redundancy of transcription factors explains why most binding targets of a transcription factor are not affected when the transcription factor is knocked out. <i>BMC Systems Biology</i> , 2015, 9, S2.	3.0	22
11273	Disentangling the multigenic and pleiotropic nature of molecular function. <i>BMC Systems Biology</i> , 2015, 9, S3.	3.0	9
11274	Linked annotations: a middle ground for manual curation of biomedical databases and text corpora. <i>BMC Proceedings</i> , 2015, 9, .	1.8	5

#	ARTICLE	IF	CITATIONS
11275	Identification association of drug-disease by using functional gene module for breast cancer. <i>BMC Medical Genomics</i> , 2015, 8, S3.	0.7	7
11276	Multiple target drug cocktail design for attacking the core network markers of four cancers using ligand-based and structure-based virtual screening methods. <i>BMC Medical Genomics</i> , 2015, 8, S4.	0.7	15
11277	The administration of intranasal live attenuated influenza vaccine induces changes in the nasal microbiota and nasal epithelium gene expression profiles. <i>Microbiome</i> , 2015, 3, 74.	4.9	64
11278	Complete genome sequence of the chromate-reducing bacterium <i>Thermoanaerobacter thermohydrosulfuricus</i> strain BSB-33. <i>Standards in Genomic Sciences</i> , 2015, 10, 74.	1.5	15
11279	The complete genome sequence and emendation of the hyperthermophilic, obligate iron-reducing archaeon <i>Geoglobus ahangari</i> strain 234T. <i>Standards in Genomic Sciences</i> , 2015, 10, 77.	1.5	24
11280	Transcriptome sequencing of three <i>Pseudo-nitzschia</i> species reveals comparable gene sets and the presence of Nitric Oxide Synthase genes in diatoms. <i>Scientific Reports</i> , 2015, 5, 12329.	1.6	58
11281	Large-scale identification of encystment-related proteins and genes in <i>Pseudourostyla cristata</i> . <i>Scientific Reports</i> , 2015, 5, 11360.	1.6	13
11282	Bioinformatic analysis of microRNA expression in Parkinson's disease. <i>Molecular Medicine Reports</i> , 2015, 11, 1079-1084.	1.1	13
11283	Highly proliferative primitive fetal liver hematopoietic stem cells are fueled by oxidative metabolic pathways. <i>Stem Cell Research</i> , 2015, 15, 715-721.	0.3	59
11284	High-quality genome sequence and description of <i>Bacillus ndiopicus</i> strain FF3T sp. nov.. <i>New Microbes and New Infections</i> , 2015, 8, 154-163.	0.8	10
11285	Identification of miRNAs and their targets in transgenic <i>Brassica napus</i> and its acceptor (Westar) by high-throughput sequencing and degradome analysis. <i>RSC Advances</i> , 2015, 5, 85383-85394.	1.7	11
11286	Draft genome of <i>Gemmata massiliana</i> sp. nov, a water-borne Planctomycetes species exhibiting two variants. <i>Standards in Genomic Sciences</i> , 2015, 10, 120.	1.5	35
11287	Noncontiguous finished genome sequence and description of <i>Necropsobacter massiliensis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2015, 8, 41-50.	0.8	8
11288	Noncontiguous finished genome sequence and description of <i>Diaminobutyricimonas massiliensis</i> strain FF2T sp. nov.. <i>New Microbes and New Infections</i> , 2015, 8, 31-40.	0.8	1
11289	MicroRNA sequencing detects miR-424-5p up-regulation in ovarian cancer stem cells. <i>Genes and Genomics</i> , 2015, 37, 737-742.	0.5	5
11290	A method of searching for related literature on protein structure analysis by considering a user's intention. <i>BMC Bioinformatics</i> , 2015, 16, S4.	1.2	0
11291	EXPath: a database of comparative expression analysis inferring metabolic pathways for plants. <i>BMC Genomics</i> , 2015, 16, S6.	1.2	45
11292	LncRNA2Function: a comprehensive resource for functional investigation of human lncRNAs based on RNA-seq data. <i>BMC Genomics</i> , 2015, 16, S2.	1.2	117

#	ARTICLE	IF	CITATIONS
11293	Co-modulation analysis of gene regulation in breast cancer reveals complex interplay between ESR1 and ERBB2 genes. <i>BMC Genomics</i> , 2015, 16, S19.	1.2	7
11294	Draft genome sequences for the obligate bacterial predators <i>Bacteriovorax</i> spp. of four phylogenetic clusters. <i>Standards in Genomic Sciences</i> , 2015, 10, 11.	1.5	12
11295	CompGO: an R package for comparing and visualizing Gene Ontology enrichment differences between DNA binding experiments. <i>BMC Bioinformatics</i> , 2015, 16, 275.	1.2	44
11296	Genome-wide target analysis of NEUROD2 provides new insights into regulation of cortical projection neuron migration and differentiation. <i>BMC Genomics</i> , 2015, 16, 681.	1.2	49
11297	Integrated ordination of miRNA and mRNA expression profiles. <i>BMC Genomics</i> , 2015, 16, 767.	1.2	38
11298	Blood transcriptomics of drug-naïve sporadic Parkinson's disease patients. <i>BMC Genomics</i> , 2015, 16, 876.	1.2	64
11299	Genome-wide transcriptome profiling reveals functional networks involving the <i>Plasmodium falciparum</i> drug resistance transporters PfCRT and PfMDR1. <i>BMC Genomics</i> , 2015, 16, 1090.	1.2	20
11300	Systems biology evaluation of cell-free amniotic fluid transcriptome of term and preterm infants to detect fetal maturity. <i>BMC Medical Genomics</i> , 2015, 8, 67.	0.7	25
11301	Improved orthologous databases to ease protozoan targets inference. <i>Parasites and Vectors</i> , 2015, 8, 494.	1.0	2
11302	Methylome profiling reveals functions and genes which are differentially methylated in serrated compared to conventional colorectal carcinoma. <i>Clinical Epigenetics</i> , 2015, 7, 101.	1.8	21
11303	Ambiguity and variability of database and software names in bioinformatics. <i>Journal of Biomedical Semantics</i> , 2015, 6, 29.	0.9	6
11304	A survey of computational tools for downstream analysis of proteomic and other omic datasets. <i>Human Genomics</i> , 2015, 9, 28.	1.4	16
11305	High quality draft genome sequence of <i>Brachymonas chironomi</i> AIMA4T (DSM 19884T) isolated from a <i>Chironomus</i> sp. egg mass. <i>Standards in Genomic Sciences</i> , 2015, 10, 29.	1.5	2
11306	High-quality permanent draft genome sequence of the <i>Parapiptadenia rigida</i> -nodulating <i>Burkholderia</i> sp. strain UYPR1.413. <i>Standards in Genomic Sciences</i> , 2015, 10, 31.	1.5	2
11307	Draft-genome sequence of <i>Shewanella</i> algae strain C6G3. <i>Standards in Genomic Sciences</i> , 2015, 10, 43.	1.5	7
11308	High quality draft genome sequence of <i>Bacteroides barnesiae</i> type strain BL2T (DSM 18169T) from chicken caecum. <i>Standards in Genomic Sciences</i> , 2015, 10, 48.	1.5	4
11309	High-quality permanent draft genome sequence of the <i>Lebeckia</i> - nodulating <i>Burkholderia dilworthii</i> strain WSM3556T. <i>Standards in Genomic Sciences</i> , 2015, 10, 64.	1.5	1
11310	Draft genome sequence of the extremely halophilic archaeon <i>Haladaptatus cibarius</i> type strain D43T isolated from fermented seafood. <i>Standards in Genomic Sciences</i> , 2015, 10, 53.	1.5	4

#	ARTICLE	IF	CITATIONS
11311	Complete genome sequence of <i>Vibrio anguillarum</i> strain NB10, a virulent isolate from the Gulf of Bothnia. <i>Standards in Genomic Sciences</i> , 2015, 10, 60.	1.5	15
11312	Draft genome sequence of a nitrate-reducing, o-phthalate degrading bacterium, <i>Azoarcus</i> sp. strain PA01T. <i>Standards in Genomic Sciences</i> , 2015, 10, 90.	1.5	26
11313	High quality draft genomic sequence of <i>Flavobacterium enshiense</i> DK69T and comparison among <i>Flavobacterium</i> genomes. <i>Standards in Genomic Sciences</i> , 2015, 10, 92.	1.5	2
11314	High-quality draft genome sequence of <i>Gracilimonas tropica</i> CL-CB462T (DSM 19535T), isolated from a <i>Synechococcus</i> culture. <i>Standards in Genomic Sciences</i> , 2015, 10, 98.	1.5	3
11315	A multilevel pan-cancer map links gene mutations to cancer hallmarks. <i>Chinese Journal of Cancer</i> , 2015, 34, 439-49.	4.9	38
11316	Virtual pathway explorer (viPEr) and pathway enrichment analysis tool (PEANuT): creating and analyzing focus networks to identify cross-talk between molecules and pathways. <i>BMC Genomics</i> , 2015, 16, 790.	1.2	7
11317	Deep sequencing of Danish Holstein dairy cattle for variant detection and insight into potential loss-of-function variants in protein coding genes. <i>BMC Genomics</i> , 2015, 16, 1043.	1.2	32
11318	Developing expressed sequence tag libraries and the discovery of simple sequence repeat markers for two species of raspberry (<i>Rubus</i> L.). <i>BMC Plant Biology</i> , 2015, 15, 258.	1.6	13
11319	Integrative analyses of proteomics and RNA transcriptomics implicate mitochondrial processes, protein folding pathways and GWAS loci in Parkinson disease. <i>BMC Medical Genomics</i> , 2015, 9, 5.	0.7	103
11320	Extensive rewiring of epithelial-stromal co-expression networks in breast cancer. <i>Genome Biology</i> , 2015, 16, 128.	3.8	48
11321	Prediction of problematic complexes from PPI networks: sparse, embedded, and small complexes. <i>Biology Direct</i> , 2015, 10, 40.	1.9	23
11322	High-quality permanent draft genome sequence of the <i>Lebeckia ambigua</i> -nodulating <i>Burkholderia</i> sp. strain WSM4176. <i>Standards in Genomic Sciences</i> , 2015, 10, 79.	1.5	5
11323	Partial genome sequence of <i>Thioalkalivibrio thiocyanodenitrificans</i> ARhD 1T, a chemolithoautotrophic haloalkaliphilic sulfur-oxidizing bacterium capable of complete denitrification. <i>Standards in Genomic Sciences</i> , 2015, 10, 84.	1.5	2
11324	Complete genome sequence of <i>Paracoccus marcusii</i> phage vB_PmaS-R3 isolated from the South China Sea. <i>Standards in Genomic Sciences</i> , 2015, 10, 94.	1.5	9
11325	UniRef clusters: a comprehensive and scalable alternative for improving sequence similarity searches. <i>Bioinformatics</i> , 2015, 31, 926-932.	1.8	1,223
11326	CATH FunFHMMer web server: protein functional annotations using functional family assignments. <i>Nucleic Acids Research</i> , 2015, 43, W148-W153.	6.5	59
11327	Draft genome sequences of <i>Chrysosporthe austroafricana</i> , <i>Diplodia scrobiculata</i> , <i>Fusarium nygamai</i> , <i>Leptographium lundbergii</i> , <i>Limonomyces culmigenus</i> , <i>Stagonosporopsis tanacetii</i> , and <i>Thielaviopsis punctulata</i> . <i>IMA Fungus</i> , 2015, 6, 233-248.	1.7	46
11328	Gene Expression Profile of the Neonatal Female Mouse Brain After Administration of Testosterone Propionate. <i>Journal of Sexual Medicine</i> , 2015, 12, 887-896.	0.3	2

#	ARTICLE	IF	CITATIONS
11329	Genome-wide analysis of androgen receptor binding sites in prostate cancer cells. <i>Experimental and Therapeutic Medicine</i> , 2015, 9, 2319-2324.	0.8	16
11330	Integrated microRNA-mRNA analysis revealing the potential roles of microRNAs in tongue squamous cell cancer. <i>Molecular Medicine Reports</i> , 2015, 12, 885-894.	1.1	14
11331	Identifying overlapping mutated driver pathways by constructing gene networks in cancer. <i>BMC Bioinformatics</i> , 2015, 16, S3.	1.2	21
11332	High-quality permanent draft genome sequence of the <i>Parapiptadenia rigida</i> -nodulating <i>Cupriavidus</i> sp. strain UYPR2.512. <i>Standards in Genomic Sciences</i> , 2015, 10, 13.	1.5	6
11333	Genome sequence of the <i>Roseovarius mucosus</i> type strain (DSM 17069T), a bacteriochlorophyll a-containing representative of the marine <i>Roseobacter</i> group isolated from the dinoflagellate <i>Alexandrium ostenfeldii</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 17.	1.5	12
11334	Complete genome sequence and description of <i>Salinispira pacifica</i> gen. nov., sp. nov., a novel spirochaete isolated from a hypersaline microbial mat. <i>Standards in Genomic Sciences</i> , 2015, 10, 7.	1.5	38
11335	Revisiting operons: an analysis of the landscape of transcriptional units in <i>E. coli</i> . <i>BMC Bioinformatics</i> , 2015, 16, 356.	1.2	39
11336	Cross-tissue and cross-species analysis of gene expression in skeletal muscle and electric organ of African weakly-electric fish (Teleostei; Mormyridae). <i>BMC Genomics</i> , 2015, 16, 668.	1.2	38
11337	Genomic insight into <i>Aquimarina longa</i> SWO24T: its ultra-oligotrophic adapting mechanisms and biogeochemical functions. <i>BMC Genomics</i> , 2015, 16, 772.	1.2	13
11338	Identification of novel and conserved microRNAs in <i>Panax notoginseng</i> roots by high-throughput sequencing. <i>BMC Genomics</i> , 2015, 16, 835.	1.2	38
11339	The distribution and impact of common copy-number variation in the genome of the domesticated apple, <i>Malus x domestica</i> Borkh. <i>BMC Genomics</i> , 2015, 16, 848.	1.2	21
11340	A human 3' UTR clone collection to study post-transcriptional gene regulation. <i>BMC Genomics</i> , 2015, 16, 1036.	1.2	7
11341	Protein aggregation, structural disorder and RNA-binding ability: a new approach for physico-chemical and gene ontology classification of multiple datasets. <i>BMC Genomics</i> , 2015, 16, 1071.	1.2	14
11342	Fair evaluation of global network aligners. <i>Algorithms for Molecular Biology</i> , 2015, 10, 19.	0.3	18
11343	A co-culture genome-wide RNAi screen with mammary epithelial cells reveals transmembrane signals required for growth and differentiation. <i>Breast Cancer Research</i> , 2015, 17, 4.	2.2	24
11344	Draft genome sequence of <i>Methylibium</i> sp. strain T29, a novel fuel oxygenate-degrading bacterial isolate from Hungary. <i>Standards in Genomic Sciences</i> , 2015, 10, 39.	1.5	9
11345	Non contiguous-finished genome sequence and description of <i>Bacillus jeddahensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 47.	1.5	22
11346	High quality draft genomic sequence of <i>Arenimonas donghaensis</i> DSM 18148T. <i>Standards in Genomic Sciences</i> , 2015, 10, 59.	1.5	6

#	ARTICLE	IF	CITATIONS
11347	High quality draft genomes of the <i>Mycoplasma mycoides</i> subsp. <i>mycoides</i> challenge strains Afad ^Å and B237. <i>Standards in Genomic Sciences</i> , 2015, 10, 89.	1.5	21
11348	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. strain WSM1743 - an effective microsymbiont of an <i>Indigofera</i> sp. growing in Australia. <i>Standards in Genomic Sciences</i> , 2015, 10, 87.	1.5	1
11349	Working draft genome sequence of the mesophilic acetate oxidizing bacterium <i>Syntrophaceticus schinkii</i> strain Sp3. <i>Standards in Genomic Sciences</i> , 2015, 10, 99.	1.5	19
11350	Draft genome sequence of <i>Cellulomonas carbonis</i> T26T and comparative analysis of six <i>Cellulomonas</i> genomes. <i>Standards in Genomic Sciences</i> , 2015, 10, 104.	1.5	5
11351	Complete genome sequence of <i>Staphylococcus aureus</i> , strain LLRI_Eymole1/1, isolated from a Kenyan dromedary camel. <i>Standards in Genomic Sciences</i> , 2015, 10, 109.	1.5	16
11352	Complete genome sequence of the thermophilic Acidobacteria, <i>Pyrimonas methylaliphatogenes</i> type strain K22T. <i>Standards in Genomic Sciences</i> , 2015, 10, 101.	1.5	17
11353	Complete genome sequence of <i>Salinicoccus halodurans</i> H3B36, isolated from the Qaidam Basin in China. <i>Standards in Genomic Sciences</i> , 2015, 10, 116.	1.5	7
11354	mycoCLAP, the database for characterized lignocellulose-active proteins of fungal origin: resource and text mining curation support. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, .	1.4	32
11355	An Ebola virus-centered knowledge base. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav049.	1.4	13
11356	Proteome profile of salt gland ^Å rich epidermis extracted from a salt ^Å tolerant tree species. <i>Electrophoresis</i> , 2015, 36, 2473-2481.	1.3	2
11357	Gene set analysis: A step ^Å by ^Å step guide. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2015, 168, 517-527.	1.1	66
11358	A quantitative proteomic analysis of cellular responses to high glucose media in Chinese hamster ovary cells. <i>Biotechnology Progress</i> , 2015, 31, 1026-1038.	1.3	30
11359	Uncovering the abilities of <i>Agaricus bisporus</i> to degrade plant biomass throughout its life cycle. <i>Environmental Microbiology</i> , 2015, 17, 3098-3109.	1.8	49
11360	A genome-wide scan for copy number variations using high-density single nucleotide polymorphism array in Simmental cattle. <i>Animal Genetics</i> , 2015, 46, 289-298.	0.6	39
11361	Genome ^Å wide association and genome partitioning reveal novel genomic regions underlying variation in gastrointestinal nematode burden in a wild bird. <i>Molecular Ecology</i> , 2015, 24, 4175-4192.	2.0	20
11362	Central role of <i>FaGAMYB</i> in the transition of the strawberry receptacle from development to ripening. <i>New Phytologist</i> , 2015, 208, 482-496.	3.5	62
11363	Regulation of flowering time by the histone deacetylase <i>HDA5</i> in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2015, 82, 925-936.	2.8	94
11364	Gram-positive and gram-negative subcellular localization using rotation forest and physicochemical-based features. <i>BMC Bioinformatics</i> , 2015, 16, S1.	1.2	26

#	ARTICLE	IF	CITATIONS
11365	Computational algorithms to predict Gene Ontology annotations. BMC Bioinformatics, 2015, 16, S4.	1.2	24
11366	Comparison of microarray expression profiles between follicular variant of papillary thyroid carcinomas and follicular adenomas of the thyroid. BMC Genomics, 2015, 16, S7.	1.2	40
11367	IIIDB: a database for isoform-isoform interactions and isoform network modules. BMC Genomics, 2015, 16, S10.	1.2	31
11368	Pinpointing disease genes through phenomic and genomic data fusion. BMC Genomics, 2015, 16, S3.	1.2	14
11369	Integrating experimental and literature protein-protein interaction data for protein complex prediction. BMC Genomics, 2015, 16, S4.	1.2	11
11370	FunPat: function-based pattern analysis on RNA-seq time series data. BMC Genomics, 2015, 16, S2.	1.2	63
11371	Systems analysis of gene ontology and biological pathways involved in post-myocardial infarction responses. BMC Genomics, 2015, 16, S18.	1.2	9
11372	Multiple signatures of a disease in potential biomarker space: Getting the signatures consensus and identification of novel biomarkers. BMC Genomics, 2015, 16, S2.	1.2	5
11373	Discovery and characterization of long intergenic non-coding RNAs (lincRNA) module biomarkers in prostate cancer: an integrative analysis of RNA-Seq data. BMC Genomics, 2015, 16, S3.	1.2	50
11374	Conditional entropy in variation-adjusted windows detects selection signatures associated with expression quantitative trait loci (eQTLs). BMC Genomics, 2015, 16, S8.	1.2	3
11375	Bicluster Sampled Coherence Metric (BSCM) provides an accurate environmental context for phenotype predictions. BMC Systems Biology, 2015, 9, S1.	3.0	4
11376	Performance of case-control rare copy number variation annotation in classification of autism. BMC Medical Genomics, 2015, 8, S7.	0.7	15
11377	Draft genome sequence of Halomonas lutea strain YIM 91125T (DSM 23508T) isolated from the alkaline Lake Ebinur in Northwest China. Standards in Genomic Sciences, 2015, 10, 1.	1.5	65
11378	Draft genome sequence and characterization of Desulfitobacterium hafniense PCE-S. Standards in Genomic Sciences, 2015, 10, 15.	1.5	25
11379	Genome sequence of the soil bacterium Corynebacterium callunae type strain DSM 20147T. Standards in Genomic Sciences, 2015, 10, 5.	1.5	8
11380	Complete genome sequence of Roseophage vB_DshP-R1, which infects Dinoroseobacter shibae DFL12. Standards in Genomic Sciences, 2015, 10, 6.	1.5	13
11381	High quality draft genome sequence and analysis of Pontibacter roseus type strain SRC-1T (DSM 17521T) isolated from muddy waters of a drainage system in Chandigarh, India. Standards in Genomic Sciences, 2015, 10, 8.	1.5	6
11382	High quality genome sequence and description of Enterobacter mori strain 5â€“4, isolated from a mixture of formation water and crude-oil. Standards in Genomic Sciences, 2015, 10, 9.	1.5	6

#	ARTICLE	IF	CITATIONS
11383	Reconstruction of novel transcription factor regulons through inference of their binding sites. BMC Bioinformatics, 2015, 16, 299.	1.2	3
11384	A reverse-engineering approach to dissect post-translational modulators of transcription factor's activity from transcriptional data. BMC Bioinformatics, 2015, 16, 279.	1.2	7
11385	htsint: a Python library for sequencing pipelines that combines data through gene set generation. BMC Bioinformatics, 2015, 16, 307.	1.2	1
11386	Interlog protein network: an evolutionary benchmark of protein interaction networks for the evaluation of clustering algorithms. BMC Bioinformatics, 2015, 16, 319.	1.2	16
11387	Estimating cumulative pathway effects on risk for age-related macular degeneration using mixed linear models. BMC Bioinformatics, 2015, 16, 329.	1.2	9
11388	GOTA: GO term annotation of biomedical literature. BMC Bioinformatics, 2015, 16, 346.	1.2	20
11389	Novel gene sets improve set-level classification of prokaryotic gene expression data. BMC Bioinformatics, 2015, 16, 348.	1.2	1
11390	An assessment of catalytic residue 3D ensembles for the prediction of enzyme function. BMC Bioinformatics, 2015, 16, 359.	1.2	3
11391	Analysis of 5' 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
11392	De novo sequencing and assembly analysis of transcriptome in the Sodom apple (<i>Calotropis gigantea</i>). BMC Genomics, 2015, 16, 723.	1.2	20
11393	TSS seq based core promoter architecture in blood feeding Tsetse fly (<i>Glossina morsitans morsitans</i>) vector of Trypanosomiasis. BMC Genomics, 2015, 16, 722.	1.2	6
11394	Deciphering the association between gene function and spatial gene-gene interactions in 3D human genome conformation. BMC Genomics, 2015, 16, 880.	1.2	17
11395	Investigating inter-chromosomal regulatory relationships through a comprehensive meta-analysis of matched copy number and transcriptomics data sets. BMC Genomics, 2015, 16, 967.	1.2	11
11396	De novo transcriptome reconstruction and annotation of the Egyptian rousette bat. BMC Genomics, 2015, 16, 1033.	1.2	42
11397	Development and validation of a mixed-tissue oligonucleotide DNA microarray for Atlantic bluefin tuna, <i>Thunnus thynnus</i> (Linnaeus, 1758). BMC Genomics, 2015, 16, 1007.	1.2	8
11398	Transcriptomics of diapause in an isogenic self-fertilizing vertebrate. BMC Genomics, 2015, 16, 989.	1.2	12
11399	IRES-dependent translated genes in fungi: computational prediction, phylogenetic conservation and functional association. BMC Genomics, 2015, 16, 1059.	1.2	10
11400	Dintor: functional annotation of genomic and proteomic data. BMC Genomics, 2015, 16, 1081.	1.2	10

#	ARTICLE	IF	CITATIONS
11401	MycobASE: expanding the functional annotation coverage of mycobacterial genomes. <i>BMC Genomics</i> , 2015, 16, 1102.	1.2	10
11402	Using host-pathogen protein interactions to identify and characterize <i>Francisella tularensis</i> virulence factors. <i>BMC Genomics</i> , 2015, 16, 1106.	1.2	33
11403	Implications of ethylene biosynthesis and signaling in soybean drought stress tolerance. <i>BMC Plant Biology</i> , 2015, 15, 213.	1.6	110
11404	MetAnnotate: function-specific taxonomic profiling and comparison of metagenomes. <i>BMC Biology</i> , 2015, 13, 92.	1.7	39
11405	Horizontal gene transfer in bdelloid rotifers is ancient, ongoing and more frequent in species from desiccating habitats. <i>BMC Biology</i> , 2015, 13, 90.	1.7	76
11406	A high-resolution gene expression atlas of epistasis between gene-specific transcription factors exposes potential mechanisms for genetic interactions. <i>BMC Biology</i> , 2015, 13, 112.	1.7	21
11407	Gene-expression signature functional annotation of breast cancer tumours in function of age. <i>BMC Medical Genomics</i> , 2015, 8, 80.	0.7	6
11408	Microarray analysis of Long non-coding RNA expression profiles in human gastric cells and tissues with <i>Helicobacter pylori</i> infection. <i>BMC Medical Genomics</i> , 2015, 8, 84.	0.7	51
11409	Identification of enhanced hydrogen and ethanol <i>Escherichia coli</i> producer strains in a glycerol-based medium by screening in single-knock out mutant collections. <i>Microbial Cell Factories</i> , 2015, 14, 93.	1.9	22
11410	Targeting PBK/TOPK decreases growth and survival of glioma initiating cells in vitro and attenuates tumor growth in vivo. <i>Molecular Cancer</i> , 2015, 14, 121.	7.9	72
11411	PDON: Parkinson's disease ontology for representation and modeling of the Parkinson's disease knowledge domain. <i>Theoretical Biology and Medical Modelling</i> , 2015, 12, 20.	2.1	29
11412	Gene activity in primary T cells infected with HIV89.6: intron retention and induction of genomic repeats. <i>Retrovirology</i> , 2015, 12, 79.	0.9	40
11413	Quantitative proteomics identifies 38 proteins that are differentially expressed in cucumber in response to cucumber green mottle mosaic virus infection. <i>Virology Journal</i> , 2015, 12, 216.	1.4	17
11414	De novo deletions and duplications of 17q25.3 cause susceptibility to cardiovascular malformations. <i>Orphanet Journal of Rare Diseases</i> , 2015, 10, 75.	1.2	10
11415	Principal component gene set enrichment (PCGSE). <i>BioData Mining</i> , 2015, 8, 25.	2.2	22
11416	Angptl4 is upregulated under inflammatory conditions in the bone marrow of mice, expands myeloid progenitors, and accelerates reconstitution of platelets after myelosuppressive therapy. <i>Journal of Hematology and Oncology</i> , 2015, 8, 64.	6.9	23
11417	Confrontation of fibroblasts with cancer cells in vitro: gene network analysis of transcriptome changes and differential capacity to inhibit tumor growth. <i>Journal of Experimental and Clinical Cancer Research</i> , 2015, 34, 62.	3.5	11
11418	The sialyl-glycolipid stage-specific embryonic antigen 4 marks a subpopulation of chemotherapy-resistant breast cancer cells with mesenchymal features. <i>Breast Cancer Research</i> , 2015, 17, 146.	2.2	54

#	ARTICLE	IF	CITATIONS
11419	Draft genome of <i>Brugia pahangi</i> : high similarity between <i>B. pahangi</i> and <i>B. malayi</i> . <i>Parasites and Vectors</i> , 2015, 8, 451.	1.0	19
11420	Differential sialotranscriptomes of unfed and fed <i>Rhipicephalus haemaphysaloides</i> , with particular regard to differentially expressed genes of cysteine proteases. <i>Parasites and Vectors</i> , 2015, 8, 597.	1.0	39
11421	PanFP: pangenome-based functional profiles for microbial communities. <i>BMC Research Notes</i> , 2015, 8, 479.	0.6	38
11422	ChemDIS: a chemicalâ€“disease inference system based on chemicalâ€“protein interactions. <i>Journal of Cheminformatics</i> , 2015, 7, 25.	2.8	13
11423	Concept selection for phenotypes and diseases using learn to rank. <i>Journal of Biomedical Semantics</i> , 2015, 6, 24.	0.9	11
11424	Ontology-based representation and analysis of host- <i>Brucella</i> interactions. <i>Journal of Biomedical Semantics</i> , 2015, 6, 37.	0.9	8
11425	RDF2Graph a tool to recover, understand and validate the ontology of an RDF resource. <i>Journal of Biomedical Semantics</i> , 2015, 6, 39.	0.9	13
11426	The endogenous molecular clock orchestrates the temporal separation of substrate metabolism in skeletal muscle. <i>Skeletal Muscle</i> , 2015, 5, 17.	1.9	128
11427	Circadian rhythm influences genome-wide transcriptional responses to 1311 in a tissue-specific manner in mice. <i>EJNMMI Research</i> , 2015, 5, 75.	1.1	12
11428	Exploring soybean metabolic pathways based on probabilistic graphical model and knowledge-based methods. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2015, 2015, 5.	1.4	3
11429	A close look at protein function prediction evaluation protocols. <i>GigaScience</i> , 2015, 4, 41.	3.3	18
11430	The role of breast-feeding in infant immune system: a systems perspective on the intestinal microbiome. <i>Microbiome</i> , 2015, 3, 41.	4.9	81
11431	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Ai1a-2; a microsymbiont of <i>Andira inermis</i> discovered in Costa Rica. <i>Standards in Genomic Sciences</i> , 2015, 10, 33.	1.5	2
11432	Complete genome sequence of <i>Actinobacillus equuli</i> subspecies <i>equuli</i> ATCC 19392T. <i>Standards in Genomic Sciences</i> , 2015, 10, 32.	1.5	8
11433	Draft genome of <i>Myxosarcina</i> sp. strain G11, a baeocytous cyanobacterium associated with the marine sponge <i>Terpios hoshinota</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 28.	1.5	9
11434	Complete genome sequence of <i>Salmonella enterica</i> subspecies <i>arizonae</i> str. RKS2983. <i>Standards in Genomic Sciences</i> , 2015, 10, 30.	1.5	9
11435	Non-contiguous finished genome sequence and description of <i>Clostridium ihumii</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 63.	1.5	11
11436	Permanent draft genome sequence of sulfoquinovose-degrading <i>Pseudomonas putida</i> strain SQ1. <i>Standards in Genomic Sciences</i> , 2015, 10, 42.	1.5	6

#	ARTICLE	IF	CITATIONS
11437	Genome sequence of the haloarchaeon <i>Haloterrigena jeotgali</i> type strain A29T isolated from salt-fermented food. <i>Standards in Genomic Sciences</i> , 2015, 10, 49.	1.5	4
11438	Genome sequence of the pink pigmented marine bacterium <i>Loktanella hongkongensis</i> type strain (UST950701), a representative of the <i>Roseobacter</i> group. <i>Standards in Genomic Sciences</i> , 2015, 10, 51.	1.5	1
11439	High-quality permanent draft genome sequence of the extremely osmotolerant diphenol degrading bacterium <i>Halotalea alkalilenta</i> AW-7T, and emended description of the genus <i>Halotalea</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 52.	1.5	5
11440	Complete genome sequence of the thermophilic <i>Thermus</i> sp. CCB_US3_UF1 from a hot spring in Malaysia. <i>Standards in Genomic Sciences</i> , 2015, 10, 76.	1.5	6
11441	Complete genome sequence of <i>Bacillus thuringiensis</i> strain HD521. <i>Standards in Genomic Sciences</i> , 2015, 10, 62.	1.5	18
11442	Genome sequence of a native-feather degrading extremely thermophilic Eubacterium, <i>Fervidobacterium islandicum</i> AW-1. <i>Standards in Genomic Sciences</i> , 2015, 10, 71.	1.5	19
11443	Genome sequence of <i>Anoxybacillus ayderensis</i> AB04T isolated from the Ayder hot spring in Turkey. <i>Standards in Genomic Sciences</i> , 2015, 10, 70.	1.5	14
11444	Draft genome sequence of <i>Halomonas meridiana</i> R1t3 isolated from the surface microbiota of the Caribbean Elkhorn coral <i>Acropora palmata</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 75.	1.5	19
11445	Genomic information of the arsenic-resistant bacterium <i>Lysobacter arseniciresistens</i> type strain ZS79T and comparison of <i>Lysobacter</i> draft genomes. <i>Standards in Genomic Sciences</i> , 2015, 10, 88.	1.5	6
11446	Complete genome sequence of <i>Mycobacterium tuberculosis</i> K from a Korean high school outbreak, belonging to the Beijing family. <i>Standards in Genomic Sciences</i> , 2015, 10, 78.	1.5	26
11447	High-quality permanent draft genome sequence of the <i>Mimosa asperata</i> - nodulating <i>Cupriavidus</i> sp. strain AMP6. <i>Standards in Genomic Sciences</i> , 2015, 10, 80.	1.5	2
11448	Genome sequence of <i>Oceanobacillus picturae</i> strain S1, an halophilic bacterium first isolated in human gut. <i>Standards in Genomic Sciences</i> , 2015, 10, 91.	1.5	16
11449	Genome sequence and description of <i>Pantoea septica</i> strain FF5. <i>Standards in Genomic Sciences</i> , 2015, 10, 103.	1.5	5
11450	High quality draft genome sequence of the moderately halophilic bacterium <i>Pontibacillus yanchengensis</i> Y32T and comparison among <i>Pontibacillus</i> genomes. <i>Standards in Genomic Sciences</i> , 2015, 10, 93.	1.5	5
11451	Genome sequence of <i>Pedobacter glucosidilyticus</i> DD6b, isolated from zooplankton <i>Daphnia magna</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 100.	1.5	11
11452	Complete genome sequence of bacteriophage P26218 infecting <i>Rhodospirillum rubrum</i> sp. strain IMCC26218. <i>Standards in Genomic Sciences</i> , 2015, 10, 111.	1.5	7
11453	High-quality draft genome sequence of a new phytase-producing microorganism <i>Pantoea</i> sp. 3.5.1. <i>Standards in Genomic Sciences</i> , 2015, 10, 95.	1.5	3
11454	Complete genome sequence of <i>Bacillus cereus</i> FORC_005, a food-borne pathogen from the soy sauce braised fish-cake with quail-egg. <i>Standards in Genomic Sciences</i> , 2015, 10, 97.	1.5	7

#	ARTICLE	IF	CITATIONS
11455	Complete genome sequencing of <i>Dehalococcoides</i> sp. strain UCH007 using a differential reads picking method. <i>Standards in Genomic Sciences</i> , 2015, 10, 102.	1.5	18
11456	Genome sequence and description of the anaerobic lignin-degrading bacterium <i>Tolomonas lignolytica</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 106.	1.5	43
11457	Draft genome sequence of <i>Janthinobacterium lividum</i> strain MTR reveals its mechanism of capnophilic behavior. <i>Standards in Genomic Sciences</i> , 2015, 10, 110.	1.5	29
11458	Complete genome of <i>Pseudomonas chlororaphis</i> strain UFB2, a soil bacterium with antibacterial activity against bacterial canker pathogen of tomato. <i>Standards in Genomic Sciences</i> , 2015, 10, 117.	1.5	42
11459	Complete genome sequence and characterization of the haloacid-degrading <i>Burkholderia caribensis</i> MBA4. <i>Standards in Genomic Sciences</i> , 2015, 10, 114.	1.5	6
11460	Draft genome sequence of <i>Halopiger salifodinae</i> KCY07-B2T, an extremely halophilic archaeon isolated from a salt mine. <i>Standards in Genomic Sciences</i> , 2015, 10, 124.	1.5	2
11461	Genome sequence of <i>Lysobacter dokdonensis</i> DS-58T, a gliding bacterium isolated from soil in Dokdo, Korea. <i>Standards in Genomic Sciences</i> , 2015, 10, 123.	1.5	3
11462	Genome sequence of a dissimilatory Fe(III)-reducing bacterium <i>Geobacter soli</i> type strain GSS01T. <i>Standards in Genomic Sciences</i> , 2015, 10, 118.	1.5	22
11463	Complete genome sequence of the molybdenum-resistant bacterium <i>Bacillus subtilis</i> strain LM 4 ² . <i>Standards in Genomic Sciences</i> , 2015, 10, 127.	1.5	2
11464	Effects of subsampling on characteristics of RNA-seq data from triple-negative breast cancer patients. <i>Chinese Journal of Cancer</i> , 2015, 34, 427-38.	4.9	4
11465	Using Ontology Fingerprints to disambiguate gene name entities in the biomedical literature. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav034-bav034.	1.4	9
11466	CerebralWeb: a Cytoscape.js plug-in to visualize networks stratified by subcellular localization. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav041.	1.4	7
11467	Human cell adhesion molecules: annotated functional subtypes and overrepresentation of addiction-associated genes. <i>Annals of the New York Academy of Sciences</i> , 2015, 1349, 83-95.	1.8	33
11468	Unrestricted modification search reveals lysine methylation as major modification induced by tissue formalin fixation and paraffin embedding. <i>Proteomics</i> , 2015, 15, 2568-2579.	1.3	40
11469	Quantitative proteomics using SILAC: Principles, applications, and developments. <i>Proteomics</i> , 2015, 15, 3175-3192.	1.3	158
11470	Autoantibodies targeting glomerular annexin A2 identify patients with proliferative lupus nephritis. <i>Proteomics - Clinical Applications</i> , 2015, 9, 1012-1020.	0.8	37
11471	The enzymatic nature of an anonymous protein sequence cannot reliably be inferred from superfamily level structural information alone. <i>Protein Science</i> , 2015, 24, 643-650.	3.1	3
11472	Coiled-coil length: Size does matter. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 2162-2169.	1.5	16

#	ARTICLE	IF	CITATIONS
11473	Genome-Wide Identification of MESP1 Targets Demonstrates Primary Regulation Over Mesendoderm Gene Activity. <i>Stem Cells</i> , 2015, 33, 3254-3265.	1.4	26
11474	An Integrated Multiomics Approach to Identify Candidate Antigens for Serodiagnosis of Human Onchocerciasis*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3224-3233.	2.5	12
11475	Transcriptome Analysis of Minimal Residual Disease in Subtypes of Pediatric B Cell Acute Lymphoblastic Leukemia. <i>Clinical Medicine Insights: Oncology</i> , 2015, 9, CMO.S17049.	0.6	4
11476	Protein and small non-coding RNA-enriched extracellular vesicles are released by the pathogenic blood fluke <i>Schistosoma mansoni</i> . <i>Journal of Extracellular Vesicles</i> , 2015, 4, 28665.	5.5	140
11477	Permanent draft genome sequence of <i>Acidiphilium</i> sp. JA12-A1. <i>Standards in Genomic Sciences</i> , 2015, 10, 56.	1.5	26
11478	The evolution of standards and data management practices in systems biology. <i>Molecular Systems Biology</i> , 2015, 11, 851.	3.2	35
11479	Improved-high-quality draft genome sequence of <i>Rhodococcus</i> sp. JG-3, a eurypsychrophilic Actinobacteria from Antarctic Dry Valley permafrost. <i>Standards in Genomic Sciences</i> , 2015, 10, 61.	1.5	11
11480	Cabut/ <i>dTIEG</i> associates with the transcription factor Yorkie for growth control. <i>EMBO Reports</i> , 2015, 16, 362-369.	2.0	12
11481	Exome analysis of a family with Wolff-Parkinson-White syndrome identifies a novel disease locus. <i>American Journal of Medical Genetics, Part A</i> , 2015, 167, 2975-2984.	0.7	17
11482	Membrane protein isolation and identification by covalent binding for proteome research. <i>Proteomics</i> , 2015, 15, 3892-3900.	1.3	5
11483	toxome: an integrated omics data warehouse for <i>Toxoplasma gondii</i> systems biology research. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav066.	1.4	7
11484	PhenoMiner: from text to a database of phenotypes associated with OMIM diseases. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav104.	1.4	29
11485	Large-scale identification of secretome glycoproteins recognized by <i>Wisteria floribunda</i> agglutinin: A glycoproteomic approach to biomarker discovery. <i>Proteomics</i> , 2015, 15, 2921-2933.	1.3	18
11486	REVIEW: Predictive ecology in a changing world. <i>Journal of Applied Ecology</i> , 2015, 52, 1293-1310.	1.9	237
11487	Generating a focused view of disease ontology cancer terms for pan-cancer data integration and analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav032-bav032.	1.4	40
11488	miRSponge: a manually curated database for experimentally supported miRNA sponges and ceRNAs. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav098.	1.4	112
11489	Gene Expression in HIV-Associated Neurocognitive Disorders. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2015, 70, 479-488.	0.9	31
11490	Temperature- and sex-related effects of serine protease alleles on larval development in the Glanville fritillary butterfly. <i>Journal of Evolutionary Biology</i> , 2015, 28, 2224-2235.	0.8	14

#	ARTICLE	IF	CITATIONS
11491	Protein-protein interaction network of gene expression in the hydrocortisone-treated keloid. <i>International Journal of Dermatology</i> , 2015, 54, 549-554.	0.5	6
11492	Genome-wide analysis of long noncoding RNA expression profiles in patients with nonalcoholic fatty liver disease. <i>IUBMB Life</i> , 2015, 67, 847-852.	1.5	53
11493	GeneStoryTeller: a mobile app for quick and comprehensive information retrieval of human genes. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav048.	1.4	0
11494	Deep Question Answering for protein annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav081.	1.4	17
11495	MAPanalyzer: a novel online tool for analyzing microtubule-associated proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	23
11496	Building a Human Health Risk Assessment Ontology (RsO): A Proposed Framework. <i>Risk Analysis</i> , 2015, 35, 2087-2101.	1.5	3
11497	Chemoproteomic Evaluation of the Polyacetylene Callyspongynic Acid. <i>Chemistry - A European Journal</i> , 2015, 21, 10721-10728.	1.7	20
11498	Co-controllability of drug-disease-gene network. <i>New Journal of Physics</i> , 2015, 17, 085009.	1.2	17
11499	Ontology application and use at the ENCODE DCC. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	42
11500	AtmiRNET: a web-based resource for reconstructing regulatory networks of Arabidopsis microRNAs. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav042.	1.4	18
11501	kpath: integration of metabolic pathway linked data. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav053.	1.4	8
11502	Kiwifruit Information Resource (KIR): a comparative platform for kiwifruit genomics. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav113.	1.4	14
11503	Alteration in abundance of specific membrane proteins of <i>Aggregatibacter actinomycetemcomitans</i> is attributed to deletion of the inner membrane protein MorC. <i>Proteomics</i> , 2015, 15, 1859-1867.	1.3	14
11504	Microparticles released from <i>Mycobacterium tuberculosis</i> -infected human macrophages contain increased levels of the type I interferon inducible proteins including ISG15. <i>Proteomics</i> , 2015, 15, 3020-3029.	1.3	35
11505	Large-scale identification of membrane proteins with properties favorable for crystallization. <i>Protein Science</i> , 2015, 24, 1756-1763.	3.1	2
11506	Extracellular heat shock protein 70 promotes osteogenesis of human mesenchymal stem cells through activation of the ERK signaling pathway. <i>FEBS Letters</i> , 2015, 589, 4088-4096.	1.3	46
11507	Pilocytic Astrocytoma (PMA) Shows Significant Differences in Gene Expression vs. Pilocytic Astrocytoma (PA) and Variable Tendency Toward Maturation to PA. <i>Brain Pathology</i> , 2015, 25, 429-440.	2.1	28
11508	Transcriptional changes during <i>Daphnia pulex</i> development indicate that the maturation decision resembles a rate more than a threshold. <i>Journal of Evolutionary Biology</i> , 2015, 28, 944-958.	0.8	6

#	ARTICLE	IF	CITATIONS
11509	LMDs-based approach for efficient top-k local ligand-binding site search. <i>International Journal of Data Mining and Bioinformatics</i> , 2015, 12, 417.	0.1	0
11510	A methodology for ontology update in the semantic grid environment. <i>Concurrency Computation Practice and Experience</i> , 2015, 27, 782-808.	1.4	12
11513	Prioritising Lexical Patterns to Increase Axiomatisation in Biomedical Ontologies. <i>Methods of Information in Medicine</i> , 2015, 54, 56-64.	0.7	4
11514	Role of network biology and network medicine in early detection of cancer. , 0, , 457-463.		0
11515	The Prognostic Value of Cell Cycle Gene Expression Signatures in Muscle Invasive, High-Grade Bladder Cancer. <i>Bladder Cancer</i> , 2015, 1, 45-63.	0.2	7
11516	Genome-wide Massive Sequencing in Embryonic Stem Cell Biology:Recent Insights and Challenges. <i>Journal of Stem Cell Research & Therapy</i> , 2015, 05, .	0.3	0
11517	Partial least squares-based gene expression analysis in preeclampsia. <i>Genetics and Molecular Research</i> , 2015, 14, 6598-6604.	0.3	5
11518	Genome-wide pathway analysis in glioma. <i>Neoplasma</i> , 2015, 62, 230-238.	0.7	10
11519	Transcriptome Analysis and Discovery of Genes Involved in Immune Pathways from Coelomocytes of Sea Cucumber (<i>Apostichopus japonicus</i>) after <i>Vibrio splendidus</i> Challenge. <i>International Journal of Molecular Sciences</i> , 2015, 16, 16347-16377.	1.8	50
11520	Application of biclustering of gene expression data and gene set enrichment analysis methods to identify potentially disease causing nanomaterials. <i>Beilstein Journal of Nanotechnology</i> , 2015, 6, 2438-2448.	1.5	49
11521	Screening of crucial long non-coding RNAs in oral epithelial dysplasia by serial analysis of gene expression. <i>Genetics and Molecular Research</i> , 2015, 14, 11729-11738.	0.3	6
11522	Draft genome sequence of <i>Mesotoga</i> strain PhosAC3, a mesophilic member of the bacterial order Thermotogales, isolated from a digester treating phosphogypsum in Tunisia. <i>Standards in Genomic Sciences</i> , 2015, 10, 12.	1.5	8
11523	Gene expression profile analysis of colorectal cancer to investigate potential mechanisms using bioinformatics. <i>OncoTargets and Therapy</i> , 2015, 8, 745.	1.0	13
11524	Role of NSC319726 in ovarian cancer based on the bioinformatics analyses. <i>OncoTargets and Therapy</i> , 2015, 8, 3757.	1.0	5
11525	Identification of biomarkers for metastatic osteosarcoma based on DNA microarray data. <i>Neoplasma</i> , 2015, 62, 365-371.	0.7	9
11526	A New Study on Biclustering Tools, Biclusters Validation and Evaluation Functions. <i>International Journal of Computer Science & Engineering Survey</i> , 2015, 6, 01-13.	0.2	5
11527	Association of genetic and psychological factors with persistent pain after cosmetic thoracic surgery. <i>Journal of Pain Research</i> , 2015, 8, 829.	0.8	10
11528	Analysis of the Human Proteome in Subcutaneous and Visceral Fat Depots in Diabetic and Non-diabetic Patients with Morbid Obesity. <i>Journal of Proteomics and Bioinformatics</i> , 2015, 08, 133-141.	0.4	13

#	ARTICLE	IF	CITATIONS
11529	In silico characterization of hypothetical proteins from <i>Paracoccidioides lutzii</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 17416-17425.	0.3	15
11530	Genome-wide identification of copy number variations in Holstein cattle from Baja California, Mexico, using high-density SNP genotyping arrays. <i>Genetics and Molecular Research</i> , 2015, 14, 11848-11859.	0.3	12
11531	Herb Network Analysis for a Famous TCM Doctor's Prescriptions on Treatment of Rheumatoid Arthritis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2015, 2015, 1-9.	0.5	17
11532	In Vivo Molecular Responses of Fast and Slow Muscle Fibers to Lipopolysaccharide in a Teleost Fish, the Rainbow Trout (<i>Oncorhynchus mykiss</i>). <i>Biology</i> , 2015, 4, 67-87.	1.3	15
11533	Molecular Effects of Irradiation (Cobalt-60) on the Control of <i>Panonychus citri</i> (Acari: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Td (Tet	1.8	4
11534	The eNanoMapper database for nanomaterial safety information. <i>Beilstein Journal of Nanotechnology</i> , 2015, 6, 1609-1634.	1.5	92
11535	Construction of a full-length cDNA library and analysis of expressed sequence tags in white jute (<i>Corchorus capsularis</i> L.). <i>African Journal of Biotechnology</i> , 2015, 14, 1928-1935.	0.3	3
11536	Differential mRNA expression profiling of oral squamous cell carcinoma by high-throughput RNA sequencing. <i>Journal of Biomedical Research</i> , 2015, 29, 397.	0.7	17
11537	Applied ontology: The next decade begins. <i>Applied Ontology</i> , 2015, 10, 1-4.	1.0	23
11538	Proteomic Analysis of Embryonic and Young Human Vitreous. , 2015, 56, 7036.		14
11539	Genome-wide pathway analysis in amyotrophic lateral sclerosis. <i>Genetics and Molecular Research</i> , 2015, 14, 6429-6438.	0.3	3
11540	Analysis of the gene-protein interaction network in glioma. <i>Genetics and Molecular Research</i> , 2015, 14, 14196-14206.	0.3	8
11541	Screening of potential diagnostic markers and therapeutic targets against colorectal cancer. <i>OncoTargets and Therapy</i> , 2015, 8, 1691.	1.0	22
11542	Investigation of genes in chronic and acute morphine-treated mice using microarray datasets. <i>Genetics and Molecular Research</i> , 2015, 14, 10193-10205.	0.3	1
11543	De novo assembly, functional annotation, and marker development of Asian pear (<i>Pyrus pyrifolia</i>) fruit transcriptome through massively parallel sequencing. <i>Genetics and Molecular Research</i> , 2015, 14, 18344-18355.	0.3	1
11544	Determination of the mechanism of action of repetitive halothane exposure on rat brain tissues using a combined method of microarray gene expression profiling and bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2015, 12, 8071-8076.	1.1	1
11545	Tools for visualization and analysis of molecular networks, pathways, and -omics data. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2015, 8, 11.	1.6	50
11546	Transcriptome characterization and large-scale identification of SSR/SNP markers in symbiotic nitrogen fixation crop faba bean (<i>Vicia faba</i> L.). <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2015, 39, 459-469.	0.8	4

#	ARTICLE	IF	CITATIONS
11547	Transcriptome Profiling of Rust Resistance in Switchgrass Using RNA-Seq Analysis. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0075.	1.6	20
11548	Suppression of transcriptional drift extends <i>C. elegans</i> lifespan by postponing the onset of mortality. <i>ELife</i> , 2015, 4, e08833.	2.8	76
11549	A Survey on the Computational Approaches to Identify Drug Targets in the Postgenomic Era. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	52
11550	Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 19.	2.0	72
11551	Bioinformatics and Moonlighting Proteins. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 90.	2.0	25
11552	Natalie 2.0: Sparse Global Network Alignment as a Special Case of Quadratic Assignment. <i>Algorithms</i> , 2015, 8, 1035-1051.	1.2	21
11553	Differential DNA Methylation in Relation to Age and Health Risks of Obesity. <i>International Journal of Molecular Sciences</i> , 2015, 16, 16816-16832.	1.8	43
11554	Proteins and Their Interacting Partners: An Introduction to Protein-Ligand Binding Site Prediction Methods. <i>International Journal of Molecular Sciences</i> , 2015, 16, 29829-29842.	1.8	66
11555	Data Integration for Microarrays: Enhanced Inference for Gene Regulatory Networks. <i>Microarrays (Basel, Switzerland)</i> , 2015, 4, 255-269.	1.4	3
11556	Protective Effect of 2,4,5-Trihydroxy-5,2-dibromo diphenylmethanone, a New Halophenol, against Hydrogen Peroxide-Induced EA.hy926 Cells Injury. <i>Molecules</i> , 2015, 20, 14254-14264.	1.7	9
11557	Characterization of Global Transcriptome Using Illumina Paired-End Sequencing and Development of EST-SSR Markers in Two Species of <i>Gynostemma</i> (Cucurbitaceae). <i>Molecules</i> , 2015, 20, 21214-21231.	1.7	12
11558	Gene Expression, Protein Function and Pathways of <i>Arabidopsis thaliana</i> Responding to Silver Nanoparticles in Comparison to Silver Ions, Cold, Salt, Drought, and Heat. <i>Nanomaterials</i> , 2015, 5, 436-467.	1.9	104
11559	Hidden among the crowd: differential DNA methylation-expression correlations in cancer occur at important oncogenic pathways. <i>Frontiers in Genetics</i> , 2015, 6, 163.	1.1	16
11560	Cosplicing network analysis of mammalian brain RNA-Seq data utilizing WGCNA and Mantel correlations. <i>Frontiers in Genetics</i> , 2015, 6, 174.	1.1	48
11561	PrOnto database : GO term functional dissimilarity inferred from biological data. <i>Frontiers in Genetics</i> , 2015, 6, 200.	1.1	8
11562	Moving from capstones toward cornerstones: successes and challenges in applying systems biology to identify mechanisms of autism spectrum disorders. <i>Frontiers in Genetics</i> , 2015, 6, 301.	1.1	14
11563	AnGeLi: A Tool for the Analysis of Gene Lists from Fission Yeast. <i>Frontiers in Genetics</i> , 2015, 6, 330.	1.1	65
11564	Novel Primary Immunodeficiency Candidate Genes Predicted by the Human Gene Connectome. <i>Frontiers in Immunology</i> , 2015, 6, 142.	2.2	54

#	ARTICLE	IF	CITATIONS
11565	Differential Expression of microRNAs in Thymic Epithelial Cells from <i>Trypanosoma cruzi</i> Acutely Infected Mice: Putative Role in Thymic Atrophy. <i>Frontiers in Immunology</i> , 2015, 6, 428.	2.2	47
11566	Integrated inference and evaluation of host-fungi interaction networks. <i>Frontiers in Microbiology</i> , 2015, 6, 764.	1.5	63
11567	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1. <i>Frontiers in Microbiology</i> , 2015, 6, 978.	1.5	83
11568	Metagenomic sequencing of marine periphyton: taxonomic and functional insights into biofilm communities. <i>Frontiers in Microbiology</i> , 2015, 6, 1192.	1.5	49
11569	RNA-seq de novo Assembly Reveals Differential Gene Expression in <i>Glossina palpalis gambiense</i> Infected with <i>Trypanosoma brucei gambiense</i> vs. Non-Infected and Self-Cured Flies. <i>Frontiers in Microbiology</i> , 2015, 6, 1259.	1.5	26
11570	Expression of ionotropic receptors in terrestrial hermit crab's olfactory sensory neurons. <i>Frontiers in Cellular Neuroscience</i> , 2014, 8, 448.	1.8	34
11571	The deafness gene <i>DFNA5</i> induces programmed cell death through mitochondria and MAPK-related pathways. <i>Frontiers in Cellular Neuroscience</i> , 2015, 9, 231.	1.8	47
11572	Gene expression profiling for human iPS-derived motor neurons from sporadic ALS patients reveals a strong association between mitochondrial functions and neurodegeneration. <i>Frontiers in Cellular Neuroscience</i> , 2015, 9, 289.	1.8	51
11573	A scalable neuroinformatics data flow for electrophysiological signals using MapReduce. <i>Frontiers in Neuroinformatics</i> , 2015, 9, 4.	1.3	14
11574	Epigenetic modulation of brain gene networks for cocaine and alcohol abuse. <i>Frontiers in Neuroscience</i> , 2015, 9, 176.	1.4	69
11575	A FreeSurfer view of the cortical transcriptome generated from the Allen Human Brain Atlas. <i>Frontiers in Neuroscience</i> , 2015, 9, 323.	1.4	93
11576	High-quality permanent draft genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> strain GB30; an effective microsymbiont of <i>Pisum sativum</i> growing in Poland. <i>Standards in Genomic Sciences</i> , 2015, 10, 36.	1.5	3
11577	High quality draft genome sequence of <i>Flavobacterium rivuli</i> type strain WB 3.3-2T (DSM 21788T), a valuable source of polysaccharide decomposing enzymes. <i>Standards in Genomic Sciences</i> , 2015, 10, 46.	1.5	16
11578	High quality draft genome sequence of <i>Corynebacterium ulceribovis</i> type strain IMMIB-L1395T (DSM) Tj ETQq1 1 0,784314 rgBT /Overd	1.5	1
11579	High quality draft genomic sequence of <i>Flaviumibacter solisilvae</i> 3-3T. <i>Standards in Genomic Sciences</i> , 2015, 10, 66.	1.5	3
11580	Complete genome sequence of the phenanthrene-degrading soil bacterium <i>Delftia acidovorans</i> Cs1-4. <i>Standards in Genomic Sciences</i> , 2015, 10, 55.	1.5	43
11581	The Wnt signaling network in cancer. , 0, , 222-255.		0
11582	Bioinformatics analyses of differentially expressed genes associated with bisphosphonate-related osteonecrosis of the jaw in patients with multiple myeloma. <i>OncoTargets and Therapy</i> , 2015, 8, 2681.	1.0	12

#	ARTICLE	IF	CITATIONS
11583	Abnormal gene expression profile reveals the common key signatures associated with clear cell renal cell carcinoma: a meta-analysis. <i>Genetics and Molecular Research</i> , 2015, 14, 2216-2224.	0.3	4
11584	MSL: A Measure to Evaluate Three-dimensional Patterns in Gene Expression Data. <i>Evolutionary Bioinformatics</i> , 2015, 11, EBO.S25822.	0.6	16
11585	Identification of the key genes connected with plasma cells of multiple myeloma using expression profiles. <i>OncoTargets and Therapy</i> , 2015, 8, 1795.	1.0	8
11586	Pathway-Based Analysis of Genome-Wide siRNA Screens Reveals the Regulatory Landscape of App Processing. <i>PLoS ONE</i> , 2015, 10, e0115369.	1.1	19
11587	Quality Measures for Gene Expression Biclusters. <i>PLoS ONE</i> , 2015, 10, e0115497.	1.1	36
11588	HPOSim: An R Package for Phenotypic Similarity Measure and Enrichment Analysis Based on the Human Phenotype Ontology. <i>PLoS ONE</i> , 2015, 10, e0115692.	1.1	55
11589	Reconstructing Genome-Wide Protein-Protein Interaction Networks Using Multiple Strategies with Homologous Mapping. <i>PLoS ONE</i> , 2015, 10, e0116347.	1.1	8
11590	Properties of Protein Drug Target Classes. <i>PLoS ONE</i> , 2015, 10, e0117955.	1.1	97
11591	Phenotypic Responses of Differentiated Asthmatic Human Airway Epithelial Cultures to Rhinovirus. <i>PLoS ONE</i> , 2015, 10, e0118286.	1.1	61
11592	Differential Gene Expression in Ovaries of Qira Black Sheep and Hetian Sheep Using RNA-Seq Technique. <i>PLoS ONE</i> , 2015, 10, e0120170.	1.1	60
11593	Lessons Learned from Whole Exome Sequencing in Multiplex Families Affected by a Complex Genetic Disorder, Intracranial Aneurysm. <i>PLoS ONE</i> , 2015, 10, e0121104.	1.1	32
11594	Modes of Interaction between Individuals Dominate the Topologies of Real World Networks. <i>PLoS ONE</i> , 2015, 10, e0121248.	1.1	4
11595	<i>Plasmodium knowlesi</i> Genome Sequences from Clinical Isolates Reveal Extensive Genomic Dimorphism. <i>PLoS ONE</i> , 2015, 10, e0121303.	1.1	54
11596	Tensor GSVD of Patient- and Platform-Matched Tumor and Normal DNA Copy-Number Profiles Uncovers Chromosome Arm-Wide Patterns of Tumor-Exclusive Platform-Consistent Alterations Encoding for Cell Transformation and Predicting Ovarian Cancer Survival. <i>PLoS ONE</i> , 2015, 10, e0121396.	1.1	37
11597	Alternative Polyadenylation Allows Differential Negative Feedback of Human miRNA miR-579 on Its Host Gene ZFR. <i>PLoS ONE</i> , 2015, 10, e0121507.	1.1	24
11598	Transcriptome Assembly, Gene Annotation and Tissue Gene Expression Atlas of the Rainbow Trout. <i>PLoS ONE</i> , 2015, 10, e0121778.	1.1	53
11599	Analysis of Genomic Regions of <i>Trichoderma harzianum</i> IOC-3844 Related to Biomass Degradation. <i>PLoS ONE</i> , 2015, 10, e0122122.	1.1	17
11600	De Novo Characterization of Fall Dormant and Nondormant Alfalfa (<i>Medicago sativa</i> L.) Leaf Transcriptome and Identification of Candidate Genes Related to Fall Dormancy. <i>PLoS ONE</i> , 2015, 10, e0122170.	1.1	36

#	ARTICLE	IF	CITATIONS
11601	A New Method for Discovering Disease-Specific MiRNA-Target Regulatory Networks. PLoS ONE, 2015, 10, e0122473.	1.1	9
11602	Binary Gene Expression Patterning of the Molt Cycle: The Case of Chitin Metabolism. PLoS ONE, 2015, 10, e0122602.	1.1	25
11603	Construction of an Ortholog Database Using the Semantic Web Technology for Integrative Analysis of Genomic Data. PLoS ONE, 2015, 10, e0122802.	1.1	11
11604	Toll-Like Receptor Signaling in Vertebrates: Testing the Integration of Protein, Complex, and Pathway Data in the Protein Ontology Framework. PLoS ONE, 2015, 10, e0122978.	1.1	2
11605	ClusTrack: Feature Extraction and Similarity Measures for Clustering of Genome-Wide Data Sets. PLoS ONE, 2015, 10, e0123261.	1.1	3
11606	Molecular Signatures of Nicotinoid-Pathogen Synergy in the Termite Gut. PLoS ONE, 2015, 10, e0123391.	1.1	17
11607	Effect of Vitrification on the MicroRNA Transcriptome in Mouse Blastocysts. PLoS ONE, 2015, 10, e0123451.	1.1	22
11608	MeDiA: Mean Distance Association and Its Applications in Nonlinear Gene Set Analysis. PLoS ONE, 2015, 10, e0124620.	1.1	0
11609	From Gigabyte to Kilobyte: A Bioinformatics Protocol for Mining Large RNA-Seq Transcriptomics Data. PLoS ONE, 2015, 10, e0125000.	1.1	7
11610	Network-based Phenome-Genome Association Prediction by Bi-Random Walk. PLoS ONE, 2015, 10, e0125138.	1.1	35
11611	Sequence Analysis of Insecticide Action and Detoxification-Related Genes in the Insect Pest Natural Enemy <i>Pardosa pseudoannulata</i> . PLoS ONE, 2015, 10, e0125242.	1.1	29
11612	Label-Free Protein-RNA Interactome Analysis Identifies Khsrp Signaling Downstream of the p38/Mk2 Kinase Complex as a Critical Modulator of Cell Cycle Progression. PLoS ONE, 2015, 10, e0125745.	1.1	32
11613	Transcriptome Analysis Comparison of Lipid Biosynthesis in the Leaves and Developing Seeds of <i>Brassica napus</i> . PLoS ONE, 2015, 10, e0126250.	1.1	23
11614	Assembly of a Comprehensive Regulatory Network for the Mammalian Circadian Clock: A Bioinformatics Approach. PLoS ONE, 2015, 10, e0126283.	1.1	43
11615	Quantitative Proteomic Analysis Reveals That Anti-Cancer Effects of Selenium-Binding Protein 1 In Vivo Are Associated with Metabolic Pathways. PLoS ONE, 2015, 10, e0126285.	1.1	23
11616	Gene Ontology and KEGG Pathway Enrichment Analysis of a Drug Target-Based Classification System. PLoS ONE, 2015, 10, e0126492.	1.1	50
11617	Randomized Trial of Glucosamine and Chondroitin Supplementation on Inflammation and Oxidative Stress Biomarkers and Plasma Proteomics Profiles in Healthy Humans. PLoS ONE, 2015, 10, e0117534.	1.1	58
11618	Clinical Data Integration Model. <i>Methods of Information in Medicine</i> , 2015, 54, 16-23.	0.7	30

#	ARTICLE	IF	CITATIONS
11619	RNA Sequence Analysis of Human Huntington Disease Brain Reveals an Extensive Increase in Inflammatory and Developmental Gene Expression. <i>PLoS ONE</i> , 2015, 10, e0143563.	1.1	150
11620	Transcriptome Sequencing of <i>Codonopsis pilosula</i> and Identification of Candidate Genes Involved in Polysaccharide Biosynthesis. <i>PLoS ONE</i> , 2015, 10, e0117342.	1.1	35
11621	Identifying Driver Genomic Alterations in Cancers by Searching Minimum-Weight, Mutually Exclusive Sets. <i>PLoS Computational Biology</i> , 2015, 11, e1004257.	1.5	18
11622	Genome Modeling System: A Knowledge Management Platform for Genomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004274.	1.5	83
11623	Time-Course Gene Set Analysis for Longitudinal Gene Expression Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004310.	1.5	60
11624	Revealing Pathway Dynamics in Heart Diseases by Analyzing Multiple Differential Networks. <i>PLoS Computational Biology</i> , 2015, 11, e1004332.	1.5	43
11625	Ten Simple Rules for Experimentsâ€™ Provenance. <i>PLoS Computational Biology</i> , 2015, 11, e1004384.	1.5	13
11626	Curation of the Mammalian Palmitoylome Indicates a Pivotal Role for Palmitoylation in Diseases and Disorders of the Nervous System and Cancers. <i>PLoS Computational Biology</i> , 2015, 11, e1004405.	1.5	120
11627	Genome-Wide Detection and Analysis of Multifunctional Genes. <i>PLoS Computational Biology</i> , 2015, 11, e1004467.	1.5	36
11628	Beyond the E-Value: Stratified Statistics for Protein Domain Prediction. <i>PLoS Computational Biology</i> , 2015, 11, e1004509.	1.5	19
11629	Gene Prioritization by Compressive Data Fusion and Chaining. <i>PLoS Computational Biology</i> , 2015, 11, e1004552.	1.5	22
11630	Identification of Chemical Inhibitors of β^2 -Catenin-Driven Liver Tumorigenesis in Zebrafish. <i>PLoS Genetics</i> , 2015, 11, e1005305.	1.5	67
11631	YAP1 Exerts Its Transcriptional Control via TEAD-Mediated Activation of Enhancers. <i>PLoS Genetics</i> , 2015, 11, e1005465.	1.5	296
11632	A Large-Scale Functional Analysis of Putative Target Genes of Mating-Type Loci Provides Insight into the Regulation of Sexual Development of the Cereal Pathogen <i>Fusarium graminearum</i> . <i>PLoS Genetics</i> , 2015, 11, e1005486.	1.5	121
11633	Transcriptional and Linkage Analyses Identify Loci that Mediate the Differential Macrophage Response to Inflammatory Stimuli and Infection. <i>PLoS Genetics</i> , 2015, 11, e1005619.	1.5	21
11634	Time-Dependent Transcriptional Changes in Axenic <i>Giardia duodenalis</i> Trophozoites. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004261.	1.3	16
11635	A Novel Chitin Binding Crayfish Molar Tooth Protein with Elasticity Properties. <i>PLoS ONE</i> , 2015, 10, e0127871.	1.1	9
11636	ProteINSIDE to Easily Investigate Proteomics Data from Ruminants: Application to Mine Proteome of Adipose and Muscle Tissues in Bovine Foetuses. <i>PLoS ONE</i> , 2015, 10, e0128086.	1.1	33

#	ARTICLE	IF	CITATIONS
11637	Self-Organizing Feature Maps Identify Proteins Critical to Learning in a Mouse Model of Down Syndrome. PLoS ONE, 2015, 10, e0129126.	1.1	88
11638	Exploring Differentially Expressed Genes and Natural Antisense Transcripts in Sheep (<i>Ovis aries</i>) Skin with Different Wool Fiber Diameters by Digital Gene Expression Profiling. PLoS ONE, 2015, 10, e0129249.	1.1	19
11639	Gene Expression Signature in Adipose Tissue of Acromegaly Patients. PLoS ONE, 2015, 10, e0129359.	1.1	19
11640	Transcriptomic Analysis Reveals Possible Influences of ABA on Secondary Metabolism of Pigments, Flavonoids and Antioxidants in Tomato Fruit during Ripening. PLoS ONE, 2015, 10, e0129598.	1.1	79
11641	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
11642	Isolation, Characterization and Biological Properties of Membrane Vesicles Produced by the Swine Pathogen <i>Streptococcus suis</i> . PLoS ONE, 2015, 10, e0130528.	1.1	49
11643	Physical Features of Intracellular Proteins that Moonlight on the Cell Surface. PLoS ONE, 2015, 10, e0130575.	1.1	75
11644	Identification of Candidate Adherent-Invasive <i>E. coli</i> Signature Transcripts by Genomic/Transcriptomic Analysis. PLoS ONE, 2015, 10, e0130902.	1.1	40
11645	Proteomic Characterisation of the Salt Gland-Enriched Tissues of the Mangrove Tree Species <i>Avicennia officinalis</i> . PLoS ONE, 2015, 10, e0133386.	1.1	17
11646	An Integrative Approach for Mapping Differentially Expressed Genes and Network Components Using Novel Parameters to Elucidate Key Regulatory Genes in Colorectal Cancer. PLoS ONE, 2015, 10, e0133901.	1.1	11
11647	FROG - Fingerprinting Genomic Variation Ontology. PLoS ONE, 2015, 10, e0134693.	1.1	3
11648	De Novo Transcriptome Analysis of <i>Allium cepa</i> L. (Onion) Bulb to Identify Allergens and Epitopes. PLoS ONE, 2015, 10, e0135387.	1.1	18
11649	Diversified Control Paths: A Significant Way Disease Genes Perturb the Human Regulatory Network. PLoS ONE, 2015, 10, e0135491.	1.1	6
11650	Impaired Cell Cycle Regulation in a Natural Equine Model of Asthma. PLoS ONE, 2015, 10, e0136103.	1.1	24
11651	Proteins with Intrinsically Disordered Domains Are Preferentially Recruited to Polyglutamine Aggregates. PLoS ONE, 2015, 10, e0136362.	1.1	31
11652	Bioinformatics-Based Identification of MicroRNA-Regulated and Rheumatoid Arthritis-Associated Genes. PLoS ONE, 2015, 10, e0137551.	1.1	22
11653	Modeling the Regulatory Mechanisms by Which NLRX1 Modulates Innate Immune Responses to <i>Helicobacter pylori</i> Infection. PLoS ONE, 2015, 10, e0137839.	1.1	32
11654	Assessing the Metabolic Diversity of <i>Streptococcus</i> from a Protein Domain Point of View. PLoS ONE, 2015, 10, e0137908.	1.1	8

#	ARTICLE	IF	CITATIONS
11655	Global Identification of MicroRNAs and Their Targets in Barley under Salinity Stress. PLoS ONE, 2015, 10, e0137990.	1.1	71
11656	A Semi-Supervised Approach for Refining Transcriptional Signatures of Drug Response and Repositioning Predictions. PLoS ONE, 2015, 10, e0139446.	1.1	39
11657	Transcriptomic Analysis of Ovaries from Pigs with High And Low Litter Size. PLoS ONE, 2015, 10, e0139514.	1.1	45
11658	Comparative Transcriptome Analysis of the Less-Dormant Taiwanese Pear and the Dormant Japanese Pear during Winter Season. PLoS ONE, 2015, 10, e0139595.	1.1	20
11659	The Effect of Statins on Blood Gene Expression in COPD. PLoS ONE, 2015, 10, e0140022.	1.1	16
11660	Proteomic Analysis of Anti-Cancerous Scopularide Production by a Marine Microascus brevicaulis Strain and Its UV Mutant. PLoS ONE, 2015, 10, e0140047.	1.1	14
11661	Naturally Occurring Stilbenoid TSG Reverses Non-Alcoholic Fatty Liver Diseases via Gut-Liver Axis. PLoS ONE, 2015, 10, e0140346.	1.1	37
11662	Identification of Novel and Conserved miRNAs from Extreme Halophyte, <i>Oryza coarctata</i> , a Wild Relative of Rice. PLoS ONE, 2015, 10, e0140675.	1.1	42
11663	Identification, Characterization, and Diel Pattern of Expression of Canonical Clock Genes in <i>Nephrops norvegicus</i> (Crustacea: Decapoda) Eyestalk. PLoS ONE, 2015, 10, e0141893.	1.1	37
11664	De Novo Assembly and Characterization of the Invasive Northern Pacific Seastar Transcriptome. PLoS ONE, 2015, 10, e0142003.	1.1	16
11665	Identification of Putative Nuclear Receptors and Steroidogenic Enzymes in Murray-Darling Rainbowfish (<i>Melanotaenia fluviatilis</i>) Using RNA-Seq and De Novo Transcriptome Assembly. PLoS ONE, 2015, 10, e0142636.	1.1	2
11666	Transcriptome Analysis Revealed Highly Expressed Genes Encoding Secondary Metabolite Pathways and Small Cysteine-Rich Proteins in the Sclerotium of <i>Lignosus rhinocerotis</i> . PLoS ONE, 2015, 10, e0143549.	1.1	17
11667	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. PLoS ONE, 2015, 10, e0144176.	1.1	1
11668	Schizophrenia-Associated MIR204 Regulates Noncoding RNAs and Affects Neurotransmitter and Ion Channel Gene Sets. PLoS ONE, 2015, 10, e0144428.	1.1	12
11669	Gene Expression Analysis of Plum pox virus (Sharka) Susceptibility/Resistance in Apricot (<i>Prunus</i>) Tj ETQq0 0 0 rgBT ₁ /Overlock ₁₀ Tf 50 1	1.1	25
11670	Reproducible Analysis of Post-Translational Modifications in Proteomes—Application to Human Mutations. PLoS ONE, 2015, 10, e0144692.	1.1	9
11671	Cyclophilin C Participates in the US2-Mediated Degradation of Major Histocompatibility Complex Class I Molecules. PLoS ONE, 2015, 10, e0145458.	1.1	9
11672	p38 Mitogen-Activated Protein Kinase Pathway Regulates Genes during Proliferation and Differentiation in Oligodendrocytes. PLoS ONE, 2015, 10, e0145843.	1.1	17

#	ARTICLE	IF	CITATIONS
11673	The role of markup for enabling interoperability in health informatics. <i>Frontiers in Physiology</i> , 2015, 6, 152.	1.3	3
11674	A novel, dynamic pattern-based analysis of NF- κ B binding during the priming phase of liver regeneration reveals switch-like functional regulation of target genes. <i>Frontiers in Physiology</i> , 2015, 6, 189.	1.3	8
11675	Pathway Analysis: State of the Art. <i>Frontiers in Physiology</i> , 2015, 6, 383.	1.3	227
11676	Transcriptomic landscape of <i>Pueraria lobata</i> demonstrates potential for phytochemical study. <i>Frontiers in Plant Science</i> , 2015, 6, 426.	1.7	21
11677	Proteomic analysis and candidate allergenic proteins in <i>Populus deltoides</i> CL. α 2KCN8 mature pollen. <i>Frontiers in Plant Science</i> , 2015, 6, 548.	1.7	14
11678	Acetylation of cell wall is required for structural integrity of the leaf surface and exerts a global impact on plant stress responses. <i>Frontiers in Plant Science</i> , 2015, 6, 550.	1.7	22
11679	Transcriptome profiling reveals differential gene expression in proanthocyanidin biosynthesis associated with red/green skin color mutant of pear (<i>Pyrus communis</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 795.	1.7	53
11680	Dynamic transcription profiles of α -Qinguan apple (<i>Malus domestica</i>) leaves in response to <i>Marssonina coronaria</i> inoculation. <i>Frontiers in Plant Science</i> , 2015, 6, 842.	1.7	16
11681	Changes in the nuclear proteome of developing wheat (<i>Triticum aestivum</i> L.) grain. <i>Frontiers in Plant Science</i> , 2015, 6, 905.	1.7	13
11682	RNA Sequencing Analysis of the <i>msl2msl3</i> , <i>crl</i> , and <i>ggps1</i> Mutants Indicates that Diverse Sources of Plastid Dysfunction Do Not Alter Leaf Morphology Through a Common Signaling Pathway. <i>Frontiers in Plant Science</i> , 2015, 6, 1148.	1.7	6
11683	Contextualizing the Genes Altered in Bladder Neoplasms in Pediatric and Teen Patients Allows Identifying Two Main Classes of Biological Processes Involved and New Potential Therapeutic Targets. <i>Current Genomics</i> , 2015, 17, 33-61.	0.7	3
11685	Effectiveness and Usability of Bioinformatics Tools to Analyze Pathways Associated with miRNA Expression. <i>Cancer Informatics</i> , 2015, 14, CIN.S32716.	0.9	8
11686	Bioinformatics Approach Reveals Systematic Mechanism Underlying Lung Adenocarcinoma. <i>Tumori</i> , 2015, 101, 281-286.	0.6	10
11687	Identification of the Interaction Network of Hub Genes for Melanoma Treated with Vemurafenib Based on Microarray Data. <i>Tumori</i> , 2015, 101, 368-374.	0.6	5
11688	Article Commentary: Predictive Modeling of Drug Treatment in the Area of Personalized Medicine. <i>Cancer Informatics</i> , 2015, 14s4, CIN.S19330.	0.9	11
11689	High-Throughput Sequencing Reveals Diverse Sets of Conserved, Nonconserved, and Species-Specific miRNAs in <i>Jute</i> . <i>International Journal of Genomics</i> , 2015, 2015, 1-14.	0.8	14
11690	A Systematic Evaluation of Feature Selection and Classification Algorithms Using Simulated and Real miRNA Sequencing Data. <i>Computational and Mathematical Methods in Medicine</i> , 2015, 2015, 1-11.	0.7	8
11691	An Improved Method for Completely Uncertain Biological Network Alignment. <i>BioMed Research International</i> , 2015, 2015, 1-11.	0.9	1

#	ARTICLE	IF	CITATIONS
11692	Prediction of Drug Indications Based on Chemical Interactions and Chemical Similarities. <i>BioMed Research International</i> , 2015, 2015, 1-14.	0.9	3
11693	Dietary Nitrate Is a Modifier of Vascular Gene Expression in Old Male Mice. <i>Oxidative Medicine and Cellular Longevity</i> , 2015, 2015, 1-12.	1.9	13
11694	Identification of Gene Biomarkers for Distinguishing Small-Cell Lung Cancer from Non-Small-Cell Lung Cancer Using a Network-Based Approach. <i>BioMed Research International</i> , 2015, 2015, 1-8.	0.9	12
11695	Human Gene Expression in Uncomplicated <i>Plasmodium falciparum</i> Malaria. <i>Journal of Immunology Research</i> , 2015, 2015, 1-10.	0.9	17
11696	Identification of Chemical Toxicity Using Ontology Information of Chemicals. <i>Computational and Mathematical Methods in Medicine</i> , 2015, 2015, 1-5.	0.7	2
11697	Identification of Subtype Specific miRNA-mRNA Functional Regulatory Modules in Matched miRNA-mRNA Expression Data: Multiple Myeloma as a Case. <i>BioMed Research International</i> , 2015, 2015, 1-15.	0.9	5
11698	$\langle \text{mml:math} \text{ xmlns:mml="http://www.w3.org/1998/Math/MathML" id="M1"} \rangle \langle \text{mml:mrow} \rangle \langle \text{mml:mi} \rangle K \langle \text{mml:mi} \rangle \langle \text{mml:mrow} \rangle \langle \text{mml:math} \rangle$ -Profiles: A Nonlinear Clustering Method for Pattern Detection in High Dimensional Data. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	10
11699	<i>De Novo</i> Assembly of the Pea (<i>Pisum sativum</i> L.) Nodule Transcriptome. <i>International Journal of Genomics</i> , 2015, 2015, 1-11.	0.8	25
11700	A Glimpse to Background and Characteristics of Major Molecular Biological Networks. <i>BioMed Research International</i> , 2015, 2015, 1-14.	0.9	12
11701	A Whole-Genome Microarray Study of <i>Arabidopsis thaliana</i> Semisolid Callus Cultures Exposed to Microgravity and Nonmicrogravity Related Spaceflight Conditions for 5 Days on Board of Shenzhou 8. <i>BioMed Research International</i> , 2015, 2015, 1-15.	0.9	42
11702	Coexpression Pattern Analysis of NPM1-Associated Genes in Chronic Myelogenous Leukemia. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	7
11703	Improving the Understanding of Pathogenesis of Human Papillomavirus 16 via Mapping Protein-Protein Interaction Network. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	8
11704	Identification of a New <i>Alcaligenes faecalis</i> Strain MOR02 and Assessment of Its Toxicity and Pathogenicity to Insects. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	30
11705	Genome-Wide Gene Expression in relation to Age in Large Laboratory Cohorts of <i>Drosophila melanogaster</i> . <i>Genetics Research International</i> , 2015, 2015, 1-19.	2.0	30
11706	An extracellular biochemical screen reveals that FLRTs and Unc5s mediate neuronal subtype recognition in the retina. <i>ELife</i> , 2015, 4, e08149.	2.8	45
11707	HIV Tat controls RNA Polymerase II and the epigenetic landscape to transcriptionally reprogram target immune cells. <i>ELife</i> , 2015, 4, .	2.8	47
11708	SHOPIN. <i>Advances in Protein Chemistry and Structural Biology</i> , 2015, 101, 323-349.	1.0	2
11709	Protein Complex Discovery by Interaction Filtering from Protein Interaction Networks Using Mutual Rank Coexpression and Sequence Similarity. <i>BioMed Research International</i> , 2015, 2015, 1-7.	0.9	1

#	ARTICLE	IF	CITATIONS
11710	An Overview of Biomolecular Event Extraction from Scientific Documents. Computational and Mathematical Methods in Medicine, 2015, 2015, 1-19.	0.7	13
11711	Multi-Instance Multilabel Learning with Weak-Label for Predicting Protein Function in Electricigens. BioMed Research International, 2015, 2015, 1-9.	0.9	0
11712	Developing of the Computer Method for Annotation of Bacterial Genes. Advances in Bioinformatics, 2015, 2015, 1-9.	5.7	15
11713	Recovering Drug-Induced Apoptosis Subnetwork from Connectivity Map Data. BioMed Research International, 2015, 2015, 1-11.	0.9	11
11714	Comparative Meta-Analysis of Transcriptomics Data during Cellular Senescence and <i>In Vivo</i> Tissue Ageing. Oxidative Medicine and Cellular Longevity, 2015, 2015, 1-17.	1.9	17
11715	RecRWR: A Recursive Random Walk Method for Improved Identification of Diseases. BioMed Research International, 2015, 2015, 1-7.	0.9	1
11716	Combined Analysis of SNP Array Data Identifies Novel CNV Candidates and Pathways in Ependymoma and Mesothelioma. BioMed Research International, 2015, 2015, 1-10.	0.9	3
11717	Transcriptional changes between uninfamed ulcerative colitis and familial adenomatous polyposis pouch mucosa can be attributed to an altered immune response. Acta Biochimica Polonica, 2015, 62, 69-75.	0.3	7
11718	Fair evaluation of global network aligners. , 2015, , .		1
11720	Ontologies in Metabolomics. Metabolomics: Open Access, 2015, 05, .	0.1	0
11721	Identifying communities from multiplex biological networks. PeerJ, 2015, 3, e1525.	0.9	57
11722	Analysis of expressed sequence tags from cDNA library of Fusarium culmorum infected barley (Hordeum vulgare L.) roots. Bioinformatics, 2015, 11, 34-38.	0.2	4
11723	Molecular Genetic Approaches to Studying the Externalizing Spectrum. , 2015, , .		0
11724	The BRCA1/2-directed miRNA signature predicts a good prognosis in ovarian cancer patients with wild-type BRCA1/2. Oncotarget, 2015, 6, 2397-2406.	0.8	36
11725	Application of Functional Genomics for Bovine Respiratory Disease Diagnostics. Bioinformatics and Biology Insights, 2015, 9s2, BBI.S30525.	1.0	7
11726	A multi-functional analyzer uses parameter constraints to improve the efficiency of model-based gene-set analysis. Annals of Applied Statistics, 2015, 9, .	0.5	6
11727	Taxonomy and Genetic Differentiation among Wild and Cultivated Germplasm of <i>Solanum</i> sect. <i>Petota</i> . Plant Genome, 2015, 8, eplantgenome2014.06.0025.	1.6	52
11728	Genetic alterations of JAK/STAT cascade and histone modification in extranodal NK/T-cell lymphoma nasal type. Oncotarget, 2015, 6, 17764-17776.	0.8	136

#	ARTICLE	IF	CITATIONS
11729	A panel of induced pluripotent stem cells from chimpanzees: a resource for comparative functional genomics. <i>ELife</i> , 2015, 4, e07103.	2.8	114
11731	Comparative Transcriptome Analyses Reveal Core Parasitism Genes and Suggest Gene Duplication and Repurposing as Sources of Structural Novelty. <i>Molecular Biology and Evolution</i> , 2015, 32, 767-790.	3.5	137
11732	The Avian Transcriptome Response to Malaria Infection. <i>Molecular Biology and Evolution</i> , 2015, 32, 1255-1267.	3.5	83
11733	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2015, 43, D6-D17.	6.5	275
11734	BioAssay Research Database (BARD): chemical biology and probe-development enabled by structured metadata and result types. <i>Nucleic Acids Research</i> , 2015, 43, D1163-D1170.	6.5	20
11735	The Comparative Toxicogenomics Database's 10th year anniversary: update 2015. <i>Nucleic Acids Research</i> , 2015, 43, D914-D920.	6.5	342
11736	Genetic Determinants of Depression. <i>Harvard Review of Psychiatry</i> , 2015, 23, 1-18.	0.9	132
11737	De novo assembly, transcriptome characterization, lignin accumulation and anatomic characteristics: novel insights into lignin biosynthesis during celery leaf development. <i>Scientific Reports</i> , 2015, 5, 8259.	1.6	78
11738	A statistically inferred microRNA network identifies breast cancer target miR-940 as an actin cytoskeleton regulator. <i>Scientific Reports</i> , 2015, 5, 8336.	1.6	28
11739	Identification of hybrid node and link communities in complex networks. <i>Scientific Reports</i> , 2015, 5, 8638.	1.6	36
11740	Metazoans evolved by taking domains from soluble proteins to expand intercellular communication network. <i>Scientific Reports</i> , 2015, 5, 9576.	1.6	8
11741	What helminth genomes have taught us about parasite evolution. <i>Parasitology</i> , 2015, 142, S85-S97.	0.7	75
11742	Multidimensional Fractionation Is a Requirement for Quantitation of Golgi-Resident Glycosylation Enzymes from Cultured Human Cells. <i>Journal of Proteome Research</i> , 2015, 14, 747-755.	1.8	2
11743	An allelic series of miR-17 ^{-1/492} mutant mice uncovers functional specialization and cooperation among members of a microRNA polycistron. <i>Nature Genetics</i> , 2015, 47, 766-775.	9.4	101
11744	microRNA regulatory mechanism by which PLLA aligned nanofibers influence PC12 cell differentiation. <i>Journal of Neural Engineering</i> , 2015, 12, 046010.	1.8	19
11745	The semantic web in translational medicine: current applications and future directions. <i>Briefings in Bioinformatics</i> , 2015, 16, 89-103.	3.2	37
11746	SimSeq: a nonparametric approach to simulation of RNA-sequence datasets. <i>Bioinformatics</i> , 2015, 31, 2131-2140.	1.8	55
11747	Gene selection for the reconstruction of stem cell differentiation trees: a linear programming approach. <i>Bioinformatics</i> , 2015, 31, 2676-2682.	1.8	0

#	ARTICLE	IF	CITATIONS
11748	Small <sc>RNA</sc> deep sequencing reveals the important role of micro<sc>RNA</sc>s in the halophyte <i>Halostachys caspica</i> . <i>Plant Biotechnology Journal</i> , 2015, 13, 395-408.	4.1	37
11749	From Raw Data to Biological Discoveries: A Computational Analysis Pipeline for Mass Spectrometry-Based Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1820-1826.	1.2	17
11750	Secretome protein signature of human gastrointestinal stromal tumor cells. <i>Experimental Cell Research</i> , 2015, 336, 158-170.	1.2	6
11751	The History of Salivary Diagnostics. , 2015, , 17-31.		1
11752	Methods for protein complex prediction and their contributions towards understanding the organisation, function and dynamics of complexes. <i>FEBS Letters</i> , 2015, 589, 2590-2602.	1.3	66
11753	Genetic variants and risk of gastric cancer: a pathway analysis of a genome-wide association study. <i>SpringerPlus</i> , 2015, 4, 215.	1.2	13
11754	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Th.b2, a microsymbiont of <i>Amphicarpaea bracteata</i> collected in Johnson City, New York. <i>Standards in Genomic Sciences</i> , 2015, 10, 24.	1.5	2
11755	The Classification and Evolution of Enzyme Function. <i>Biophysical Journal</i> , 2015, 109, 1082-1086.	0.2	95
11756	Functional Organization of the Genome May Shape the Species Boundary in the House Mouse. <i>Molecular Biology and Evolution</i> , 2015, 32, 1208-1220.	3.5	65
11757	Comprehensively Evaluating cis -Regulatory Variation in the Human Prostate Transcriptome by Using Gene-Level Allele-Specific Expression. <i>American Journal of Human Genetics</i> , 2015, 96, 869-882.	2.6	37
11758	Horsetails Are Ancient Polyploids: Evidence from <i>Equisetum giganteum</i> . <i>Plant Cell</i> , 2015, 27, 1567-1578.	3.1	78
11759	Approaching the axiomatic enrichment of the Gene Ontology from a lexical perspective. <i>Artificial Intelligence in Medicine</i> , 2015, 65, 35-48.	3.8	9
11760	Tree shrew database (TreeshrewDB): a genomic knowledge base for the Chinese tree shrew. <i>Scientific Reports</i> , 2014, 4, 7145.	1.6	34
11761	New Heuristics for Clustering Large Biological Networks. <i>Lecture Notes in Computer Science</i> , 2015, , 309-319.	1.0	1
11762	Primer to Analysis of Genomic Data Using R. <i>Use R!</i> , 2015, , .	0.3	11
11763	Hippocampal Proteomic and Metabonomic Abnormalities in Neurotransmission, Oxidative Stress, and Apoptotic Pathways in a Chronic Phencyclidine Rat Model. <i>Journal of Proteome Research</i> , 2015, 14, 3174-3187.	1.8	14
11764	Diverse array-designed modes of combination therapies in Fangjiomics. <i>Acta Pharmacologica Sinica</i> , 2015, 36, 680-688.	2.8	25
11765	Controllability and observability analysis for vertex domination centrality in directed networks. <i>Scientific Reports</i> , 2014, 4, 5399.	1.6	29

#	ARTICLE	IF	CITATIONS
11766	Gene expression studies of a human monocyte cell line identify dissimilarities between differently manufactured glatiramoids. <i>Scientific Reports</i> , 2015, 5, 10191.	1.6	14
11767	Evolution of an Epigenetic Gene Ensemble within the Genus <i>Anopheles</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 901-915.	1.1	8
11768	Gemcitabine resistant pancreatic cancer cell lines acquire an invasive phenotype with collateral hypersensitivity to histone deacetylase inhibitors. <i>Cancer Biology and Therapy</i> , 2015, 16, 43-51.	1.5	50
11769	In Silico Post Genome-Wide Association Studies Analysis of C-Reactive Protein Loci Suggests an Important Role for Interferons. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 487-497.	5.1	24
11770	Simultaneous Enrichment of Plasma Soluble and Extracellular Vesicular Glycoproteins Using Prolonged Ultracentrifugation-Electrostatic Repulsion-hydrophilic Interaction Chromatography (PUC-ERLIC) Approach*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1657-1671.	2.5	28
11771	Ontology Based Document Clustering Using MapReduce. <i>International Journal of Database Management Systems</i> , 2015, 7, 01-12.	0.2	7
11772	Dynamic transcriptome profiles of skeletal muscle tissue across 11 developmental stages for both Tongcheng and Yorkshire pigs. <i>BMC Genomics</i> , 2015, 16, 377.	1.2	64
11773	Coronaviruses. <i>Methods in Molecular Biology</i> , 2015, 1282, v.	0.4	102
11775	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
11776	High quality reference genome of drumstick tree (<i>Moringa oleifera</i> Lam.), a potential perennial crop. <i>Science China Life Sciences</i> , 2015, 58, 627-638.	2.3	53
11777	Ontology-based approach for structural design considering low embodied energy and carbon. <i>Energy and Buildings</i> , 2015, 102, 75-90.	3.1	36
11778	10-Hydroxy-2-decenoic acid inhibiting the proliferation of fibroblast-like synoviocytes by PI3K-AKT pathway. <i>International Immunopharmacology</i> , 2015, 28, 97-104.	1.7	13
11779	Single cell subtractive transcriptomics for identification of cell-specifically expressed candidate genes of pyrrolizidine alkaloid biosynthesis. <i>Phytochemistry</i> , 2015, 117, 17-24.	1.4	7
11780	Analysis of protein expression changes of the Vero E6 cells infected with classic PEDV strain CV777 by using quantitative proteomic technique. <i>Journal of Virological Methods</i> , 2015, 218, 27-39.	1.0	44
11781	Draft genome sequence of Strain ATCC 17802T, the type strain of <i>Vibrio parahaemolyticus</i> . <i>Marine Genomics</i> , 2015, 24, 203-205.	0.4	9
11782	MAPK feedback encodes a switch and timer for tunable stress adaptation in yeast. <i>Science Signaling</i> , 2015, 8, ra5.	1.6	46
11783	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
11784	Bioinformatics and Biomedical Engineering. <i>Lecture Notes in Computer Science</i> , 2015, , .	1.0	3

#	ARTICLE	IF	CITATIONS
11785	A comprehensive map of genome-wide gene regulation in <i>Mycobacterium tuberculosis</i> . <i>Scientific Data</i> , 2015, 2, 150010.	2.4	55
11786	FCMM: A comparative metagenomic approach for functional characterization of multiple metagenome samples. <i>Journal of Microbiological Methods</i> , 2015, 115, 121-128.	0.7	2
11787	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
11788	MicroRNA expression profiles and networks in mouse lung infected with H1N1 influenza virus. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1885-1897.	1.0	13
11789	Genome-wide transcriptome analysis of mRNAs and microRNAs in Dorset and Small Tail Han sheep to explore the regulation of fecundity. <i>Molecular and Cellular Endocrinology</i> , 2015, 402, 32-42.	1.6	64
11790	Transcriptomics of mRNA and egg quality in farmed fish: Some recent developments and future directions. <i>General and Comparative Endocrinology</i> , 2015, 221, 23-30.	0.8	58
11791	Transcriptome analysis in <i>Cucumis sativus</i> identifies genes involved in multicellular trichome development. <i>Genomics</i> , 2015, 105, 296-303.	1.3	26
11792	Identification of lung cancer miRNA-miRNA co-regulation networks through a progressive data refining approach. <i>Journal of Theoretical Biology</i> , 2015, 380, 271-279.	0.8	18
11793	Novel Findings from CNVs Implicate Inhibitory and Excitatory Signaling Complexes in Schizophrenia. <i>Neuron</i> , 2015, 86, 1203-1214.	3.8	173
11794	Genome-wide distribution of superoxide dismutase (SOD) gene families in <i>Sorghum bicolor</i> . <i>Turkish Journal of Biology</i> , 2015, 39, 49-59.	2.1	55
11795	From the static interactome to dynamic protein complexes: Three challenges. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1571001.	0.3	30
11796	Genome sequence and description of the mosquitocidal and heavy metal tolerant strain <i>Lysinibacillus sphaericus</i> CBAM5. <i>Standards in Genomic Sciences</i> , 2015, 10, 2.	1.5	42
11797	Complete genome sequence of the fish pathogen <i>Flavobacterium psychrophilum</i> ATCC 49418T. <i>Standards in Genomic Sciences</i> , 2015, 10, 3.	1.5	24
11798	Moment based gene set tests. <i>BMC Bioinformatics</i> , 2015, 16, 132.	1.2	6
11799	Determining minimum set of driver nodes in protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2015, 16, 146.	1.2	51
11800	Linking gene expression to phenotypes via pathway information. <i>Journal of Biomedical Semantics</i> , 2015, 6, 17.	0.9	26
11801	Annotation-based feature extraction from sets of SBML models. <i>Journal of Biomedical Semantics</i> , 2015, 6, 20.	0.9	13
11802	High quality draft genome sequence of <i>Leucobacter chironomi</i> strain MM2LBT (DSM 19883T) isolated from a <i>Chironomus</i> sp. egg mass. <i>Standards in Genomic Sciences</i> , 2015, 10, 21.	1.5	8

#	ARTICLE	IF	CITATIONS
11803	Complete genome sequence of endophytic nitrogen-fixing <i>Klebsiella variicola</i> strain DX120E. <i>Standards in Genomic Sciences</i> , 2015, 10, 22.	1.5	66
11804	Genetic Evidence That Intratumoral T-cell Proliferation and Activation Are Associated with Recurrence and Survival in Patients with Resected Colorectal Liver Metastases. <i>Cancer Immunology Research</i> , 2015, 3, 380-388.	1.6	30
11805	Ascorbic Acid-Induced Cardiac Differentiation of Murine Pluripotent Stem Cells: Transcriptional Profiling and Effect of a Small Molecule Synergist of Wnt/ β^2 -Catenin Signaling Pathway. <i>Cellular Physiology and Biochemistry</i> , 2015, 36, 810-830.	1.1	23
11806	Systematic discovery and characterization of stress-related microRNA genes in <i>Oryza sativa</i> . <i>Biologia (Poland)</i> , 2015, 70, 75-84.	0.8	1
11807	Semantic Similarity from Natural Language and Ontology Analysis. <i>Synthesis Lectures on Human Language Technologies</i> , 2015, 8, 1-254.	2.3	127
11808	Computational Methods in Epigenetics. , 2015, , 153-180.		0
11809	PolySearch2: a significantly improved text-mining system for discovering associations between human diseases, genes, drugs, metabolites, toxins and more. <i>Nucleic Acids Research</i> , 2015, 43, W535-W542.	6.5	143
11810	Literature Mining and Ontology Mapping Applied to Big Data. , 2015, , 184-208.		2
11811	Integrating ontologies of rare diseases and radiological diagnosis. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1164-1168.	2.2	8
11813	Phosphoproteomic Analysis of the Highly-Metastatic Hepatocellular Carcinoma Cell Line, MHCC97-H. <i>International Journal of Molecular Sciences</i> , 2015, 16, 4209-4225.	1.8	22
11814	SIFTER search: a web server for accurate phylogeny-based protein function prediction. <i>Nucleic Acids Research</i> , 2015, 43, W141-W147.	6.5	39
11815	Proteomic Enrichment Analysis of Psychotic and Affective Disorders Reveals Common Signatures in Presynaptic Glutamatergic Signaling and Energy Metabolism. <i>International Journal of Neuropsychopharmacology</i> , 2015, 18, .	1.0	44
11816	Novel Gene-Ontology Based Distance-Metric for Function-Prediction via Clustering in Protein-Interaction-Networks. <i>Advances in Intelligent Systems and Computing</i> , 2015, , 167-176.	0.5	0
11817	Dnmt1 is essential to maintain progenitors in the perinatal intestinal epithelium. <i>Development (Cambridge)</i> , 2015, 142, 2163-2172.	1.2	60
11818	Expression of Human Skin-Specific Genes Defined by Transcriptomics and Antibody-Based Profiling. <i>Journal of Histochemistry and Cytochemistry</i> , 2015, 63, 129-141.	1.3	63
11819	Extreme multifunctional proteins identified from a human protein interaction network. <i>Nature Communications</i> , 2015, 6, 7412.	5.8	101
11820	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. <i>Nature Communications</i> , 2015, 6, 7208.	5.8	178
11821	A semantic approach for knowledge capture of MicroRNA-Target gene interactions. , 2015, , .		10

#	ARTICLE	IF	CITATIONS
11822	DISim: Ontology-driven simulation of biomedical data integration tasks. , 2015, , .		2
11823	A hybrid semantic similarity measure for gene ontology based on offspring and path length. , 2015, , .		3
11824	Identification of function modules in protein-protein interaction networks by modularity optimization method. , 2015, , .		2
11825	The anatomical distribution of genetic associations. Nucleic Acids Research, 2015, 43, 10804-10820.	6.5	37
11826	Functional Implications of Biochemical and Molecular Characteristics of Donation After Circulatory Death Livers. Transplantation Direct, 2015, 1, 1-9.	0.8	3
11827	Using aggregate taxonomies to summarize SNOMED CT evolution. , 2015, , .		3
11828	GO-based Gene Expression Cluster Validation. , 2015, , .		0
11829	A ranking-based approach for hierarchical classification. , 2015, , .		7
11830	Identifying driver genomic alterations in cancers by searching minimum-weight, mutually exclusive sets. , 2015, , .		1
11831	Biclustering analysis of gene expression data using multi-objective evolutionary algorithms. , 2015, , .		4
11832	Global analyses revealed age-related alterations in innate immune responses after stimulation of pathogen recognition receptors. Aging Cell, 2015, 14, 421-432.	3.0	155
11833	The arabidopsis information resource: Making and mining the "gold standard" annotated reference plant genome. Genesis, 2015, 53, 474-485.	0.8	884
11834	BioModels: Content, Features, Functionality, and Use. CPT: Pharmacometrics and Systems Pharmacology, 2015, 4, 55-68.	1.3	56
11835	Molecular Mechanisms Mediating Retinal Reactive Gliosis Following Bone Marrow Mesenchymal Stem Cell Transplantation. Stem Cells, 2015, 33, 3006-3016.	1.4	64
11836	Improving network topology-based protein interactome mapping via collaborative filtering. Knowledge-Based Systems, 2015, 90, 23-32.	4.0	52
11837	Multidisciplinary Collaboration to Facilitate Hypotheses Generation in Huntington's Disease. , 2015, , .		3
11838	Cross-organism analysis using InterMine. Genesis, 2015, 53, 547-560.	0.8	31
11839	An Ontology-Based Approach for Retrieving Information from Disparate Sectors in Government: The Patent System as an Exemplar. , 2015, , .		2

#	ARTICLE	IF	CITATIONS
11840	A computer information system for genetic data analysis on the basis of a permutation test. , 2015, , .		0
11841	Genome-wide identification of the <i>Phaseolus vulgaris</i> sRNAome using small RNA and degradome sequencing. <i>BMC Genomics</i> , 2015, 16, 423.	1.2	49
11842	Transcriptional response of Atlantic salmon families to <i>Piscirickettsia salmonis</i> infection highlights the relevance of the iron-deprivation defence system. <i>BMC Genomics</i> , 2015, 16, 495.	1.2	94
11843	Genome-wide association study revealed a promising region and candidate genes for eggshell quality in an F2 resource population. <i>BMC Genomics</i> , 2015, 16, 565.	1.2	29
11844	RNA sequencing from human neutrophils reveals distinct transcriptional differences associated with chronic inflammatory states. <i>BMC Medical Genomics</i> , 2015, 8, 55.	0.7	61
11845	RNA-seq analysis of <i>Macrobrachium rosenbergii</i> hepatopancreas in response to <i>Vibrio parahaemolyticus</i> infection. <i>Gut Pathogens</i> , 2015, 7, 6.	1.6	66
11846	Distal 10q trisomy with copy number gain in chromosome region 10q23.1â€“10q25.1: the Wnt signaling pathway is the most pertinent to the gene content in the region of copy number gain: a case report. <i>BMC Research Notes</i> , 2015, 8, 250.	0.6	5
11847	Codon and Amino Acid Usage Are Shaped by Selection Across Divergent Model Organisms of the Pancrustacea. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2307-2321.	0.8	20
11848	Similarity-based relaxed instance queries. <i>Journal of Applied Logic</i> , 2015, 13, 480-508.	1.1	12
11849	Using Semantic Association to Extend and Infer Literature-Oriented Relativity Between Terms. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 1219-1226.	1.9	7
11850	Genome sequence of <i>Clostridium sporogenes</i> DSM 795T, an amino acid-degrading, nontoxic surrogate of neurotoxin-producing <i>Clostridium botulinum</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 40.	1.5	13
11851	Linking Phenotypes and Modes of Action Through High-Content Screen Fingerprints. <i>Assay and Drug Development Technologies</i> , 2015, 13, 415-427.	0.6	67
11852	L-GRAAL: Lagrangian graphlet-based network aligner. <i>Bioinformatics</i> , 2015, 31, 2182-2189.	1.8	112
11853	Exploring the structure and function of temporal networks with dynamic graphlets. <i>Bioinformatics</i> , 2015, 31, i171-i180.	1.8	75
11854	Improving compoundâ€™protein interaction prediction by building up highly credible negative samples. <i>Bioinformatics</i> , 2015, 31, i221-i229.	1.8	201
11855	PAGER: constructing PAGs and new PAGâ€™PAG relationships for network biology. <i>Bioinformatics</i> , 2015, 31, i250-i257.	1.8	21
11856	OVA: integrating molecular and physical phenotype data from multiple biomedical domain ontologies with variant filtering for enhanced variant prioritization. <i>Bioinformatics</i> , 2015, 31, 3822-3829.	1.8	24
11857	Two <i>Theobroma cacao</i> genotypes with contrasting pathogen tolerance show aberrant transcriptional and ROS responses after salicylic acid treatment. <i>Journal of Experimental Botany</i> , 2015, 66, 6245-6258.	2.4	29

#	ARTICLE	IF	CITATIONS
11858	Key Role of Amino Acid Repeat Expansions in the Functional Diversification of Duplicated Transcription Factors. <i>Molecular Biology and Evolution</i> , 2015, 32, 2263-2272.	3.5	24
11859	PheNetic: network-based interpretation of molecular profiling data. <i>Nucleic Acids Research</i> , 2015, 43, W244-W250.	6.5	24
11860	CellWhere: graphical display of interaction networks organized on subcellular localizations. <i>Nucleic Acids Research</i> , 2015, 43, W571-W575.	6.5	23
11861	Babelomics 5.0: functional interpretation for new generations of genomic data. <i>Nucleic Acids Research</i> , 2015, 43, W117-W121.	6.5	114
11862	DIANA-miRPath v3.0: deciphering microRNA function with experimental support. <i>Nucleic Acids Research</i> , 2015, 43, W460-W466.	6.5	1,494
11863	FNTM: a server for predicting functional networks of tissues in mouse. <i>Nucleic Acids Research</i> , 2015, 43, W182-W187.	6.5	25
11864	Haploinsufficiency predictions without study bias. <i>Nucleic Acids Research</i> , 2015, 43, e101-e101.	6.5	54
11865	Multidimensional gene search with Genehopper. <i>Nucleic Acids Research</i> , 2015, 43, W98-W103.	6.5	17
11866	MyProteinNet: build up-to-date protein interaction networks for organisms, tissues and user-defined contexts. <i>Nucleic Acids Research</i> , 2015, 43, W258-W263.	6.5	49
11867	Gene target specificity of the Super Elongation Complex (SEC) family: how HIV-1 Tat employs selected SEC members to activate viral transcription. <i>Nucleic Acids Research</i> , 2015, 43, 5868-5879.	6.5	65
11868	High-quality permanent draft genome sequence of <i>Rhizobium sullae</i> strain WSM1592; a <i>Hedysarum coronarium</i> microsymbiont from Sassari, Italy. <i>Standards in Genomic Sciences</i> , 2015, 10, 44.	1.5	9
11869	PKDE4J: Entity and relation extraction for public knowledge discovery. <i>Journal of Biomedical Informatics</i> , 2015, 57, 320-332.	2.5	88
11870	SSWAP: Enabling Transaction-Time Reasoning for Semantic Workflows. <i>Computer</i> , 2015, 48, 60-68.	1.2	0
11871	Microbial Proteome Profiling and Systems Biology: Applications to <i>Mycobacterium tuberculosis</i> . <i>Advances in Experimental Medicine and Biology</i> , 2015, 883, 235-254.	0.8	9
11872	UNIPred: Unbalance-Aware Network Integration and Prediction of Protein Functions. <i>Journal of Computational Biology</i> , 2015, 22, 1057-1074.	0.8	17
11873	Signature automation of UMLS concepts: An un-supervised named entity recognition framework for classification of DNA and RNA in biological text. , 2015, , .		0
11874	Large-scale transcriptome sequencing reveals novel expression patterns for key sex-related genes in a sex-changing fish. <i>Biology of Sex Differences</i> , 2015, 6, 26.	1.8	100
11875	Complete genome sequence of bacteriophage P8625, the first lytic phage that infects <i>Verrucomicrobia</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 96.	1.5	1

#	ARTICLE	IF	CITATIONS
11877	Big Data in <i>Caenorhabditis elegans</i> : <i>quo vadis</i> ?. <i>Molecular Biology of the Cell</i> , 2015, 26, 3909-3914.	0.9	8
11878	Every Site Counts: Submitting Transcription Factor-Binding Site Information through the CollecTF Portal. <i>Journal of Bacteriology</i> , 2015, 197, 2454-2457.	1.0	4
11879	BiobankConnect: software to rapidly connect data elements for pooled analysis across biobanks using ontological and lexical indexing. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 65-75.	2.2	24
11880	Genomic islands of speciation separate cichlid ecomorphs in an East African crater lake. <i>Science</i> , 2015, 350, 1493-1498.	6.0	330
11881	Mechanisms of stem cell osteogenic differentiation on TiO ₂ nanotubes. <i>Colloids and Surfaces B: Biointerfaces</i> , 2015, 136, 779-785.	2.5	33
11882	Sparse omics-network regularization to increase interpretability and performance of linear classification models. , 2015, , .		0
11883	A domain ontology for the Non-Coding RNA field. , 2015, , .		0
11884	A model selection criterion for model-based clustering of annotated gene expression data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 413-28.	0.2	0
11885	Assessing protein-protein interactions based on the semantic similarity of interacting proteins. <i>International Journal of Data Mining and Bioinformatics</i> , 2015, 13, 75.	0.1	8
11886	SCAN: A Smart Application Platform for Empowering Parallelizations of Big Genomic Data Analysis in Clouds. , 2015, , .		0
11887	VizEpis : A visualization and mapping tool for interpreting epistasis. , 2015, , .		2
11888	Draft genome sequence of <i>Bacillus azotoformans</i> MEV2011, a (Co-) denitrifying strain unable to grow with oxygen. <i>Standards in Genomic Sciences</i> , 2015, 10, 4.	1.5	4
11889	Towards improved genome-scale metabolic network reconstructions: unification, transcript specificity and beyond. <i>Briefings in Bioinformatics</i> , 2015, 17, bbv100.	3.2	19
11890	DESO: Addressing volume and variety in large-scale criminal cases. <i>Digital Investigation</i> , 2015, 15, 72-82.	3.2	17
11891	Complete genome of the marine bacterium <i>Wenzhouxiangella marina</i> KCTC 42284T. <i>Marine Genomics</i> , 2015, 24, 277-280.	0.4	10
11892	Transcriptional Dynamics Driving MAMP-Triggered Immunity and Pathogen Effector-Mediated Immunosuppression in <i>Arabidopsis</i> Leaves Following Infection with <i>Pseudomonas syringae</i> pv tomato DC3000. <i>Plant Cell</i> , 2015, 27, 3038-3064.	3.1	148
11893	Identification of phenotypic networks based on whole transcriptome by comparative network decomposition. , 2015, , .		0
11894	Engineering dynamic cell cycle control with synthetic small molecule-responsive RNA devices. <i>Journal of Biological Engineering</i> , 2015, 9, 21.	2.0	22

#	ARTICLE	IF	CITATIONS
11895	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. <i>Journal of Experimental Botany</i> , 2015, 66, 5351-5365.	2.4	72
11896	Haem-activated promiscuous targeting of artemisinin in <i>Plasmodium falciparum</i> . <i>Nature Communications</i> , 2015, 6, 10111.	5.8	486
11897	Comparative genome analysis of <i>Lysinibacillus B1-CDA</i> , a bacterium that accumulates arsenic. <i>Genomics</i> , 2015, 106, 384-392.	1.3	17
11898	Deep sequencing reveals cell-type-specific patterns of single-cell transcriptome variation. <i>Genome Biology</i> , 2015, 16, 122.	13.9	95
11899	Sample size reassessment for a two-stage design controlling the false discovery rate. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 429-42.	0.2	3
11900	Predicting Subcellular Localization of Proteins by Bioinformatic Algorithms. <i>Current Topics in Microbiology and Immunology</i> , 2015, 404, 129-158.	0.7	10
11901	Reduced Supply of Monocyte-Derived Macrophages Leads to a Transition from Nodular to Diffuse Lesions and Tissue Cell Activation in Silica-Induced Pulmonary Fibrosis in Mice. <i>American Journal of Pathology</i> , 2015, 185, 2923-2938.	1.9	26
11902	Phylogeny, Morphology, and Metabolic and Invasive Capabilities of Epicellular Fish <i>Coccidium Goussia janae</i> . <i>Protist</i> , 2015, 166, 659-676.	0.6	16
11903	A survey of semantic similarity and its application to social network analysis. , 2015, , .		15
11904	Partial genome sequence of the haloalkaliphilic soda lake bacterium <i>Thioalkalivibrio thiocyanoxidans</i> ARh 2T. <i>Standards in Genomic Sciences</i> , 2015, 10, 85.	1.5	13
11905	Complete genome sequence of <i>Thioalkalivibrio paradoxus</i> type strain ARh 1T, an obligately chemolithoautotrophic haloalkaliphilic sulfur-oxidizing bacterium isolated from a Kenyan soda lake. <i>Standards in Genomic Sciences</i> , 2015, 10, 105.	1.5	5
11907	High-Throughput Transcriptome Analysis of Plant Stress Responses. , 2015, , 195-209.		0
11908	Novel structural co-expression analysis linking the NPM1-associated ribosomal biogenesis network to chronic myelogenous leukemia. <i>Scientific Reports</i> , 2015, 5, 10973.	1.6	14
11909	An integrated strategy for functional analysis of microbial communities based on gene ontology and 16S rRNA gene. <i>International Journal of Data Mining and Bioinformatics</i> , 2015, 13, 63.	0.1	4
11910	Gene expression profile analysis of ventilator-associated pneumonia. <i>Molecular Medicine Reports</i> , 2015, 12, 7455-7462.	1.1	4
11911	Efficient exploration of pan-cancer networks by generalized covariance selection and interactive web content. <i>Nucleic Acids Research</i> , 2015, 43, e98-e98.	6.5	16
11912	Towards rule-based metabolic databases: a requirement analysis based on KEGG. <i>International Journal of Data Mining and Bioinformatics</i> , 2015, 13, 289.	0.1	2
11913	KENeV : A web-application for the automated reconstruction and visualization of the enriched metabolic and signaling super-pathways deriving from genomic experiments. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 248-255.	1.9	11

#	ARTICLE	IF	CITATIONS
11914	Screening of human chromosome 21 genes in the dorsolateral prefrontal cortex of individuals with Down syndrome. <i>Molecular Medicine Reports</i> , 2015, 11, 1235-1239.	1.1	4
11915	Synthetic Quantitative Array Technology Identifies the Ubp3-Bre5 Deubiquitinase Complex as a Negative Regulator of Mitophagy. <i>Cell Reports</i> , 2015, 10, 1215-1225.	2.9	57
11916	Dynamics in Transcriptomics: Advancements in RNA-seq Time Course and Downstream Analysis. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 469-477.	1.9	74
11917	Identifying binary protein-protein interactions from affinity purification mass spectrometry data. <i>BMC Genomics</i> , 2015, 16, 745.	1.2	11
11918	A concept ideation framework for medical device design. <i>Journal of Biomedical Informatics</i> , 2015, 55, 218-230.	2.5	32
11919	The organic osmolyte betaine induces keratin 2 expression in rat epidermal keratinocytes – A genome-wide study in UVB irradiated organotypic 3D cultures. <i>Toxicology in Vitro</i> , 2015, 30, 462-475.	1.1	5
11920	Gene-disease association through topological and biological feature integration. , 2015, , .		0
11921	Sparse Markov chain-based semi-supervised multi-instance multi-label method for protein function prediction. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1543001.	0.3	4
11922	Enhancing domain specific language implementations through ontology. , 2015, , .		6
11923	Identification of multi-target effects of Huaier aqueous extract via microarray profiling in triple-negative breast cancer cells. <i>International Journal of Oncology</i> , 2015, 46, 2047-2056.	1.4	16
11924	Data quality issues in big data. , 2015, , .		19
11925	High-quality permanent draft genome sequence of <i>Ensifer meliloti</i> strain 4H41, an effective salt- and drought-tolerant microsymbiont of <i>Phaseolus vulgaris</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 34.	1.5	4
11926	The complete genome, structural proteome, comparative genomics and phylogenetic analysis of a broad host lytic bacteriophage Φ D3 infecting pectinolytic <i>Dickeya</i> spp.. <i>Standards in Genomic Sciences</i> , 2015, 10, 68.	1.5	16
11927	Complete genome sequences of bacteriophages P12002L and P12002S, two lytic phages that infect a marine <i>Polaribacter</i> strain. <i>Standards in Genomic Sciences</i> , 2015, 10, 82.	1.5	25
11928	High-quality permanent draft genome sequence of <i>Ensifer medicae</i> strain WSM244, a microsymbiont isolated from <i>Medicago polymorpha</i> growing in alkaline soil. <i>Standards in Genomic Sciences</i> , 2015, 10, 126.	1.5	1
11929	Expression profile analysis of microRNAs and downregulated miR-486-5p and miR-30a-5p in non-small cell lung cancer. <i>Oncology Reports</i> , 2015, 34, 1779-1786.	1.2	54
11930	Genomic analysis of <i>Luteimonas abyssi</i> XH031T: insights into its adaption to the seafloor environment of South Pacific Gyre and ecological role in biogeochemical cycle. <i>BMC Genomics</i> , 2015, 16, 1092.	1.2	22
11931	Genome sequence of <i>Bradyrhizobium</i> sp. WSM1253; a microsymbiont of <i>Ornithopus compressus</i> from the Greek Island of Sifnos. <i>Standards in Genomic Sciences</i> , 2015, 10, 113.	1.5	3

#	ARTICLE	IF	CITATIONS
11932	Epistatic Analysis of Clarkson Disease. <i>Procedia Computer Science</i> , 2015, 51, 725-734.	1.2	6
11933	Proteomics and glycoproteomics of pluripotent stem cell surface proteins. <i>Proteomics</i> , 2015, 15, 1152-1163.	1.3	4
11934	Improved bone defect healing by a superagonistic GDF5 variant derived from a patient with multiple synostoses syndrome. <i>Bone</i> , 2015, 73, 111-119.	1.4	12
11935	The eyestalk transcriptome of red swamp crayfish <i>Procambarus clarkii</i> . <i>Gene</i> , 2015, 557, 28-34.	1.0	60
11936	An immune-enriched oligo-microarray analysis of gene expression in Manila clam (<i>Venerupis</i>). <i>Journal of Proteomics</i> , 2015, 15, 275-286.	1.6	30
11937	An efficient algorithm for pairwise local alignment of protein interaction networks. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550003.	0.3	0
11938	GeneFriends: a human RNA-seq-based gene and transcript co-expression database. <i>Nucleic Acids Research</i> , 2015, 43, D1124-D1132.	6.5	108
11939	Chemometrics methods for the analysis of genomics, transcriptomics, proteomics, metabolomics, and metagenomics datasets. <i>Journal of Proteomics</i> , 2015, 15, 37-60.		1
11940	Computational Peptidology. <i>Methods in Molecular Biology</i> , 2015, .	0.4	14
11941	Asymmetry within and around the human planum temporale is sexually dimorphic and influenced by genes involved in steroid hormone receptor activity. <i>Cortex</i> , 2015, 62, 41-55.	1.1	114
11942	Genetic Contributions to Urgency Urinary Incontinence in Women. <i>Journal of Urology</i> , 2015, 193, 2020-2027.	0.2	24
11943	Augmentation of multiple protein kinase activities associated with secondary imatinib resistance in gastrointestinal stromal tumors as revealed by quantitative phosphoproteome analysis. <i>Journal of Proteomics</i> , 2015, 115, 132-142.	1.2	19
11944	High-throughput transcriptome analysis of barley (<i>Hordeum vulgare</i>) exposed to excessive boron. <i>Gene</i> , 2015, 557, 71-81.	1.0	50
11945	Comparative analysis of the uropathogenic <i>Escherichia coli</i> surface proteome by tandem mass-spectrometry of artificially induced outer membrane vesicles. <i>Journal of Proteomics</i> , 2015, 115, 93-106.	1.2	33
11946	Complete mitogenome of the edible sea urchin <i>Loxechinus albus</i> : genetic structure and comparative genomics within Echinozoa. <i>Molecular Biology Reports</i> , 2015, 42, 1081-1089.	1.0	6
11947	The KnownLeaf literature curation system captures knowledge about <i>Arabidopsis</i> leaf growth and development and facilitates integrated data mining. <i>Current Plant Biology</i> , 2015, 2, 1-11.	2.3	7
11948	Dose-specific transcriptional responses in thyroid tissue in mice after ¹³¹ I administration. <i>Nuclear Medicine and Biology</i> , 2015, 42, 263-268.	0.3	19
11949	A new data architecture for advancing life cycle assessment. <i>International Journal of Life Cycle Assessment</i> , 2015, 20, 520-526.	2.2	20

#	ARTICLE	IF	CITATIONS
11950	Large-scale exploration and analysis of drug combinations. <i>Bioinformatics</i> , 2015, 31, 2007-2016.	1.8	127
11951	Pantograph: A template-based method for genome-scale metabolic model reconstruction. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550006.	0.3	29
11952	Incorporating computational resources in a cancer research program. <i>Human Genetics</i> , 2015, 134, 467-478.	1.8	2
11953	Predicting Protein Function Using Multiple Kernels. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 219-233.	1.9	27
11954	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
11955	In silico mining, characterization and cross-species transferability of EST-SSR markers for European hazelnut (<i>Corylus avellana</i> L.). <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	29
11956	Yeast Mitochondrial Protein-Protein Interactions Reveal Diverse Complexes and Disease-Relevant Functional Relationships. <i>Journal of Proteome Research</i> , 2015, 14, 1220-1237.	1.8	18
11957	The penalized biclustering model and related algorithms. <i>Journal of Applied Statistics</i> , 2015, 42, 1255-1277.	0.6	9
11958	Natural Genetic Variation for Acclimation of Photosynthetic Light Use Efficiency to Growth Irradiance in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2015, 167, 1412-1429.	2.3	78
11959	A multiobjective memetic algorithm for PPI network alignment. <i>Bioinformatics</i> , 2015, 31, 1988-1998.	1.8	50
11960	Crucial microRNAs and genes of human primary breast cancer explored by microRNA-mRNA integrated analysis. <i>Tumor Biology</i> , 2015, 36, 5571-5579.	0.8	27
11961	FungiFun2: a comprehensive online resource for systematic analysis of gene lists from fungal species. <i>Bioinformatics</i> , 2015, 31, 445-446.	1.8	228
11962	Negative feedback buffers effects of regulatory variants. <i>Molecular Systems Biology</i> , 2015, 11, 785.	3.2	33
11963	Identification of Key Genes Associated with Colorectal Cancer Based on the Transcriptional Network. <i>Pathology and Oncology Research</i> , 2015, 21, 719-725.	0.9	5
11964	Transcriptome profiling of the hypothalamus during prelaying and laying periods in Sichuan white geese (<i>Anser cygnoides</i>). <i>Animal Science Journal</i> , 2015, 86, 800-805.	0.6	20
11965	Genome-wide survey of the seagrass <i>Zostera muelleri</i> suggests modification of the ethylene signalling network. <i>Journal of Experimental Botany</i> , 2015, 66, 1489-1498.	2.4	46
11966	Uncovering disease-disease relationships through the incomplete interactome. <i>Science</i> , 2015, 347, 1257601.	6.0	1,219
11967	Analysis of Parkinson's disease pathophysiology using an integrated genomics-bioinformatics approach. <i>Pathophysiology</i> , 2015, 22, 15-29.	1.0	19

#	ARTICLE	IF	CITATIONS
11968	Kuwaiti population subgroup of nomadic Bedouin ancestryâ€”Whole genome sequence and analysis. <i>Genomics Data</i> , 2015, 3, 116-127.	1.3	26
11969	Towards the taxonomic categorization and recognition of nanoparticle shapes. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2015, 11, 457-465.	1.7	11
11970	Visualization of proteomics data using R and Bioconductor. <i>Proteomics</i> , 2015, 15, 1375-1389.	1.3	47
11971	Walking on multiple disease-gene networks to prioritize candidate genes. <i>Journal of Molecular Cell Biology</i> , 2015, 7, 214-230.	1.5	65
11972	Proteomic profile of dormancy within <i>Staphylococcus epidermidis</i> biofilms using iTRAQ and label-free strategies. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 2751-2762.	1.7	20
11973	Evolution of novel wood decay mechanisms in Agaricales revealed by the genome sequences of <i>Fistulina hepatica</i> and <i>Cylindrobasidium torrendii</i> . <i>Fungal Genetics and Biology</i> , 2015, 76, 78-92.	0.9	141
11974	Cross-talk between ER and HER2 regulates c-MYC-mediated glutamine metabolism in aromatase inhibitor resistant breast cancer cells. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2015, 149, 118-127.	1.2	71
11975	Mitofusin 2 is required to maintain mitochondrial coenzyme Q levels. <i>Journal of Cell Biology</i> , 2015, 208, 429-442.	2.3	180
11976	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653
11977	Proteome profile of the endomembrane of developing coleoptiles from switchgrass (<i>Panicum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.3	6
11978	Pancreatic Beta Cells Are Highly Susceptible to Oxidative and ER Stresses during the Development of Diabetes. <i>Journal of Proteome Research</i> , 2015, 14, 688-699.	1.8	30
11979	Insights on the Evolution of Mycoparasitism from the Genome of <i>Clonostachys rosea</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 465-480.	1.1	150
11980	Comparative computational analysis of pluripotency in human and mouse stem cells. <i>Scientific Reports</i> , 2015, 5, 7927.	1.6	16
11981	Transâ€”Proteomic Pipeline, a standardized data processing pipeline for largeâ€”scale reproducible proteomics informatics. <i>Proteomics - Clinical Applications</i> , 2015, 9, 745-754.	0.8	319
11982	Analysis of differential gene expression under low-temperature stress in Nile tilapia (<i>Oreochromis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	44
11983	Characterization of microRNA profile in human cumulus granulosa cells: Identification of microRNAs that regulate Notch signaling and are associated with PCOS. <i>Molecular and Cellular Endocrinology</i> , 2015, 404, 26-36.	1.6	122
11984	Physiological and cell morphology adaptation of <i>Bacillus subtilis</i> at nearâ€”zero specific growth rates: a transcriptome analysis. <i>Environmental Microbiology</i> , 2015, 17, 346-363.	1.8	26
11985	MAGIC: An Automated N-Linked Glycoprotein Identification Tool Using a Y1-Ion Pattern Matching Algorithm and <i>In Silico</i> MS ² Approach. <i>Analytical Chemistry</i> , 2015, 87, 2466-2473.	3.2	67

#	ARTICLE	IF	CITATIONS
11986	Autophagy Regulatory Network " A systems-level bioinformatics resource for studying the mechanism and regulation of autophagy. <i>Autophagy</i> , 2015, 11, 155-165.	4.3	89
11987	ASSIGN: context-specific genomic profiling of multiple heterogeneous biological pathways. <i>Bioinformatics</i> , 2015, 31, 1745-1753.	1.8	28
11988	Functional and Phylogenetic Characterization of Proteins Detected in Various Nematode Intestinal Compartments*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 812-827.	2.5	23
11989	Multiset Statistics for Gene Set Analysis. <i>Annual Review of Statistics and Its Application</i> , 2015, 2, 95-111.	4.1	10
11990	Upregulation of Gingival Tissue miR-200b in Obese Periodontitis Subjects. <i>Journal of Dental Research</i> , 2015, 94, 59S-69S.	2.5	37
11991	Bias in microRNA functional enrichment analysis. <i>Bioinformatics</i> , 2015, 31, 1592-1598.	1.8	100
11992	The transcriptomic profile of ovarian cancer grading. <i>Cancer Medicine</i> , 2015, 4, 56-64.	1.3	2
11993	Degradation science: Mesoscopic evolution and temporal analytics of photovoltaic energy materials. <i>Current Opinion in Solid State and Materials Science</i> , 2015, 19, 212-226.	5.6	51
11994	Network analysis of gene expression in peripheral blood identifies mTOR and NF- κ B pathways involved in antipsychotic-induced extrapyramidal symptoms. <i>Pharmacogenomics Journal</i> , 2015, 15, 452-460.	0.9	18
11995	Fumarate induces redox-dependent senescence by modifying glutathione metabolism. <i>Nature Communications</i> , 2015, 6, 6001.	5.8	208
11996	An Extensive Evaluation of Decision Tree-Based Hierarchical Multilabel Classification Methods and Performance Measures. <i>Computational Intelligence</i> , 2015, 31, 1-46.	2.1	21
11997	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015, 43, D447-D452.	6.5	9,029
11998	TRPC3 channels critically regulate hippocampal excitability and contextual fear memory. <i>Behavioural Brain Research</i> , 2015, 281, 69-77.	1.2	51
12000	Chromatin decompaction by the nucleosomal binding protein HMG5 impairs nuclear sturdiness. <i>Nature Communications</i> , 2015, 6, 6138.	5.8	115
12001	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
12002	Early markers of Fabry disease revealed by proteomics. <i>Molecular BioSystems</i> , 2015, 11, 1543-1551.	2.9	51
12003	Effects of copy number variable regions on local gene expression in white blood cells of Mexican Americans. <i>European Journal of Human Genetics</i> , 2015, 23, 1229-1235.	1.4	7
12004	Global Network Alignment in the Context of Aging. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 40-52.	1.9	46

#	ARTICLE	IF	CITATIONS
12005	limma powers differential expression analyses for RNA-sequencing and microarray studies. <i>Nucleic Acids Research</i> , 2015, 43, e47-e47.	6.5	26,032
12006	ACPP: A Web Server for Prediction and Design of Anti-cancer Peptides. <i>International Journal of Peptide Research and Therapeutics</i> , 2015, 21, 99-106.	0.9	76
12007	High Fidelity Between Saliva Proteomics and the Biologic State of Salivary Glands Defines Biomarker Signatures for Primary Sjögren's Syndrome. <i>Arthritis and Rheumatology</i> , 2015, 67, 1084-1095.	2.9	87
12008	Genome-wide association study of antibody level response to NDV and IBV in Jinghai yellow chicken based on SLAF-seq technology. <i>Journal of Applied Genetics</i> , 2015, 56, 365-373.	1.0	22
12009	A copy number variation map of the human genome. <i>Nature Reviews Genetics</i> , 2015, 16, 172-183.	7.7	707
12010	Integration of a prognostic gene module with a drug sensitivity module to identify drugs that could be repurposed for breast cancer therapy. <i>Computers in Biology and Medicine</i> , 2015, 61, 163-171.	3.9	4
12011	Differential transcriptional response to antibiotics by <i>Pseudomonas putida</i> ... <i>DOT</i> ... <i>T1E</i> . <i>Environmental Microbiology</i> , 2015, 17, 3251-3262.	1.8	32
12012	The Origin of CDR H3 Structural Diversity. <i>Structure</i> , 2015, 23, 302-311.	1.6	78
12013	GlycoMine: a machine learning-based approach for predicting N-, C- and O-linked glycosylation in the human proteome. <i>Bioinformatics</i> , 2015, 31, 1411-1419.	1.8	167
12014	The draft genome of Tibetan hulless barley reveals adaptive patterns to the high stressful Tibetan Plateau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1095-1100.	3.3	147
12015	Identification of Low Temperature Stress Regulated Transcript Sequences and Gene Families in Italian Cypress. <i>Molecular Biotechnology</i> , 2015, 57, 407-418.	1.3	5
12016	The Unipept metaproteomics analysis pipeline. <i>Proteomics</i> , 2015, 15, 1437-1442.	1.3	114
12017	RNA Bioinformatics. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	3
12018	A disease module in the interactome explains disease heterogeneity, drug response and captures novel pathways and genes in asthma. <i>Human Molecular Genetics</i> , 2015, 24, 3005-3020.	1.4	162
12019	Unravelling adverse reactions to NSAIDs using systems biology. <i>Trends in Pharmacological Sciences</i> , 2015, 36, 172-180.	4.0	24
12020	Coupling enrichment methods with proteomics for understanding and treating disease. <i>Proteomics - Clinical Applications</i> , 2015, 9, 33-47.	0.8	18
12021	Transcriptome characterization and SSR discovery in large-scale loach <i>Paramisgurnus dabryanus</i> (Cobitidae, Cypriniformes). <i>Gene</i> , 2015, 557, 201-208.	1.0	36
12022	Integrated genome sequence and linkage map of physic nut (<i>Jatropha curcas</i> L.), a biodiesel plant. <i>Plant Journal</i> , 2015, 81, 810-821.	2.8	149

#	ARTICLE	IF	CITATIONS
12023	Genome-scale quantitative characterization of bacterial protein localization dynamics throughout the cell cycle. <i>Molecular Microbiology</i> , 2015, 95, 64-79.	1.2	53
12024	The clinicopathological and gene expression patterns associated with ulceration of primary melanoma. <i>Pigment Cell and Melanoma Research</i> , 2015, 28, 94-104.	1.5	26
12025	A unigene set for European beech (<i>Fagus sylvatica</i> L.) and its use to decipher the molecular mechanisms involved in dormancy regulation. <i>Molecular Ecology Resources</i> , 2015, 15, 1192-1204.	2.2	35
12026	Transcriptional analysis of adaptation to high glucose concentrations in <i>Zymomonas mobilis</i> . <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 2009-2022.	1.7	23
12027	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	6.5	1,205
12028	Gremlin 1 Identifies a Skeletal Stem Cell with Bone, Cartilage, and Reticular Stromal Potential. <i>Cell</i> , 2015, 160, 269-284.	13.5	535
12029	Event-based text mining for biology and functional genomics. <i>Briefings in Functional Genomics</i> , 2015, 14, 213-230.	1.3	58
12030	Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , 2015, 6, 5890.	5.8	706
12031	Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell-type-specific expression. <i>Genome Research</i> , 2015, 25, 544-557.	2.4	74
12032	Genome sequences as the type material for taxonomic descriptions of prokaryotes. <i>Systematic and Applied Microbiology</i> , 2015, 38, 217-222.	1.2	107
12033	p54 ^{nrb} /NONO Regulates Cyclic AMP-Dependent Glucocorticoid Production by Modulating Phosphodiesterase mRNA Splicing and Degradation. <i>Molecular and Cellular Biology</i> , 2015, 35, 1223-1237.	1.1	35
12034	Clinical Proteomics. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	1
12035	FUN-L: gene prioritization for RNAi screens: Fig. 1.. <i>Bioinformatics</i> , 2015, 31, 2052-2053.	1.8	9
12036	Computational Prediction of Riboswitches. <i>Methods in Enzymology</i> , 2015, 553, 287-312.	0.4	7
12037	Graphical algorithm for integration of genetic and biological data: proof of principle using psoriasis as a model. <i>Bioinformatics</i> , 2015, 31, 1243-1249.	1.8	10
12038	Defining the transcriptomic landscape of <i>Candida glabrata</i> by RNA-Seq. <i>Nucleic Acids Research</i> , 2015, 43, 1392-1406.	6.5	74
12039	Methylomic trajectories across human fetal brain development. <i>Genome Research</i> , 2015, 25, 338-352.	2.4	250
12040	Guidance for RNA-seq co-expression network construction and analysis: safety in numbers. <i>Bioinformatics</i> , 2015, 31, 2123-2130.	1.8	203

#	ARTICLE	IF	CITATIONS
12041	Sparse expression bases in cancer reveal tumor drivers. <i>Nucleic Acids Research</i> , 2015, 43, 1332-1344.	6.5	27
12042	Neuronal CRTG-1 Governs Systemic Mitochondrial Metabolism and Lifespan via a Catecholamine Signal. <i>Cell</i> , 2015, 160, 842-855.	13.5	175
12043	Agent-Based Modeling and Translational Systems Biology. , 2015, , 111-135.		1
12044	Identifying microRNA-mRNA regulatory network in gemcitabine-resistant cells derived from human pancreatic cancer cells. <i>Tumor Biology</i> , 2015, 36, 4525-4534.	0.8	29
12045	<i>APOBEC3B</i> expression in breast cancer reflects cellular proliferation, while a deletion polymorphism is associated with immune activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2841-2846.	3.3	118
12046	Data Imputation in Epistatic MAPs by Network-Guided Matrix Completion. <i>Journal of Computational Biology</i> , 2015, 22, 595-608.	0.8	11
12047	Transcriptional profiling defines dynamics of parasite tissue sequestration during malaria infection. <i>Genome Medicine</i> , 2015, 7, 19.	3.6	77
12048	Mycofumigation by the Volatile Organic Compound-Producing Fungus <i>Muscodor albus</i> Induces Bacterial Cell Death through DNA Damage. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1147-1156.	1.4	53
12049	Isolation, characterization and functional annotation of the salt tolerance genes through screening the high-quality cDNA library of the halophytic green alga <i>Dunaliella salina</i> (Chlorophyta). <i>Annals of Microbiology</i> , 2015, 65, 1293-1302.	1.1	9
12050	A GS-CORE algorithm for performing a reduction test on multiple gene sets and their core genes. <i>Computational Statistics</i> , 2015, 30, 29-41.	0.8	0
12051	Identification of Differently Expressed Genes with Specific SNP Loci for Breast Cancer by the Integration of SNP and Gene Expression Profiling Analyses. <i>Pathology and Oncology Research</i> , 2015, 21, 469-475.	0.9	7
12052	Pathways associated with lignin biosynthesis in lignomaniac jute fibres. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1523-1542.	1.0	39
12053	Berberine ameliorates nonalcoholic fatty liver disease by a global modulation of hepatic mRNA and lncRNA expression profiles. <i>Journal of Translational Medicine</i> , 2015, 13, 24.	1.8	92
12054	Candidate gene markers associated with cold tolerance in vegetative stage of rice (<i>Oryza sativa</i> L.). <i>Euphytica</i> , 2015, 203, 385-398.	0.6	10
12055	A systems genetics study of swine illustrates mechanisms underlying human phenotypic traits. <i>BMC Genomics</i> , 2015, 16, 88.	1.2	28
12056	RNA-Seq-based toxicogenomic assessment of fresh frozen and formalin-fixed tissues yields similar mechanistic insights. <i>Journal of Applied Toxicology</i> , 2015, 35, 766-780.	1.4	22
12057	The role of transcriptome resilience in resistance of corals to bleaching. <i>Molecular Ecology</i> , 2015, 24, 1467-1484.	2.0	137
12058	A Pilot Proteomic Analysis of Salivary Biomarkers in Autism Spectrum Disorder. <i>Autism Research</i> , 2015, 8, 338-350.	2.1	73

#	ARTICLE	IF	CITATIONS
12059	The shortest path is not the one you know: application of biological network resources in precision oncology research. <i>Mutagenesis</i> , 2015, 30, 191-204.	1.0	37
12060	The human Drugâ€“Diseaseâ€“Gene Network. <i>Information Sciences</i> , 2015, 306, 70-80.	4.0	21
12061	Identification of Target Genes Regulated by KSHV miRNAs in KSHV-Infected Lymphoma Cells. <i>Pathology and Oncology Research</i> , 2015, 21, 875-880.	0.9	10
12062	Annocript: a flexible pipeline for the annotation of transcriptomes able to identify putative long noncoding RNAs. <i>Bioinformatics</i> , 2015, 31, 2199-2201.	1.8	94
12063	A model to investigate SNPsâ€™ interaction in GWAS studies. <i>Journal of Neural Transmission</i> , 2015, 122, 145-153.	1.4	3
12064	Predicting protein complexes from weighted proteinâ€“protein interaction graphs with a novel unsupervised methodology: Evolutionary enhanced Markov clustering. <i>Artificial Intelligence in Medicine</i> , 2015, 63, 181-189.	3.8	26
12065	Therapeutic opportunities within the DNA damage response. <i>Nature Reviews Cancer</i> , 2015, 15, 166-180.	12.8	442
12066	Identification of copy number variations in Qinchuan cattle using BovineHD Genotyping Beadchip array. <i>Molecular Genetics and Genomics</i> , 2015, 290, 319-327.	1.0	48
12067	Temporal endogenous gene expression profiles in response to polymer-mediated transfection and profile comparison to lipid-mediated transfection. <i>Journal of Gene Medicine</i> , 2015, 17, 33-53.	1.4	7
12068	Summary of the BioLINK SIG 2013 meeting at ISMB/ECCB 2013. <i>Bioinformatics</i> , 2015, 31, 297-298.	1.8	1
12069	Untangling the origin of viruses and their impact on cellular evolution. <i>Annals of the New York Academy of Sciences</i> , 2015, 1341, 61-74.	1.8	30
12070	Identification of important interacting proteins (IIPs) in <i>Plasmodium falciparum</i> using large-scale interaction network analysis and in-silico knock-out studies. <i>Malaria Journal</i> , 2015, 14, 70.	0.8	29
12071	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	3.8	687
12072	Genome analysis of <i>Flaviramulus ichthyoenteri</i> Th78T in the family Flavobacteriaceae: insights into its quorum quenching property and potential roles in fish intestine. <i>BMC Genomics</i> , 2015, 16, 38.	1.2	22
12073	Analytical workflow profiling gene expression in murine macrophages. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550010.	0.3	8
12074	Whole-genome sequence of the Tibetan frog <i>Nanorana parkeri</i> and the comparative evolution of tetrapod genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1257-62.	3.3	159
12075	Beyond protein expression, MOPED goes multi-omics. <i>Nucleic Acids Research</i> , 2015, 43, D1145-D1151.	6.5	17
12076	Mining Host-Pathogen Protein Interactions to Characterize <i>Burkholderia mallei</i> Infectivity Mechanisms. <i>PLoS Computational Biology</i> , 2015, 11, e1004088.	1.5	34

#	ARTICLE	IF	CITATIONS
12077	Mapping the global mRNA transcriptome during development of the murine first molar. <i>Frontiers in Genetics</i> , 2015, 6, 47.	1.1	7
12078	Summarizing and visualizing structural changes during the evolution of biomedical ontologies using a Diff Abstraction Network. <i>Journal of Biomedical Informatics</i> , 2015, 56, 127-144.	2.5	14
12079	A Disease Module Detection (DIAMOND) Algorithm Derived from a Systematic Analysis of Connectivity Patterns of Disease Proteins in the Human Interactome. <i>PLoS Computational Biology</i> , 2015, 11, e1004120.	1.5	310
12080	Techniques for transferring host-pathogen protein interactions knowledge to new tasks. <i>Frontiers in Microbiology</i> , 2015, 6, 36.	1.5	22
12081	The Zinc-Finger Antiviral Protein ZAP Inhibits LINE and Alu Retrotransposition. <i>PLoS Genetics</i> , 2015, 11, e1005121.	1.5	119
12082	Incidence and physiological relevance of protein thiol switches. <i>Biological Chemistry</i> , 2015, 396, 389-399.	1.2	48
12083	Regulation of flavonol content and composition in (Syrah—Pinot Noir) mature grapes: integration of transcriptional profiling and metabolic quantitative trait locus analyses. <i>Journal of Experimental Botany</i> , 2015, 66, 4441-4453.	2.4	58
12084	The Novel Ribonucleotide Reductase Inhibitor COH29 Inhibits DNA Repair In Vitro. <i>Molecular Pharmacology</i> , 2015, 87, 996-1005.	1.0	20
12085	Describing the Breakbone Fever: IDODEN, an Ontology for Dengue Fever. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003479.	1.3	13
12086	Classification by integrating plant stress response gene expression data with biological knowledge. <i>Mathematical Biosciences</i> , 2015, 266, 65-72.	0.9	8
12088	Tracking global gene expression responses in T cell differentiation. <i>Gene</i> , 2015, 569, 259-266.	1.0	20
12089	High-quality draft genome sequences of five anaerobic oral bacteria and description of <i>Peptoanaerobacter stomatis</i> gen. nov., sp. nov., a new member of the family Peptostreptococcaceae. <i>Standards in Genomic Sciences</i> , 2015, 10, 37.	1.5	21
12090	C-It-Loci: a knowledge database for tissue-enriched loci. <i>Bioinformatics</i> , 2015, 31, 3537-3543.	1.8	30
12091	Evolutionary Divergence of Gene and Protein Expression in the Brains of Humans and Chimpanzees. <i>Genome Biology and Evolution</i> , 2015, 7, 2276-2288.	1.1	41
12092	Chronic ethanol consumption induces mitochondrial protein acetylation and oxidative stress in the kidney. <i>Redox Biology</i> , 2015, 6, 33-40.	3.9	49
12093	Genome-Wide Profiling of TRACK Kidneys Shows Similarity to the Human ccRCC Transcriptome. <i>Molecular Cancer Research</i> , 2015, 13, 870-878.	1.5	19
12094	RNA-seq for gene identification and transcript profiling in relation to root growth of bermudagrass (<i>Cynodon dactylon</i>) under salinity stress. <i>BMC Genomics</i> , 2015, 16, 575.	1.2	67
12095	Linear Discriminant Analysis Identifies Mitochondrially Localized Proteins in <i>Neurospora crassa</i> . <i>Journal of Proteome Research</i> , 2015, 14, 3900-3911.	1.8	6

#	ARTICLE	IF	CITATIONS
12096	Evidence of perturbations of the cytokine network in preterm labor. <i>American Journal of Obstetrics and Gynecology</i> , 2015, 213, 836.e1-836.e18.	0.7	141
12097	Gene network inference by fusing data from diverse distributions. <i>Bioinformatics</i> , 2015, 31, i230-i239.	1.8	34
12098	Pathologic Mechanical Stress and Endotoxin Exposure Increases Lung Endothelial Microparticle Shedding. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2015, 52, 193-204.	1.4	68
12099	Kiwi genome provides insights into evolution of a nocturnal lifestyle. <i>Genome Biology</i> , 2015, 16, 147.	3.8	68
12100	Phosphoproteomic analysis of kinase-deficient mice reveals multiple TAK1 targets in osteoclast differentiation. <i>Biochemical and Biophysical Research Communications</i> , 2015, 463, 1284-1290.	1.0	12
12101	Analysis of copy number variations by SNP50 BeadChip array in Chinese sheep. <i>Genomics</i> , 2015, 106, 295-300.	1.3	18
12102	Acute myocardial infarction activates distinct inflammation and proliferation pathways in circulating monocytes, prior to recruitment, and identified through conserved transcriptional responses in mice and humans. <i>European Heart Journal</i> , 2015, 36, 1923-1934.	1.0	88
12103	Application of comparative biology in GO functional annotation: the mouse model. <i>Mammalian Genome</i> , 2015, 26, 574-583.	1.0	11
12104	Developmental exposure to ethanol increases the neuronal vulnerability to oxygen and glucose deprivation in cerebellar granule cell cultures. <i>Brain Research</i> , 2015, 1614, 1-13.	1.1	14
12105	Proteomic profiling of hyperplasia/atypia and adenoma-induced by NNK in mouse lung identified multiple proteins as potential biomarkers for early detection. <i>EuPA Open Proteomics</i> , 2015, 9, 23-33.	2.5	1
12106	Towards a PBMC "virogram assay" for precision medicine: Concordance between ex vivo and in vivo viral infection transcriptomes. <i>Journal of Biomedical Informatics</i> , 2015, 55, 94-103.	2.5	18
12107	A new test for part of high dimensional regression coefficients. <i>Journal of Multivariate Analysis</i> , 2015, 137, 187-203.	0.5	6
12108	Skin mucus proteome of gilthead sea bream: A non-invasive method to screen for welfare indicators. <i>Fish and Shellfish Immunology</i> , 2015, 46, 426-435.	1.6	74
12109	ClustVis: a web tool for visualizing clustering of multivariate data using Principal Component Analysis and heatmap. <i>Nucleic Acids Research</i> , 2015, 43, W566-W570.	6.5	2,762
12111	A rule-based expert system for inferring functional annotation. <i>Applied Soft Computing Journal</i> , 2015, 35, 373-385.	4.1	5
12112	A first insight into the spleen transcriptome of the nototheniid fish <i>Lepidonotothen nudifrons</i> : Resource description and functional overview. <i>Marine Genomics</i> , 2015, 24, 237-239.	0.4	14
12113	Whole exome sequencing in extended families with autism spectrum disorder implicates four candidate genes. <i>Human Genetics</i> , 2015, 134, 1055-1068.	1.8	49
12114	Signaling network of lipids as a comprehensive scaffold for omics data integration in sputum of COPD patients. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2015, 1851, 1383-1393.	1.2	27

#	ARTICLE	IF	CITATIONS
12115	Identification of neurodegenerative factors using translatoeacuteregulatory network analysis. <i>Nature Neuroscience</i> , 2015, 18, 1325-1333.	7.1	113
12116	Identification of reproducible drug-resistance-related dysregulated genes in small-scale cancer cell line experiments. <i>Scientific Reports</i> , 2015, 5, 11895.	1.6	11
12117	Extracellular protein analysis of activated sludge and their functions in wastewater treatment plant by shotgun proteomics. <i>Scientific Reports</i> , 2015, 5, 12041.	1.6	43
12118	<i>Functional Genomics.</i> , 2015, , 223-245.		0
12119	Protein function prediction using guilty by association from interaction networks. <i>Amino Acids</i> , 2015, 47, 2583-2592.	1.2	40
12120	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
12121	Functional Networks of Highest-Connected Splice Isoforms: From The Chromosome 17 Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3484-3491.	1.8	28
12122	GreedyPlus: An Algorithm for the Alignment of Interface Interaction Networks. <i>Scientific Reports</i> , 2015, 5, 12074.	1.6	0
12123	Impact of heuristics in clustering large biological networks. <i>Computational Biology and Chemistry</i> , 2015, 59, 28-36.	1.1	1
12124	Proteomic Approach to Identify Nuclear Proteins in Wheat Grain. <i>Journal of Proteome Research</i> , 2015, 14, 4432-4439.	1.8	16
12125	Best behaviour? Ontologies and the formal description of animal behaviour. <i>Mammalian Genome</i> , 2015, 26, 540-547.	1.0	4
12126	Ontology-Mediated Query Answering with Data-Tractable Description Logics. <i>Lecture Notes in Computer Science</i> , 2015, , 218-307.	1.0	48
12127	Automated gene function prediction through gene multifunctionality in biological networks. <i>Neurocomputing</i> , 2015, 162, 48-56.	3.5	14
12128	Genes Caught In Flagranti: Integrating Renal Transcriptional Profiles With Genotypes and Phenotypes. <i>Seminars in Nephrology</i> , 2015, 35, 237-244.	0.6	1
12129	Cellular Proteome Dynamics during Differentiation of Human Primary Myoblasts. <i>Journal of Proteome Research</i> , 2015, 14, 3348-3361.	1.8	30
12130	Anxiety as a neurodevelopmental disorder in a neuronal subpopulation: Evidence from gene expression data. <i>Psychiatry Research</i> , 2015, 228, 729-740.	1.7	15
12131	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. <i>PLoS Computational Biology</i> , 2015, 11, e1004220.	1.5	158
12132	Development of an Ontology for Periodontitis. <i>Journal of Biomedical Semantics</i> , 2015, 6, 30.	0.9	6

#	ARTICLE	IF	CITATIONS
12133	Distinct differences in global gene expression profiles in non-implanted blastocysts and blastocysts resulting in live birth. <i>Gene</i> , 2015, 571, 212-220.	1.0	20
12134	Combining metagenomics, metatranscriptomics and viromics to explore novel microbial interactions: towards a systems-level understanding of human microbiome. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 390-401.	1.9	182
12135	Olfactory drug effects approached from human-derived data. <i>Drug Discovery Today</i> , 2015, 20, 1398-1406.	3.2	28
12136	Systems biology and gene networks in neurodevelopmental and neurodegenerative disorders. <i>Nature Reviews Genetics</i> , 2015, 16, 441-458.	7.7	378
12137	Transcriptome analysis of the biofilm formed by methicillin-susceptible <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2015, 5, 11997.	1.6	75
12138	Draft genome of <i>Bacillus</i> sp. A053 isolated from the Arctic seawater with antimicrobial activity. <i>Marine Genomics</i> , 2015, 22, 19-21.	0.4	2
12139	Causal Modeling of Cancer-Stromal Communication Identifies PAPP A as a Novel Stroma-Secreted Factor Activating NF- κ B Signaling in Hepatocellular Carcinoma. <i>PLoS Computational Biology</i> , 2015, 11, e1004293.	1.5	22
12140	Evolutionary Constraint and Disease Associations of Post-Translational Modification Sites in Human Genomes. <i>PLoS Genetics</i> , 2015, 11, e1004919.	1.5	69
12141	MetaRank: Ranking Microbial Taxonomic Units or Functional Groups for Comparative Analysis of Metagenomes. , 2015, , 442-447.		0
12142	The pathway not taken: understanding omics data in the perinatal context. <i>American Journal of Obstetrics and Gynecology</i> , 2015, 213, 59.e1-59.e172.	0.7	16
12143	TRIB3 enhances cell viability during glucose deprivation in HEK293-derived cells by upregulating IGF2R, a novel nutrient deficiency survival factor. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2015, 1853, 2492-2505.	1.9	17
12144	Endothelial transcriptomic changes induced by oxidized low density lipoprotein disclose an up-regulation of Jak-Stat pathway. <i>Vascular Pharmacology</i> , 2015, 73, 104-114.	1.0	8
12145	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. <i>PLoS Genetics</i> , 2015, 11, e1004898.	1.5	82
12146	Global Genome and Transcriptome Analyses of <i>Magnaporthe oryzae</i> Epidemic Isolate 98-06 Uncover Novel Effectors and Pathogenicity-Related Genes, Revealing Gene Gain and Loss Dynamics in Genome Evolution. <i>PLoS Pathogens</i> , 2015, 11, e1004801.	2.1	148
12147	A global network-based protocol for functional inference of hypothetical proteins in <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Microbiological Methods</i> , 2015, 116, 44-52.	0.7	5
12148	Differentially expressed protein-coding genes and long noncoding RNA in early-stage lung cancer. <i>Tumor Biology</i> , 2015, 36, 9969-9978.	0.8	26
12149	The Janus kinase inhibitor JTE-052 improves skin barrier function through suppressing signal transducer and activator of transcription 3 signaling. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 667-677.e7.	1.5	195
12150	Genome-Wide Localization Study of Yeast Pex11 Identifies Peroxisome-Mitochondria Interactions through the ERMES Complex. <i>Journal of Molecular Biology</i> , 2015, 427, 2072-2087.	2.0	131

#	ARTICLE	IF	CITATIONS
12151	INGA: protein function prediction combining interaction networks, domain assignments and sequence similarity. <i>Nucleic Acids Research</i> , 2015, 43, W134-W140.	6.5	73
12152	Next generation sequencing of sex-specific genes in the livers of obese ZSF1 rats. <i>Genomics</i> , 2015, 106, 204-213.	1.3	15
12153	Rice Xa21 primed genes and pathways that are critical for combating bacterial blight infection. <i>Scientific Reports</i> , 2015, 5, 12165.	1.6	36
12154	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015, 6, 7866.	5.8	676
12155	Towards understanding the molecular basis of cockroach tergal gland morphogenesis. A transcriptomic approach. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 63, 104-112.	1.2	8
12156	Transcriptomic insight into the immune defenses in the ghost moth, <i>Hepialus xiaojinensis</i> , during an <i>Ophiocordyceps sinensis</i> fungal infection. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 64, 1-15.	1.2	44
12157	A genome-wide screening and SNPs-to-genes approach to identify novel genetic risk factors associated with frontotemporal dementia. <i>Neurobiology of Aging</i> , 2015, 36, 2904.e13-2904.e26.	1.5	48
12158	Elevated levels of adaption in <i>Helicobacter pylori</i> genomes from Japan; a link to higher incidences of gastric cancer?. <i>Evolution, Medicine and Public Health</i> , 2015, 2015, 88-105.	1.1	6
12159	Prioritization of candidate disease genes by combining topological similarity and semantic similarity. <i>Journal of Biomedical Informatics</i> , 2015, 57, 1-5.	2.5	16
12160	Advances in natural language processing. <i>Science</i> , 2015, 349, 261-266.	6.0	926
12161	Ligand-Target Prediction by Structural Network Biology Using nAnnoLyze. <i>PLoS Computational Biology</i> , 2015, 11, e1004157.	1.5	16
12162	Biomarker-based classification of bacterial and fungal whole-blood infections in a genome-wide expression study. <i>Frontiers in Microbiology</i> , 2015, 6, 171.	1.5	30
12163	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
12164	A Two-Stage Geometric Method for Pruning Unreliable Links in Protein-Protein Networks. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 528-534.	2.2	62
12165	Next-generation transcriptome analysis in transgenic birch overexpressing and suppressing APETALA1 sheds lights in reproduction development and diterpenoid biosynthesis. <i>Plant Cell Reports</i> , 2015, 34, 1663-1680.	2.8	6
12166	Principles for the organization of gene-sets. <i>Computational Biology and Chemistry</i> , 2015, 59, 139-149.	1.1	10
12167	System-wide identification of wild-type SUMO-2 conjugation sites. <i>Nature Communications</i> , 2015, 6, 7289.	5.8	97
12168	Collation and analyses of DNA-binding protein domain families from sequence and structural databanks. <i>Molecular BioSystems</i> , 2015, 11, 1110-1118.	2.9	5

#	ARTICLE	IF	CITATIONS
12169	Characterization of the Tyrosine Kinase-Regulated Proteome in Breast Cancer by Combined use of RNA interference (RNAi) and Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC) Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2479-2492.	2.5	17
12170	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035.	1.5	107
12171	Autoantibody profile of patients infected with knowlesi malaria. <i>Clinica Chimica Acta</i> , 2015, 448, 33-38.	0.5	8
12172	Enabling Scientific Collaboration and Discovery Through the Use of Data Standardization. <i>IEEE Transactions on Plasma Science</i> , 2015, 43, 1190-1193.	0.6	3
12173	E2F8 promotes hepatic steatosis through FABP3 expression in diet-induced obesity in zebrafish. <i>Nutrition and Metabolism</i> , 2015, 12, 17.	1.3	36
12174	Exploiting ontology graph for predicting sparsely annotated gene function. <i>Bioinformatics</i> , 2015, 31, i357-i364.	1.8	97
12175	Proteomic analysis on zoxamide-induced sensitivity changes in <i>Phytophthora cactorum</i> . <i>Pesticide Biochemistry and Physiology</i> , 2015, 123, 9-18.	1.6	6
12176	Quantitative Proteomics of Human Fibroblasts with I1061T Mutation in Niemann-Pick C1 (NPC1) Protein Provides Insights into the Disease Pathogenesis*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1734-1749.	2.5	41
12177	The post-genomic era of biological network alignment. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2015, 2015, 3.	1.4	60
12178	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
12179	Gene Networks Underlying Convergent and Pleiotropic Phenotypes in a Large and Systematically-Phenotyped Cohort with Heterogeneous Developmental Disorders. <i>PLoS Genetics</i> , 2015, 11, e1005012.	1.5	14
12180	Improving 3D Genome Reconstructions Using Orthologous and Functional Constraints. <i>PLoS Computational Biology</i> , 2015, 11, e1004298.	1.5	10
12181	An Integrated Approach to Reconstructing Genome-Scale Transcriptional Regulatory Networks. <i>PLoS Computational Biology</i> , 2015, 11, e1004103.	1.5	23
12182	Transcriptome profiling analysis of naked carp (<i>Gymnocypris przewalskii</i>) provides insights into the immune-related genes in highland fish. <i>Fish and Shellfish Immunology</i> , 2015, 46, 366-377.	1.6	36
12183	An LXR- NCOA5 gene regulatory complex directs inflammatory cross-talk-dependent repression of macrophage cholesterol efflux. <i>EMBO Journal</i> , 2015, 34, 1244-1258.	3.5	35
12184	Identification and Functional Analysis of Healing Regulators in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2015, 11, e1004965.	1.5	8
12185	OntoBio: A Biodiversity Domain Ontology for Amazonian Biological Collected Objects. , 2015, , .		7
12186	ComPPI: a cellular compartment-specific database for protein-protein interaction network analysis. <i>Nucleic Acids Research</i> , 2015, 43, D485-D493.	6.5	116

#	ARTICLE	IF	CITATIONS
12187	Incorporating g-gap dipeptide composition and position specific scoring matrix for identifying antioxidant proteins. , 2015, , .		6
12188	Tracking Temporal Community Strength in Dynamic Networks. IEEE Transactions on Knowledge and Data Engineering, 2015, 27, 3125-3137.	4.0	20
12189	A Computational Approach to Identifying Gene-microRNA Modules in Cancer. PLoS Computational Biology, 2015, 11, e1004042.	1.5	35
12190	Human primordial germ cell commitment <i>in vitro</i> associates with a unique PRDM14 expression profile. EMBO Journal, 2015, 34, 1009-1024.	3.5	122
12191	Label-free quantitative proteomic analysis reveals strong involvement of complement alternative and terminal pathways in human glomerular sclerotic lesions. Journal of Proteomics, 2015, 123, 89-100.	1.2	5
12192	Global Transcriptome Analysis Reveals Acclimation-Primed Processes Involved in the Acquisition of Desiccation Tolerance in <i>Boea hygrometrica</i> . Plant and Cell Physiology, 2015, 56, 1429-1441.	1.5	54
12193	Structural and Functional Diversity of Peptide Toxins from Tarantula <i>Haplopelma hainanum</i> (<i>Ornithoctonus hainana</i>) Venom Revealed by Transcriptomic, Peptidomic, and Patch Clamp Approaches. Journal of Biological Chemistry, 2015, 290, 14192-14207.	1.6	18
12194	The Genetic Basis of Peripheral Arterial Disease. Circulation Research, 2015, 116, 1551-1560.	2.0	68
12195	Microbial communities, extracellular proteomics and polysaccharides: A comparative investigation on biofilm and suspended sludge. Bioresource Technology, 2015, 190, 21-28.	4.8	76
12196	VR-BFDT: A variance reduction based binary fuzzy decision tree induction method for protein function prediction. Journal of Theoretical Biology, 2015, 377, 10-24.	0.8	2
12197	Emerging molecular networks common in ionizing radiation, immune and inflammatory responses by employing bioinformatics approaches. Cancer Letters, 2015, 368, 164-172.	3.2	60
12198	Identification and characterization of novel serum microRNAs in unstable angina pectoris and subclinical atherosclerotic patients. Experimental Cell Research, 2015, 333, 220-227.	1.2	4
12199	Transcriptome analysis reveals the potential mechanism of the albino skin development in pufferfish <i>Takifugu obscurus</i> . In Vitro Cellular and Developmental Biology - Animal, 2015, 51, 572-577.	0.7	2
12200	Establishment and characterization of models of chemotherapy resistance in colorectal cancer: Towards a predictive signature of chemoresistance. Molecular Oncology, 2015, 9, 1169-1185.	2.1	91
12201	Choose wisely: Network, ontology and annotation resources for the analysis of <i>Staphylococcus aureus</i> omics data. International Journal of Medical Microbiology, 2015, 305, 339-347.	1.5	3
12202	Cellular processes involved in human epidermal cells exposed to extremely low frequency electric fields. Cellular Signalling, 2015, 27, 889-898.	1.7	12
12203	Microarray gene expression analysis reveals major differences between <i>Toxocara canis</i> and <i>Toxocara cati</i> neurotoxocarosis and involvement of <i>T. canis</i> in lipid biosynthetic processes. International Journal for Parasitology, 2015, 45, 495-503.	1.3	19
12204	Long noncoding ribonucleic acid specific for distant metastasis of gastric cancer is associated with <i>TRIM16</i> expression and facilitates tumor cell invasion <i>in vitro</i> . Journal of Gastroenterology and Hepatology (Australia), 2015, 30, 1367-1375.	1.4	19

#	ARTICLE	IF	CITATIONS
12205	Mutation analysis in patients with total sperm immotility. <i>Journal of Assisted Reproduction and Genetics</i> , 2015, 32, 893-902.	1.2	36
12206	Genetic conflict reflected in tissue-specific maps of genomic imprinting in human and mouse. <i>Nature Genetics</i> , 2015, 47, 544-549.	9.4	221
12207	High-mobility group box 1 accelerates lipopolysaccharide-induced lung fibroblast proliferation in vitro: involvement of the NF- κ B signaling pathway. <i>Laboratory Investigation</i> , 2015, 95, 635-647.	1.7	34
12208	Concordant dysregulation of miR-5p and miR-3p arms of the same precursor microRNA may be a mechanism in inducing cell proliferation and tumorigenesis: a lung cancer study. <i>Rna</i> , 2015, 21, 1055-1065.	1.6	36
12209	Genome-wide Analysis of Body Proportion Classifies Height-Associated Variants by Mechanism of Action and Implicates Genes Important for Skeletal Development. <i>American Journal of Human Genetics</i> , 2015, 96, 695-708.	2.6	67
12210	De novo transcriptome assembly of <i>Ipomoea nil</i> using Illumina sequencing for gene discovery and SSR marker identification. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1873-1884.	1.0	21
12211	Predicting the Pro-Longevity or Anti-Longevity Effect of Model Organism Genes with New Hierarchical Feature Selection Methods. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 262-275.	1.9	34
12212	Sequencing of allotetraploid cotton (<i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.	9.4	1,560
12213	Biochemical functional predictions for protein structures of unknown or uncertain function. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 182-191.	1.9	77
12214	Constructing Conceptual Knowledge Artefacts. , 2015, , .		8
12215	Genome-wide identification and analysis of <i>Catharanthus roseus</i> RLK1-like kinases in rice. <i>Planta</i> , 2015, 241, 603-613.	1.6	55
12216	Comparative transcriptome analysis of the petal degeneration mutant pdm in Chinese cabbage (<i>Brassica campestris</i> ssp. <i>pekinensis</i>) using RNA-Seq. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1833-1847.	1.0	30
12217	Reduced expression of miRNA-1237-3p associated with poor survival of spinal chordoma patients. <i>European Spine Journal</i> , 2015, 24, 1738-1746.	1.0	49
12218	MassExodus: modeling evolving networks in harsh environments. <i>Data Mining and Knowledge Discovery</i> , 2015, 29, 1211-1232.	2.4	3
12220	I-GSEA4GWAS v2: a web server for functional analysis of SNPs in trait-associated pathways identified from genome-wide association study. <i>Protein and Cell</i> , 2015, 6, 221-224.	4.8	23
12221	Mass-spectrometry-based characterization of oxidations in proteins. <i>Free Radical Research</i> , 2015, 49, 477-493.	1.5	12
12222	Inhibition of Hedgehog signaling pathway impedes cancer cell proliferation by promotion of autophagy. <i>European Journal of Cell Biology</i> , 2015, 94, 223-233.	1.6	17
12223	The resurrection genome of <i>Boea hygrometrica</i> : A blueprint for survival of dehydration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5833-5837.	3.3	132

#	ARTICLE	IF	CITATIONS
12224	Uncovering the novel characteristics of Asian honey bee, <i>Apis cerana</i> , by whole genome sequencing. BMC Genomics, 2015, 16, 1.	1.2	1,445
12225	Integrating multiple networks for protein function prediction. BMC Systems Biology, 2015, 9, S3.	3.0	23
12226	Investigating the utility of clinical outcome-guided mutual information network in network-based Cox regression. BMC Systems Biology, 2015, 9, S8.	3.0	8
12227	Abiotic stress and genome dynamics: specific genes and transposable elements response to iron excess in rice. Rice, 2015, 8, 13.	1.7	87
12228	Fast and robust group-wise eQTL mapping using sparse graphical models. BMC Bioinformatics, 2015, 16, 2.	1.2	11
12229	Predicting protein functions using incomplete hierarchical labels. BMC Bioinformatics, 2015, 16, 1.	1.2	436
12230	MeSH ORA framework: R/Bioconductor packages to support MeSH over-representation analysis. BMC Bioinformatics, 2015, 16, 45.	1.2	40
12231	Aber-OWL: a framework for ontology-based data access in biology. BMC Bioinformatics, 2015, 16, 26.	1.2	68
12232	Measuring semantic similarities by combining gene ontology annotations and gene co-function networks. BMC Bioinformatics, 2015, 16, 44.	1.2	39
12233	BiNChE: A web tool and library for chemical enrichment analysis based on the ChEBI ontology. BMC Bioinformatics, 2015, 16, 56.	1.2	35
12234	Spectral gene set enrichment (SGSE). BMC Bioinformatics, 2015, 16, 70.	1.2	6
12235	DomSign: a top-down annotation pipeline to enlarge enzyme space in the protein universe. BMC Bioinformatics, 2015, 16, 96.	1.2	6
12236	A de novo transcriptome of the noble scallop, <i>Chlamys nobilis</i> , focusing on mining transcripts for carotenoid-based coloration. BMC Genomics, 2015, 16, 44.	1.2	54
12237	Characterization of tissue-specific differential DNA methylation suggests distinct modes of positive and negative gene expression regulation. BMC Genomics, 2015, 16, 49.	1.2	132
12238	Transcriptomic analysis of hepatic responses to testosterone deficiency in miniature pigs fed a high-cholesterol diet. BMC Genomics, 2015, 16, 59.	1.2	28
12239	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. BMC Genomics, 2015, 16, 112.	1.2	49
12240	Predicting response to multidrug regimens in cancer patients using cell line experiments and regularised regression models. BMC Cancer, 2015, 15, 235.	1.1	44
12241	Mimoza: web-based semantic zooming and navigation in metabolic networks. BMC Systems Biology, 2015, 9, 10.	3.0	5

#	ARTICLE	IF	CITATIONS
12242	Plasmodium knowlesi gene expression differs in ex vivo compared to in vitro blood-stage cultures. <i>Malaria Journal</i> , 2015, 14, 110.	0.8	31
12243	Deeper insight into chronic kidney disease-related atherosclerosis: comparative proteomic studies of blood plasma using 2DE and mass spectrometry. <i>Journal of Translational Medicine</i> , 2015, 13, 20.	1.8	25
12244	Chemokine-mediated inflammation in the degenerating retina is coordinated by MÄ¼ller cells, activated microglia, and retinal pigment epithelium. <i>Journal of Neuroinflammation</i> , 2015, 12, 8.	3.1	117
12245	An ontology approach to comparative phenomics in plants. <i>Plant Methods</i> , 2015, 11, 10.	1.9	53
12246	Analysis of long non-coding RNAs highlights tissue-specific expression patterns and epigenetic profiles in normal and psoriatic skin. <i>Genome Biology</i> , 2015, 16, 24.	3.8	204
12247	Expression of multiple horizontally acquired genes is a hallmark of both vertebrate and invertebrate genomes. <i>Genome Biology</i> , 2015, 16, 50.	3.8	226
12248	An atlas of mouse CD4+ T cell transcriptomes. <i>Biology Direct</i> , 2015, 10, 14.	1.9	82
12249	An epigenetic map of age-associated autosomal loci in northern European families at high risk for the metabolic syndrome. <i>Clinical Epigenetics</i> , 2015, 7, 12.	1.8	28
12250	Similarity-based search of model organism, disease and drug effect phenotypes. <i>Journal of Biomedical Semantics</i> , 2015, 6, 6.	0.9	8
12251	Completing the is-a structure in light-weight ontologies. <i>Journal of Biomedical Semantics</i> , 2015, 6, 12.	0.9	8
12252	eNanoMapper: harnessing ontologies to enable data integration for nanomaterial risk assessment. <i>Journal of Biomedical Semantics</i> , 2015, 6, 10.	0.9	63
12253	Evaluating a variety of text-mined features for automatic protein function prediction with GOstruct. <i>Journal of Biomedical Semantics</i> , 2015, 6, 9.	0.9	20
12254	Transcriptional response in normal mouse tissues after i.v. 211At administration - response related to absorbed dose, dose rate, and time. <i>EJNMMI Research</i> , 2015, 5, 1.	1.1	46
12255	The OMA orthology database in 2015: function predictions, better plant support, synteny view and other improvements. <i>Nucleic Acids Research</i> , 2015, 43, D240-D249.	6.5	201
12256	Extracting high confidence protein interactions from affinity purification data: At the crossroads. <i>Journal of Proteomics</i> , 2015, 118, 63-80.	1.2	30
12257	ENViz: a Cytoscape App for integrated statistical analysis and visualization of sample-matched data with multiple data types. <i>Bioinformatics</i> , 2015, 31, 1683-1685.	1.8	12
12258	Effects of microgravity on DNA damage response in <i>Caenorhabditis elegans</i> during Shenzhou-8 spaceflight. <i>International Journal of Radiation Biology</i> , 2015, 91, 531-539.	1.0	27
12259	Dissection of the styleâ€™s response to pollination using transcriptome profiling in self-compatible (<i>Solanum pimpinellifolium</i>) and self-incompatible (<i>Solanum chilense</i>) tomato species. <i>BMC Plant Biology</i> , 2015, 15, 119.	1.6	20

#	ARTICLE	IF	CITATIONS
12260	High quality draft genome sequence of <i>Meganema perideroedes</i> str. Gr1T and a proposal for its reclassification to the family Meganemaceae fam. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 23.	1.5	15
12261	Capturing domain knowledge from multiple sources: the rare bone disorders use case. <i>Journal of Biomedical Semantics</i> , 2015, 6, 21.	0.9	2
12262	Non-Negative Matrix Factorization with Auxiliary Information on Overlapping Groups. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2015, 27, 1615-1628.	4.0	13
12263	Drawing on millions of biomedical journal publications to do predictive biology. , 2015, , .		0
12264	Topology-function conservation in protein-protein interaction networks. <i>Bioinformatics</i> , 2015, 31, 1632-1639.	1.8	62
12265	Identifying entities from scientific publications: A comparison of vocabulary- and model-based methods. <i>Journal of Informetrics</i> , 2015, 9, 455-465.	1.4	12
12266	Long non-coding RNA discovery across the genus <i>Anopheles</i> reveals conserved secondary structures within and beyond the <i>Gambiae</i> complex. <i>BMC Genomics</i> , 2015, 16, 337.	1.2	85
12267	Proteomics and Metabolomics as Large-Scale Phenotyping Tools. , 2015, , 125-139.		1
12268	Identification of conserved drought-adaptive genes using a cross-species meta-analysis approach. <i>BMC Plant Biology</i> , 2015, 15, 111.	1.6	90
12269	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Tv2a.2, a microsymbiont of <i>Tachigali versicolor</i> discovered in Barro Colorado Island of Panama. <i>Standards in Genomic Sciences</i> , 2015, 10, 27.	1.5	5
12270	Complete genome sequence of <i>Pseudomonas fluorescens</i> strain PICF7, an indigenous root endophyte from olive (<i>Olea europaea</i> L.) and effective biocontrol agent against <i>Verticillium dahliae</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 10.	1.5	60
12271	Heritability, SNP- and Gene-Based Analyses of Cannabis Use Initiation and Age at Onset. <i>Behavior Genetics</i> , 2015, 45, 503-513.	1.4	25
12272	A novel method for identifying disease associated protein complexes based on functional similarity protein complex networks. <i>Algorithms for Molecular Biology</i> , 2015, 10, 14.	0.3	18
12273	Interpolation based consensus clustering for gene expression time series. <i>BMC Bioinformatics</i> , 2015, 16, 117.	1.2	12
12274	Database of Gene Co-Regulation (dGCR): A Web Tool for Analysing Patterns of Gene Co-regulation across Publicly Available Expression Data. <i>Journal of Genomics</i> , 2015, 3, 29-35.	0.6	8
12275	Burden Analysis of Rare Microdeletions Suggests a Strong Impact of Neurodevelopmental Genes in Genetic Generalised Epilepsies. <i>PLoS Genetics</i> , 2015, 11, e1005226.	1.5	91
12277	LAILAPS: The Plant Science Search Engine. <i>Plant and Cell Physiology</i> , 2015, 56, e8-e8.	1.5	7
12278	PomBase 2015: updates to the fission yeast database. <i>Nucleic Acids Research</i> , 2015, 43, D656-D661.	6.5	95

#	ARTICLE	IF	CITATIONS
12279	Analysis of human upstream open reading frames and impact on gene expression. <i>Human Genetics</i> , 2015, 134, 605-612.	1.8	39
12280	Neuronal identity genes regulated by super-enhancers are preferentially down-regulated in the striatum of Huntington's disease mice. <i>Human Molecular Genetics</i> , 2015, 24, 3481-3496.	1.4	84
12281	Identifying causal regulatory SNPs in ChIP-seq enhancers. <i>Nucleic Acids Research</i> , 2015, 43, 225-236.	6.5	50
12282	SiPAN: simultaneous prediction and alignment of protein-protein interaction networks. <i>Bioinformatics</i> , 2015, 31, 2356-2363.	1.8	9
12283	An immunoproteomic approach for characterization of dormancy within <i>Staphylococcus epidermidis</i> biofilms. <i>Molecular Immunology</i> , 2015, 65, 429-435.	1.0	19
12284	Segmentation of biological multivariate time-series data. <i>Scientific Reports</i> , 2015, 5, 8937.	1.6	25
12285	Extensive microRNA-mediated crosstalk between lncRNAs and mRNAs in mouse embryonic stem cells. <i>Genome Research</i> , 2015, 25, 655-666.	2.4	95
12286	Genome-wide computational determination of the human metalloproteome. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 931-939.	1.5	11
12287	Large-scale whole-genome sequencing of the Icelandic population. <i>Nature Genetics</i> , 2015, 47, 435-444.	9.4	663
12288	iTRAQ-based quantitative analysis of hippocampal postsynaptic density-associated proteins in a rat chronic mild stress model of depression. <i>Neuroscience</i> , 2015, 298, 220-292.	1.1	64
12289	Gene network coherence based on prior knowledge using direct and indirect relationships. <i>Computational Biology and Chemistry</i> , 2015, 56, 142-151.	1.1	11
12290	Rethinking the Niche of Upper-Atmosphere Bacteria: Draft Genome Sequences of <i>Bacillus aryabhattai</i> C765 and <i>Bacillus aerophilus</i> C772, Isolated from Rice Fields. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
12291	Functional dissection of virus-human crosstalk mediated by miRNAs based on the VmiReg database. <i>Molecular BioSystems</i> , 2015, 11, 1319-1328.	2.9	12
12292	Widespread Proteome Remodeling and Aggregation in Aging <i>C.Âelegans</i> . <i>Cell</i> , 2015, 161, 919-932.	13.5	478
12293	Transcriptome assembly, profiling and differential gene expression analysis of the halophyte <i>Suaeda fruticosa</i> provides insights into salt tolerance. <i>BMC Genomics</i> , 2015, 16, 353.	1.2	62
12294	Transcriptome profiling of trichome-less reveals genes associated with multicellular trichome development in <i>Cucumis sativus</i> . <i>Molecular Genetics and Genomics</i> , 2015, 290, 2007-2018.	1.0	25
12295	High spatial resolution proteomic comparison of the brain in humans and chimpanzees. <i>Journal of Comparative Neurology</i> , 2015, 523, 2043-2061.	0.9	18
12296	In silico identification, characterization and expression analysis of miRNAs in <i>Cannabis sativa</i> L.. <i>Plant Gene</i> , 2015, 2, 17-24.	1.4	23

#	ARTICLE	IF	CITATIONS
12297	Bioinformatics analyses of significant prognostic risk markers for thyroid papillary carcinoma. <i>Tumor Biology</i> , 2015, 36, 7457-7463.	0.8	14
12298	Machine learning applications in genetics and genomics. <i>Nature Reviews Genetics</i> , 2015, 16, 321-332.	7.7	1,334
12299	Rough Based Symmetrical Clustering for Gene Expression Profile Analysis. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 360-367.	2.2	5
12300	The red coral (<i>Corallium rubrum</i>) transcriptome: a new resource for population genetics and local adaptation studies. <i>Molecular Ecology Resources</i> , 2015, 15, 1205-1215.	2.2	47
12301	Complete genome of <i>Bacillus</i> sp. Pc3 isolated from the Antarctic seawater with antimicrobial activity. <i>Marine Genomics</i> , 2015, 20, 1-2.	0.4	5
12302	Key challenges for the creation and maintenance of specialist protein resources. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1005-1013.	1.5	13
12304	Evolutionary Dynamics of GLD-1 mRNA Complexes in <i>Caenorhabditis</i> Nematodes. <i>Genome Biology and Evolution</i> , 2015, 7, 314-335.	1.1	7
12305	A new vision of evaluating gene expression signatures. <i>Computational Biology and Chemistry</i> , 2015, 57, 54-60.	1.1	1
12306	Genome-Wide Association Study of Behavioral Disinhibition in a Selected Adolescent Sample. <i>Behavior Genetics</i> , 2015, 45, 375-381.	1.4	55
12307	A primer to frequent itemset mining for bioinformatics. <i>Briefings in Bioinformatics</i> , 2015, 16, 216-231.	3.2	102
12308	Identification of potential therapeutic target genes, key miRNAs and mechanisms in acute myeloid leukemia based on bioinformatics analysis. <i>Medical Oncology</i> , 2015, 32, 152.	1.2	9
12309	Triticeae Resources in Ensembl Plants. <i>Plant and Cell Physiology</i> , 2015, 56, e3-e3.	1.5	59
12310	Immunoreactive pattern of <i>Staphylococcus epidermidis</i> biofilm against human whole saliva. <i>Electrophoresis</i> , 2015, 36, 1228-1233.	1.3	3
12311	[FeFe]-Hydrogenase Maturation: Insights into the Role HydE Plays in Dithiomethylamine Biosynthesis. <i>Biochemistry</i> , 2015, 54, 1807-1818.	1.2	57
12313	Genome Mapping and Genomics in Human and Non-Human Primates. , 2015, , .		0
12314	Predicting protein interface residues using easily accessible on-line resources. <i>Briefings in Bioinformatics</i> , 2015, 16, 1025-1034.	3.2	47
12315	Disease Gene Prioritization Using Network and Feature. <i>Journal of Computational Biology</i> , 2015, 22, 313-323.	0.8	12
12316	Spatially resolved, highly multiplexed RNA profiling in single cells. <i>Science</i> , 2015, 348, aaa6090.	6.0	1,689

#	ARTICLE	IF	CITATIONS
12317	Characterization of proteins in <i>S. cerevisiae</i> with subcellular localizations. <i>Molecular BioSystems</i> , 2015, 11, 1360-1369.	2.9	2
12318	High-density genetic map construction and identification of a locus controlling weeping trait in an ornamental woody plant (<i>Prunus mume</i> Sieb. et Zucc). <i>DNA Research</i> , 2015, 22, 183-191.	1.5	187
12319	Bridging topological and functional information in protein interaction networks by short loops profiling. <i>Scientific Reports</i> , 2015, 5, 8540.	1.6	19
12320	A New Semantic Functional Similarity over Gene Ontology. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 322-334.	1.9	8
12321	Identification of Protein Complexes from Tandem Affinity Purification/Mass Spectrometry Data via Biased Random Walk. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 455-466.	1.9	3
12322	Development of an informatics infrastructure for data exchange of biomolecular simulations: Architecture, data models and ontology. <i>SAR and QSAR in Environmental Research</i> , 2015, 26, 577-593.	1.0	2
12323	A bioinformatics approach to distinguish plant parasite and host transcriptomes in interface tissue by classifying RNA-Seq reads. <i>Plant Methods</i> , 2015, 11, 34.	1.9	23
12324	Elucidation of the CHO Super-Ome (CHO-SO) by Proteoinformatics. <i>Journal of Proteome Research</i> , 2015, 14, 4687-4703.	1.8	35
12325	Encoding of Fundamental Chemical Entities of Organic Reactivity Interest using chemical ontology and XML. <i>Journal of Molecular Graphics and Modelling</i> , 2015, 61, 30-43.	1.3	6
12326	Heimler Syndrome Is Caused by Hypomorphic Mutations in the Peroxisome-Biogenesis Genes PEX1 and PEX6. <i>American Journal of Human Genetics</i> , 2015, 97, 535-545.	2.6	103
12328	Age-driven modulation of tRNA-derived fragments in <i>Drosophila</i> and their potential targets. <i>Biology Direct</i> , 2015, 10, 51.	1.9	78
12329	Label-Free LC-MS/MS Proteomic Analysis of Cerebrospinal Fluid Identifies Protein/Pathway Alterations and Candidate Biomarkers for Amyotrophic Lateral Sclerosis. <i>Journal of Proteome Research</i> , 2015, 14, 4486-4501.	1.8	83
12330	Recent findings and technological advances in phosphoproteomics for cells and tissues. <i>Expert Review of Proteomics</i> , 2015, 12, 469-487.	1.3	70
12331	Fuzzy Inference-Based Ontology Matching Using Upper Ontology. <i>Communications in Computer and Information Science</i> , 2015, , 392-402.	0.4	3
12332	Genomic alterations in <i>BCL2L1</i> and <i>DLC1</i> contribute to drug sensitivity in gastric cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12492-12497.	3.3	46
12333	Dynamic changes of RNA-sequencing expression for precision medicine: N-of-1-pathways Mahalanobis distance within pathways of single subjects predicts breast cancer survival. <i>Bioinformatics</i> , 2015, 31, i293-i302.	1.8	30
12334	Somatic mutation in single human neurons tracks developmental and transcriptional history. <i>Science</i> , 2015, 350, 94-98.	6.0	486
12335	High throughput profiling of the cotton bollworm <i>Helicoverpa armigera</i> immunotranscriptome during the fungal and bacterial infections. <i>BMC Genomics</i> , 2015, 16, 321.	1.2	100

#	ARTICLE	IF	CITATIONS
12336	Transcriptome and venom proteome of the box jellyfish <i>Chironex fleckeri</i> . BMC Genomics, 2015, 16, 407.	1.2	103
12337	The <i>Medicago sativa</i> gene index 1.2: a web-accessible gene expression atlas for investigating expression differences between <i>Medicago sativa</i> subspecies. BMC Genomics, 2015, 16, 502.	1.2	54
12338	Transcriptome analysis of the Holly mangrove <i>Acanthus ilicifolius</i> and its terrestrial relative, <i>Acanthus leucostachyus</i> , provides insights into adaptation to intertidal zones. BMC Genomics, 2015, 16, 605.	1.2	46
12339	KI 2015: Advances in Artificial Intelligence. Lecture Notes in Computer Science, 2015, , .	1.0	2
12340	Human pluripotent stem cell-derived neural constructs for predicting neural toxicity. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12516-12521.	3.3	288
12341	Proteome-wide quantitative multiplexed profiling of protein expression: carbon-source dependency in <i>Saccharomyces cerevisiae</i> . Molecular Biology of the Cell, 2015, 26, 4063-4074.	0.9	62
12342	Associations of SNPs located at candidate genes to bovine growth traits, prioritized with an interaction networks construction approach. BMC Genetics, 2015, 16, 91.	2.7	16
12343	POTION: an end-to-end pipeline for positive Darwinian selection detection in genome-scale data through phylogenetic comparison of protein-coding genes. BMC Genomics, 2015, 16, 567.	1.2	44
12344	An Integrated Framework for Functional Annotation of Protein Structural Domains. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 902-913.	1.9	24
12345	Using Semantic Similarities and csbl.go for Analyzing Microarray Data. Methods in Molecular Biology, 2015, 1375, 105-116.	0.4	1
12346	Sparse multi-view matrix factorization: a multivariate approach to multiple tissue comparisons. Bioinformatics, 2015, 31, 3163-3171.	1.8	6
12347	A mutation profile for top- <i>k</i> patient search exploiting Gene-Ontology and orthogonal non-negative matrix factorization. Bioinformatics, 2015, 31, 3653-3659.	1.8	12
12348	Long-range evolutionary constraints reveal cis-regulatory interactions on the human X chromosome. Nature Communications, 2015, 6, 6904.	5.8	31
12349	Molecular transitions from papillomavirus infection to cervical precancer and cancer: Role of stromal estrogen receptor signaling. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3255-64.	3.3	197
12350	PathwaysWeb: a gene pathways API with directional interactions, expanded gene ontology, and versioning. Bioinformatics, 2016, 32, 312-314.	1.8	3
12351	Network analysis reveals stage-specific changes in zebrafish embryo development using time course whole transcriptome profiling and prior biological knowledge. BioData Mining, 2015, 8, 26.	2.2	1
12352	Genome-Wide Screen Reveals Valosin-Containing Protein Requirement for Coronavirus Exit from Endosomes. Journal of Virology, 2015, 89, 11116-11128.	1.5	54
12353	Representing virus-host interactions and other multi-organism processes in the Gene Ontology. BMC Microbiology, 2015, 15, 146.	1.3	33

#	ARTICLE	IF	CITATIONS
12354	A genome-scale mining strategy for recovering novel rapidly-evolving nuclear single-copy genes for addressing shallow-scale phylogenetics in <i>Hydrangea</i> . <i>BMC Evolutionary Biology</i> , 2015, 15, 132.	3.2	20
12355	Unravelling the genome of Holy basil: an "incomparable" elixir of life of traditional Indian medicine. <i>BMC Genomics</i> , 2015, 16, 413.	1.2	60
12356	Target prediction utilising negative bioactivity data covering large chemical space. <i>Journal of Cheminformatics</i> , 2015, 7, 51.	2.8	109
12357	Functional classification of CATH superfamilies: a domain-based approach for protein function annotation. <i>Bioinformatics</i> , 2015, 31, 3460-3467.	1.8	93
12358	Draft Genome Sequence of <i>Gluconobacter oxydans</i> NL71, a Strain That Efficiently Biocatalyzes Xylose to Xylonic Acid at a High Concentration. <i>Genome Announcements</i> , 2015, 3, .	0.8	17
12359	Draft genome sequence of marine-derived <i>Streptomyces</i> sp. TP-A0598, a producer of anti-MRSA antibiotic lydicamycins. <i>Standards in Genomic Sciences</i> , 2015, 10, 58.	1.5	25
12360	A Feature Selection Approach for Evaluate the Inference of GRNs Through Biological Data Integration - A Case Study on <i>A. Thaliana</i> . <i>Lecture Notes in Computer Science</i> , 2015, , 667-675.	1.0	0
12361	Visual analysis of biological data-knowledge networks. <i>BMC Bioinformatics</i> , 2015, 16, 135.	1.2	29
12362	Using Gene Ontology to describe the role of the neurexin-neurologin-SHANK complex in human, mouse and rat and its relevance to autism. <i>BMC Bioinformatics</i> , 2015, 16, 186.	1.2	17
12363	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
12364	Orthology for comparative genomics in the mouse genome database. <i>Mammalian Genome</i> , 2015, 26, 305-313.	1.0	9
12365	PPDB: A Tool for Investigation of Plants Physiology Based on Gene Ontology. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2015, 7, 295-308.	2.2	2
12366	GO2TR: a gene ontology-based workflow to generate target regions for target enrichment experiments. <i>Conservation Genetics Resources</i> , 2015, 7, 851-857.	0.4	5
12368	Evolutionary insights from de novo transcriptome assembly and SNP discovery in California white oaks. <i>BMC Genomics</i> , 2015, 16, 552.	1.2	31
12369	Less pronounced response to exercise in healthy relatives to type 2 diabetic subjects compared with controls. <i>Journal of Applied Physiology</i> , 2015, 119, 953-960.	1.2	13
12370	DECODE: an integrated differential co-expression and differential expression analysis of gene expression data. <i>BMC Bioinformatics</i> , 2015, 16, 182.	1.2	45
12371	Reference genome of wild goat (<i>capra aegagrus</i>) and sequencing of goat breeds provide insight into genic basis of goat domestication. <i>BMC Genomics</i> , 2015, 16, 431.	1.2	103
12372	Generating and evaluating a ranked candidate gene list for potential vertebrate heart field regulators. <i>Genomics Data</i> , 2015, 6, 199-201.	1.3	8

#	ARTICLE	IF	CITATIONS
12373	Longevity Genes Revealed by Integrative Analysis of Isoform-Specific <i>daf-16/FoxO</i> Mutants of <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2015, 201, 613-629.	1.2	63
12374	Analyzing alternative splicing data of splice junction arrays from Parkinson patients' leukocytes before and after deep brain stimulation as compared with control donors. <i>Genomics Data</i> , 2015, 5, 340-343.	1.3	9
12375	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
12376	Comparative analysis of anti-viral transcriptomics reveals novel effects of influenza immune antagonism. <i>BMC Immunology</i> , 2015, 16, 46.	0.9	19
12377	On predicting transport proteins and their substrates for the reconstruction of metabolic networks. , 2015, , .		1
12378	Evolutionary computation for disease gene association. , 2015, , .		4
12379	Genome-wide pathway analysis for diabetic nephropathy in type 1 diabetes. <i>Endocrine Research</i> , 2015, 41, 1-7.	0.6	6
12380	Transcriptome sequencing and annotation of the polychaete <i>Hermodice carunculata</i> (Annelida, Tj ETQq1 1 0.784314 rgBT /Overlock 23	1.2	23
12381	Effects of β -catenin on differentially expressed genes in multiple myeloma. <i>Journal of Huazhong University of Science and Technology [Medical Sciences]</i> , 2015, 35, 546-552.	1.0	4
12382	KnowEnG: a knowledge engine for genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1115-1119.	2.2	13
12383	A density-based clustering approach for identifying overlapping protein complexes with functional preferences. <i>BMC Bioinformatics</i> , 2015, 16, 174.	1.2	24
12384	Predicting protein function via downward random walks on a gene ontology. <i>BMC Bioinformatics</i> , 2015, 16, 271.	1.2	22
12385	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
12386	Avoiding abundance bias in the functional annotation of posttranslationally modified proteins. <i>Nature Methods</i> , 2015, 12, 1003-1004.	9.0	60
12387	The human gene damage index as a gene-level approach to prioritizing exome variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13615-13620.	3.3	213
12388	A framework for ontology-based question answering with application to parasite immunology. <i>Journal of Biomedical Semantics</i> , 2015, 6, 31.	0.9	23
12389	Mouse Genome Informatics (MGI): reflecting on 25 years. <i>Mammalian Genome</i> , 2015, 26, 272-284.	1.0	34
12390	SimiRa: A tool to identify coregulation between microRNAs and RNA-binding proteins. <i>RNA Biology</i> , 2015, 12, 998-1009.	1.5	14

#	ARTICLE	IF	CITATIONS
12391	Identification and characterization of long non-coding RNAs involved in osmotic and salt stress in <i>Medicago truncatula</i> using genome-wide high-throughput sequencing. <i>BMC Plant Biology</i> , 2015, 15, 131.	1.6	181
12392	Proteomic profile of KSR1-regulated signalling in response to genotoxic agents in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2015, 151, 555-568.	1.1	10
12393	Detecting protein complexes using gene expression biclusters. , 2015, , .		0
12394	Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. <i>GigaScience</i> , 2015, 4, 38.	3.3	84
12395	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. <i>Molecular Systems Biology</i> , 2015, 11, 799.	3.2	102
12396	Unique ability of pandemic influenza to downregulate the genes involved in neuronal disorders. <i>Molecular Biology Reports</i> , 2015, 42, 1377-1390.	1.0	27
12397	Epigenomic evolution in diffuse large B-cell lymphomas. <i>Nature Communications</i> , 2015, 6, 6921.	5.8	111
12398	BioMiner: Paving the Way for Personalized Medicine. <i>Cancer Informatics</i> , 2015, 14, CIN.S20910.	0.9	9
12399	A fuzzy document clustering approach based on domain-specified ontology. <i>Data and Knowledge Engineering</i> , 2015, 100, 148-166.	2.1	19
12400	GESSE: Predicting Drug Side Effects from Drug-Target Relationships. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 1804-1823.	2.5	23
12401	RC3H1 post-transcriptionally regulates A20 mRNA and modulates the activity of the IKK/NF- κ B pathway. <i>Nature Communications</i> , 2015, 6, 7367.	5.8	99
12402	Survey of genome sequences in a wild sweet potato, <i>Ipomoea trifida</i> (H. B. K.) G. Don. <i>DNA Research</i> , 2015, 22, 171-179.	1.5	107
12403	Malleable nature of mRNA-protein compositional complementarity and its functional significance. <i>Nucleic Acids Research</i> , 2015, 43, 3012-3021.	6.5	7
12404	Comparative transcriptome resources of eleven <i>Primulina</i> species, a group of "stone plants" from a biodiversity hot spot. <i>Molecular Ecology Resources</i> , 2015, 15, 619-632.	2.2	45
12405	Expressed sequence tags 454 sequencing and biomineralization gene expression for pearl sac of the pearl oyster, <i>Pinctada fucata martensii</i> . <i>Aquaculture Research</i> , 2015, 46, 745-758.	0.9	19
12406	Genomic evidence for role of inversion <i>3<sc>RP</sc></i> of <i>Drosophila melanogaster</i> in facilitating climate change adaptation. <i>Molecular Ecology</i> , 2015, 24, 2423-2432.	2.0	53
12407	Antisense suppression of <i>LOX3</i> gene expression in rice endosperm enhances seed longevity. <i>Plant Biotechnology Journal</i> , 2015, 13, 526-539.	4.1	64
12408	Myeloid <i>STAT3</i> promotes formation of colitis-associated colorectal cancer in mice. <i>Oncolmmunology</i> , 2015, 4, e998529.	2.1	24

#	ARTICLE	IF	CITATIONS
12409	Building Transcriptional Association Networks in Cytoscape with <i>RegNetC</i> . IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 823-824.	1.9	1
12410	RNA-Seq UD: A bioinformatics platform for RNA-Seq analysis. , 2015, , .		0
12411	Rapid acclimation of juvenile corals to CO ₂ -mediated acidification by upregulation of heat shock protein and Bcl-2 genes. Molecular Ecology, 2015, 24, 438-452.	2.0	101
12412	Discovering weighted motifs in gene co-expression networks. , 2015, , .		2
12413	Proteomic analysis of Eimeria acervulina sporozoite proteins interaction with duodenal epithelial cells by shotgun LC-MS/MS. Molecular and Biochemical Parasitology, 2015, 202, 29-33.	0.5	31
12414	Comparative proteomic analysis using 2D-MS/MS reveals the mechanism of Fuzhuan brick tea extract against hepatic fat accumulation in rats with nonalcoholic fatty liver disease. Electrophoresis, 2015, 36, 2002-2016.	1.3	25
12415	Analysis of Human Triallelic SNPs by Next-Generation Sequencing. Annals of Human Genetics, 2015, 79, 275-281.	0.3	23
12416	Temporal endogenous gene expression profiles in response to lipid-mediated transfection. Journal of Gene Medicine, 2015, 17, 14-32.	1.4	8
12417	Metaproteomics of complex microbial communities in biogas plants. Microbial Biotechnology, 2015, 8, 749-763.	2.0	98
12418	The Plant Genome Integrative Explorer Resource: PlantGen.org. New Phytologist, 2015, 208, 1149-1156.	3.5	282
12419	Explore the hidden treasure in protein-protein interaction networks: An iterative model for predicting protein functions. Journal of Bioinformatics and Computational Biology, 2015, 13, 1550026.	0.3	4
12420	Microarray profiling of long non-coding RNA (lncRNA) associated with hypertrophic cardiomyopathy. BMC Cardiovascular Disorders, 2015, 15, 62.	0.7	49
12421	Revealing the Underlying Mechanism of Diabetic Nephropathy Viewed by Microarray Analysis. Experimental and Clinical Endocrinology and Diabetes, 2015, 123, 353-359.	0.6	7
12422	Proteomic changes of the porcine small intestine in response to chronic heat stress. Journal of Molecular Endocrinology, 2015, 55, 277-293.	1.1	43
12423	Transcriptomic changes in the plant pathogenic fungus Rhizoctonia solani AG-3 in response to the antagonistic bacteria Serratia proteamaculans and Serratia plymuthica. BMC Genomics, 2015, 16, 630.	1.2	97
12424	Urothelial cancer gene regulatory networks inferred from large-scale RNAseq, Bead and Oligo gene expression data. BMC Systems Biology, 2015, 9, 21.	3.0	11
12425	Evolving-Pattern Analysis of Transient and Long-Term Biomarkers for Cancers: Hepatocellular Carcinoma as a Case. Interdisciplinary Sciences, Computational Life Sciences, 2015, 7, 414-422.	2.2	1
12426	De novo sequencing and characterization of the Bradysia odoriphaga (Diptera: Sciaridae) larval transcriptome. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 16, 20-27.	0.4	13

#	ARTICLE	IF	CITATIONS
12427	Functional relevance for type 1 diabetes mellitus-associated genetic variants by using integrative analyses. <i>Human Immunology</i> , 2015, 76, 753-758.	1.2	10
12428	MGFM: a novel tool for detection of tissue and cell specific marker genes from microarray gene expression data. <i>BMC Genomics</i> , 2015, 16, 645.	1.2	10
12429	Computing the origin and evolution of the ribosome from its structure " Uncovering processes of macromolecular accretion benefiting synthetic biology. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 427-447.	1.9	26
12430	DNA-binding protein prediction using plant specific support vector machines: validation and application of a new genome annotation tool. <i>Nucleic Acids Research</i> , 2015, 43, e158-e158.	6.5	20
12431	Malignant pleural mesothelioma: history, controversy and future of a manmade epidemic. <i>European Respiratory Review</i> , 2015, 24, 115-131.	3.0	136
12432	Identifying and characterising key alternative splicing events in <i>Drosophila</i> development. <i>BMC Genomics</i> , 2015, 16, 608.	1.2	9
12433	The human cardiac and skeletal muscle proteomes defined by transcriptomics and antibody-based profiling. <i>BMC Genomics</i> , 2015, 16, 475.	1.2	58
12434	Integrated network analysis and logistic regression modeling identify stage-specific genes in Oral Squamous Cell Carcinoma. <i>BMC Medical Genomics</i> , 2015, 8, 39.	0.7	12
12435	High-quality genome sequence and description of <i>Bacillus dielmoensis</i> strain FF4T sp. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 41.	1.5	18
12436	An Ancient Yeast for Young Geneticists: A Primer on the <i>Schizosaccharomyces pombe</i> Model System. <i>Genetics</i> , 2015, 201, 403-423.	1.2	180
12437	Different Temporal Effects of Ebola Virus VP35 and VP24 Proteins on Global Gene Expression in Human Dendritic Cells. <i>Journal of Virology</i> , 2015, 89, 7567-7583.	1.5	50
12438	Partial depletion of yolk during zebrafish embryogenesis changes the dynamics of methionine cycle and metabolic genes. <i>BMC Genomics</i> , 2015, 16, 427.	1.2	6
12439	Whole transcriptome profiling of the vernalization process in <i>Lilium longiflorum</i> (cultivar White) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 2	1.2	45
12440	Essential protein identification based on essential protein-protein interaction prediction by Integrated Edge Weights. <i>Methods</i> , 2015, 83, 51-62.	1.9	25
12441	Comparative transcriptional profiling analysis of developing melon (<i>Cucumis melo</i> L.) fruit from climacteric and non-climacteric varieties. <i>BMC Genomics</i> , 2015, 16, 440.	1.2	62
12442	mapDIA: Preprocessing and statistical analysis of quantitative proteomics data from data independent acquisition mass spectrometry. <i>Journal of Proteomics</i> , 2015, 129, 108-120.	1.2	149
12443	Aberrant DNA methylation in non-small cell lung cancer-associated fibroblasts. <i>Carcinogenesis</i> , 2015, 36, bgv146.	1.3	84
12444	IMP 2.0: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. <i>Nucleic Acids Research</i> , 2015, 43, W128-W133.	6.5	60

#	ARTICLE	IF	CITATIONS
12445	Identification of in vitro and in vivo disconnects using transcriptomic data. BMC Genomics, 2015, 16, 615.	1.2	13
12446	Identification and transcriptomic profiling of genes involved in increasing sugar content during salt stress in sweet sorghum leaves. BMC Genomics, 2015, 16, 534.	1.2	144
12447	LARVA: an integrative framework for large-scale analysis of recurrent variants in noncoding annotations. Nucleic Acids Research, 2015, 43, 8123-8134.	6.5	72
12448	Genome sequences of copper resistant and sensitive Enterococcus faecalis strains isolated from copper-fed pigs in Denmark. Standards in Genomic Sciences, 2015, 10, 35.	1.5	25
12449	Genome Sequence of Phytophthora fragariae var. fragariae, a Quarantine Plant-Pathogenic Fungus. Genome Announcements, 2015, 3, .	0.8	20
12450	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. Nature Medicine, 2015, 21, 1018-1027.	15.2	212
12451	A Combined Omics Approach to Generate the Surface Atlas of Human Naive CD4+ T Cells during Early T-Cell Receptor Activation. Molecular and Cellular Proteomics, 2015, 14, 2085-2102.	2.5	40
12452	The role of ontologies in biological and biomedical research: a functional perspective. Briefings in Bioinformatics, 2015, 16, 1069-1080.	3.2	199
12453	The Phenome-Wide Distribution of Genetic Variance. American Naturalist, 2015, 186, 15-30.	1.0	26
12454	TCF12 is mutated in anaplastic oligodendroglioma. Nature Communications, 2015, 6, 7207.	5.8	42
12455	Comparative Genomics of a Bacterivorous Green Alga Reveals Evolutionary Causalities and Consequences of Phago-Mixotrophic Mode of Nutrition. Genome Biology and Evolution, 2015, 7, 3047-3061.	1.1	36
12456	Single-Cell RNA-Seq with Waterfall Reveals Molecular Cascades underlying Adult Neurogenesis. Cell Stem Cell, 2015, 17, 360-372.	5.2	680
12457	Node sampling for protein complex estimation in bait-prey graphs. Statistical Applications in Genetics and Molecular Biology, 2015, 14, 391-411.	0.2	0
12458	Predicting Future Scientific Discoveries Based on a Networked Analysis of the Past Literature. , 2015, , .		22
12459	Specific miRNA and its target in neutrophils after traumatic injury. Acta Biochimica Et Biophysica Sinica, 2015, 47, 749-754.	0.9	5
12460	Genetic Analysis of Association Between Calcium Signaling and Hippocampal Activation, Memory Performance in the Young and Old, and Risk for Sporadic Alzheimer Disease. JAMA Psychiatry, 2015, 72, 1029.	6.0	23
12461	Development and application of wide-range gradient gel electrophoresis to proteome analysis. Analytical Methods, 2015, 7, 8109-8115.	1.3	6
12462	Hybrid Simulations of Heterogeneous Biochemical Models in SBML. ACM Transactions on Modeling and Computer Simulation, 2015, 25, 1-22.	0.6	4

#	ARTICLE	IF	CITATIONS
12463	Bioinformatics analysis of transcription profiling of sepsis. <i>European Journal of Inflammation</i> , 2015, 13, 82-90.	0.2	0
12464	Intelligent Computing Theories and Methodologies. <i>Lecture Notes in Computer Science</i> , 2015, , .	1.0	2
12465	Estimating a Ranked List of Human Genetic Diseases by Associating Phenotype-Gene with Gene-Disease Bipartite Graphs. <i>ACM Transactions on Intelligent Systems and Technology</i> , 2015, 6, 1-21.	2.9	5
12466	Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 2207-2217.	1.1	101
12467	Potential role of differentially expressed lncRNAs in the pathogenesis of oral squamous cell carcinoma. <i>Archives of Oral Biology</i> , 2015, 60, 1581-1587.	0.8	40
12468	Enhanced SDC-assisted digestion coupled with lipid chromatography-tandem mass spectrometry for shotgun analysis of membrane proteome. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2015, 1002, 144-151.	1.2	12
12469	MicroRNA Let-7i Negatively Regulates Cardiac Inflammation and Fibrosis. <i>Hypertension</i> , 2015, 66, 776-785.	1.3	98
12470	The <i>Brassica rapa</i> Genome. <i>Compendium of Plant Genomes</i> , 2015, , .	0.3	8
12471	Computational Systems Toxicology. <i>Methods in Pharmacology and Toxicology</i> , 2015, , .	0.1	5
12472	Thalamic WNT3 Secretion Spatiotemporally Regulates the Neocortical Ribosome Signature and mRNA Translation to Specify Neocortical Cell Subtypes. <i>Journal of Neuroscience</i> , 2015, 35, 10911-10926.	1.7	50
12473	Approximate block coordinate descent for large scale hierarchical classification. , 2015, , .		2
12474	Identification of stable reference genes in differentiating human pluripotent stem cells. <i>Physiological Genomics</i> , 2015, 47, 232-239.	1.0	18
12475	Expression Quantitative Trait Loci Acting Across Multiple Tissues Are Enriched in Inherited Risk for Coronary Artery Disease. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 305-315.	5.1	39
12476	Proteomic analysis of <i>Vibrio metschnikovii</i> under cold stress using a quadrupole Orbitrap mass spectrometer. <i>Research in Microbiology</i> , 2015, 166, 618-625.	1.0	9
12477	Genome-wide association analyses based on whole-genome sequencing in Sardinia provide insights into regulation of hemoglobin levels. <i>Nature Genetics</i> , 2015, 47, 1264-1271.	9.4	66
12478	The distribution pattern of genetic variation in the transcript isoforms of the alternatively spliced protein-coding genes in the human genome. <i>Molecular BioSystems</i> , 2015, 11, 1378-1388.	2.9	16
12479	High-Quality draft genome sequence of the Lotus spp. microsymbiont <i>Mesorhizobium loti</i> strain CJ3Sym. <i>Standards in Genomic Sciences</i> , 2015, 10, 54.	1.5	2
12480	sRNAtoolbox: an integrated collection of small RNA research tools. <i>Nucleic Acids Research</i> , 2015, 43, W467-W473.	6.5	238

#	ARTICLE	IF	CITATIONS
12481	Prepatterning of differentiation-driven nuclear lamin A/C-associated chromatin domains by GlcNAcylated histone H2B. <i>Genome Research</i> , 2015, 25, 1825-1835.	2.4	75
12482	Transcriptomic Signatures Mirror the Lack of the Fecundity/Longevity Trade-Off in Ant Queens. <i>Molecular Biology and Evolution</i> , 2015, 32, msv186.	3.5	43
12483	Changes in microRNAs associated with Twist-1 and Bcl-2 overexpression identify signaling pathways. <i>Experimental and Molecular Pathology</i> , 2015, 99, 524-532.	0.9	10
12484	Proteomic and Biochemical Studies of Lysine Malonylation Suggest Its Malonic Aciduria-associated Regulatory Role in Mitochondrial Function and Fatty Acid Oxidation. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3056-3071.	2.5	143
12485	Pervasive pleiotropy between psychiatric disorders and immune disorders revealed by integrative analysis of multiple GWAS. <i>Human Genetics</i> , 2015, 134, 1195-1209.	1.8	72
12486	Biclustering on expression data: A review. <i>Journal of Biomedical Informatics</i> , 2015, 57, 163-180.	2.5	201
12487	Virtual microdissection identifies distinct tumor- and stroma-specific subtypes of pancreatic ductal adenocarcinoma. <i>Nature Genetics</i> , 2015, 47, 1168-1178.	9.4	1,491
12488	A survey on knowledge representation in materials science and engineering: An ontological perspective. <i>Computers in Industry</i> , 2015, 73, 8-22.	5.7	32
12489	Identification of module biomarkers from the dysregulated ceRNA- <i>ceRNA</i> interaction network in lung adenocarcinoma. <i>Molecular BioSystems</i> , 2015, 11, 3048-3058.	2.9	50
12490	The genetics of human autoimmune disease: A perspective on progress in the field and future directions. <i>Journal of Autoimmunity</i> , 2015, 64, 1-12.	3.0	80
12491	Efficient MUS Enumeration of Horn Formulae with Applications to Axiom Pinpointing. <i>Lecture Notes in Computer Science</i> , 2015, , 324-342.	1.0	15
12492	Gene expression during zombie ant biting behavior reflects the complexity underlying fungal parasitic behavioral manipulation. <i>BMC Genomics</i> , 2015, 16, 620.	1.2	107
12493	In search of key genes associated with endometriosis using bioinformatics approach. <i>European Journal of Obstetrics, Gynecology and Reproductive Biology</i> , 2015, 194, 119-124.	0.5	17
12494	Computational functional genomics based analysis of pain-relevant micro-RNAs. <i>Human Genetics</i> , 2015, 134, 1221-1238.	1.8	3
12495	Methods of processing mass spectrometry data to identify peptides and proteins. <i>Moscow University Chemistry Bulletin</i> , 2015, 70, 211-222.	0.2	0
12496	A systems biology approach for the identification of significantly perturbed genes. , 2015, , .		6
12497	Big Data Analytics. <i>Lecture Notes in Computer Science</i> , 2015, , .	1.0	4
12498	Multi-omics Multi-scale Big Data Analytics for Cancer Genomics. <i>Lecture Notes in Computer Science</i> , 2015, , 228-243.	1.0	3

#	ARTICLE	IF	CITATIONS
12499	Overflow metabolism in <i>Escherichia coli</i> results from efficient proteome allocation. <i>Nature</i> , 2015, 528, 99-104.	13.7	566
12500	The epigenomic landscape of African rainforest hunter-gatherers and farmers. <i>Nature Communications</i> , 2015, 6, 10047.	5.8	75
12501	Applicability of gene expression and systems biology to develop pharmacogenetic predictors; antipsychotic-induced extrapyramidal symptoms as an example. <i>Pharmacogenomics</i> , 2015, 16, 1975-1988.	0.6	11
12502	Protein-protein interaction network analysis and identifying regulation microRNAs in asthmatic children. <i>Allergologia Et Immunopathologia</i> , 2015, 43, 584-592.	1.0	13
12503	Shared and unique mutational gene co-occurrences in cancers. <i>Biochemical and Biophysical Research Communications</i> , 2015, 465, 777-783.	1.0	2
12504	Rat malignant fibrous histiocytoma (MFH)-derived cloned cell lines (MT-8 and MT-9) show different differentiation in mesenchymal stem cell lineage. <i>Experimental and Toxicologic Pathology</i> , 2015, 67, 499-507.	2.1	4
12505	The effect of antibiotic exposure on eicosanoid generation from arachidonic acid and gene expression in a primitive chordate, <i>Branchiostoma belcheri</i> . <i>FEBS Open Bio</i> , 2015, 5, 615-624.	1.0	3
12506	Increased hepatocellular protein carbonylation in human end-stage alcoholic cirrhosis. <i>Free Radical Biology and Medicine</i> , 2015, 89, 1144-1153.	1.3	14
12507	Using distant supervised learning to identify protein subcellular localizations from full-text scientific articles. <i>Journal of Biomedical Informatics</i> , 2015, 57, 134-144.	2.5	15
12508	Multimodal probabilistic generative models for time-course gene expression data and Gene Ontology (GO) tags. <i>Mathematical Biosciences</i> , 2015, 268, 80-91.	0.9	2
12509	Discovery of toxin-encoding genes from the false viper <i>Macropisthodon rudis</i> , a rear-fanged snake, by transcriptome analysis of venom gland. <i>Toxicon</i> , 2015, 106, 72-78.	0.8	9
12510	Characterization of whole-genome autosomal differences of DNA methylation between men and women. <i>Epigenetics and Chromatin</i> , 2015, 8, 43.	1.8	176
12511	Genomic insights into the evolutionary origin of Myxozoa within Cnidaria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14912-14917.	3.3	193
12512	Diversity in protein domain superfamilies. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 40-49.	1.5	38
12513	Mitochondrial Involvement in Vertebrate Speciation? The Case of Mito-nuclear Genetic Divergence in Chameleons. <i>Genome Biology and Evolution</i> , 2015, 7, 3322-3336.	1.1	49
12514	Draft genomic sequence of a selenite-reducing bacterium, <i>Paenirhodobacter enshiensis</i> DW2-9T. <i>Standards in Genomic Sciences</i> , 2015, 10, 38.	1.5	4
12515	Perivascular Mesenchymal Stem Cells From the Adult Human Brain Harbor No Intrinsic Neuroectodermal but High Mesodermal Differentiation Potential. <i>Stem Cells Translational Medicine</i> , 2015, 4, 1223-1233.	1.6	17
12516	Prediction of the anti-inflammatory mechanisms of curcumin by module-based protein interaction network analysis. <i>Acta Pharmaceutica Sinica B</i> , 2015, 5, 590-595.	5.7	29

#	ARTICLE	IF	CITATIONS
12517	Transcriptomic analysis of cobalt stress in the marine yeast <i>Debaryomyces hansenii</i> . FEMS Yeast Research, 2015, 15, fov099.	1.1	4
12518	Identification of genes related to learning and memory in the brain transcriptome of the mollusc, <i>Hermissenda crassicornis</i> . Learning and Memory, 2015, 22, 617-621.	0.5	13
12519	Transcriptional regulators form diverse groups with context-dependent regulatory functions. Nature, 2015, 528, 147-151.	13.7	169
12520	Complete genome sequence of <i>Propionibacterium freudenreichii</i> DSM 20271T. Standards in Genomic Sciences, 2015, 10, 83.	1.5	23
12521	DeCoaD: determining correlations among diseases using protein interaction networks. BMC Research Notes, 2015, 8, 226.	0.6	16
12522	A Chemical Proteomics Approach for Global Analysis of Lysine Monomethylome Profiling *. Molecular and Cellular Proteomics, 2015, 14, 329-339.	2.5	58
12523	The cell envelope proteome of <i>Aggregatibacter actinomycetemcomitans</i> . Molecular Oral Microbiology, 2015, 30, 97-110.	1.3	9
12524	Enhanced Cardiac Akt/Protein Kinase B Signaling Contributes to Pathological Cardiac Hypertrophy in Part by Impairing Mitochondrial Function via Transcriptional Repression of Mitochondrion-Targeted Nuclear Genes. Molecular and Cellular Biology, 2015, 35, 831-846.	1.1	84
12525	RNA-seq reveals regional differences in transcriptome response to heat stress in the marine snail <i>Cyprina stultorum</i> . Molecular Ecology, 2015, 24, 610-627.	2.0	145
12526	Role of Lamin B1 in Chromatin Instability. Molecular and Cellular Biology, 2015, 35, 884-898.	1.1	63
12527	New insights into the wheat chromosome 4D structure and virtual gene order, revealed by survey pyrosequencing. Plant Science, 2015, 233, 200-212.	1.7	20
12528	Comprehensive large-scale assessment of intrinsic protein disorder. Bioinformatics, 2015, 31, 201-208.	1.8	154
12529	Analysis of Protein Interaction Networks for the Detection of Candidate Hepatitis B and C Biomarkers. IEEE Journal of Biomedical and Health Informatics, 2015, 19, 181-189.	3.9	16
12530	RAMONA: a Web application for gene set analysis on multilevel omics data. Bioinformatics, 2015, 31, 128-130.	1.8	7
12531	Global ontology research progress: a bibliometric analysis. Aslib Journal of Information Management, 2015, 67, 27-54.	1.3	21
12532	Proteomic Analysis and Identification of Cellular Interactors of the Giant Ubiquitin Ligase HERC2. Journal of Proteome Research, 2015, 14, 953-966.	1.8	45
12533	Enhancer-core-promoter specificity separates developmental and housekeeping gene regulation. Nature, 2015, 518, 556-559.	13.7	402
12534	AtCAST3.0 Update: A Web-Based Tool for Analysis of Transcriptome Data by Searching Similarities in Gene Expression Profiles. Plant and Cell Physiology, 2015, 56, e7-e7.	1.5	14

#	ARTICLE	IF	CITATIONS
12535	Activation of Type II Cells into Regenerative Stem Cell Antigen-1 ⁺ Cells during Alveolar Repair. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2015, 53, 113-124.	1.4	41
12536	ProKinO: A Unified Resource for Mining the Cancer Kinome. <i>Human Mutation</i> , 2015, 36, 175-186.	1.1	47
12537	Bioinformatics of cardiovascular miRNA biology. <i>Journal of Molecular and Cellular Cardiology</i> , 2015, 89, 3-10.	0.9	20
12538	Population transcriptomics of human malaria parasites reveals the mechanism of artemisinin resistance. <i>Science</i> , 2015, 347, 431-435.	6.0	362
12539	Pathway-level disease data mining through hyper-box principles. <i>Mathematical Biosciences</i> , 2015, 260, 25-34.	0.9	5
12540	Transcriptomic Analysis of Temperature Responses of <i>Aspergillus kawachii</i> during Barley Koji Production. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1353-1363.	1.4	33
12541	Fourteen years of plant proteomics reflected in <i>Proteomics</i> : Moving from model species and 2DE-based approaches to orphan species and gel-free platforms. <i>Proteomics</i> , 2015, 15, 1089-1112.	1.3	91
12542	Analysis of expressed sequence tags (ESTs) from a normalized cDNA library and isolation of EST simple sequence repeats from the invasive cotton mealybug <i>Phenacoccus solenopsis</i> . <i>Insect Science</i> , 2015, 22, 761-767.	1.5	5
12543	Knowledge based word-concept model estimation and refinement for biomedical text mining. <i>Journal of Biomedical Informatics</i> , 2015, 53, 300-307.	2.5	20
12544	Contribution of bioinformatics prediction in microRNA-based cancer therapeutics. <i>Advanced Drug Delivery Reviews</i> , 2015, 81, 94-103.	6.6	47
12545	Comparative transcriptome analysis of the lichen-forming fungus <i>Endocarpon pusillum</i> elucidates its drought adaptation mechanisms. <i>Science China Life Sciences</i> , 2015, 58, 89-100.	2.3	34
12546	A novel common variant in DCST2 is associated with length in early life and height in adulthood. <i>Human Molecular Genetics</i> , 2015, 24, 1155-1168.	1.4	109
12547	Accurate in silico identification of species-specific acetylation sites by integrating protein sequence-derived and functional features. <i>Scientific Reports</i> , 2014, 4, 5765.	1.6	71
12548	Sinbase: An Integrated Database to Study Genomics, Genetics and Comparative Genomics in <i>Sesamum indicum</i> . <i>Plant and Cell Physiology</i> , 2015, 56, e2-e2.	1.5	46
12549	Gene Ontology Consortium: going forward. <i>Nucleic Acids Research</i> , 2015, 43, D1049-D1056.	6.5	2,743
12550	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
12551	RNA-Seq analysis of differentially expressed genes in rice under varied nitrogen supplies. <i>Gene</i> , 2015, 555, 305-317.	1.0	80
12552	Molecular Landscape of <i>Helopeltis theivora</i> Induced Transcriptome and Defense Gene Expression in Tea. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1042-1057.	1.0	9

#	ARTICLE	IF	CITATIONS
12554	Genomic expression profiling of NK cells in health and disease. <i>European Journal of Immunology</i> , 2015, 45, 661-678.	1.6	13
12555	Integrating Proteomics Profiling Data Sets: A Network Perspective. <i>Methods in Molecular Biology</i> , 2015, 1243, 237-253.	0.4	5
12556	Comparative Transcriptomics of Convergent Evolution: Different Genes but Conserved Pathways Underlie Caste Phenotypes across Lineages of Eusocial Insects. <i>Molecular Biology and Evolution</i> , 2015, 32, 690-703.	3.5	161
12557	OrthoDB v8: update of the hierarchical catalog of orthologs and the underlying free software. <i>Nucleic Acids Research</i> , 2015, 43, D250-D256.	6.5	303
12558	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
12559	Comparative pathway and network analysis of brain transcriptome changes during adult aging and in Parkinson's disease. <i>Neurobiology of Disease</i> , 2015, 74, 1-13.	2.1	76
12560	Predicting the potential ankylosing spondylitis-related genes utilizing bioinformatics approaches. <i>Rheumatology International</i> , 2015, 35, 973-979.	1.5	17
12562	Gene duplication of type-B ARR transcription factors systematically extends transcriptional regulatory structures in <i>Arabidopsis</i> . <i>Scientific Reports</i> , 2015, 4, 7197.	1.6	9
12563	Transcriptome analysis elucidates key developmental components of bryozoan lophophore development. <i>Scientific Reports</i> , 2014, 4, 6534.	1.6	19
12564	Behavioral and Proteomic Analysis of Stress Response in Zebrafish (<i>Danio rerio</i>). <i>Journal of Proteome Research</i> , 2015, 14, 943-952.	1.8	14
12565	Searching for repetitions in biological networks: methods, resources and tools. <i>Briefings in Bioinformatics</i> , 2015, 16, 118-136.	3.2	24
12566	miRNAs are Essential for the Survival and Maturation of Cortical Interneurons. <i>Cerebral Cortex</i> , 2015, 25, 1842-1857.	1.6	23
12567	The blind men and the elephant: on meeting the problem of multiple truths in data from clustering and pattern mining perspectives. <i>Machine Learning</i> , 2015, 98, 121-155.	3.4	73
12568	Genome wide identification and expression profile in epithelial cells exposed to TiO ₂ particles. <i>Environmental Toxicology</i> , 2015, 30, 293-300.	2.1	17
12569	Arsenic hypertolerance in the protist <i>Euglena mutabilis</i> is mediated by specific transporters and functional integrity maintenance mechanisms. <i>Environmental Microbiology</i> , 2015, 17, 1941-1949.	1.8	12
12570	Annotation Enrichment Analysis: An Alternative Method for Evaluating the Functional Properties of Gene Sets. <i>Scientific Reports</i> , 2014, 4, 4191.	1.6	56
12571	Copy Number Variable MicroRNAs in Schizophrenia and Their Neurodevelopmental Gene Targets. <i>Biological Psychiatry</i> , 2015, 77, 158-166.	0.7	58
12572	Systems analysis reveals down-regulation of a network of pro-survival miRNAs drives the apoptotic response in dilated cardiomyopathy. <i>Molecular BioSystems</i> , 2015, 11, 239-251.	2.9	23

#	ARTICLE	IF	CITATIONS
12573	Identification of master genes involved in liver key functions through transcriptomics and epigenomics of methyl donor deficiency in rat: Relevance to nonalcoholic liver disease. <i>Molecular Nutrition and Food Research</i> , 2015, 59, 293-302.	1.5	41
12574	Protein-protein interaction predictions using text mining methods. <i>Methods</i> , 2015, 74, 47-53.	1.9	73
12575	Toxicogenomic analysis in the combined effect of tributyltin and benzo[a]pyrene on the development of zebrafish embryos. <i>Aquatic Toxicology</i> , 2015, 158, 157-164.	1.9	34
12576	Comprehensive characterization of cancer subtype associated long non-coding RNAs and their clinical implications. <i>Scientific Reports</i> , 2014, 4, 6591.	1.6	106
12577	Functional annotation and biological interpretation of proteomics data. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 46-54.	1.1	45
12578	Transcriptomic and proteomic analysis reveals mechanisms of embryo abortion during chrysanthemum cross breeding. <i>Scientific Reports</i> , 2015, 4, 6536.	1.6	36
12579	Deep sequencing reveals important roles of microRNAs in response to drought and salinity stress in cotton. <i>Journal of Experimental Botany</i> , 2015, 66, 789-804.	2.4	198
12580	High-resolution prediction of mouse brain connectivity using gene expression patterns. <i>Methods</i> , 2015, 73, 71-78.	1.9	29
12581	Identification of dorsal-ventral hippocampal differentiation in neonatal rats. <i>Brain Structure and Function</i> , 2015, 220, 2873-2893.	1.2	31
12582	Lectin-like molecules in transcriptome of <i>Littorina littorea</i> hemocytes. <i>Developmental and Comparative Immunology</i> , 2015, 48, 210-220.	1.0	46
12583	Profiling status epilepticus-induced changes in hippocampal RNA expression using high-throughput RNA sequencing. <i>Scientific Reports</i> , 2014, 4, 6930.	1.6	94
12585	Immune- and Ribosome-Related Genes were Associated with Systemic Vasculitis. <i>Scandinavian Journal of Immunology</i> , 2015, 81, 96-101.	1.3	9
12586	Evolutionary soft co-clustering: formulations, algorithms, and applications. <i>Data Mining and Knowledge Discovery</i> , 2015, 29, 765-791.	2.4	11
12587	In silico prediction of physical protein interactions and characterization of interactome orphans. <i>Nature Methods</i> , 2015, 12, 79-84.	9.0	148
12588	Quantitative proteome analysis of <i>Caenorhabditis elegans</i> upon exposure to nematocidal <i>Bacillus thuringiensis</i> . <i>Journal of Proteomics</i> , 2015, 113, 337-350.	1.2	53
12589	Comparative proteomic and transcriptomic profile of <i>Staphylococcus epidermidis</i> biofilms grown in glucose-enriched medium. <i>Talanta</i> , 2015, 132, 705-712.	2.9	14
12590	A multiple testing method for hypotheses structured in a directed acyclic graph. <i>Biometrical Journal</i> , 2015, 57, 123-143.	0.6	19
12591	Altered protein expression profile associated with phenotypic changes in lung fibroblasts co-cultured with gold nanoparticle-treated small airway epithelial cells. <i>Biomaterials</i> , 2015, 39, 31-38.	5.7	29

#	ARTICLE	IF	CITATIONS
12592	New FeFe-hydrogenase genes identified in a metagenomic fosmid library from a municipal wastewater treatment plant as revealed by high-throughput sequencing. <i>Research in Microbiology</i> , 2015, 166, 9-19.	1.0	12
12593	Genome-wide DNA Methylation Profiles and Their Relationships with mRNA and the microRNA Transcriptome in Bovine Muscle Tissue (<i>Bos taurine</i>). <i>Scientific Reports</i> , 2015, 4, 6546.	1.6	97
12594	Data Fusion by Matrix Factorization. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2015, 37, 41-53.	9.7	166
12595	An overview of the neurobiology of suicidal behaviors as one meta-system. <i>Molecular Psychiatry</i> , 2015, 20, 56-71.	4.1	38
12596	LocalAli: an evolutionary-based local alignment approach to identify functionally conserved modules in multiple networks. <i>Bioinformatics</i> , 2015, 31, 363-372.	1.8	32
12597	Making proteomics data accessible and reusable: Current state of proteomics databases and repositories. <i>Proteomics</i> , 2015, 15, 930-950.	1.3	181
12598	Cytoskeletal Control of Nuclear Morphology and Chromatin Organization. <i>Journal of Molecular Biology</i> , 2015, 427, 695-706.	2.0	155
12599	Analysis of gene expression changes in peach leaves in response to plum pox virus infection using RNA-seq. <i>Molecular Plant Pathology</i> , 2015, 16, 164-176.	2.0	56
12600	Genome-wide pathway analysis of a genome-wide association study on Alzheimer's disease. <i>Neurological Sciences</i> , 2015, 36, 53-59.	0.9	19
12601	Genomic Profiling of Human <i>Leishmania braziliensis</i> Lesions Identifies Transcriptional Modules Associated with Cutaneous Immunopathology. <i>Journal of Investigative Dermatology</i> , 2015, 135, 94-101.	0.3	130
12602	Pathogenicity phenomena in three model systems: from network mining to emerging system-level properties. <i>Briefings in Bioinformatics</i> , 2015, 16, 169-182.	3.2	1
12603	Genome of the halotolerant green alga <i>Chlorella</i> sp. reveals strategies for thriving under fluctuating environmental conditions. <i>Environmental Microbiology</i> , 2015, 17, 412-426.	1.8	85
12604	How to learn about gene function: text-mining or ontologies?. <i>Methods</i> , 2015, 74, 3-15.	1.9	24
12605	From pathways to networks: Connecting dots by establishing protein-protein interaction networks in signaling pathways using affinity purification and mass spectrometry. <i>Proteomics</i> , 2015, 15, 188-202.	1.3	20
12606	Insights from the cold transcriptome of <i>Physcomitrella patens</i> : global specialization pattern of conserved transcriptional regulators and identification of orphan genes involved in cold acclimation. <i>New Phytologist</i> , 2015, 205, 869-881.	3.5	84
12607	Biomedical ontologies—A review. <i>Biocybernetics and Biomedical Engineering</i> , 2015, 35, 75-86.	3.3	19
12608	Altered microglial phagocytosis in GPR34-deficient mice. <i>Glia</i> , 2015, 63, 206-215.	2.5	60
12609	Gram-positive and Gram-negative protein subcellular localization by incorporating evolutionary-based descriptors into Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2015, 364, 284-294.	0.8	232

#	ARTICLE	IF	CITATIONS
12610	Differential regulation enrichment analysis via the integration of transcriptional regulatory network and gene expression data. <i>Bioinformatics</i> , 2015, 31, 563-571.	1.8	19
12611	BurrH: a new modular DNA binding protein for genome engineering. <i>Scientific Reports</i> , 2014, 4, 3831.	1.6	45
12612	Myostatin/activin blocking combined with exercise reconditions skeletal muscle expression profile of mdx mice. <i>Molecular and Cellular Endocrinology</i> , 2015, 399, 131-142.	1.6	21
12613	Design of a 9K illumina BeadChip for polar bears (<i>Ursus maritimus</i>) from RAD and transcriptome sequencing. <i>Molecular Ecology Resources</i> , 2015, 15, 587-600.	2.2	45
12614	Integrative Clustering by Nonnegative Matrix Factorization Can Reveal Coherent Functional Groups From Gene Profile Data. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2015, 19, 698-708.	3.9	1
12615	Genome-wide analysis of <i>Sphingomonas wittichii</i> RW1 behaviour during inoculation and growth in contaminated sand. <i>ISME Journal</i> , 2015, 9, 150-165.	4.4	40
12616	Genome-wide identification of transcription factors and transcription-factor binding sites in oleaginous microalgae <i>Nannochloropsis</i> . <i>Scientific Reports</i> , 2014, 4, 5454.	1.6	75
12617	PDB-wide collection of binding data: current status of the PDBbind database. <i>Bioinformatics</i> , 2015, 31, 405-412.	1.8	375
12618	Gene expression plasticity resulting from parental leaf damage in <i>Mimulus guttatus</i> . <i>New Phytologist</i> , 2015, 205, 894-906.	3.5	22
12619	ICT Innovations 2014. <i>Advances in Intelligent Systems and Computing</i> , 2015, , .	0.5	1
12620	fabp4 is central to eight obesity associated genes: A functional gene network-based polymorphic study. <i>Journal of Theoretical Biology</i> , 2015, 364, 344-354.	0.8	33
12621	Identification of DNA-binding proteins by incorporating evolutionary information into pseudo amino acid composition via the top-n-gram approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 1720-1730.	2.0	80
12622	Exceptionally abundant exceptions: comprehensive characterization of intrinsic disorder in all domains of life. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 137-151.	2.4	314
12623	Proteomic profiling of human placenta-derived mesenchymal stem cells upon transforming LIM mineralization protein-1 stimulation. <i>Cytotechnology</i> , 2015, 67, 285-297.	0.7	2
12624	Organellar proteome analyses of ricin toxin-treated HeLa cells. <i>Toxicology and Industrial Health</i> , 2016, 32, 1166-1178.	0.6	2
12625	GeneRank-based partly adaptive group-penalised multinomial regression for microarray classification. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 16, 252.	0.1	0
12626	Discovering low-connectivity essential proteins based on protein-protein interaction network. <i>International Journal of High Performance Systems Architecture</i> , 2016, 6, 171.	0.2	0
12627	Draft Genome Sequence of <i>Pseudoalteromonas tetraodonis</i> Strain MQS005, a Bacterium with Potential Quorum-Sensing Regulation. <i>Genome Announcements</i> , 2016, 4, .	0.8	2

#	ARTICLE	IF	CITATIONS
12628	Web-based hybrid-dimensional Visualization and Exploration of Cytological Localization Scenarios. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 47-58.	1.0	4
12629	Complete Genome Sequence of <i>Brevibacterium linens</i> BS258, a Potential Marine Actinobacterium for Environmental Remediation via Microbially Induced Calcite Precipitation. <i>Journal of Oceanography and Marine Research</i> , 2016, 04, .	0.1	8
12631	Chemical Similarity Networks for Drug Discovery. , 0, , .		5
12632	Health Concept and Knowledge Management: Twenty-five Years of Evolution. <i>Yearbook of Medical Informatics</i> , 2016, 25, S32-S41.	0.8	12
12633	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
12634	The Classification of SiniDecoction Pattern in Traditional Chinese Medicine by Gene Expression Profiling. <i>Evidence-based Complementary and Alternative Medicine</i> , 2016, 2016, 1-13.	0.5	4
12635	Gene Expression Analysis of Fibroblasts from Patients with Bipolar Disorder. <i>Journal of Neuropsychopharmacology & Mental Health</i> , 2016, 01, .	0.1	0
12636	Predicting Diagnostic Gene Biomarkers for Non-Small-Cell Lung Cancer. <i>BioMed Research International</i> , 2016, 2016, 1-8.	0.9	5
12637	Annotating the Function of the Human Genome with Gene Ontology and Disease Ontology. <i>BioMed Research International</i> , 2016, 2016, 1-8.	0.9	16
12638	Identification of differentially expressed genes in salivary adenoid cystic carcinoma cells associated with metastasis. <i>Archives of Medical Science</i> , 2016, 4, 881-888.	0.4	15
12639	Identification of disturbed pathways in heart failure based on Gibbs sampling and pathway enrichment analysis. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	6
12640	Gene-Disease Interaction Retrieval from Multiple Sources: A Network Based Method. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	5
12641	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. <i>Frontiers in Microbiology</i> , 2016, 7, 238.	1.5	66
12642	Using predictive specificity to determine when gene set analysis is biologically meaningful. <i>Nucleic Acids Research</i> , 2017, 45, gkw957.	6.5	32
12643	Sparse models for imaging genetics. , 2016, , 129-151.		2
12644	Selective forces and mutational biases drive stop codon usage in the human genome: a comparison with sense codon usage. <i>BMC Genomics</i> , 2016, 17, 366.	1.2	25
12645	Genome-wide characterization of non-reference transposons in crops suggests non-random insertion. <i>BMC Genomics</i> , 2016, 17, 536.	1.2	13
12646	Transcriptomics of liver and muscle in Holstein cows genetically divergent for fertility highlight differences in nutrient partitioning and inflammation processes. <i>BMC Genomics</i> , 2016, 17, 603.	1.2	18

#	ARTICLE	IF	CITATIONS
12647	In Vitro Model for Hepatotoxicity Studies Based on Primary Human Hepatocyte Cultivation in a Perfused 3D Bioreactor System. <i>International Journal of Molecular Sciences</i> , 2016, 17, 584.	1.8	19
12648	Sexually Dimorphic Gene Expression Associated with Growth and Reproduction of Tongue Sole (<i>Cynoglossus semilaevis</i>) Revealed by Brain Transcriptome Analysis. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1402.	1.8	15
12649	PeanutBase and Other Bioinformatic Resources for Peanut. , 2016, , 241-252.		46
12650	Advancing Exposure Science through Chemical Data Curation and Integration in the Comparative Toxicogenomics Database. <i>Environmental Health Perspectives</i> , 2016, 124, 1592-1599.	2.8	39
12651	Gene expression profiling analysis of the role of miR-22 in clear cell ovarian cancer. <i>Neoplasma</i> , 2016, 63, 856-864.	0.7	5
12652	Integrated Analysis of Expression Profile Based on Differentially Expressed Genes in Middle Cerebral Artery Occlusion Animal Models. <i>International Journal of Molecular Sciences</i> , 2016, 17, 776.	1.8	12
12653	Transcriptome Sequencing of <i>Gynostemma pentaphyllum</i> to Identify Genes and Enzymes Involved in Triterpenoid Biosynthesis. <i>International Journal of Genomics</i> , 2016, 2016, 1-10.	0.8	8
12654	De novo Transcriptome Sequencing of Cold-treated Kentucky Bluegrass (<i>Poa pratensis</i>) and Analysis of the Genes Involved in Cold Tolerance. <i>Journal of Horticulture</i> , 2016, 3, .	0.3	3
12655	Network analysis reveals potential markers for pediatric adrenocortical carcinoma. <i>OncoTargets and Therapy</i> , 2016, Volume 9, 4569-4581.	1.0	33
12656	Comparative analysis of the liver tissue transcriptomes of Mongolian and Lanzhou fat-tailed sheep. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	11
12657	De novo assembly and analysis of changes in the protein-coding transcriptome of the freshwater shrimp <i>Paratya australiensis</i> (Decapoda: Atyidae) in response to acid sulfate drainage water. <i>BMC Genomics</i> , 2016, 17, 890.	1.2	12
12658	Genetic variants and risk of prostate cancer using pathway analysis of a genome-wide association study. <i>Neoplasma</i> , 2016, 63, 629-634.	0.7	10
12659	Transcriptome responses to temperature, water availability and photoperiod are conserved among mature trees of two divergent Douglas-fir provenances from a coastal and an interior habitat. <i>BMC Genomics</i> , 2016, 17, 682.	1.2	26
12660	Development of an in vitro human liver system for interrogating nonalcoholic steatohepatitis. <i>JCI Insight</i> , 2016, 1, e90954.	2.3	98
12661	The green ash transcriptome and identification of genes responding to abiotic and biotic stresses. <i>BMC Genomics</i> , 2016, 17, 702.	1.2	32
12662	Enhancing Interpretability of Gene Signatures with Prior Biological Knowledge. <i>Microarrays (Basel)</i> Tj ETQq1 1 0.784314 rgBT ₃ /Overlock	1.4	3
12663	Ontology Update in the Cognitive Model of Ontology Learning. <i>ITM Web of Conferences</i> , 2016, 7, 05010.	0.4	0
12664	Bioinformatics analysis of the gene expression profile of hepatocellular carcinoma: preliminary results. <i>Wspolczesna Onkologia</i> , 2016, 1, 20-27.	0.7	8

#	ARTICLE	IF	CITATIONS
12665	Integration and Weighing of Omics Data for Obesity. <i>Journal of Diabetes & Metabolism</i> , 2016, 7, .	0.2	0
12666	Laying a Community-Based Foundation for Data-Driven Semantic Standards in Environmental Health Sciences. <i>Environmental Health Perspectives</i> , 2016, 124, 1136-1140.	2.8	21
12667	Practical aspects of NGS-based pathways analysis for personalized cancer science and medicine. <i>Oncotarget</i> , 2016, 7, 52493-52516.	0.8	15
12668	Text mining resources for the life sciences. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, .	1.4	44
12669	Interconnections Between RNA-Processing Pathways Revealed by a Sequencing-Based Genetic Screen for Pre-mRNA Splicing Mutants in Fission Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1513-1523.	0.8	14
12670	Microbial culturomics unravels the halophilic microbiota repertoire of table salt: description of <i>Gracilibacillus massiliensis</i> sp. nov.. <i>Microbial Ecology in Health and Disease</i> , 2016, 27, 32049.	3.8	54
12671	Data-intensive drug development in the information age: applications of Systems Biology/Pharmacology/Toxicology. <i>Journal of Toxicological Sciences</i> , 2016, 41, SP15-SP25.	0.7	4
12672	Knowledge Representation and Management: a Linked Data Perspective. <i>Yearbook of Medical Informatics</i> , 2016, 25, 178-183.	0.8	17
12673	Complete Genome Sequence of <i>Pontibacter akesuensis</i> Strain AKS 1 T , Which Exhibits Robust Nutrient Metabolism in Harsh Environments. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
12674	Analyzing and Visualizing Genomic Complexity for the Derivation of the Emergent Molecular Networks. <i>International Journal of Monitoring and Surveillance Technologies Research</i> , 2016, 4, 30-49.	0.3	18
12675	Comparative Genomics of <i>H. pylori</i> and Non- <i>Pylori Helicobacter</i> Species to Identify New Regions Associated with Its Pathogenicity and Adaptability. <i>BioMed Research International</i> , 2016, 2016, 1-15.	0.9	20
12676	Clinical Application of a Modular Genomics Technique in Systemic Lupus Erythematosus: Progress towards Precision Medicine. <i>International Journal of Genomics</i> , 2016, 2016, 1-7.	0.8	11
12677	Classification of Non-Small Cell Lung Cancer Using Significance Analysis of Microarray-Gene Set Reduction Algorithm. <i>BioMed Research International</i> , 2016, 2016, 1-8.	0.9	14
12678	Identification and Characterization of Small Noncoding RNAs in Genome Sequences of the Edible Fungus <i>Pleurotus ostreatus</i> . <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	38
12679	Identification of the Key Genes and Pathways in Esophageal Carcinoma. <i>Gastroenterology Research and Practice</i> , 2016, 2016, 1-11.	0.7	19
12680	Leveraging Comparative Genomics to Identify and Functionally Characterize Genes Associated with Sperm Phenotypes in <i>Python bivittatus</i> (Burmese Python). <i>Genetics Research International</i> , 2016, 2016, 1-16.	2.0	0
12681	Differentially Expressed miRNAs in Tumor, Adjacent, and Normal Tissues of Lung Adenocarcinoma. <i>BioMed Research International</i> , 2016, 2016, 1-10.	0.9	28
12682	Hipposeq: a comprehensive RNA-seq database of gene expression in hippocampal principal neurons. <i>ELife</i> , 2016, 5, e14997.	2.8	355

#	ARTICLE	IF	CITATIONS
12683	Androgen Modulates Functions of Endothelial Progenitor Cells through Activated Egr1 Signaling. <i>Stem Cells International</i> , 2016, 2016, 1-16.	1.2	12
12684	Reconstruction of the Fatty Acid Biosynthetic Pathway of <i>Exiguobacterium antarcticum</i> B7 Based on Genomic and Bibliomic Data. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	5
12685	Assessing the Gene Content of the Megagenome: Sugar Pine (<i>Pinus lambertiana</i>). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3787-3802.	0.8	51
12686	Identification and Evolutionary Analysis of Potential Candidate Genes in a Human Eating Disorder. <i>BioMed Research International</i> , 2016, 2016, 1-11.	0.9	7
12687	Aberrant LncRNA Expression Profile in a Contusion Spinal Cord Injury Mouse Model. <i>BioMed Research International</i> , 2016, 2016, 1-10.	0.9	35
12688	Transcriptomic Profiling Using Next Generation Sequencing - Advances, Advantages, and Challenges. , O, , .		8
12689	Lamina Associated Polypeptide 1 (LAP1) Interactome and Its Functional Features. <i>Membranes</i> , 2016, 6, 8.	1.4	19
12690	Transcriptome Sequencing and Development of Genic SSR Markers of an Endangered Chinese Endemic Genus <i>Dipteronia</i> Oliver (<i>Aceraceae</i>). <i>Molecules</i> , 2016, 21, 166.	1.7	24
12691	Regulatory complexity revealed by integrated cytological and RNA-seq analyses of meiotic substages in mouse spermatocytes. <i>BMC Genomics</i> , 2016, 17, 628.	1.2	35
12692	An Integrated Analysis of the Genome-Wide Profiles of DNA Methylation and mRNA Expression Defining the Side Population of a Human Malignant Mesothelioma Cell Line. <i>Journal of Cancer</i> , 2016, 7, 1668-1679.	1.2	22
12693	The genetic basis for ecological adaptation of the Atlantic herring revealed by genome sequencing. <i>ELife</i> , 2016, 5, .	2.8	143
12694	A transcriptional blueprint for a spiral-cleaving embryo. <i>BMC Genomics</i> , 2016, 17, 552.	1.2	20
12695	Systems Perturbation Analysis of a Large-Scale Signal Transduction Model Reveals Potentially Influential Candidates for Cancer Therapeutics. <i>Frontiers in Bioengineering and Biotechnology</i> , 2016, 4, 10.	2.0	29
12696	Label-Free Proteomics Assisted by Affinity Enrichment for Elucidating the Chemical Reactivity of the Liver Mitochondrial Proteome toward Adduction by the Lipid Electrophile 4-hydroxy-2-nonenal (HNE). <i>Frontiers in Chemistry</i> , 2016, 4, 2.	1.8	21
12697	Proteome-Wide Effect of 17- β -Estradiol and Lipoxin A4 in an Endometriotic Epithelial Cell Line. <i>Frontiers in Endocrinology</i> , 2015, 6, 192.	1.5	3
12698	Genome-Wide Expression Profiling Reveals S100B as Biomarker for Invasive Aspergillosis. <i>Frontiers in Microbiology</i> , 2016, 7, 320.	1.5	9
12699	Differential Biphasic Transcriptional Host Response Associated with Coevolution of Hemagglutinin Quasispecies of Influenza A Virus. <i>Frontiers in Microbiology</i> , 2016, 7, 1167.	1.5	11
12700	Nitrogen Metabolism and Growth Enhancement in Tomato Plants Challenged with <i>Trichoderma harzianum</i> Expressing the <i>Aspergillus nidulans</i> Acetamidase <i>amdS</i> Gene. <i>Frontiers in Microbiology</i> , 2016, 7, 1182.	1.5	34

#	ARTICLE	IF	CITATIONS
12701	Genome Sequence of <i>Pseudomonas koreensis</i> CRS05-R5, an Antagonistic Bacterium Isolated from Rice Paddy Field. <i>Frontiers in Microbiology</i> , 2016, 7, 1756.	1.5	20
12702	SUR1 Receptor Interaction with Hesperidin and Linarin Predicts Possible Mechanisms of Action of <i>Valeriana officinalis</i> in Parkinson. <i>Frontiers in Aging Neuroscience</i> , 2016, 8, 97.	1.7	27
12703	A Pathway Proteomic Profile of Ischemic Stroke Survivors Reveals Innate Immune Dysfunction in Association with Mild Symptoms of Depression – A Pilot Study. <i>Frontiers in Neurology</i> , 2016, 7, 85.	1.1	34
12704	Gene Prioritization for Imaging Genetics Studies Using Gene Ontology and a Stratified False Discovery Rate Approach. <i>Frontiers in Neuroinformatics</i> , 2016, 10, 14.	1.3	7
12705	Expression Profiles and Biological Roles of miR-196a in Swine. <i>Genes</i> , 2016, 7, 5.	1.0	10
12706	Comparative Transcriptome Profile of the Cytoplasmic Male Sterile and Fertile Floral Buds of Radish (<i>Raphanus sativus</i> L.). <i>International Journal of Molecular Sciences</i> , 2016, 17, 42.	1.8	29
12707	Active and Repressive Chromatin-Associated Proteome after MPA Treatment and the Role of Midkine in Epithelial Monolayer Permeability. <i>International Journal of Molecular Sciences</i> , 2016, 17, 597.	1.8	4
12708	Chronic Heat Stress Induces Immune Response, Oxidative Stress Response, and Apoptosis of Finishing Pig Liver: A Proteomic Approach. <i>International Journal of Molecular Sciences</i> , 2016, 17, 393.	1.8	79
12709	Human Milk Cells Contain Numerous miRNAs that May Change with Milk Removal and Regulate Multiple Physiological Processes. <i>International Journal of Molecular Sciences</i> , 2016, 17, 956.	1.8	58
12710	<i>Piriformospora indica</i> Stimulates Root Metabolism of <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2016, 17, 1091.	1.8	35
12711	Gene Set ⁺ -Based Integrative Analysis Revealing Two Distinct Functional Regulation Patterns in Four Common Subtypes of Epithelial Ovarian Cancer. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1272.	1.8	15
12712	Maternal Chromium Restriction Leads to Glucose Metabolism Imbalance in Mice Offspring through Insulin Signaling and Wnt Signaling Pathways. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1767.	1.8	22
12713	Identification and Characterization of MicroRNAs in the Liver of Blunt Snout Bream (<i>Megalobrama</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 17, 1972.	1.8	14
12714	Human Intervention Study to Assess the Effects of Supplementation with Olive Leaf Extract on Peripheral Blood Mononuclear Cell Gene Expression. <i>International Journal of Molecular Sciences</i> , 2016, 17, 2019.	1.8	24
12715	Functional Annotations of Paralogs: A Blessing and a Curse. <i>Life</i> , 2016, 6, 39.	1.1	45
12716	Generalized enrichment analysis improves the detection of adverse drug events from the biomedical literature. <i>BMC Bioinformatics</i> , 2016, 17, 250.	1.2	9
12717	Statistical inference for time course RNA-Seq data using a negative binomial mixed-effect model. <i>BMC Bioinformatics</i> , 2016, 17, 324.	1.2	21
12718	Fusing literature and full network data improves disease similarity computation. <i>BMC Bioinformatics</i> , 2016, 17, 326.	1.2	16

#	ARTICLE	IF	CITATIONS
12719	GeneSCF: a real-time based functional enrichment tool with support for multiple organisms. BMC Bioinformatics, 2016, 17, 365.	1.2	87
12720	CicerTransDB 1.0: a resource for expression and functional study of chickpea transcription factors. BMC Plant Biology, 2016, 16, 169.	1.6	16
12721	Conservation and diversification of the transcriptomes of adult <i>Paragonimus westermani</i> and <i>P. skrjabini</i> . Parasites and Vectors, 2016, 9, 497.	1.0	10
12722	Identification and characterization of miRNAs and targets in flax (<i>Linum usitatissimum</i>) under saline, alkaline, and saline-alkaline stresses. BMC Plant Biology, 2016, 16, 124.	1.6	57
12723	Innate immune defects in HIV permissive cell lines. Retrovirology, 2016, 13, 43.	0.9	17
12724	Community-Reviewed Biological Network Models for Toxicology and Drug Discovery Applications. Gene Regulation and Systems Biology, 2016, 10, GRSB.S39076.	2.3	10
12725	Permutation test implementation for testing set of genetic hypotheses using GPU. , 2016, , .		0
12726	m6A-Driver: Identifying Context-Specific mRNA m6A Methylation-Driven Gene Interaction Networks. PLoS Computational Biology, 2016, 12, e1005287.	1.5	38
12727	Biosynthesis of Antibiotic Leucinostatins in Bio-control Fungus <i>Purpureocillium lilacinum</i> and Their Inhibition on <i>Phytophthora</i> Revealed by Genome Mining. PLoS Pathogens, 2016, 12, e1005685.	2.1	122
12728	The Genome of the Toluene-Degrading <i>Pseudomonas veronii</i> Strain 1YdBTEX2 and Its Differential Gene Expression in Contaminated Sand. PLoS ONE, 2016, 11, e0165850.	1.1	24
12729	Structural and Functional Characterization of a <i>Caenorhabditis elegans</i> Genetic Interaction Network within Pathways. PLoS Computational Biology, 2016, 12, e1004738.	1.5	3
12730	AuPairWise: A Method to Estimate RNA-Seq Replicability through Co-expression. PLoS Computational Biology, 2016, 12, e1004868.	1.5	11
12731	Single-Cell Co-expression Analysis Reveals Distinct Functional Modules, Co-regulation Mechanisms and Clinical Outcomes. PLoS Computational Biology, 2016, 12, e1004892.	1.5	36
12732	Integrating Transcriptomic and Proteomic Data Using Predictive Regulatory Network Models of Host Response to Pathogens. PLoS Computational Biology, 2016, 12, e1005013.	1.5	24
12733	Targeted Next-Generation Sequencing Identifies a Recurrent Mutation in MCPH1 Associating with Hereditary Breast Cancer Susceptibility. PLoS Genetics, 2016, 12, e1005816.	1.5	22
12734	Comprehensive Transcriptome Analysis of Sex-Biased Expressed Genes Reveals Discrete Biological and Physiological Features of Male and Female <i>Schistosoma japonicum</i> . PLoS Neglected Tropical Diseases, 2016, 10, e0004684.	1.3	43
12735	The <i>Anisakis</i> Transcriptome Provides a Resource for Fundamental and Applied Studies on Allergy-Causing Parasites. PLoS Neglected Tropical Diseases, 2016, 10, e0004845.	1.3	41
12736	The Effects of Ivermectin on <i>Brugia malayi</i> Females In Vitro: A Transcriptomic Approach. PLoS Neglected Tropical Diseases, 2016, 10, e0004929.	1.3	26

#	ARTICLE	IF	CITATIONS
12737	dEMBF: A Comprehensive Database of Enzymes of Microalgal Biofuel Feedstock. PLoS ONE, 2016, 11, e0146158.	1.1	12
12738	Advanced Running Performance by Genetic Predisposition in Male Dummerstorf Marathon Mice (DUhTP) Reveals Higher Sterol Regulatory Element-Binding Protein (SREBP) Related mRNA Expression in the Liver and Higher Serum Levels of Progesterone. PLoS ONE, 2016, 11, e0146748.	1.1	6
12739	Rapid Identification of Candidate Genes for Seed Weight Using the SLAF-Seq Method in Brassica napus. PLoS ONE, 2016, 11, e0147580.	1.1	70
12740	Prediction of Candidate Drugs for Treating Pancreatic Cancer by Using a Combined Approach. PLoS ONE, 2016, 11, e0149896.	1.1	6
12741	miR-130b-3p Modulates Epithelial-Mesenchymal Crosstalk in Lung Fibrosis by Targeting IGF-1. PLoS ONE, 2016, 11, e0150418.	1.1	45
12742	Transcriptome Profiling of Two Asparagus Bean (<i>Vigna unguiculata</i> subsp. <i>sesquipedalis</i>) Cultivars Differing in Chilling Tolerance under Cold Stress. PLoS ONE, 2016, 11, e0151105.	1.1	26
12743	Activation of Myenteric Glia during Acute Inflammation In Vitro and In Vivo. PLoS ONE, 2016, 11, e0151335.	1.1	69
12744	System-Wide Associations between DNA-Methylation, Gene Expression, and Humoral Immune Response to Influenza Vaccination. PLoS ONE, 2016, 11, e0152034.	1.1	53
12745	Spaceflight Activates Lipotoxic Pathways in Mouse Liver. PLoS ONE, 2016, 11, e0152877.	1.1	69
12746	A Novel Prioritization Method in Identifying Recurrent Venous Thromboembolism-Related Genes. PLoS ONE, 2016, 11, e0153006.	1.1	4
12747	Coordinated Evolution of Transcriptional and Post-Transcriptional Regulation for Mitochondrial Functions in Yeast Strains. PLoS ONE, 2016, 11, e0153523.	1.1	9
12748	The Ontology for Biomedical Investigations. PLoS ONE, 2016, 11, e0154556.	1.1	217
12749	Six Tissue Transcriptomics Reveals Specific Immune Suppression in Spleen by Dietary Polyunsaturated Fatty Acids. PLoS ONE, 2016, 11, e0155099.	1.1	13
12750	Transcription Analysis of the Myometrium of Labouring and Non-Labouring Women. PLoS ONE, 2016, 11, e0155413.	1.1	40
12751	Massive Shift in Gene Expression during Transitions between Developmental Stages of the Gall Midge, <i>Mayetiola Destructor</i> . PLoS ONE, 2016, 11, e0155616.	1.1	8
12752	Insights into Sexual Precocity of Female Oriental River Prawn <i>Macrobrachium nipponense</i> through Transcriptome Analysis. PLoS ONE, 2016, 11, e0157173.	1.1	13
12753	De novo Transcriptome Analysis of Chinese Citrus Fly, <i>Bactrocera minax</i> (Diptera: Tephritidae), by High-Throughput Illumina Sequencing. PLoS ONE, 2016, 11, e0157656.	1.1	13
12754	A Mechanistic Beta-Binomial Probability Model for mRNA Sequencing Data. PLoS ONE, 2016, 11, e0157828.	1.1	8

#	ARTICLE	IF	CITATIONS
12755	The De Novo Transcriptome and Its Functional Annotation in the Seed Beetle <i>Callosobruchus maculatus</i> . PLoS ONE, 2016, 11, e0158565.	1.1	52
12756	Whole Genome Pathway Analysis Identifies an Association of Cadmium Response Gene Loss with Copy Number Variation in Mutant p53 Bearing Uterine Endometrial Carcinomas. PLoS ONE, 2016, 11, e0159114.	1.1	7
12757	De Novo Assembly and Developmental Transcriptome Analysis of the Small White Butterfly <i>Pieris rapae</i> . PLoS ONE, 2016, 11, e0159258.	1.1	24
12758	Transcriptomic Analysis of Multipurpose Timber Yielding Tree <i>Neolamarckia cadamba</i> during Xylogenesis Using RNA-Seq. PLoS ONE, 2016, 11, e0159407.	1.1	26
12759	Comparison of miRNAs and Their Targets in Seed Development between Two Maize Inbred Lines by High-Throughput Sequencing and Degradome Analysis. PLoS ONE, 2016, 11, e0159810.	1.1	7
12760	NF-Y Binding Site Architecture Defines a C-Fos Targeted Promoter Class. PLoS ONE, 2016, 11, e0160803.	1.1	17
12761	Systems Analysis of Early Host Gene Expression Provides Clues for Transient <i>Mycobacterium avium</i> ssp <i>avium</i> vs. Persistent <i>Mycobacterium avium</i> ssp <i>paratuberculosis</i> Intestinal Infections. PLoS ONE, 2016, 11, e0161946.	1.1	12
12762	The Pre-Eclampsia Ontology: A Disease Ontology Representing the Domain Knowledge Specific to Pre-Eclampsia. PLoS ONE, 2016, 11, e0162828.	1.1	7
12763	Transcriptome Profile of the Chicken Thrombocyte: New Implications as an Advanced Immune Effector Cell. PLoS ONE, 2016, 11, e0163890.	1.1	25
12764	Dissecting the Origin of Breast Cancer Subtype Stem Cell and the Potential Mechanism of Malignant Transformation. PLoS ONE, 2016, 11, e0165001.	1.1	11
12765	Identification of Genes Discriminating Multiple Sclerosis Patients from Controls by Adapting a Pathway Analysis Method. PLoS ONE, 2016, 11, e0165543.	1.1	4
12766	De Novo Sequencing and Comparative Analysis of <i>Schima superba</i> Seedlings to Explore the Response to Drought Stress. PLoS ONE, 2016, 11, e0166975.	1.1	3
12767	Insecticidal Activity of <i>Melaleuca alternifolia</i> Essential Oil and RNA-Seq Analysis of <i>Sitophilus zeamais</i> Transcriptome in Response to Oil Fumigation. PLoS ONE, 2016, 11, e0167748.	1.1	85
12768	Prediction of Possible Biomarkers and Novel Pathways Conferring Risk to Post-Traumatic Stress Disorder. PLoS ONE, 2016, 11, e0168404.	1.1	12
12769	Comparative genomic and transcriptomic analyses of the Fuzhuan brick tea-fermentation fungus <i>Aspergillus cristatus</i> . BMC Genomics, 2016, 17, 428.	1.2	55
12770	Identification of Potential Biomarkers for Rhegmatogenous Retinal Detachment Associated with Choroidal Detachment by Vitreous iTRAQ-Based Proteomic Profiling. International Journal of Molecular Sciences, 2016, 17, 2052.	1.8	18
12771	Transcriptome Analysis of Differentially Expressed Genes Involved in Proanthocyanidin Accumulation in the Rhizomes of <i>Fagopyrum dibotrys</i> and an Irradiation-Induced Mutant. Frontiers in Physiology, 2016, 7, 100.	1.3	16
12772	Physiological Adjustments and Circulating MicroRNA Reprogramming Are Involved in Early Acclimatization to High Altitude in Chinese Han Males. Frontiers in Physiology, 2016, 7, 601.	1.3	11

#	ARTICLE	IF	CITATIONS
12773	Network Analysis-Based Approach for Exploring the Potential Diagnostic Biomarkers of Acute Myocardial Infarction. <i>Frontiers in Physiology</i> , 2016, 7, 615.	1.3	49
12774	Multi-Omics Approach Identifies Molecular Mechanisms of Plant-Fungus Mycorrhizal Interaction. <i>Frontiers in Plant Science</i> , 2015, 6, 1061.	1.7	39
12775	Transcriptome Analysis of Brassica rapa Near-Isogenic Lines Carrying Clubroot-Resistant and Susceptible Alleles in Response to Plasmodiophora brassicae during Early Infection. <i>Frontiers in Plant Science</i> , 2015, 6, 1183.	1.7	118
12776	Commentary: Comparative Transcriptome Analysis of Raphanus sativus Tissues. <i>Frontiers in Plant Science</i> , 2015, 6, 1191.	1.7	2
12777	Sequencing, De novo Assembly, Functional Annotation and Analysis of Phyllanthus amarus Leaf Transcriptome Using the Illumina Platform. <i>Frontiers in Plant Science</i> , 2016, 6, 1199.	1.7	25
12778	Physiological Characterization and Comparative Transcriptome Analysis of a Slow-Growing Reduced-Thylakoid Mutant of Chinese Cabbage (Brassica campestris ssp. pekinensis). <i>Frontiers in Plant Science</i> , 2016, 7, 3.	1.7	9
12779	De novo Transcriptome Assembly of Floral Buds of Pineapple and Identification of Differentially Expressed Genes in Response to Ethephon Induction. <i>Frontiers in Plant Science</i> , 2016, 7, 203.	1.7	17
12780	Transcriptome Analysis of Differentially Expressed Genes Provides Insight into Stolon Formation in Tulipa edulis. <i>Frontiers in Plant Science</i> , 2016, 7, 409.	1.7	27
12781	Learning from Co-expression Networks: Possibilities and Challenges. <i>Frontiers in Plant Science</i> , 2016, 7, 444.	1.7	268
12782	Transcriptome-Assisted Label-Free Quantitative Proteomics Analysis Reveals Novel Insights into Piper nigrum-Phytophthora capsici Phytopathosystem. <i>Frontiers in Plant Science</i> , 2016, 7, 785.	1.7	29
12783	Identification of miRNAs Involved in Stolon Formation in Tulipa edulis by High-Throughput Sequencing. <i>Frontiers in Plant Science</i> , 2016, 7, 852.	1.7	4
12784	Genome-Wide Sequence Variation Identification and Floral-Associated Trait Comparisons Based on the Re-sequencing of the Nagafu No. 2 and Qinguan Varieties of Apple (Malus domestica Borkh.). <i>Frontiers in Plant Science</i> , 2016, 7, 908.	1.7	33
12785	Comparative Transcriptome Analysis Reveals Heat-Responsive Genes in Chinese Cabbage (Brassica rapa). <i>Frontiers in Plant Science</i> , 2016, 7, 1046.	1.7	46
12786	Partial Activation of SA- and JA-Defensive Pathways in Strawberry upon Colletotrichum acutatum Interaction. <i>Frontiers in Plant Science</i> , 2016, 7, 1036.	1.7	55
12787	Identification and Comparative Analysis of Differential Gene Expression in Soybean Leaf Tissue under Drought and Flooding Stress Revealed by RNA-Seq. <i>Frontiers in Plant Science</i> , 2016, 7, 1044.	1.7	116
12788	Highlighting the Need for Systems-Level Experimental Characterization of Plant Metabolic Enzymes. <i>Frontiers in Plant Science</i> , 2016, 7, 1127.	1.7	2
12789	Transcriptome Analysis of Sucrose Metabolism during Bulb Swelling and Development in Onion (Allium cepa L.). <i>Frontiers in Plant Science</i> , 2016, 7, 1425.	1.7	49
12790	Transcriptome Analysis and Ultrastructure Observation Reveal that Hawthorn Fruit Softening Is due to Cellulose/Hemicellulose Degradation. <i>Frontiers in Plant Science</i> , 2016, 7, 1524.	1.7	35

#	ARTICLE	IF	CITATIONS
12791	Differential Gene Expression in <i>Rhododendron fortunei</i> Roots Colonized by an Ericoid Mycorrhizal Fungus and Increased Nitrogen Absorption and Plant Growth. <i>Frontiers in Plant Science</i> , 2016, 7, 1594.	1.7	21
12792	Modeling Rice Metabolism: From Elucidating Environmental Effects on Cellular Phenotype to Guiding Crop Improvement. <i>Frontiers in Plant Science</i> , 2016, 7, 1795.	1.7	18
12793	Identity, proliferation capacity, genomic stability and novel senescence markers of mesenchymal stem cells isolated from low volume of human bone marrow. <i>Oncotarget</i> , 2016, 7, 10788-10802.	0.8	41
12794	OCT4 Remodels the Phenotype and Promotes Angiogenesis of HUVECs by Changing the Gene Expression Profile. <i>International Journal of Medical Sciences</i> , 2016, 13, 386-394.	1.1	8
12795	eQTL mapping. , 0, , 208-228.		0
12796	Saffron-Based Crocin Prevents Early Lesions of Liver Cancer: In vivo, In vitro and Network Analyses. <i>Recent Patents on Anti-Cancer Drug Discovery</i> , 2016, 11, 121-133.	0.8	70
12797	Bioinformatics Tools in Epigenomics Studies. , 2016, , 73-107.		1
12798	Expression profile analysis of long noncoding RNA in HER-2-enriched subtype breast cancer by next-generation sequencing and bioinformatics. <i>OncoTargets and Therapy</i> , 2016, 9, 761.	1.0	79
12799	Finding Low-Conductance sets with Dense interactions (FLCD) for better protein complex prediction. , 2016, , .		0
12800	Medical Big Data Analysis in Hospital Information System. , 0, , .		7
12802	Smell of pain: intersection of nociception and olfaction. <i>Pain</i> , 2016, 157, 2152-2157.	2.0	23
12803	A genome-wide association study of copy number variations with umbilical hernia in swine. <i>Animal Genetics</i> , 2016, 47, 298-305.	0.6	36
12804	Genome-wide association mapping and pathway analysis of leukosis incidence in a US Holstein cattle population. <i>Animal Genetics</i> , 2016, 47, 395-407.	0.6	25
12805	Transcriptional signature induced by a metastasis-promoting c-Myc mutant in a human breast cell line. <i>FEBS Journal</i> , 2016, 283, 1669-1688.	2.2	8
12806	Molecular serum signature of treatment resistant depression. <i>Psychopharmacology</i> , 2016, 233, 3051-3059.	1.5	20
12807	Epigenome-wide DNA methylation analysis implicates neuronal and inflammatory signaling pathways in adult murine hepatic tumorigenesis following perinatal exposure to bisphenol A. <i>Environmental and Molecular Mutagenesis</i> , 2016, 57, 435-446.	0.9	10
12808	An overview of innovations and industrial solutions in Protein Microarray Technology. <i>Proteomics</i> , 2016, 16, 1297-1308.	1.3	34
12809	Comparative analyses of quaternary arrangements in homo-oligomeric proteins in superfamilies: Functional implications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1190-1202.	1.5	3

#	ARTICLE	IF	CITATIONS
12810	Transcriptomic response to injury sheds light on the physiological costs of reproduction in ant queens. <i>Molecular Ecology</i> , 2016, 25, 1972-1985.	2.0	12
12811	Plasma proteomics for the assessment of acute renal transplant rejection. <i>Life Sciences</i> , 2016, 158, 111-120.	2.0	13
12812	Prostate Cancer-Associated Kallikrein-Related Peptidase 4 Activates Matrix Metalloproteinase-1 and Thrombospondin-1. <i>Journal of Proteome Research</i> , 2016, 15, 2466-2478.	1.8	30
12813	RegenBase: a knowledge base of spinal cord injury biology for translational research. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw040.	1.4	14
12814	Combinatorial <i>Cis</i> -regulation in <i>Saccharomyces</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 653-667.	0.8	10
12815	Early leukocyte gene expression associated with age, burn size, and inhalation injury in severely burned adults. <i>Journal of Trauma and Acute Care Surgery</i> , 2016, 80, 250-257.	1.1	26
12816	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
12817	Middle age has a significant impact on gene expression during skin wound healing in male mice. <i>Biogerontology</i> , 2016, 17, 763-770.	2.0	4
12818	Using PSEA-Quant for Protein Set Enrichment Analysis of Quantitative Mass Spectrometry-Based Proteomics. <i>Current Protocols in Bioinformatics</i> , 2016, 53, 13.28.1-13.28.16.	25.8	8
12819	Hybrid Measure of Agreement and Expertise for Ontology Matching in Lieu of a Reference Ontology. <i>International Journal of Intelligent Systems</i> , 2016, 31, 502-525.	3.3	4
12820	Wikidata as a semantic framework for the Gene Wiki initiative. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw015.	1.4	47
12821	EXTRACT: interactive extraction of environment metadata and term suggestion for metagenomic sample annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw005.	1.4	40
12822	Gene expression under thermal stress varies across a geographical range expansion front. <i>Molecular Ecology</i> , 2016, 25, 1141-1156.	2.0	73
12823	Transcriptomic profiling of <i>Alexandrium fundyense</i> during physical interaction with or exposure to chemical signals from the parasite <i>Amoebophrya</i> . <i>Molecular Ecology</i> , 2016, 25, 1294-1307.	2.0	22
12824	Molecular mechanisms of postmating prezygotic reproductive isolation uncovered by transcriptome analysis. <i>Molecular Ecology</i> , 2016, 25, 2592-2608.	2.0	33
12825	Dynamic metabolic and transcriptomic profiling of methyl jasmonate-treated hairy roots reveals synthetic characters and regulators of lignan biosynthesis in <i>Isatis indigotica</i> . <i>Plant Biotechnology Journal</i> , 2016, 14, 2217-2227.	4.1	51
12826	The genome of black raspberry (<i>Rubus occidentalis</i>). <i>Plant Journal</i> , 2016, 87, 535-547.	2.8	111
12827	State-of-the-art housekeeping proteins for quantitative western blotting: Revisiting the first draft of the human proteome. <i>Proteomics</i> , 2016, 16, 1863-1867.	1.3	27

#	ARTICLE	IF	CITATIONS
12828	Histone deacetylase gene expression profiles are associated with outcomes in blunt trauma patients. <i>Journal of Trauma and Acute Care Surgery</i> , 2016, 80, 26-33.	1.1	14
12829	Shotgun proteomic analysis of <i>Bombyx mori</i> brain: emphasis on regulation of behavior and development of the nervous system. <i>Insect Science</i> , 2016, 23, 15-27.	1.5	3
12830	Bioinformatics Analyses of Differentially Expressed Genes Associated with Acute Myocardial Infarction. <i>Cardiovascular Therapeutics</i> , 2016, 34, 67-75.	1.1	14
12831	<scp>GAMDB</scp>: a web resource to connect microRNAs with autophagy in gerontology. <i>Cell Proliferation</i> , 2016, 49, 246-251.	2.4	10
12832	The advantage of laser capture microdissection over whole tissue analysis in proteomic profiling studies. <i>Proteomics</i> , 2016, 16, 1474-1485.	1.3	38
12833	Adaptation to nocturnality – learning from avian genomes. <i>BioEssays</i> , 2016, 38, 694-703.	1.2	13
12834	Transcriptome analysis reveals a diverse family of kinesins essential for spermatogenesis in the fern <i>Marsilea</i> . <i>Cytoskeleton</i> , 2016, 73, 145-159.	1.0	16
12835	The Disease Portals, disease gene annotation and the RGD disease ontology at the Rat Genome Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw034.	1.4	20
12836	Patterns of differentially expressed genes in oral mucosal lesions visualised under autofluorescence (VELscope [®]). <i>Oral Diseases</i> , 2016, 22, 285-296.	1.5	18
12837	Generation of Human Lens Epithelial-Like Cells From Patient-Specific Induced Pluripotent Stem Cells. <i>Journal of Cellular Physiology</i> , 2016, 231, 2555-2562.	2.0	19
12838	Peptide-based systems analysis of inflammation induced myeloid-derived suppressor cells reveals diverse signaling pathways. <i>Proteomics</i> , 2016, 16, 1881-1888.	1.3	16
12839	DrugTargetInspector: An assistance tool for patient treatment stratification. <i>International Journal of Cancer</i> , 2016, 138, 1765-1776.	2.3	8
12840	Identification of featured biomarkers in breast cancer with microRNA microarray. <i>Archives of Gynecology and Obstetrics</i> , 2016, 294, 1047-1053.	0.8	11
12841	DAPPLE 2: a Tool for the Homology-Based Prediction of Post-Translational Modification Sites. <i>Journal of Proteome Research</i> , 2016, 15, 2760-2767.	1.8	20
12842	Persistent alterations of gene expression profiling of human peripheral blood mononuclear cells from smokers. <i>Molecular Carcinogenesis</i> , 2016, 55, 1424-1437.	1.3	4
12843	Review on proteomics for food authentication. <i>Journal of Proteomics</i> , 2016, 147, 212-225.	1.2	136
12844	Proteomic profile of mouse fibroblasts exposed to pure magnesium extract. <i>Materials Science and Engineering C</i> , 2016, 69, 522-531.	3.8	9
12845	Genome-Wide Identification of Regulatory Sequences Undergoing Accelerated Evolution in the Human Genome. <i>Molecular Biology and Evolution</i> , 2016, 33, 2565-2575.	3.5	64

#	ARTICLE	IF	CITATIONS
12846	Suppressing Farnesyl Diphosphate Synthase Alters Chloroplast Development and Triggers Sterol-Dependent Induction of Jasmonate- and Fe-Related Responses. <i>Plant Physiology</i> , 2016, 172, 93-117.	2.3	32
12847	An Integrated Clinico-transcriptomic Approach Identifies a Central Role of the Heme Degradation Pathway for Septic Complications after Trauma. <i>Annals of Surgery</i> , 2016, 264, 1125-1134.	2.1	13
12848	<sc>SMC</sc>3 may play an important role in atopic asthma development. <i>Clinical Respiratory Journal</i> , 2016, 10, 469-476.	0.6	6
12849	The Zfh3-Mediated Axis Regulates Sleep and Interval Timing in Mice. <i>Cell Reports</i> , 2016, 16, 615-621.	2.9	33
12850	Insight : An ontology-based integrated database and analysis platform for epilepsy self-management research. <i>International Journal of Medical Informatics</i> , 2016, 94, 21-30.	1.6	10
12851	Metaproteomic data analysis at a glance: advances in computational microbial community proteomics. <i>Expert Review of Proteomics</i> , 2016, 13, 757-769.	1.3	67
12852	Preâ€<sc>mRNA</sc> splicing is modulated by antifungal drugs in the filamentous fungus <i>Neurospora crassa</i>. <i>FEBS Open Bio</i> , 2016, 6, 358-368.	1.0	18
12853	Landscape of expression profiles in esophageal carcinoma by The Cancer Genome Atlas data. <i>Ecological Management and Restoration</i> , 2016, 29, 920-928.	0.2	26
12854	Alternative splicing enhances transcriptome complexity in desiccating seeds. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 947-958.	4.1	26
12855	Genomic and phenotypic differentiation of <i>Arabidopsis thaliana</i> along altitudinal gradients in the North Italian Alps. <i>Molecular Ecology</i> , 2016, 25, 3574-3592.	2.0	47
12856	<sc><i>D</i></sc> <i>eâ€%novo</i> analysis of the transcriptome of <sc><i>P</i></sc> <i>ratylenchus zae</i> to identify transcripts for proteins required for structural integrity, sensation, locomotion and parasitism. <i>Molecular Plant Pathology</i> , 2016, 17, 532-552.	2.0	27
12857	Heterozygote Advantage Is a Common Outcome of Adaptation in <i>Saccharomyces cerevisiae</i>. <i>Genetics</i> , 2016, 203, 1401-1413.	1.2	38
12858	dbWGFP: a database and web server of human whole-genome single nucleotide variants and their functional predictions. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw024.	1.4	27
12859	CoDNaS 2.0: a comprehensive database of protein conformational diversity in the native state. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw038.	1.4	60
12860	From data repositories to submission portals: rethinking the role of domain-specific databases in CollecTF. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw055.	1.4	20
12861	<sc>GEMC</sc> 1 is a critical regulator of multiciliated cell differentiation. <i>EMBO Journal</i> , 2016, 35, 942-960.	3.5	91
12862	Draft genome sequences of three <i>Xanthomonas translucens</i> pathovar reference strains (pv.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 T. <i>Genomic Sciences</i> , 2016, 11, 50.	1.5	6
12863	Whole-transcriptome response to water stress in a California endemic oak, <i>Quercus lobata</i>. <i>Tree Physiology</i> , 2017, 37, 632-644.	1.4	37

#	ARTICLE	IF	CITATIONS
12864	Pathway-Specific Polygenic Risk Scores as Predictors of Amyloid- β^2 Deposition and Cognitive Function in a Sample at Increased Risk for Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2016, 55, 473-484.	1.2	93
12865	Protein Function Detection Based on Machine Learning: Survey and Possible Solutions. , 2016, , .		0
12866	Propagation on Molecular Interaction Networks: Prediction of Effective Drug Combinations and Biomarkers in Cancer Treatment. <i>Current Pharmaceutical Design</i> , 2016, 22, 1-1.	0.9	2
12867	Comparative transcriptome analysis revealing dormant conidia and germination associated genes in <i>Aspergillus</i> species: an essential role for AtfA in conidial dormancy. <i>BMC Genomics</i> , 2016, 17, 358.	1.2	67
12868	The Interaction Network Ontology-supported modeling and mining of complex interactions represented with multiple keywords in biomedical literature. <i>BioData Mining</i> , 2016, 9, 41.	2.2	7
12869	Construction of a large collection of small genome variations in French dairy and beef breeds using whole-genome sequences. <i>Genetics Selection Evolution</i> , 2016, 48, 87.	1.2	15
12871	Distinct properties of proteases and nucleases in the gut, salivary gland and saliva of southern green stink bug, <i>Nezara viridula</i> . <i>Scientific Reports</i> , 2016, 6, 27587.	1.6	64
12872	Genome-wide analysis of miRNAs in the ovaries of Jining Grey and Laiwu Black goats to explore the regulation of fecundity. <i>Scientific Reports</i> , 2016, 6, 37983.	1.6	44
12873	Microarray analysis of differentially-expressed genes and linker genes associated with the molecular mechanism of colorectal cancer. <i>Oncology Letters</i> , 2016, 12, 3250-3258.	0.8	19
12874	Changes in the Membrane-Associated Proteins of Exosomes Released from Human Macrophages after <i>Mycobacterium tuberculosis</i> Infection. <i>Scientific Reports</i> , 2016, 6, 37975.	1.6	51
12875	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
12876	Complete genome sequence of <i>Pseudomonas citronellolis</i> P3B5, a candidate for microbial phyllo-remediation of hydrocarbon-contaminated sites. <i>Standards in Genomic Sciences</i> , 2016, 11, 75.	1.5	49
12877	Deregulated expression of HDAC9 in B-cells promotes development of lymphoproliferative disease and lymphoma. <i>DMM Disease Models and Mechanisms</i> , 2016, 9, 1483-1495.	1.2	37
12878	New insights into the <i>Plasmodium vivax</i> transcriptome using RNA-Seq. <i>Scientific Reports</i> , 2016, 6, 20498.	1.6	65
12879	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
12880	Cocaine promotes primary human astrocyte proliferation via JNK-dependent up-regulation of cyclin A2. <i>Restorative Neurology and Neuroscience</i> , 2016, 34, 965-976.	0.4	10
12881	A Network of Splice Isoforms for the Mouse. <i>Scientific Reports</i> , 2016, 6, 24507.	1.6	17
12882	Large-scale correlation mining for biomolecular network discovery. , 2016, , 409-436.		1

#	ARTICLE	IF	CITATIONS
12883	Bioinformatics analysis of molecular mechanisms involved in intervertebral disc degeneration induced by TNF- α and IL-1 β . <i>Molecular Medicine Reports</i> , 2016, 13, 2925-2931.	1.1	13
12884	Identifying protein complexes via multi-network clustering. , 2016, , .		1
12885	Visualization of multiple experiment gene set analysis. , 2016, , .		0
12886	Var2GO: a web-based tool for gene variants selection. <i>BMC Bioinformatics</i> , 2016, 17, 376.	1.2	7
12887	The utilization of the OmniSearch semantic search tool to explore various microRNA regulation mechanisms in osteoarthritis. , 2016, , .		0
12888	Venom gland transcriptome analyses of two freshwater stingrays (Myliobatiformes): Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 54 24	1.6	24
12889	Arsenic resistance strategy in <i>Pantoea</i> sp. IMH: Organization, function and evolution of ars genes. <i>Scientific Reports</i> , 2016, 6, 39195.	1.6	10
12890	Schizophrenia genes discovery by mining the minimum spanning trees from multi-dimensional imaging genomic data integration. , 2016, , .		3
12891	Microarray expression profile analysis of aberrant long non-coding RNAs in esophageal squamous cell carcinoma. <i>International Journal of Oncology</i> , 2016, 48, 2543-2557.	1.4	34
12892	RNA-seq-based evaluation of bicolor tepal pigmentation in Asiatic hybrid lilies (<i>Lilium</i> spp.). <i>BMC Genomics</i> , 2016, 17, 611.	1.2	65
12893	Gene expression changes triggered by end-of-day far-red light treatment on early developmental stages of <i>Eustoma grandiflorum</i> (Raf.) Shinn.. <i>Scientific Reports</i> , 2016, 5, 17864.	1.6	8
12894	DisSim: an online system for exploring significant similar diseases and exhibiting potential therapeutic drugs. <i>Scientific Reports</i> , 2016, 6, 30024.	1.6	53
12895	Access technology to high performance resources by means of information systems. , 2016, , .		0
12896	Draft Genome Sequence of <i>Lactobacillus plantarum</i> XJ25 Isolated from Chinese Red Wine. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
12897	Embedding feature selection for large-scale hierarchical classification. , 2016, , .		9
12898	Functions in Basic Formal Ontology. <i>Applied Ontology</i> , 2016, 11, 103-128.	1.0	31
12899	Fuel: Representing function structure and function dependencies with a UML profile for function modeling. <i>Applied Ontology</i> , 2016, 11, 155-203.	1.0	4
12900	A network-based pathway-expanding approach for pathway analysis. <i>BMC Bioinformatics</i> , 2016, 17, 536.	1.2	4

#	ARTICLE	IF	CITATIONS
12901	An integrated analysis of cancer genes in thyroid cancer. <i>Oncology Reports</i> , 2016, 35, 962-970.	1.2	17
12902	Identification of genes for controlling swine adipose deposition by integrating transcriptome, whole-genome resequencing, and quantitative trait loci data. <i>Scientific Reports</i> , 2016, 6, 23219.	1.6	49
12903	Comparative transcriptome analyses of seven anurans reveal functions and adaptations of amphibian skin. <i>Scientific Reports</i> , 2016, 6, 24069.	1.6	36
12904	Ensemble cuckoo search biclustering of the gene expression data. , 2016, , .		1
12905	Discovery of biomarkers in rare diseases: innovative approaches by predictive and personalized medicine. <i>EPMA Journal</i> , 2016, 7, 24.	3.3	28
12906	On Ontology-Based Diagnosis and Defeasibility. , 2016, , .		4
12907	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
12908	Transcriptome analysis of maize resistance to <i>Fusarium graminearum</i> . <i>BMC Genomics</i> , 2016, 17, 477.	1.2	42
12909	Axiomatisation of general concept inclusions from finite interpretations. <i>Journal of Applied Non-Classical Logics</i> , 2016, 26, 1-46.	0.4	8
12910	Draft genome sequence of <i>Streptomyces</i> sp. MWW064 for elucidating the rakicidin biosynthetic pathway. <i>Standards in Genomic Sciences</i> , 2016, 11, 83.	1.5	11
12911	Draft genome sequence of <i>Streptomyces</i> sp. TP-A0867, an alchivemycin producer. <i>Standards in Genomic Sciences</i> , 2016, 11, 85.	1.5	10
12912	Network Modeling of Heterogeneous Datasets. , 2016, , 211-217.		0
12913	Functional characterization of three trehalase genes regulating the chitin metabolism pathway in rice brown planthopper using RNA interference. <i>Scientific Reports</i> , 2016, 6, 27841.	1.6	69
12914	Expression and methylation patterns partition luminal-A breast tumors into distinct prognostic subgroups. <i>Breast Cancer Research</i> , 2016, 18, 74.	2.2	75
12915	Insights from the draft genome of the subsection V (Stigonematales) cyanobacterium <i>Hapalosiphon</i> sp. Strain MRB220 associated with 2-MIB production. <i>Standards in Genomic Sciences</i> , 2016, 11, 58.	1.5	8
12916	Graphlet-based Characterization of Directed Networks. <i>Scientific Reports</i> , 2016, 6, 35098.	1.6	68
12917	Corrigendum to: Integrated transcriptomics and metabolomics reveal induction of hierarchies of resistance genes in potato against late blight. <i>Functional Plant Biology</i> , 2016, 43, 1205.	1.1	0
12918	Protein complex detection based on partially shared multi-view clustering. <i>BMC Bioinformatics</i> , 2016, 17, 371.	1.2	10

#	ARTICLE	IF	CITATIONS
12919	De-novo protein function prediction using DNA binding and RNA binding proteins as a test case. <i>Nature Communications</i> , 2016, 7, 13424.	5.8	22
12920	Permanent draft genome of strain ESFC-1: ecological genomics of a newly discovered lineage of filamentous diazotrophic cyanobacteria. <i>Standards in Genomic Sciences</i> , 2016, 11, 53.	1.5	4
12921	Characterization and phosphoproteomic analysis of a human immortalized podocyte model of Fabry disease generated using CRISPR/Cas9 technology. <i>American Journal of Physiology - Renal Physiology</i> , 2016, 311, F1015-F1024.	1.3	19
12922	Alternative splicing in tomato pollen in response to heat stress. <i>DNA Research</i> , 2017, 24, dsw051.	1.5	55
12923	Gene Ontology Based Clustering Analysis for Functionally Linked Genes and Cross-Species Comparison for SSR Biomarkers. , 2016, , .		0
12924	Novel loci and pathways significantly associated with longevity. <i>Scientific Reports</i> , 2016, 6, 21243.	1.6	145
12925	Driver gene classification reveals a substantial overrepresentation of tumor suppressors among very large chromatin-regulating proteins. <i>Scientific Reports</i> , 2016, 6, 38988.	1.6	22
12926	Evolution of chemosensory gene families in arthropods: Insight from the first inclusive comparative transcriptome analysis across spider appendages. <i>Genome Biology and Evolution</i> , 2017, 9, evw296.	1.1	43
12927	Evolutionary Histories of Gene Families in Angiosperm Trees. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 121-137.	0.3	0
12928	Kinase impact assessment in the landscape of fusion genes that retain kinase domains: a pan-cancer study. <i>Briefings in Bioinformatics</i> , 2016, 19, bbw127.	3.2	19
12929	From Berman and Hafner's teleological context to Baude and Sachs's interpretive defaults: an ontological challenge for the next decades of AI and Law. <i>Artificial Intelligence and Law</i> , 2016, 24, 371-385.	3.0	4
12930	Sixty-five years of the long march in protein secondary structure prediction: the final stretch?. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw129.	3.2	168
12931	Hypoxia-driven splicing into noncoding isoforms regulates the DNA damage response. <i>Npj Genomic Medicine</i> , 2016, 1, 16020.	1.7	22
12932	Gene regulatory network inference using PLS-based methods. <i>BMC Bioinformatics</i> , 2016, 17, 545.	1.2	46
12933	Comprehensive analysis of the long noncoding RNA HOXA11-AS gene interaction regulatory network in NSCLC cells. <i>Cancer Cell International</i> , 2016, 16, 89.	1.8	55
12934	Analysis of Annotation and Differential Expression Methods used in RNA-seq Studies in Crustacean Systems. <i>Integrative and Comparative Biology</i> , 2016, 56, 1067-1079.	0.9	20
12935	VHLdb: A database of von Hippel-Lindau protein interactors and mutations. <i>Scientific Reports</i> , 2016, 6, 31128.	1.6	36
12936	Machine Learning for Health Informatics. <i>Lecture Notes in Computer Science</i> , 2016, , .	1.0	27

#	ARTICLE	IF	CITATIONS
12937	Analysis of representative organ-specific genes and promoters of rice using a 3â€™ ORF-oriented long oligomer microarray. <i>Journal of Plant Biology</i> , 2016, 59, 579-593.	0.9	8
12938	Co-expression analysis and identification of fecundity-related long non-coding RNAs in sheep ovaries. <i>Scientific Reports</i> , 2016, 6, 39398.	1.6	74
12939	An Ensemble Based in Silico Prediction of <i>Saccharomyces Cerevisiae</i> Proteins under Mitochondrion Organization. , 2016, , .		0
12940	Genome-Wide Functional Identification of Maximal Consensus Patterns Derived from Multiple Species piRNAs. , 2016, , .		3
12941	TopolCSim: a new semantic similarity measure based on gene ontology. <i>BMC Bioinformatics</i> , 2016, 17, 296.	1.2	24
12942	GOAL: the comprehensive gene ontology analysis layer. <i>Science China Information Sciences</i> , 2016, 59, 1.	2.7	1
12943	<i>Bursaphelenchus xylophilus</i> and <i>B. mucronatus</i> secretomes: a comparative proteomic analysis. <i>Scientific Reports</i> , 2016, 6, 39007.	1.6	25
12944	Dual-seq transcriptomics reveals the battle for iron during <i>Pseudomonas aeruginosa</i> acute murine pneumonia. <i>Scientific Reports</i> , 2016, 6, 39172.	1.6	126
12945	From comorbidities of chronic obstructive pulmonary disease to identification of shared molecular mechanisms by data integration. <i>BMC Bioinformatics</i> , 2016, 17, 441.	1.2	20
12946	Identification of Development-Related Genes in the Ovaries of Adult <i>Harmonia axyridis</i> (Pallas) Lady Beetles Using a Time- Series Analysis by RNA-seq. <i>Scientific Reports</i> , 2016, 6, 39109.	1.6	14
12947	Cardiovascular proteomics in the era of big data: experimental and computational advances. <i>Clinical Proteomics</i> , 2016, 13, 23.	1.1	9
12948	Genes encoding intrinsic disorder in Eukaryota have high GC content. <i>Intrinsically Disordered Proteins</i> , 2016, 4, e1262225.	1.9	25
12949	Hum-mPLOC 3.0: prediction enhancement of human protein subcellular localization through modeling the hidden correlations of gene ontology and functional domain features. <i>Bioinformatics</i> , 2017, 33, 843-853.	1.8	88
12950	Population structure and minimum core genome typing of <i>Legionella pneumophila</i> . <i>Scientific Reports</i> , 2016, 6, 21356.	1.6	28
12951	Effects of early feeding on the host rumen transcriptome and bacterial diversity in lambs. <i>Scientific Reports</i> , 2016, 6, 32479.	1.6	148
12952	Studying the Microbiome: â€œOmicsâ€•Made Accessible. <i>Seminars in Liver Disease</i> , 2016, 36, 306-311.	1.8	4
12953	Transcriptome analysis reveals global regulation in response to CO2 supplementation in oleaginous microalga <i>Coccomyxa subellipsoidea</i> C-169. <i>Biotechnology for Biofuels</i> , 2016, 9, 151.	6.2	53
12954	An interâ€•species proteinâ€•protein interaction network across vast evolutionary distance. <i>Molecular Systems Biology</i> , 2016, 12, 865.	3.2	42

#	ARTICLE	IF	CITATIONS
12955	Searching the Mouse Genome Informatics (MGI) Resources for Information on Mouse Biology from Genotype to Phenotype. <i>Current Protocols in Bioinformatics</i> , 2016, 56, 1.7.1-1.7.16.	25.8	8
12956	Modern Proteomics – Sample Preparation, Analysis and Practical Applications. <i>Advances in Experimental Medicine and Biology</i> , 2016, , .	0.8	13
12957	Processing Neurology Clinical Data for Knowledge Discovery: Scalable Data Flows Using Distributed Computing. <i>Lecture Notes in Computer Science</i> , 2016, , 303-318.	1.0	1
12958	Integrative modelling of tumour DNA methylation quantifies the contribution of metabolism. <i>Nature Communications</i> , 2016, 7, 13666.	5.8	37
12959	Bioinformatics Tools for Proteomics Data Interpretation. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 281-341.	0.8	20
12960	Survey of the genome of <i>Pogostemon cablin</i> provides insights into its evolutionary history and sesquiterpenoid biosynthesis. <i>Scientific Reports</i> , 2016, 6, 26405.	1.6	21
12961	High-throughput sequencing reveals differential regulation of miRNAs in fenoxaprop-P-ethyl-resistant <i>Beckmannia syzigachne</i> . <i>Scientific Reports</i> , 2016, 6, 28725.	1.6	19
12962	Gene expression profiling analysis reveals a crucial gene regulating metabolism in adventitious roots of neem (<i>Azadirachta indica</i>). <i>RSC Advances</i> , 2016, 6, 114889-114898.	1.7	4
12963	Draft genome sequence of subterranean clover, a reference for genus <i>Trifolium</i> . <i>Scientific Reports</i> , 2016, 6, 30358.	1.6	33
12964	Hypoxia increases genome-wide bivalent epigenetic marking by specific gain of H3K27me3. <i>Epigenetics and Chromatin</i> , 2016, 9, 46.	1.8	63
12965	Suppressive subtractive hybridization reveals different gene expression between high and low virulence strains of <i>Cladosporium cladosporioides</i> . <i>Microbial Pathogenesis</i> , 2016, 100, 276-284.	1.3	1
12966	Tomato Databases. <i>Compendium of Plant Genomes</i> , 2016, , 245-255.	0.3	0
12967	The Asian arowana (<i>Scleropages formosus</i>) genome provides new insights into the evolution of an early lineage of teleosts. <i>Scientific Reports</i> , 2016, 6, 24501.	1.6	89
12968	Eliciting the Functional Taxonomy from protein annotations and taxa. <i>Scientific Reports</i> , 2016, 6, 31971.	1.6	14
12969	Distinct and Shared Determinants of Cardiomyocyte Contractility in Multi-Lineage Competent Ethnically Diverse Human iPSCs. <i>Scientific Reports</i> , 2016, 6, 37637.	1.6	20
12970	Identification of critical paralog groups with indispensable roles in the regulation of signaling flow. <i>Scientific Reports</i> , 2016, 6, 38588.	1.6	8
12972	Towards an open grapevine information system. <i>Horticulture Research</i> , 2016, 3, 16056.	2.9	34
12973	Ovarian transcriptomic study reveals the differential regulation of miRNAs and lncRNAs related to fecundity in different sheep. <i>Scientific Reports</i> , 2016, 6, 35299.	1.6	69

#	ARTICLE	IF	CITATIONS
12974	Gene expression and metabolism preceding soft scald, a chilling injury of "Honeycrisp" apple fruit. BMC Genomics, 2016, 17, 798.	1.2	28
12975	Enhanced resistance of PsbS-deficient rice (<i>Oryza sativa</i> L.) to fungal and bacterial pathogens. Journal of Plant Biology, 2016, 59, 616-626.	0.9	13
12976	The exploration of network motifs as potential drug targets from post-translational regulatory networks. Scientific Reports, 2016, 6, 20558.	1.6	13
12977	The complete mitochondrial genome of sponge <i>Tethya</i> sp. (Demospongiae, Tethyida, Tethyidae). Mitochondrial DNA Part B: Resources, 2016, 1, 472-474.	0.2	2
12978	shRNA target prediction informed by comprehensive enquiry (SPICE): a supporting system for high-throughput screening of shRNA library. Eurasip Journal on Bioinformatics and Systems Biology, 2016, 2016, 7.	1.4	2
12979	Screening for genes, transcription factors and miRNAs associated with the myogenic and osteogenic differentiation of human adipose tissue-derived stem cells. International Journal of Molecular Medicine, 2016, 38, 1839-1849.	1.8	9
12980	A draft genome sequence of <i>Pseudomonas veronii</i> R4: a grapevine (<i>Vitis vinifera</i> L.) root-associated strain with high biocontrol potential. Standards in Genomic Sciences, 2016, 11, 76.	1.5	12
12981	Ontology extension based on axiomatic cognitive model for Ontology learning. , 2016, , .		1
12982	RDF SKETCH MAPS - KNOWLEDGE COMPLEXITY REDUCTION FOR PRECISION MEDICINE ANALYTICS. , 2016, , .		5
12983	Draft genome sequence of <i>Fusicladium effusum</i> , cause of pecan scab. Standards in Genomic Sciences, 2016, 11, 36.	1.5	19
12984	First Draft Assembly and Annotation of the Genome of a California Endemic Oak <i>Quercus lobata</i> (Fagaceae). G3: Genes, Genomes, Genetics, 2016, 6, 3485-3495.	0.8	95
12985	Datasets for the validation of the "in vivo" siRNA-silencing of CD40 and for the detection of new markers of atherosclerosis progression in ApoE-deficient mice. Data in Brief, 2016, 9, 1105-1112.	0.5	4
12986	Jumping across biomedical contexts using compressive data fusion. Bioinformatics, 2016, 32, i90-i100.	1.8	24
12987	Prediction of FAD binding sites in electron transport proteins according to efficient radial basis function networks and significant amino acid pairs. BMC Bioinformatics, 2016, 17, 298.	1.2	50
12988	Data integration to prioritize drugs using genomics and curated data. BioData Mining, 2016, 9, 21.	2.2	14
12989	Transcriptome and Gene Expression Analysis of <i>Cylas formicarius</i> (Coleoptera: Brentidae) During Different Development Stages. Journal of Insect Science, 2016, 16, .	0.6	14
12990	Systematic Exploration of the Glycoproteome of the Beneficial Gut Isolate <i>Lactobacillus rhamnosus</i> GG. Journal of Molecular Microbiology and Biotechnology, 2016, 26, 345-358.	1.0	12
12992	DisSetSim: An online system for calculating similarity between disease sets. , 2016, , .		2

#	ARTICLE	IF	CITATIONS
12993	Towards recognition of protein function based on its structure using deep convolutional networks. , 2016, , .		11
12994	L1000CDS2: LINCS L1000 characteristic direction signatures search engine. Npj Systems Biology and Applications, 2016, 2, .	1.4	250
12995	A comprehensive (biological and computational) investigation on the role of microRNA::mRNA regulations performed in chronic obstructive pulmonary disease and lung cancer. , 2016, , .		5
12996	Feature selection based on functional group structure for microRNA expression data analysis. , 2016, , .		0
12997	InfDisSim: A novel method for measuring disease similarity based on information flow. , 2016, , .		2
12998	On the Evolutionary Significance of the Mantle Margin in Pteriomorphian Bivalves. American Malacological Bulletin, 2016, 34, 148-159.	0.2	7
12999	Between-species differences in gene copy number are enriched among functions critical for adaptive evolution in Arabidopsis halleri. BMC Genomics, 2016, 17, 1034.	1.2	28
13000	Identification of genes with nonsynonymous SNP in Jeju horse by whole-genome resequencing reveals a functional role for immune response1. Journal of Animal Science, 2016, 94, 895-901.	0.2	4
13001	Innovative microRNA-lncRNA-mRNA co-expression analysis to understand the pathogenesis and progression of diabetic kidney disease. , 2016, , .		0
13002	Bone and Cartilage Regeneration. Stem Cells in Clinical Applications, 2016, , .	0.4	1
13003	Draft Genome Sequence of <i>Botryosphaeria dothidea</i> , the Pathogen of Apple Ring Rot. Genome Announcements, 2016, 4, .	0.8	19
13004	Rhizobium etli bacteroids engineered for Vitreoscilla hemoglobin expression alleviate oxidative stress in common bean nodules that reprogramme global gene expression. Plant Biotechnology Reports, 2016, 10, 463-474.	0.9	3
13005	Non-targeted transcriptomic effects upon thyroid irradiation: similarity between in-field and out-of-field responses varies with tissue type. Scientific Reports, 2016, 6, 30738.	1.6	7
13006	A methodology for disease gene association using centrality measures. , 2016, , .		2
13007	Identification of the disease-associated genes in periodontitis using the co-expression network. Molecular Biology, 2016, 50, 124-131.	0.4	2
13008	Integrative Biological Databases. Translational Bioinformatics, 2016, , 295-307.	0.0	0
13009	Recruitment of the Mammalian Histone-modifying EMSY Complex to Target Genes Is Regulated by ZNF131. Journal of Biological Chemistry, 2016, 291, 7313-7324.	1.6	35
13010	50Âyears of Arabidopsis research: highlights and future directions. New Phytologist, 2016, 209, 921-944.	3.5	186

#	ARTICLE	IF	CITATIONS
13011	Unbiased identification of substrates of protein tyrosine phosphatase ptp ϵ 3 in <i>C. elegans</i> . <i>Molecular Oncology</i> , 2016, 10, 910-920.	2.1	16
13012	Designing biomedical proteomics experiments: state-of-the-art and future perspectives. <i>Expert Review of Proteomics</i> , 2016, 13, 495-511.	1.3	13
13013	Gene-Disease Prioritization Through Cost-Sensitive Graph-Based Methodologies. <i>Lecture Notes in Computer Science</i> , 2016, , 739-751.	1.0	2
13014	Network Ranking Assisted Semantic Data Mining. <i>Lecture Notes in Computer Science</i> , 2016, , 752-764.	1.0	0
13016	Proteomic Profiling: Data Mining and Analyses. <i>Translational Bioinformatics</i> , 2016, , 133-173.	0.0	0
13017	De novo assembly and characterization of the <i>Trichuris trichiura</i> adult worm transcriptome using Ion Torrent sequencing. <i>Acta Tropica</i> , 2016, 159, 132-141.	0.9	14
13018	CCAR1 5' UTR as a natural miRancer of miR-1254 overrides tamoxifen resistance. <i>Cell Research</i> , 2016, 26, 655-673.	5.7	62
13019	Human fibroblasts display a differential focal adhesion phenotype relative to chimpanzee. <i>Evolution, Medicine and Public Health</i> , 2016, 2016, 110-116.	1.1	6
13020	Comparison of differential gene expression to water stress among bacteria with relevant pollutant degradation properties. <i>Environmental Microbiology Reports</i> , 2016, 8, 91-102.	1.0	16
13021	High-quality genome sequence and description of <i>Chryseobacterium senegalense</i> sp. nov.. <i>New Microbes and New Infections</i> , 2016, 10, 93-100.	0.8	4
13022	Longevity-modulating effects of symbiosis: insights from <i>Drosophila</i> – <i>Wolbachia</i> interaction. <i>Biogerontology</i> , 2016, 17, 785-803.	2.0	22
13023	A dataset for assessing temporal changes in gene expression during the aging process of adult <i>Drosophila melanogaster</i> . <i>Data in Brief</i> , 2016, 7, 1652-1657.	0.5	0
13024	Post-transcriptional and translational regulation modulates gene co-expression behavior in more synchronized pace to carry out molecular function in the cell. <i>Gene</i> , 2016, 587, 163-168.	1.0	2
13025	DIANA-mirExTra v2.0: Uncovering microRNAs and transcription factors with crucial roles in NGS expression data. <i>Nucleic Acids Research</i> , 2016, 44, W128-W134.	6.5	43
13026	Bioinformatics Based Approaches to Study Virus–Host Interactions During Chikungunya Virus Infection. <i>Methods in Molecular Biology</i> , 2016, 1426, 195-200.	0.4	1
13027	Traveling on discrete embeddings of gene expression. <i>Artificial Intelligence in Medicine</i> , 2016, 70, 1-11.	3.8	1
13028	A Genome-Scale Database and Reconstruction of <i>Caenorhabditis elegans</i> Metabolism. <i>Cell Systems</i> , 2016, 2, 312-322.	2.9	46
13029	TBBPA exposure during a sensitive developmental window produces neurobehavioral changes in larval zebrafish. <i>Environmental Pollution</i> , 2016, 216, 53-63.	3.7	79

#	ARTICLE	IF	CITATIONS
13030	Gene-based and semantic structure of the Gene Ontology as a complex network. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2016, 458, 313-328.	1.2	2
13031	Transcriptome analysis of cortical tissue reveals shared sets of downregulated genes in autism and schizophrenia. <i>Translational Psychiatry</i> , 2016, 6, e817-e817.	2.4	38
13032	RNA-seq analysis of virR and revR mutants of <i>Clostridium perfringens</i> . <i>BMC Genomics</i> , 2016, 17, 391.	1.2	9
13033	The effect of growth rate on pyrazinamide activity in <i>Mycobacterium tuberculosis</i> - insights for early bactericidal activity?. <i>BMC Infectious Diseases</i> , 2016, 16, 205.	1.3	13
13034	Complete genome sequence of <i>Halanaeroarchaeum sulfurireducens</i> ™ M27-SA2, a sulfur-reducing and acetate-oxidizing haloarchaeon from the deep-sea hypersaline anoxic lake Medee. <i>Standards in Genomic Sciences</i> , 2016, 11, 35.	1.5	15
13036	Exploiting single-cell expression to characterize co-expression replicability. <i>Genome Biology</i> , 2016, 17, 101.	3.8	66
13037	Revealing the role of VEGFA in clear cell sarcoma of the kidney by protein-protein interaction network and significant pathway analysis. <i>Oncology Letters</i> , 2016, 11, 953-958.	0.8	3
13038	CGC. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2016, 10, 1-27.	2.5	9
13039	Metagenomic analysis between free-living and cultured <i>Epinephelus fuscoguttatus</i> under different environmental conditions in Indonesian waters. <i>Marine Pollution Bulletin</i> , 2016, 110, 726-734.	2.3	19
13040	Editor's Highlight: Analysis of the Effects of Cell Stress and Cytotoxicity on <i>In Vitro</i> Assay Activity Across a Diverse Chemical and Assay Space. <i>Toxicological Sciences</i> , 2016, 152, 323-339.	1.4	171
13041	Altered gene expression in the lower respiratory tract of Car6 ^{+/+} mice. <i>Transgenic Research</i> , 2016, 25, 649-664.	1.3	7
13042	Characterization of pikeperch (<i>Sander lucioperca</i>) transcriptome and development of SSR markers. <i>Biochemical Systematics and Ecology</i> , 2016, 66, 188-195.	0.6	17
13043	Construction of an immunorelated protein-protein interaction network for clarifying the mechanism of burn. <i>Burns</i> , 2016, 42, 405-413.	1.1	8
13044	Transcriptomic effects of the non-steroidal anti-inflammatory drug Ibuprofen in the marine bivalve <i>Mytilus galloprovincialis</i> Lam.. <i>Marine Environmental Research</i> , 2016, 119, 31-39.	1.1	18
13045	Comprehensive quantification of N-glycoproteome in <i>Fusarium graminearum</i> reveals intensive glycosylation changes against fungicide. <i>Journal of Proteomics</i> , 2016, 142, 82-90.	1.2	15
13046	Critical role of lysosomes in the dysfunction of human Cardiac Stem Cells obtained from failing hearts. <i>International Journal of Cardiology</i> , 2016, 216, 140-150.	0.8	16
13047	Modeling ontology evolution via Pi-Calculus. <i>Information Sciences</i> , 2016, 346-347, 286-301.	4.0	4
13048	Bioinspired Saccharide-Saccharide Interaction and Smart Polymer for Specific Enrichment of Sialylated Glycopeptides. <i>ACS Applied Materials & Interfaces</i> , 2016, 8, 13294-13302.	4.0	39

#	ARTICLE	IF	CITATIONS
13049	Sequencing and characterization of leaf transcriptomes of six diploid <i>Nicotiana</i> species. <i>Journal of Biological Research</i> , 2016, 23, 6.	2.2	13
13050	Next-generation biology: Sequencing and data analysis approaches for non-model organisms. <i>Marine Genomics</i> , 2016, 30, 3-13.	0.4	164
13051	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
13052	The global effect of exposing bakers' yeast to 5-fluoruracil and nystatin; a view to Toxichip. <i>Chemosphere</i> , 2016, 145, 470-479.	4.2	3
13053	Open PHACTS computational protocols for in silico target validation of cellular phenotypic screens: knowing the knowns. <i>MedChemComm</i> , 2016, 7, 1237-1244.	3.5	18
13054	EBI metagenomics in 2016 - an expanding and evolving resource for the analysis and archiving of metagenomic data. <i>Nucleic Acids Research</i> , 2016, 44, D595-D603.	6.5	97
13055	Transcriptomic Responses of the Interactions between <i>Clostridium cellulovorans</i> 743B and <i>Rhodospseudomonas palustris</i> CGA009 in a Cellulose-Grown Coculture for Enhanced Hydrogen Production. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4546-4559.	1.4	22
13056	Identification of the anti-tumor activity and mechanisms of nuciferine through a network pharmacology approach. <i>Acta Pharmacologica Sinica</i> , 2016, 37, 963-972.	2.8	64
13057	Differences in environmental stress response among yeasts is consistent with species-specific lifestyles. <i>Molecular Biology of the Cell</i> , 2016, 27, 1694-1705.	0.9	39
13058	Gene expression profiling identifies candidate biomarkers for active and latent tuberculosis. <i>BMC Bioinformatics</i> , 2016, 17, 3.	1.2	50
13059	Guidelines for the functional annotation of microRNAs using the Gene Ontology. <i>Rna</i> , 2016, 22, 667-676.	1.6	35
13060	Core Circadian Clock Genes Regulate Leukemia Stem Cells in AML. <i>Cell</i> , 2016, 165, 303-316.	13.5	200
13061	Cooperative Co-evolutionary Module Identification with Application to Cancer Disease Module Discovery. <i>IEEE Transactions on Evolutionary Computation</i> , 2016, , 1-1.	7.5	21
13062	Radiosensitization effect of Huaier on breast cancer cells. <i>Oncology Reports</i> , 2016, 35, 2843-2850.	1.2	22
13063	Proteins as Functional Units of Biocalcification – An Overview. <i>Key Engineering Materials</i> , 2016, 672, 183-190.	0.4	3
13064	Semantic Technologies for Managing Complex Product Information in Enterprise Systems. <i>Lecture Notes in Business Information Processing</i> , 2016, , 111-118.	0.8	1
13065	Integrating transcriptomic and metabolomic analysis to understand natural leaf senescence in sunflower. <i>Plant Biotechnology Journal</i> , 2016, 14, 719-734.	4.1	53
13066	MBPpred: Proteome-wide detection of membrane lipid-binding proteins using profile Hidden Markov Models. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 747-754.	1.1	22

#	ARTICLE	IF	CITATIONS
13067	Transcriptome profiling of immune tissues reveals habitat-specific gene expression between lake and river sticklebacks. <i>Molecular Ecology</i> , 2016, 25, 943-958.	2.0	49
13068	<i>Vibrio cholerae</i> FeoA, FeoB, and FeoC Interact To Form a Complex. <i>Journal of Bacteriology</i> , 2016, 198, 1160-1170.	1.0	34
13069	Differentially Expressed Genes in Hypericin-Containing <i>Hypericum perforatum</i> Leaf Tissues as Revealed by De Novo Assembly of RNA-Seq. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 1027-1041.	1.0	15
13070	RNA-Seq analysis of non-small cell lung cancer in female never-smokers reveals candidate cancer-associated long non-coding RNAs. <i>Pathology Research and Practice</i> , 2016, 212, 549-554.	1.0	18
13071	Transcriptomic Signature of the <i>SHATTERPROOF2</i> Expression Domain Reveals the Meristematic Nature of <i>Arabidopsis</i> Gynoecial Medial Domain. <i>Plant Physiology</i> , 2016, 171, 42-61.	2.3	32
13072	Exploring information from the topology beneath the Gene Ontology terms to improve semantic similarity measures. <i>Gene</i> , 2016, 586, 148-157.	1.0	5
13073	Adeno-associated virus gene therapy vector scAAVIGF-I for transduction of equine articular chondrocytes and RNA-seq analysis. <i>Osteoarthritis and Cartilage</i> , 2016, 24, 902-911.	0.6	15
13074	SBP2 plays an important role in the virulence changes of different artificial mutants of <i>Streptococcus suis</i> . <i>Molecular BioSystems</i> , 2016, 12, 1948-1962.	2.9	33
13075	Identification of Genes Associated with Papillary Thyroid Carcinoma (PTC) for Diagnosis by Integrated Analysis. <i>Hormone and Metabolic Research</i> , 2016, 48, 226-231.	0.7	9
13076	The Reactome pathway Knowledgebase. <i>Nucleic Acids Research</i> , 2016, 44, D481-D487.	6.5	3,319
13077	Expression profile analysis of head and neck squamous cell carcinomas using data from The Cancer Genome Atlas. <i>Molecular Medicine Reports</i> , 2016, 13, 4259-4265.	1.1	22
13078	Expression profile of long non-coding RNAs in colorectal cancer: A microarray analysis. <i>Oncology Reports</i> , 2016, 35, 2035-2044.	1.2	15
13079	Cross-Study Comparison Reveals Common Genomic, Network, and Functional Signatures of Desiccation Resistance in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 1053-1067.	3.5	26
13080	Hybrid Artificial Intelligent Systems. <i>Lecture Notes in Computer Science</i> , 2016, , .	1.0	5
13081	Complete genome of <i>Thauera humireducens</i> SgZ-1, a potential bacterium for environmental remediation and wastewater treatment. <i>Journal of Biotechnology</i> , 2016, 225, 59-60.	1.9	12
13082	The Genome and Methylome of a Subsocial Small Carpenter Bee, <i>Ceratina calcarata</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 1401-1410.	1.1	71
13084	Macrophage-secreted granulins support pancreatic cancer metastasis by inducing liver fibrosis. <i>Nature Cell Biology</i> , 2016, 18, 549-560.	4.6	329
13085	Controllability analysis of the directed human protein interaction network identifies disease genes and drug targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4976-4981.	3.3	249

#	ARTICLE	IF	CITATIONS
13086	Dissecting the proteome dynamics of the early heat stress response leading to plant survival or death in Arabidopsis. <i>Plant, Cell and Environment</i> , 2016, 39, 1264-1278.	2.8	94
13087	Identification of potential therapeutic target genes and mechanisms in head and neck squamous cell carcinoma by bioinformatics analysis. <i>Oncology Letters</i> , 2016, 11, 3009-3014.	0.8	19
13088	TRIQ: A Comprehensive Evaluation Measure for Triclustering Algorithms. <i>Lecture Notes in Computer Science</i> , 2016, , 673-684.	1.0	3
13089	Immuno-Navigator, a batch-corrected coexpression database, reveals cell type-specific gene networks in the immune system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2393-402.	3.3	58
13090	Hierarchical Feature Selection Incorporating Known and Novel Biological Information: Identifying Genomic Features Related to Prostate Cancer Recurrence. <i>Journal of the American Statistical Association</i> , 2016, 111, 1427-1439.	1.8	18
13091	Comparative Single-Cell Genomics of Chloroflexi from the Okinawa Trough Deep-Subsurface Biosphere. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3000-3008.	1.4	77
13092	Predicting Unknown Interactions Between Known Drugs and Targets via Matrix Completion. <i>Lecture Notes in Computer Science</i> , 2016, , 591-604.	1.0	4
13093	Comprehensive transcriptome analysis identifies novel molecular subtypes and subtype-specific RNAs of triple-negative breast cancer. <i>Breast Cancer Research</i> , 2016, 18, 33.	2.2	176
13094	In silico Identification and Characterization of Protein-Ligand Binding Sites. <i>Methods in Molecular Biology</i> , 2016, 1414, 1-21.	0.4	7
13095	Gene Expression Profiling Identifies Cell Proliferation and Inflammation as the Predominant Pathways Regulated by Aryl Hydrocarbon Receptor in Primary Human Fetal Lung Cells Exposed to Hyperoxia. <i>Toxicological Sciences</i> , 2016, 152, 155-168.	1.4	16
13096	Genome-wide inference of protein interaction network and its application to the study of crosstalk in Arabidopsis abscisic acid signaling. <i>Plant Physiology</i> , 2016, 171, pp.00057.2016.	2.3	27
13098	Proteome-wide dataset supporting functional study of tyrosine kinases in breast cancer. <i>Data in Brief</i> , 2016, 7, 740-746.	0.5	3
13099	Brain in situ hybridization maps as a source for reverse-engineering transcriptional regulatory networks: Alzheimer's disease insights. <i>Gene</i> , 2016, 586, 77-86.	1.0	17
13100	Transcriptome changes specifically associated with apple (<i>Malus domestica</i>) root defense response during <i>Pythium ultimum</i> infection. <i>Physiological and Molecular Plant Pathology</i> , 2016, 94, 16-26.	1.3	70
13101	Using biological networks to integrate, visualize and analyze genomics data. <i>Genetics Selection Evolution</i> , 2016, 48, 27.	1.2	86
13102	Sequencing and comparative analyses of the genomes of zoysiagrasses. <i>DNA Research</i> , 2016, 23, 171-180.	1.5	68
13103	The Cotton<i>Mitogen-Activated Protein Kinase Kinase 3</i> Functions in Drought Tolerance by Regulating Stomatal Responses and Root Growth. <i>Plant and Cell Physiology</i> , 2016, 57, 1629-1642.	1.5	83
13104	The Non-Coding RNA Ontology (NCRO): a comprehensive resource for the unification of non-coding RNA biology. <i>Journal of Biomedical Semantics</i> , 2016, 7, 24.	0.9	10

#	ARTICLE	IF	CITATIONS
13105	Evidence for two protein coding transcripts at the Igf2as locus. <i>Gene Reports</i> , 2016, 4, 60-66.	0.4	1
13106	Transcriptome analysis of grapevine shoots exposed to chilling temperature for four weeks. <i>Horticulture Environment and Biotechnology</i> , 2016, 57, 161-172.	0.7	12
13107	Ontology-Based Vaccine and Drug Adverse Event Representation and Theory-Guided Systematic Causal Network Analysis Toward Integrative Pharmacovigilance Research. <i>Current Pharmacology Reports</i> , 2016, 2, 113-128.	1.5	18
13108	Complete genome sequence of an agr-dysfunctional variant of the ST239 lineage of the methicillin-resistant <i>Staphylococcus aureus</i> strain GV69 from Brazil. <i>Standards in Genomic Sciences</i> , 2016, 11, 34.	1.5	4
13109	Standardized Profiling of The Membrane-Enriched Proteome of Mouse Dorsal Root Ganglia (DRG) Provides Novel Insights Into Chronic Pain. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2152-2168.	2.5	49
13110	Signal transduction by M3 muscarinic acetylcholine receptor in prostate cancer. <i>Oncology Letters</i> , 2016, 11, 385-392.	0.8	7
13111	A Proteomics Approach for the Identification of Novel Proteins in Extremophiles. <i>Grand Challenges in Biology and Biotechnology</i> , 2016, , 303-319.	2.4	1
13112	SoftPanel: a website for grouping diseases and related disorders for generation of customized panels. <i>BMC Bioinformatics</i> , 2016, 17, 153.	1.2	4
13113	Experiences with Aber-OWL, an Ontology Repository with OWL EL Reasoning. <i>Lecture Notes in Computer Science</i> , 2016, , 81-86.	1.0	0
13114	The omic approach to parasitic trematode research—a review of techniques and developments within the past 50 years. <i>Parasitology Research</i> , 2016, 115, 2523-2543.	0.6	10
13115	Understanding the progression of atherosclerosis through gene profiling and co-expression network analysis in Apob tm2Sgy Ldlr tm1Her double knockout mice. <i>Genomics</i> , 2016, 107, 239-247.	1.3	14
13116	Genome-Wide Functional Annotation of Human Protein-Coding Splice Variants Using Multiple Instance Learning. <i>Journal of Proteome Research</i> , 2016, 15, 1747-1753.	1.8	31
13117	Genome-wide association study for endocrine fertility traits using single nucleotide polymorphism arrays and sequence variants in dairy cattle. <i>Journal of Dairy Science</i> , 2016, 99, 5470-5485.	1.4	39
13118	Developmental Acquisition of Regulomes Underlies Innate Lymphoid Cell Functionality. <i>Cell</i> , 2016, 165, 1120-1133.	13.5	273
13119	Expression Profiles of miRNA Subsets Distinguish Human Colorectal Carcinoma and Normal Colonic Mucosa. <i>Clinical and Translational Gastroenterology</i> , 2016, 7, e152.	1.3	82
13120	Bioinformatics programs are 31-fold over-represented among the highest impact scientific papers of the past two decades. <i>Bioinformatics</i> , 2016, 32, 2686-2691.	1.8	36
13121	Comparative Transcriptomics Indicates a Role for SHORT VEGETATIVE PHASE (SVP) Genes in <i>Mimulus guttatus</i> Vernalization Response. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1239-1249.	0.8	6
13122	Identification of surface-associated proteins of <i>Bifidobacterium animalis</i> ssp. <i>lactis</i> KLDS 2.0603 by enzymatic shaving. <i>Journal of Dairy Science</i> , 2016, 99, 5155-5172.	1.4	18

#	ARTICLE	IF	CITATIONS
13123	De novo transcriptome analysis reveals tissue-specific differences in gene expression in <i>Salix arbutifolia</i> . <i>Trees - Structure and Function</i> , 2016, 30, 1647-1655.	0.9	4
13124	Utilizing a structural meta-ontology for family-based quality assurance of the BioPortal ontologies. <i>Journal of Biomedical Informatics</i> , 2016, 61, 63-76.	2.5	17
13125	Independent and Parallel Evolution of New Genes by Gene Duplication in Two Origins of C4 Photosynthesis Provides New Insight into the Mechanism of Phloem Loading in C4 Species. <i>Molecular Biology and Evolution</i> , 2016, 33, 1796-1806.	3.5	66
13126	<i>Companion</i>: a web server for annotation and analysis of parasite genomes. <i>Nucleic Acids Research</i> , 2016, 44, W29-W34.	6.5	127
13127	Bioinformatic Analysis of Potential microRNAs in Ischemic Stroke. <i>Journal of Stroke and Cerebrovascular Diseases</i> , 2016, 25, 1753-1759.	0.7	41
13128	Comparison of module detection algorithms in protein networks and investigation of the biological meaning of predicted modules. <i>BMC Bioinformatics</i> , 2016, 17, 129.	1.2	28
13129	Network-driven plasma proteomics expose molecular changes in the Alzheimer's brain. <i>Molecular Neurodegeneration</i> , 2016, 11, 31.	4.4	34
13130	Characterization of long non-coding RNA expression profiles in lymph node metastasis of early-stage cervical cancer. <i>Oncology Reports</i> , 2016, 35, 3185-3197.	1.2	57
13131	In search of underlying mechanisms and potential drugs of melphalan-induced vascular toxicity through retinal endothelial cells using bioinformatics approach. <i>Tumor Biology</i> , 2016, 37, 6709-6718.	0.8	6
13132	Genes with high penetrance for syndromic and non-syndromic autism typically function within the nucleus and regulate gene expression. <i>Molecular Autism</i> , 2016, 7, 18.	2.6	40
13133	Non contiguous-finished genome sequence and description of <i>Microbacterium gorillae</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2016, 11, 32.	1.5	24
13134	Transcriptome characterization and gene expression analysis related to sexual dimorphism in the ghost moth, <i>Thitarodes pui</i> , a host of <i>Ophiocordyceps sinensis</i> . <i>Gene</i> , 2016, 588, 134-140.	1.0	5
13135	Evidence of recent signatures of selection during domestication in an Atlantic salmon population. <i>Marine Genomics</i> , 2016, 26, 41-50.	0.4	62
13136	Transcriptomic analyses giving insights into molecular regulation mechanisms involved in cold tolerance by <i>Epichloa</i> endophyte in seed germination of <i>Achnatherum inebrians</i> . <i>Plant Growth Regulation</i> , 2016, 80, 367-375.	1.8	51
13137	Characterizing gene sets using discriminative random walks with restart on heterogeneous biological networks. <i>Bioinformatics</i> , 2016, 32, 2167-2175.	1.8	38
13138	Transcriptomic Analyses in Zebrafish Cancer Models for Global Gene Expression and Pathway Discovery. <i>Advances in Experimental Medicine and Biology</i> , 2016, 916, 147-168.	0.8	2
13139	Cell-free Determination of Binary Complexes That Comprise Extended Protein-Protein Interaction Networks of <i>Yersinia pestis</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3220-3232.	2.5	0
13140	Draft genome sequence and annotation of <i>Lactobacillus acetotolerans</i> BM-LA14527, a beer-spoilage bacteria. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw201.	0.7	45

#	ARTICLE	IF	CITATIONS
13141	New insights in Rett syndrome using pathway analysis for transcriptomics data. Wiener Medizinische Wochenschrift, 2016, 166, 346-352.	0.5	9
13142	Identification of key pathways and genes in colorectal cancer using bioinformatics analysis. Medical Oncology, 2016, 33, 111.	1.2	112
13144	De novo sequencing and transcriptome analysis of venom glands of endoparasitoid <i>Aenasius arizonensis</i> (Girault) (= <i>Aenasius bambawalei</i> Hayat) (Hymenoptera, Encyrtidae). Toxicon, 2016, 121, 134-144.	0.8	8
13145	MicroRNA expression and gene regulation drive breast cancer progression and metastasis in PyMT mice. Breast Cancer Research, 2016, 18, 75.	2.2	14
13146	The Cell Ontology 2016: enhanced content, modularization, and ontology interoperability. Journal of Biomedical Semantics, 2016, 7, 44.	0.9	201
13147	FastProject: a tool for low-dimensional analysis of single-cell RNA-Seq data. BMC Bioinformatics, 2016, 17, 315.	1.2	59
13148	DNA methylation signature of human fetal alcohol spectrum disorder. Epigenetics and Chromatin, 2016, 9, 25.	1.8	129
13149	miR-30 Family Controls Proliferation and Differentiation of Intestinal Epithelial Cell Models by Directing a Broad Gene Expression Program That Includes SOX9 and the Ubiquitin Ligase Pathway. Journal of Biological Chemistry, 2016, 291, 15975-15984.	1.6	40
13150	Transcriptome sequencing reveals genome-wide variation in molecular evolutionary rate among ferns. BMC Genomics, 2016, 17, 692.	1.2	16
13151	De novo sequencing and transcriptome analysis of female venom glands of ectoparasitoid <i>Bracon hebetor</i> (Say.) (Hymenoptera: Braconidae). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2016, 20, 101-110.	0.4	16
13152	Mining potential biomarkers associated with space flight in <i>Caenorhabditis elegans</i> experienced Shenzhou-8 mission with multiple feature selection techniques. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2016, 791-792, 27-34.	0.4	20
13153	NEAT: an efficient network enrichment analysis test. BMC Bioinformatics, 2016, 17, 352.	1.2	41
13154	Correction of Weighted Orthology and Paralogy Relations - Complexity and Algorithmic Results. Lecture Notes in Computer Science, 2016, , 121-136.	1.0	8
13155	Revealing complex function, process and pathway interactions with high-throughput expression and biological annotation data. Molecular BioSystems, 2016, 12, 3196-3208.	2.9	0
13156	Hypomethylation coordinates antagonistically with hypermethylation in cancer development: a case study of leukemia. Human Genomics, 2016, 10, 18.	1.4	40
13157	Use of Anion Exchange Resins for One-Step Processing of Algae from Harvest to Biofuel. , 2016, , 261-284.		0
13158	Microalgae Isolation and Selection for Prospective Biodiesel Production. , 2016, , 285-304.		1
13159	<i>Candida albicans</i> triggers the expression of inflammatory genes in human umbilical vein endothelial cells. Experimental and Therapeutic Medicine, 2016, 12, 1490-1494.	0.8	2

#	ARTICLE	IF	CITATIONS
13161	Lipid Biosynthesis Coordinates a Mitochondrial-to-Cytosolic Stress Response. <i>Cell</i> , 2016, 166, 1539-1552.e16.	13.5	179
13162	The Role of Retrotransposons in Gene Family Expansions in the Human and Mouse Genomes. <i>Genome Biology and Evolution</i> , 2016, 8, 2632-2650.	1.1	23
13163	Sarcoidosis activates diverse transcriptional programs in bronchoalveolar lavage cells. <i>Respiratory Research</i> , 2016, 17, 93.	1.4	21
13164	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	3.8	308
13165	High-concentrate feeding upregulates the expression of inflammation-related genes in the ruminal epithelium of dairy cattle. <i>Journal of Animal Science and Biotechnology</i> , 2016, 7, 42.	2.1	49
13166	Draft genome sequence of <i>Acinetobacter baumannii</i> strain NCTC 13423, a multidrug-resistant clinical isolate. <i>Standards in Genomic Sciences</i> , 2016, 11, 57.	1.5	6
13167	Attenuation of transcriptional and signaling responses limits viability of <i>Saccharomyces cerevisiae</i> during periods of glucose deprivation. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2563-2575.	1.1	2
13168	Using the Tools and Resources of the RCSB Protein Data Bank. <i>Current Protocols in Bioinformatics</i> , 2016, 55, 1.9.1-1.9.35.	25.8	8
13169	Blot-MS of Carbonylated Proteins: A Tool to Identify Oxidized Proteins. <i>Methods in Molecular Biology</i> , 2016, 1449, 349-367.	0.4	2
13170	Mutual enrichment in aggregated ranked lists with applications to gene expression regulation. <i>Bioinformatics</i> , 2016, 32, i464-i472.	1.8	5
13171	Behavioral Genetic Toolkits. <i>Current Topics in Developmental Biology</i> , 2016, 119, 157-204.	1.0	46
13172	NoisyGOA: Noisy GO annotations prediction using taxonomic and semantic similarity. <i>Computational Biology and Chemistry</i> , 2016, 65, 203-211.	1.1	8
13173	Differentially expressed genes selection via Laplacian regularized low-rank representation method. <i>Computational Biology and Chemistry</i> , 2016, 65, 185-192.	1.1	14
13174	Draft genome sequence of <i>Micrococcus luteus</i> strain O'Kane implicates metabolic versatility and the potential to degrade polyhydroxybutyrates. <i>Genomics Data</i> , 2016, 9, 148-153.	1.3	5
13175	Draft genome sequence of <i>Microbacterium oleivorans</i> strain Wellendorf implicates heterotrophic versatility and bioremediation potential. <i>Genomics Data</i> , 2016, 10, 54-60.	1.3	9
13176	Creating NoSQL Biological Databases with Ontologies for Query Relaxation. <i>Procedia Computer Science</i> , 2016, 91, 460-469.	1.2	17
13177	Gene set-based integrative analysis of ovarian clear cell carcinoma. <i>Taiwanese Journal of Obstetrics and Gynecology</i> , 2016, 55, 552-557.	0.5	12
13178	Transcriptome response of wheat Norin 10 to long-term elevated CO ₂ under high yield field condition. <i>Journal of Integrative Agriculture</i> , 2016, 15, 2142-2152.	1.7	3

#	ARTICLE	IF	CITATIONS
13179	Analysis of Body-wide Unfractionated Tissue Data to Identify a Core Human Endothelial Transcriptome. <i>Cell Systems</i> , 2016, 3, 287-301.e3.	2.9	44
13180	Complete genome sequencing and comparative genomic analysis of functionally diverse <i>Lysinibacillus sphaericus</i> III(3)7. <i>Genomics Data</i> , 2016, 9, 78-86.	1.3	12
13181	Draft genome sequence and detailed analysis of <i>Pantoea eucrina</i> strain Russ and implication for opportunistic pathogenesis. <i>Genomics Data</i> , 2016, 10, 63-68.	1.3	6
13182	Stachyose is a preferential carbon source utilized by the rice false smut pathogen, <i>Villosiclava virens</i> . <i>Physiological and Molecular Plant Pathology</i> , 2016, 96, 69-76.	1.3	12
13183	Gene expression elucidates functional impact of polygenic risk for schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1442-1453.	7.1	952
13184	α -fucosylated glycoproteins form assemblies in close proximity to the nuclear pore complexes of <i>Toxoplasma gondii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11567-11572.	3.3	39
13185	Transcriptomic data reanalysis allows for a contribution of embryonic transcriptional change-induced gene expression reprogramming in transgenerational epigenetic inheritance. <i>Environmental Epigenetics</i> , 2016, 2, dww009.	0.9	3
13186	Profiling of downregulated blood-circulating miR-150-5p as a novel tumor marker for cholangiocarcinoma. <i>Tumor Biology</i> , 2016, 37, 15019-15029.	0.8	36
13187	Identification of genes in the hypothalamus-pituitary-gonad axis in the brain of Amur sturgeons (<i>Acipenser schrenckii</i>) by comparative transcriptome analysis in relation to kisspeptin treatment. <i>Gene</i> , 2016, 595, 53-61.	1.0	14
13188	De novo transcriptome sequencing-based discovery and expression analyses of verbascoside biosynthesis-associated genes in <i>Rehmannia glutinosa</i> tuberous roots. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	15
13189	Transcriptome sequencing of <i>Mycosphaerella fijiensis</i> during association with <i>Musa acuminata</i> reveals candidate pathogenicity genes. <i>BMC Genomics</i> , 2016, 17, 690.	1.2	20
13190	Arbuscular Mycorrhizal Symbiosis Requires a Phosphate Transceptor in the <i>Gigaspora margarita</i> Fungal Symbiont. <i>Molecular Plant</i> , 2016, 9, 1583-1608.	3.9	90
13191	The digital revolution in phenotyping. <i>Briefings in Bioinformatics</i> , 2016, 17, 819-830.	3.2	41
13192	Genome-wide identification of microRNAs in pomegranate (<i>Punica granatum</i> L.) by high-throughput sequencing. <i>BMC Plant Biology</i> , 2016, 16, 122.	1.6	57
13193	Genome sequence of <i>Candidatus Arsenophonus lipopteni</i> , the exclusive symbiont of a blood sucking fly <i>Lipoptena cervi</i> (Diptera: Hippoboscidae). <i>Standards in Genomic Sciences</i> , 2016, 11, 72.	1.5	46
13194	A machine-learned computational functional genomics-based approach to drug classification. <i>European Journal of Clinical Pharmacology</i> , 2016, 72, 1449-1461.	0.8	12
13195	Integrative transcriptomic analysis of NAFLD animal model reveals dysregulated genes and pathways in metabolism. <i>Gene</i> , 2016, 595, 99-108.	1.0	9
13196	Screening of gene signatures for rheumatoid arthritis and osteoarthritis based on bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2016, 14, 1587-1593.	1.1	36

#	ARTICLE	IF	CITATIONS
13197	The Adipokine-Cardiovascular-Lifestyle Network. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1785-1803.	1.2	42
13198	Activity-Dependent Changes in Gene Expression in Schizophrenia Human-Induced Pluripotent Stem Cell Neurons. <i>JAMA Psychiatry</i> , 2016, 73, 1180.	6.0	40
13199	A Reuse-Based Annotation Approach for Medical Documents. <i>Lecture Notes in Computer Science</i> , 2016, , 135-150.	1.0	8
13200	A scientist's guide for submitting data to ZFIN. <i>Methods in Cell Biology</i> , 2016, 135, 451-481.	0.5	7
13201	Logical and Semantic Modeling of Complex Biomolecular Networks. <i>Procedia Computer Science</i> , 2016, 96, 475-484.	1.2	6
13202	Gene transcription profiles associated with inter-modular hubs and connection distance in human functional magnetic resonance imaging networks. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150362.	1.8	188
13203	Bioinformatics analysis of the molecular mechanism of diffuse intrinsic pontine glioma. <i>Oncology Letters</i> , 2016, 12, 2524-2530.	0.8	23
13204	RGC-32 is expressed in the human atherosclerotic arterial wall: Role in C5b-9-induced cell proliferation and migration. <i>Experimental and Molecular Pathology</i> , 2016, 101, 221-230.	0.9	17
13205	Screening and identification of microRNA involved in unstable angina using gene-chip analysis. <i>Experimental and Therapeutic Medicine</i> , 2016, 12, 2716-2722.	0.8	5
13206	Transcriptomic characterization of differential gene expression in oral squamous cell carcinoma: a meta-analysis of publicly available microarray data sets. <i>Tumor Biology</i> , 2016, 37, 15913-15924.	0.8	10
13207	Permanent draft genome of <i>Thermithiobacillus tepidarius</i> DSM 3134T, a moderately thermophilic, obligately chemolithoautotrophic member of the Acidithiobacillia. <i>Standards in Genomic Sciences</i> , 2016, 11, 74.	1.5	15
13208	Building and analysis of protein-protein interactions related to diabetes mellitus using support vector machine, biomedical text mining and network analysis. <i>Computational Biology and Chemistry</i> , 2016, 65, 37-44.	1.1	23
13209	Dissolving capability difference based sequential extraction: A versatile tool for in-depth membrane proteome analysis. <i>Analytica Chimica Acta</i> , 2016, 945, 39-46.	2.6	11
13210	Nuclear receptors control pro-viral and antiviral metabolic responses to hepatitis C virus infection. <i>Nature Chemical Biology</i> , 2016, 12, 1037-1045.	3.9	45
13211	Microbial Succession and Flavor Production in the Fermented Dairy Beverage Kefir. <i>MSystems</i> , 2016, 1, .	1.7	202
13212	Identification of 2-oxohistidine Interacting Proteins Using E. coli Proteome Chips. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3581-3593.	2.5	3
13213	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016, 353, .	6.0	979
13216	Development and Validation of a Six-Gene Recurrence Risk Score Assay for Gastric Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 6228-6235.	3.2	40

#	ARTICLE	IF	CITATIONS
13217	Divergent Transcriptional Responses to Physiological and Xenobiotic Stress in <i>Giardia duodenalis</i> . Antimicrobial Agents and Chemotherapy, 2016, 60, 6034-6045.	1.4	33
13218	Improving information retrieval in functional analysis. Computers in Biology and Medicine, 2016, 79, 10-20.	3.9	9
13219	Finding lost genes in GWAS via integrative omics analysis reveals novel sub-networks associated with preterm birth. Human Molecular Genetics, 2016, 25, ddw325.	1.4	12
13220	Improving drug safety: From adverse drug reaction knowledge discovery to clinical implementation. Methods, 2016, 110, 14-25.	1.9	32
13221	On the study of microbial transcriptomes using second- and third-generation sequencing technologies. Journal of Microbiology, 2016, 54, 527-536.	1.3	12
13222	Epidermal growth factor-induced stimulation of proliferation and gene expression changes in the hypotrichous ciliate, <i>Stylonychia lemnae</i> . Gene, 2016, 592, 186-192.	1.0	2
13223	Different interactomes for p70-S6K1 and p54-S6K2 revealed by proteomic analysis. Proteomics, 2016, 16, 2650-2666.	1.3	23
13224	Strong down-regulation of glycoporphin genes: A host defense mechanism against rotavirus infection. Infection, Genetics and Evolution, 2016, 44, 403-411.	1.0	10
13225	In Depth Proteome Analysis of Ripening Muscadine Grape Berry cv. Carlos Reveals Proteins Associated with Flavor and Aroma Compounds. Journal of Proteome Research, 2016, 15, 2910-2923.	1.8	14
13226	An approach to comprehensive genome and proteome expression analyses in Schwann cells and neurons during peripheral nerve myelin formation. Journal of Neurochemistry, 2016, 138, 830-844.	2.1	10
13227	Global Transcriptional Analysis of Virus-Host Interactions between Phage ϕ 29 and <i>Bacillus subtilis</i> . Journal of Virology, 2016, 90, 9293-9304.	1.5	44
13228	Algorithms in Bioinformatics. Lecture Notes in Computer Science, 2016, , .	1.0	2
13229	Advancing Clinical Proteomics via Analysis Based on Biological Complexes: A Tale of Five Paradigms. Journal of Proteome Research, 2016, 15, 3167-3179.	1.8	37
13230	Discovery and characterization of miRNAs in mouse thymus responses to ionizing radiation by deep sequencing. International Journal of Radiation Biology, 2016, 92, 548-557.	1.0	5
13231	Genomic Prediction for Quantitative Traits Is Improved by Mapping Variants to Gene Ontology Categories in <i>Drosophila melanogaster</i> . Genetics, 2016, 203, 1871-1883.	1.2	96
13232	Evaluation of artificial selection in Standard Poodles using whole-genome sequencing. Mammalian Genome, 2016, 27, 599-609.	1.0	13
13233	Transcriptome sequencing and de novo characterization of Korean endemic land snail, <i>Koreanohadra kurodana</i> for functional transcripts and SSR markers. Molecular Genetics and Genomics, 2016, 291, 1999-2014.	1.0	14
13234	A unified software framework for deriving, visualizing, and exploring abstraction networks for ontologies. Journal of Biomedical Informatics, 2016, 62, 90-105.	2.5	27

#	ARTICLE	IF	CITATIONS
13235	Gene set analysis for interpreting genetic studies. <i>Human Molecular Genetics</i> , 2016, 25, R133-R140.	1.4	12
13236	When predator becomes prey: investigating the salivary transcriptome of the shark-feeding leech <i>Pontobdella macrothela</i> (Hirudinea: Piscicolidae). <i>Zoological Journal of the Linnean Society</i> , 2016, , .	1.0	10
13239	Transcriptomic Analysis of Compromise Between Air-Breathing and Nutrient Uptake of Posterior Intestine in Loach (<i>Misgurnus anguillicaudatus</i>), an Air-Breathing Fish. <i>Marine Biotechnology</i> , 2016, 18, 521-533.	1.1	16
13240	Div-Seq: Single-nucleus RNA-Seq reveals dynamics of rare adult newborn neurons. <i>Science</i> , 2016, 353, 925-928.	6.0	482
13241	<sc><i>GREM</i></sc><i>1</i> and <sc>POLE</sc> variants in hereditary colorectal cancer syndromes. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 95-106.	1.5	40
13242	Comparative genome-wide analysis reveals that <i>Burkholderia contaminans</i> 14 possesses multiple antimicrobial biosynthesis genes but not major genetic loci required for pathogenesis. <i>MicrobiologyOpen</i> , 2016, 5, 353-369.	1.2	44
13243	Process Pharmacology: A Pharmacological Data Science Approach to Drug Development and Therapy. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2016, 5, 192-200.	1.3	12
13244	In search for symmetries in the metabolism of cancer. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2016, 8, 23-35.	6.6	6
13245	Comparative transcriptome resources of two <i>Dysosma</i> species (Berberidaceae) and molecular evolution of the <sc>CYP</sc>719A gene in Podophylloideae. <i>Molecular Ecology Resources</i> , 2016, 16, 228-241.	2.2	13
13246	Food mechanical properties and dietary ecology. <i>American Journal of Physical Anthropology</i> , 2016, 159, 79-104.	2.1	62
13247	Construction of polyketide overproducing <i>Escherichia coli</i> strains via synthetic antisense RNAs based on in silico fluxome analysis and comparative transcriptome analysis. <i>Biotechnology Journal</i> , 2016, 11, 530-541.	1.8	13
13248	LncRNA-Hh Strengthen Cancer Stem Cells Generation in Twist-Positive Breast Cancer via Activation of Hedgehog Signaling Pathway. <i>Stem Cells</i> , 2016, 34, 55-66.	1.4	151
13249	Cry1Ab-expressing rice did not influence expression of fecundity-related genes in the wolf spider <i>Pardosa pseudoannulata</i> . <i>Gene</i> , 2016, 592, 1-7.	1.0	12
13250	Gene expression profile after activation of RIG-I in 5'ppp-dsRNA challenged DF1. <i>Developmental and Comparative Immunology</i> , 2016, 65, 191-200.	1.0	15
13251	Analyses of Drought-Tolerance Mechanism of Rice Based on the Transcriptome and Gene Ontology Data. , 2016, , 415-432.		2
13252	Systems Biology Approaches to Improve Drought Stress Tolerance in Plants: State of the Art and Future Challenges. , 2016, , 433-471.		1
13253	rG4-seq reveals widespread formation of G-quadruplex structures in the human transcriptome. <i>Nature Methods</i> , 2016, 13, 841-844.	9.0	314
13254	Representing and querying disease networks using graph databases. <i>BioData Mining</i> , 2016, 9, 23.	2.2	75

#	ARTICLE	IF	CITATIONS
13255	Genomics Resources for Plants. , 2016, , 29-57.		2
13256	Impact of outdated gene annotations on pathway enrichment analysis. <i>Nature Methods</i> , 2016, 13, 705-706.	9.0	113
13257	Transcriptome analysis reveals rod/cone photoreceptor specific signatures across mammalian retinas. <i>Human Molecular Genetics</i> , 2016, 25, ddw268.	1.4	36
13258	Nuclear import sequence identification in hOAS3 protein. <i>Inflammation Research</i> , 2016, 65, 895-904.	1.6	8
13259	RNA-seq analysis revealed ROS-mediated related genes involved in cadmium detoxification in the razor clam <i>Sinonovacula constricta</i> . <i>Fish and Shellfish Immunology</i> , 2016, 57, 350-361.	1.6	20
13260	Computational Approaches for Functional Prediction and Characterisation of Long Noncoding RNAs. <i>Trends in Genetics</i> , 2016, 32, 620-637.	2.9	89
13261	ModuleAlign: module-based global alignment of protein-protein interaction networks. <i>Bioinformatics</i> , 2016, 32, i658-i664.	1.8	34
13262	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. <i>Human Molecular Genetics</i> , 2016, 25, ddw288.	1.4	76
13263	Detection of selection signatures of population-specific genomic regions selected during domestication process in Jinhua pigs. <i>Animal Genetics</i> , 2016, 47, 672-681.	0.6	17
13264	RNA-sequencing profiles hippocampal gene expression in a validated model of cancer-induced depression. <i>Genes, Brain and Behavior</i> , 2016, 15, 711-721.	1.1	10
13265	Donor age and long-term culture do not negatively influence the stem potential of limbal fibroblast-like stem cells. <i>Stem Cell Research and Therapy</i> , 2016, 7, 83.	2.4	6
13266	Comparative Proteome Analysis in <i>Schizosaccharomyces pombe</i> Identifies Metabolic Targets to Improve Protein Production and Secretion. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3090-3106.	2.5	8
13267	C-DEVA: Detection, evaluation, visualization and annotation of clusters from biological networks. <i>BioSystems</i> , 2016, 150, 78-86.	0.9	11
13268	Advances in integrative statistics for logic programming. <i>International Journal of Approximate Reasoning</i> , 2016, 78, 103-115.	1.9	2
13269	Extensive complementarity between gene function prediction methods. <i>Bioinformatics</i> , 2016, 32, 3645-3653.	1.8	12
13270	Proteome-wide analysis of lysine acetylation in adult <i>Schistosoma japonicum</i> worm. <i>Journal of Proteomics</i> , 2016, 148, 202-212.	1.2	37
13271	Resolvin E1 Reverses Experimental Periodontitis and Dysbiosis. <i>Journal of Immunology</i> , 2016, 197, 2796-2806.	0.4	128
13272	Human INO80/YY1 chromatin remodeling complex transcriptionally regulates the BRCA2- and CDKN1A-interacting protein (BCCIP) in cells. <i>Protein and Cell</i> , 2016, 7, 749-760.	4.8	14

#	ARTICLE	IF	CITATIONS
13273	The proteome of normal human retrobulbar optic nerve and sclera. <i>Proteomics</i> , 2016, 16, 2592-2596.	1.3	17
13274	Gene signatures associated with adaptive humoral immunity following seasonal influenza A/H1N1 vaccination. <i>Genes and Immunity</i> , 2016, 17, 371-379.	2.2	26
13275	miRNA Profiling in Plants: Current Identification and Expression Approaches. , 2016, , 189-215.		0
13276	A Comparison of Resources for the Annotation of a <i>De Novo</i> Assembled Transcriptome in the Molting Gland (Y-Organ) of the Blackback Land Crab, <i>Gecarcinus lateralis</i> . <i>Integrative and Comparative Biology</i> , 2016, 56, 1103-1112.	0.9	17
13277	Expression profiling identifies Sertoli and Leydig cell genes as Fsh targets in adult zebrafish testis. <i>Molecular and Cellular Endocrinology</i> , 2016, 437, 237-251.	1.6	58
13278	First high quality draft genome sequence of a plant growth promoting and cold active enzyme producing psychrotrophic <i>Arthrobacter agilis</i> strain L77. <i>Standards in Genomic Sciences</i> , 2016, 11, 54.	1.5	78
13279	Codon identity regulates mRNA stability and translation efficiency during the maternal-to-paternal zygotic transition. <i>EMBO Journal</i> , 2016, 35, 2087-2103.	3.5	236
13280	A combined analysis of genome-wide expression profiling of bipolar disorder in human prefrontal cortex. <i>Journal of Psychiatric Research</i> , 2016, 82, 23-29.	1.5	6
13281	MathIOmica: An Integrative Platform for Dynamic Omics. <i>Scientific Reports</i> , 2016, 6, 37237.	1.6	35
13282	Insights into a novel nuclear function for Fascin in the regulation of the amino-acid transporter SLC3A2. <i>Scientific Reports</i> , 2016, 6, 36699.	1.6	22
13283	Compact Integration of Multi-Network Topology for Functional Analysis of Genes. <i>Cell Systems</i> , 2016, 3, 540-548.e5.	2.9	207
13284	Field Trial and Molecular Characterization of RNAi-Transgenic Tomato Plants That Exhibit Resistance to Tomato Yellow Leaf Curl Geminivirus. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 197-209.	1.4	60
13285	Candidate egg case silk genes for the spider <i>Argiope argentata</i> from differential gene expression analyses. <i>Insect Molecular Biology</i> , 2016, 25, 757-768.	1.0	11
13286	GEN3VA: aggregation and analysis of gene expression signatures from related studies. <i>BMC Bioinformatics</i> , 2016, 17, 461.	1.2	17
13287	Unravelling the genomic architecture of bull fertility in Holstein cattle. <i>BMC Genetics</i> , 2016, 17, 143.	2.7	87
13288	De novo transcriptome sequencing in <i>Monsonia burkeana</i> revealed putative genes for key metabolic pathways involved in tea quality and medicinal value. <i>3 Biotech</i> , 2016, 6, 250.	1.1	3
13289	Investigation of candidate genes for osteoarthritis based on gene expression profiles. <i>Acta Orthopaedica Et Traumatologica Turcica</i> , 2016, 50, 686-690.	0.3	9
13290	Systems analysis identifies miR-29b regulation of invasiveness in melanoma. <i>Molecular Cancer</i> , 2016, 15, 72.	7.9	21

#	ARTICLE	IF	CITATIONS
13291	ClassyFire: automated chemical classification with a comprehensive, computable taxonomy. <i>Journal of Cheminformatics</i> , 2016, 8, 61.	2.8	779
13292	Draft Genome Sequence of Fungus <i>Clonostachys rosea</i> Strain YKD0085. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
13293	The Tomato Genome. <i>Compendium of Plant Genomes</i> , 2016, , .	0.3	9
13294	High-throughput discovery of novel developmental phenotypes. <i>Nature</i> , 2016, 537, 508-514.	13.7	1,001
13295	<i>De novo</i> assembled transcriptome of horned gall aphid, <i>Schlechtendalia chinensis</i> Bell, suggest changes in functional gene expression during host alternation. <i>Entomological Research</i> , 2016, 46, 314-323.	0.6	2
13296	CellTree: an R/bioconductor package to infer the hierarchical structure of cell populations from single-cell RNA-seq data. <i>BMC Bioinformatics</i> , 2016, 17, 363.	1.2	81
13297	Genome-wide co-localization of active EGFR and downstream ERK pathway kinases mirrors mitogen-inducible RNA polymerase 2 genomic occupancy. <i>Nucleic Acids Research</i> , 2016, 44, gkw763.	6.5	23
13298	Application of Systems Biology to Neuroproteomics: The Path to Enhanced Theranostics in Traumatic Brain Injury. <i>Methods in Molecular Biology</i> , 2016, 1462, 139-155.	0.4	6
13299	Manual of Cardiovascular Proteomics. , 2016, , .		4
13300	Metagenomics as a preliminary screen for antimicrobial bioprospecting. <i>Gene</i> , 2016, 594, 248-258.	1.0	26
13301	v-Src Oncogene Induces Trop2 Proteolytic Activation via Cyclin D1. <i>Cancer Research</i> , 2016, 76, 6723-6734.	0.4	22
13302	Comparative analysis of housekeeping and tissue-specific driver nodes in human protein interaction networks. <i>BMC Bioinformatics</i> , 2016, 17, 358.	1.2	14
13303	Near complete genome sequence of the animal feed probiotic, <i>Bacillus amyloliquefaciens</i> H57. <i>Standards in Genomic Sciences</i> , 2016, 11, 60.	1.5	16
13304	Large-scale analysis of intrinsic disorder flavors and associated functions in the protein sequence universe. <i>Protein Science</i> , 2016, 25, 2164-2174.	3.1	52
13305	Draft genome sequence of pathogenic bacteria <i>Vibrio parahaemolyticus</i> strain Ba94C2, associated with acute hepatopancreatic necrosis disease isolate from South America. <i>Genomics Data</i> , 2016, 9, 143-144.	1.3	57
13306	Navigating the Phenotype Frontier: The Monarch Initiative. <i>Genetics</i> , 2016, 203, 1491-1495.	1.2	65
13307	Proteomic Network Systems Analysis. , 2016, , 321-342.		2
13308	Complete genome sequences of the <i>Serratia plymuthica</i> strains 3Rp8 and 3Re4-18, two rhizosphere bacteria with antagonistic activity towards fungal phytopathogens and plant growth promoting abilities. <i>Standards in Genomic Sciences</i> , 2016, 11, 61.	1.5	20

#	ARTICLE	IF	CITATIONS
13309	Autophagy induction stabilizes microtubules and promotes axon regeneration after spinal cord injury. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11324-11329.	3.3	144
13310	Cis-acting single nucleotide polymorphisms alter MicroRNA-mediated regulation of human brain-expressed transcripts. <i>Human Molecular Genetics</i> , 2016, 25, ddw317.	1.4	5
13311	Tissue enrichment analysis for <i>C. elegans</i> genomics. <i>BMC Bioinformatics</i> , 2016, 17, 366.	1.2	155
13312	Calpain Activity Is Essential for ATP-Driven Unconventional Vesicle-Mediated Protein Secretion and Inflammasome Activation in Human Macrophages. <i>Journal of Immunology</i> , 2016, 197, 3315-3325.	0.4	49
13313	Predicting protein subcellular localization based on information content of gene ontology terms. <i>Computational Biology and Chemistry</i> , 2016, 65, 1-7.	1.1	10
13314	A new multi-scale method to reveal hierarchical modular structures in biological networks. <i>Molecular BioSystems</i> , 2016, 12, 3724-3733.	2.9	2
13315	Positive Selection Linked with Generation of Novel Mammalian Dentition Patterns. <i>Genome Biology and Evolution</i> , 2016, 8, 2748-2759.	1.1	9
13316	De Novo Transcriptome Assembly and Sex-Biased Gene Expression in the Cyclical Parthenogenetic <i>Daphnia galeata</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 3120-3139.	1.1	38
13317	Proximity Labeling Reveals Molecular Determinants of FGFR4 Endosomal Transport. <i>Journal of Proteome Research</i> , 2016, 15, 3841-3855.	1.8	14
13318	Interferon- γ signaling promotes embryonic HSC maturation. <i>Blood</i> , 2016, 128, 204-216.	0.6	36
13320	Comparative transcriptomics of anal fin pigmentation patterns in cichlid fishes. <i>BMC Genomics</i> , 2016, 17, 712.	1.2	35
13321	Analysis of gene expression profile identifies potential biomarkers for atherosclerosis. <i>Molecular Medicine Reports</i> , 2016, 14, 3052-3058.	1.1	20
13322	Analytical Performance of a Gene Expression Classifier for Medullary Thyroid Carcinoma. <i>Thyroid</i> , 2016, 26, 1573-1580.	2.4	14
13323	The development of non-coding RNA ontology. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 15, 214.	0.1	9
13324	Reactive Oxygen Species-Associated Molecular Signature Predicts Survival in Patients with Sepsis. <i>Pulmonary Circulation</i> , 2016, 6, 196-201.	0.8	25
13325	Comparative genome analysis of the oleaginous yeast <i>Trichosporon fermentans</i> reveals its potential applications in lipid accumulation. <i>Microbiological Research</i> , 2016, 192, 203-210.	2.5	15
13326	The Resistome: A Comprehensive Database of <i>Escherichia coli</i> Resistance Phenotypes. <i>ACS Synthetic Biology</i> , 2016, 5, 1566-1577.	1.9	17
13327	Protein function in precision medicine: deep understanding with machine learning. <i>FEBS Letters</i> , 2016, 590, 2327-2341.	1.3	43

#	ARTICLE	IF	CITATIONS
13328	Developmental alcohol exposure leads to a persistent change on astrocyte secretome. <i>Journal of Neurochemistry</i> , 2016, 137, 730-743.	2.1	22
13329	A Network of Conserved Synthetic Lethal Interactions for Exploration of Precision Cancer Therapy. <i>Molecular Cell</i> , 2016, 63, 514-525.	4.5	140
13330	A highly multiplexed and sensitive RNA-seq protocol for simultaneous analysis of host and pathogen transcriptomes. <i>Nature Protocols</i> , 2016, 11, 1477-1491.	5.5	46
13331	Revisiting the role of the Gcm transcription factor, from master regulator to Swiss army knife. <i>Fly</i> , 2016, 10, 210-218.	0.9	4
13332	Identification and differential expression of microRNA in the ovaries of pigs (<i>Sus</i>). <i>Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50</i>	0.6	35
13333	Grasses suppress shoot-borne roots to conserve water during drought. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8861-8866.	3.3	111
13334	Gene Networks in Neuropsychiatric Disease. , 2016, , 161-178.		0
13335	Relative contributions of the structural and catalytic roles of Rrp6 in exosomal degradation of individual mRNAs. <i>Rna</i> , 2016, 22, 1311-1319.	1.6	11
13336	Identification of genes and signaling pathways associated with squamous cell carcinoma by bioinformatics analysis. <i>Oncology Letters</i> , 2016, 11, 1382-1390.	0.8	13
13337	Identification of key target genes and pathways in laryngeal carcinoma. <i>Oncology Letters</i> , 2016, 12, 1279-1286.	0.8	7
13338	De novo assembly and characterization of leaf transcriptome for the development of EST-SSR markers of the non-model species <i>Indigofera szechuensis</i> . <i>Biochemical Systematics and Ecology</i> , 2016, 68, 36-43.	0.6	9
13339	Identification of New Resistance Mechanisms in <i>Escherichia coli</i> against Apidaecin 1b Using Quantitative Gel- and LC-MS-Based Proteomics. <i>Journal of Proteome Research</i> , 2016, 15, 2607-2617.	1.8	14
13340	Integrated gene set analysis for microRNA studies. <i>Bioinformatics</i> , 2016, 32, 2809-2816.	1.8	23
13341	Here We Are, But Where Do We Go? A Systematic Review of Crustacean Transcriptomic Studies from 2014-2015. <i>Integrative and Comparative Biology</i> , 2016, 56, 1055-1066.	0.9	21
13342	Long noncoding RNA EGOT negatively affects the antiviral response and favors HCV replication. <i>EMBO Reports</i> , 2016, 17, 1013-1028.	2.0	109
13343	Use of RNA-seq to identify cardiac genes and gene pathways differentially expressed between dogs with and without dilated cardiomyopathy. <i>American Journal of Veterinary Research</i> , 2016, 77, 693-699.	0.3	7
13344	Novel proteases from the genome of the carnivorous plant <i>Drosera capensis</i> : Structural prediction and comparative analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1517-1533.	1.5	29
13345	Cdk3, a conjugation-specific cyclin-dependent kinase, is essential for the initiation of meiosis in <i>Tetrahymena thermophila</i> . <i>Cell Cycle</i> , 2016, 15, 2506-2514.	1.3	17

#	ARTICLE	IF	CITATIONS
13346	Histone deacetylase inhibitor induces cell apoptosis and cycle arrest in lung cancer cells via mitochondrial injury and p53 up-acetylation. <i>Cell Biology and Toxicology</i> , 2016, 32, 469-482.	2.4	81
13347	Inferring active regulatory networks from gene expression data using a combination of prior knowledge and enrichment analysis. <i>BMC Bioinformatics</i> , 2016, 17, 181.	1.2	30
13348	De Novo Deep Transcriptome Analysis of Medicinal Plants for Gene Discovery in Biosynthesis of Plant Natural Products. <i>Methods in Enzymology</i> , 2016, 576, 19-45.	0.4	31
13349	Draft genome sequence of <i>Pseudomonas moraviensis</i> strain Devor implicates metabolic versatility and bioremediation potential. <i>Genomics Data</i> , 2016, 9, 154-159.	1.3	11
13350	Transcriptome sequencing of maraena whitefish (<i>Coregonus maraena</i>). <i>Marine Genomics</i> , 2016, 29, 27-29.	0.4	9
13351	Development and validation of a 24-gene predictor of response to postoperative radiotherapy in prostate cancer: a matched, retrospective analysis. <i>Lancet Oncology</i> , The, 2016, 17, 1612-1620.	5.1	182
13352	Tissue-specific transcriptome characterization for developing tadpoles of the northern leopard frog (<i>Lithobates pipiens</i>). <i>Genomics</i> , 2016, 108, 232-240.	1.3	15
13353	Ancestral light and chloroplast regulation form the foundations for C4 gene expression. <i>Nature Plants</i> , 2016, 2, 16161.	4.7	32
13354	A novel single cell method to identify the genetic composition at a single nuclear body. <i>Scientific Reports</i> , 2016, 6, 29191.	1.6	8
13355	Evolution of the Calcium-Based Intracellular Signaling System. <i>Genome Biology and Evolution</i> , 2016, 8, 2118-2132.	1.1	35
13356	An evaluation of the accuracy and speed of metagenome analysis tools. <i>Scientific Reports</i> , 2016, 6, 19233.	1.6	278
13357	Discover the network mechanisms underlying the connections between aging and age-related diseases. <i>Scientific Reports</i> , 2016, 6, 32566.	1.6	40
13358	Identification and functional characterization of lncRNAs acting as ceRNA involved in the malignant progression of glioblastoma multiforme. <i>Oncology Reports</i> , 2016, 36, 2911-2925.	1.2	34
13359	ANGIOGENES: knowledge database for protein-coding and noncoding RNA genes in endothelial cells. <i>Scientific Reports</i> , 2016, 6, 32475.	1.6	34
13360	CisMapper: predicting regulatory interactions from transcription factor ChIP-seq data. <i>Nucleic Acids Research</i> , 2016, 45, gkw956.	6.5	23
13361	Characterization and target genes of nine human PRD-like homeobox domain genes expressed exclusively in early embryos. <i>Scientific Reports</i> , 2016, 6, 28995.	1.6	33
13362	Tissue Specificity of Human Disease Module. <i>Scientific Reports</i> , 2016, 6, 35241.	1.6	99
13363	Large-scale identification of human protein function using topological features of interaction network. <i>Scientific Reports</i> , 2016, 6, 37179.	1.6	8

#	ARTICLE	IF	CITATIONS
13364	Discovery of the molecular mechanisms of the novel chalcone-based <i>Magnaporthe oryzae</i> inhibitor C1 using transcriptomic profiling and co-expression network analysis. <i>SpringerPlus</i> , 2016, 5, 1851.	1.2	3
13365	Overexpression of CD44 is associated with the occurrence and migration of non-small cell lung cancer. <i>Molecular Medicine Reports</i> , 2016, 14, 3159-3167.	1.1	34
13366	An interactive web-based application for Comprehensive Analysis of RNAi-screen Data. <i>Nature Communications</i> , 2016, 7, 10578.	5.8	13
13367	The <i>Dendrobium catenatum</i> Lindl. genome sequence provides insights into polysaccharide synthase, floral development and adaptive evolution. <i>Scientific Reports</i> , 2016, 6, 19029.	1.6	255
13368	Expression Variations of miRNAs and mRNAs in Rice (<i>Oryza sativa</i>). <i>Genome Biology and Evolution</i> , 2016, 8, 3529-3544.	1.1	32
13369	Ontology-based collection, representation and analysis of drug-associated neuropathy adverse events. <i>Journal of Biomedical Semantics</i> , 2016, 7, 29.	0.9	22
13370	SOX7 co-regulates Wnt/ β -catenin signaling with Axin-2: both expressed at low levels in breast cancer. <i>Scientific Reports</i> , 2016, 6, 26136.	1.6	25
13371	Multi-label λ_1 , λ_2 -regularized logistic regression for predicting activation/inhibition relationships in human protein-protein interaction networks. <i>Scientific Reports</i> , 2016, 6, 36453.	1.6	2
13372	The Features of Low-Connectivity Essential Proteins. , 2016, , .		0
13373	Leaf transcriptome of two highly divergent genotypes of <i>Urochloa humidicola</i> (Poaceae), a tropical polyploid forage grass adapted to acidic soils and temporary flooding areas. <i>BMC Genomics</i> , 2016, 17, 910.	1.2	15
13374	Illumina microRNA profiles reveal the involvement of miR397a in Citrus adaptation to long-term boron toxicity via modulating secondary cell-wall biosynthesis. <i>Scientific Reports</i> , 2016, 6, 22900.	1.6	41
13375	AtPRMT5 Regulates Shoot Regeneration through Mediating Histone H4R3 Dimethylation on KRPs and Pre-mRNA Splicing of RKP in Arabidopsis. <i>Molecular Plant</i> , 2016, 9, 1634-1646.	3.9	33
13376	Chemical Proteomics and Structural Biology Define EPHA2 Inhibition by Clinical Kinase Drugs. <i>ACS Chemical Biology</i> , 2016, 11, 3400-3411.	1.6	42
13377	Human somatic cells subjected to genetic induction with six germ line-related factors display meiotic germ cell-like features. <i>Scientific Reports</i> , 2016, 6, 24956.	1.6	19
13378	Systematic investigation of transcription factors critical in the protection against cerebral ischemia by Danhong injection. <i>Scientific Reports</i> , 2016, 6, 29823.	1.6	33
13379	24-hour-restraint stress induces long-term depressive-like phenotypes in mice. <i>Scientific Reports</i> , 2016, 6, 32935.	1.6	64
13380	Comparative transcriptome profiling of longissimus muscle tissues from Qianhua Mutton Merino and Small Tail Han sheep. <i>Scientific Reports</i> , 2016, 6, 33586.	1.6	39
13381	RNA-binding profiles of <i>Drosophila</i> CPEB proteins Orb and Orb2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7030-E7038.	3.3	49

#	ARTICLE	IF	CITATIONS
13382	Dynamic DNA methylation regulates neuronal intrinsic membrane excitability. <i>Science Signaling</i> , 2016, 9, ra83.	1.6	64
13383	Genome sequence of the organohalide-respiring <i>Dehalogenimonas alkenigignens</i> type strain (IP3-3T). <i>Standards in Genomic Sciences</i> , 2016, 11, 44.	1.5	10
13384	Big Data Analytics in Genomics. , 2016, , .		7
13385	Mechanism of Arachidonic Acid Accumulation during Aging in <i>Mortierella alpina</i> : A Large-Scale Label-Free Comparative Proteomics Study. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 9124-9134.	2.4	29
13386	Cutaneous wound healing through paradoxical MAPK activation by BRAF inhibitors. <i>Nature Communications</i> , 2016, 7, 12348.	5.8	52
13387	Genome sequence of the basal haplorrhine primate <i>Tarsius syrichta</i> reveals unusual insertions. <i>Nature Communications</i> , 2016, 7, 12997.	5.8	32
13388	LEGO: a novel method for gene set over-representation analysis by incorporating network-based gene weights. <i>Scientific Reports</i> , 2016, 6, 18871.	1.6	37
13389	Quorum sensing activity of <i>Citrobacter amalonaticus</i> L8A, a bacterium isolated from dental plaque. <i>Scientific Reports</i> , 2016, 6, 20702.	1.6	18
13390	MicroRNA profiling of cisplatin-resistant oral squamous cell carcinoma cell lines enriched with cancer-stem-cell-like and epithelial-mesenchymal transition-type features. <i>Scientific Reports</i> , 2016, 6, 23932.	1.6	51
13391	eSNPO: An eQTL-based SNP Ontology and SNP functional enrichment analysis platform. <i>Scientific Reports</i> , 2016, 6, 30595.	1.6	9
13392	Neural stem cells secrete factors facilitating brain regeneration upon constitutive Raf-Erk activation. <i>Scientific Reports</i> , 2016, 6, 32025.	1.6	21
13393	Transcriptome and Metabolite analysis reveal candidate genes of the cardiac glycoside biosynthetic pathway from <i>Calotropis procera</i> . <i>Scientific Reports</i> , 2016, 6, 34464.	1.6	47
13394	RedNemo: topology-based PPI network reconstruction via repeated diffusion with neighborhood modifications. <i>Bioinformatics</i> , 2017, 33, 537-544.	1.8	6
13395	Transcriptomic analysis of the highly efficient oil-degrading bacterium <i>Acinetobacter venetianus</i> RAG-1 reveals genes important in dodecane uptake and utilization. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw224.	0.7	14
13396	Signal-Oriented Pathway Analyses Reveal a Signaling Complex as a Synthetic Lethal Target for p53 Mutations. <i>Cancer Research</i> , 2016, 76, 6785-6794.	0.4	3
13397	Identification of candidate genes for myeloma-induced osteocyte death based on microarray data. <i>Journal of Orthopaedic Surgery and Research</i> , 2016, 11, 81.	0.9	3
13398	Personalized Medicine. Europeanization and Globalization, 2016, , .	0.1	5
13399	Mapping wild-type and R345W fibulin-3 intracellular interactomes. <i>Experimental Eye Research</i> , 2016, 153, 165-169.	1.2	6

#	ARTICLE	IF	CITATIONS
13400	An endometrial gene expression signature accurately predicts recurrent implantation failure after IVF. <i>Scientific Reports</i> , 2016, 6, 19411.	1.6	141
13401	The Lungfish Transcriptome: A Glimpse into Molecular Evolution Events at the Transition from Water to Land. <i>Scientific Reports</i> , 2016, 6, 21571.	1.6	75
13402	Genome-wide detection of CNVs in Chinese indigenous sheep with different types of tails using ovine high-density 600K SNP arrays. <i>Scientific Reports</i> , 2016, 6, 27822.	1.6	69
13403	Notions of similarity for systems biology models. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw090.	3.2	17
13404	Computational Methods for Integration of Biological Data. <i>Europeanization and Globalization</i> , 2016, , 137-178.	0.1	2
13405	A Survey of Computational Methods for Protein Function Prediction. , 2016, , 225-298.		42
13406	Detection of Regulator Genes and eQTLs in Gene Networks. , 2016, , 1-23.		9
13407	RNA Sequencing Applied to Livestock Production. , 2016, , 63-94.		0
13408	BATMAN-TCM: a Bioinformatics Analysis Tool for Molecular mechANism of Traditional Chinese Medicine. <i>Scientific Reports</i> , 2016, 6, 21146.	1.6	530
13409	Microgravity induces proteomics changes involved in endoplasmic reticulum stress and mitochondrial protection. <i>Scientific Reports</i> , 2016, 6, 34091.	1.6	43
13410	ATR maintains chromosomal integrity during postnatal cerebellar neurogenesis and is required for medulloblastoma formation. <i>Development (Cambridge)</i> , 2016, 143, 4038-4052.	1.2	46
13411	Microenvironmental Gene Expression Plasticity Among Individual <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 4197-4210.	0.8	31
13412	Translational Biomedical Informatics. <i>Advances in Experimental Medicine and Biology</i> , 2016, , .	0.8	1
13413	Investigation of rare and low-frequency variants using high-throughput sequencing with pooled DNA samples. <i>Scientific Reports</i> , 2016, 6, 33256.	1.6	13
13414	Functional insights into the testis transcriptome of the edible sea urchin <i>Loxechinus albus</i> . <i>Scientific Reports</i> , 2016, 6, 36516.	1.6	17
13415	Complete genome of <i>Nitrosospira briensis</i> C-128, an ammonia-oxidizing bacterium from agricultural soil. <i>Standards in Genomic Sciences</i> , 2016, 11, 46.	1.5	22
13416	Silencing of CD40 in vivo reduces progression of experimental atherogenesis through an NF- κ B/miR-125b axis and reveals new potential mediators in the pathogenesis of atherosclerosis. <i>Atherosclerosis</i> , 2016, 255, 80-89.	0.4	41
13417	Overcoming the matched-sample bottleneck: an orthogonal approach to integrate omic data. <i>Scientific Reports</i> , 2016, 6, 29251.	1.6	25

#	ARTICLE	IF	CITATIONS
13418	Genotypes of cancer stem cells characterized by epithelial-to-mesenchymal transition and proliferation related functions. <i>Scientific Reports</i> , 2016, 6, 32523.	1.6	11
13419	Transcriptomic analysis on the formation of the viable putative non-culturable state of beer-spoilage <i>Lactobacillus acetotolerans</i> . <i>Scientific Reports</i> , 2016, 6, 36753.	1.6	74
13420	Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. <i>Genome Medicine</i> , 2016, 8, 55.	3.6	51
13421	Differentially expressed lncRNAs and mRNAs identified by microarray analysis in GBS patients vs healthy controls. <i>Scientific Reports</i> , 2016, 6, 21819.	1.6	15
13422	Whole-transcriptome analysis of UUO mouse model of renal fibrosis reveals new molecular players in kidney diseases. <i>Scientific Reports</i> , 2016, 6, 26235.	1.6	92
13423	Identification and Characterization of miRNAs in <i>Chondrus crispus</i> by High-Throughput Sequencing and Bioinformatics Analysis. <i>Scientific Reports</i> , 2016, 6, 26397.	1.6	7
13424	Tissue-specific Co-expression of Long Non-coding and Coding RNAs Associated with Breast Cancer. <i>Scientific Reports</i> , 2016, 6, 32731.	1.6	35
13425	Characterization of factors underlying the metabolic shifts in developing kernels of colored maize. <i>Scientific Reports</i> , 2016, 6, 35479.	1.6	22
13426	Imaging-genomics reveals driving pathways of MRI derived volumetric tumor phenotype features in Glioblastoma. <i>BMC Cancer</i> , 2016, 16, 611.	1.1	58
13427	The Genome of <i>Undifilum oxytropis</i> Provides Insights into Swainsonine Biosynthesis and Locomotion. <i>Scientific Reports</i> , 2016, 6, 30760.	1.6	16
13428	An integrated metagenomics pipeline for strain profiling reveals novel patterns of bacterial transmission and biogeography. <i>Genome Research</i> , 2016, 26, 1612-1625.	2.4	405
13429	Genetic Adaptation and Neandertal Admixture Shaped the Immune System of Human Populations. <i>Cell</i> , 2016, 167, 643-656.e17.	13.5	373
13430	KinView: a visual comparative sequence analysis tool for integrated kinome research. <i>Molecular BioSystems</i> , 2016, 12, 3651-3665.	2.9	47
13431	STAMS: STRING-assisted module search for genome wide association studies and application to autism. <i>Bioinformatics</i> , 2016, 32, 3815-3822.	1.8	17
13432	Identification potential biomarkers in pulmonary tuberculosis and latent infection based on bioinformatics analysis. <i>BMC Infectious Diseases</i> , 2016, 16, 500.	1.3	13
13433	Transcriptome Analysis on Monocytes from Patients with Neovascular Age-Related Macular Degeneration. <i>Scientific Reports</i> , 2016, 6, 29046.	1.6	32
13434	Differential expression of genes in the alate and apterous morphs of the brown citrus aphid, <i>Toxoptera citricida</i> . <i>Scientific Reports</i> , 2016, 6, 32099.	1.6	34
13435	Systems Biology in Animal Production and Health, Vol. 1. , 2016, , .		0

#	ARTICLE	IF	CITATIONS
13436	Gene expression profiling and bioinformatics analysis in 16HBE cells treated by chromium (VI). <i>Toxicology Letters</i> , 2016, 264, 71-78.	0.4	16
13437	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	9.4	284
13438	Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions. <i>Npj Genomic Medicine</i> , 2016, 1, .	1.7	19
13439	A network-biology perspective of microRNA function and dysfunction in cancer. <i>Nature Reviews Genetics</i> , 2016, 17, 719-732.	7.7	579
13440	Horizontal gene transfer events reshape the global landscape of arm race between viruses and homo sapiens. <i>Scientific Reports</i> , 2016, 6, 26934.	1.6	14
13441	A novel mass spectrometric strategy "BEMAP" reveals Extensive O-linked protein glycosylation in Enterotoxigenic <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2016, 6, 32016.	1.6	21
13442	Transcriptional Analysis of The Adaptive Digestive System of The Migratory Locust in Response to Plant Defensive Protease Inhibitors. <i>Scientific Reports</i> , 2016, 6, 32460.	1.6	19
13443	Emergence and evolution of inter-specific segregating retrocopies in cynomolgus monkey (<i>Macaca</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.6	2
13444	Transfer learning across ontologies for phenome"genome association prediction. <i>Bioinformatics</i> , 2017, 33, 529-536.	1.8	35
13445	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
13446	Robust Methods for Expression Quantitative Trait Loci Mapping. , 2016, , 25-88.		1
13447	Draft genome sequence of <i>Staphylococcus hominis</i> strain Hudgins isolated from human skin implicates metabolic versatility and several virulence determinants. <i>Genomics Data</i> , 2016, 10, 91-96.	1.3	2
13448	Characterization of Protein Lysine Propionylation in <i>Escherichia coli</i> : Global Profiling, Dynamic Change, and Enzymatic Regulation. <i>Journal of Proteome Research</i> , 2016, 15, 4696-4708.	1.8	50
13449	Natural variation in non-coding regions underlying phenotypic diversity in budding yeast. <i>Scientific Reports</i> , 2016, 6, 21849.	1.6	100
13450	The myocardial regenerative potential of three-dimensional engineered cardiac tissues composed of multiple human iPSC cell-derived cardiovascular cell lineages. <i>Scientific Reports</i> , 2016, 6, 29933.	1.6	95
13451	FFPred 3: feature-based function prediction for all Gene Ontology domains. <i>Scientific Reports</i> , 2016, 6, 31865.	1.6	93
13452	Long noncoding RNA linc00598 regulates CCND2 transcription and modulates the G1 checkpoint. <i>Scientific Reports</i> , 2016, 6, 32172.	1.6	13
13453	Expression of HIV-1 matrix protein p17 and association with B-cell lymphoma in HIV-1 transgenic mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13168-13173.	3.3	26

#	ARTICLE	IF	CITATIONS
13454	A Comparative Study and Analysis of DNA Sequence Classifiers for Predicting Human Diseases. , 2016, , .		3
13455	An efficient method for protein function annotation based on multilayer protein networks. Human Genomics, 2016, 10, 33.	1.4	29
13456	Exploring Human Diseases and Biological Mechanisms by Protein Structure Prediction and Modeling. Advances in Experimental Medicine and Biology, 2016, 939, 39-61.	0.8	4
13457	Computational Identification of Novel Genes: Current and Future Perspectives. Bioinformatics and Biology Insights, 2016, 10, BBI.S39950.	1.0	32
13459	A De-Novo Genome Analysis Pipeline (DeNoGAP) for large-scale comparative prokaryotic genomics studies. BMC Bioinformatics, 2016, 17, 260.	1.2	17
13460	Identification of large disjoint motifs in biological networks. BMC Bioinformatics, 2016, 17, 408.	1.2	20
13461	DBSecSys 2.0: a database of Burkholderia mallei and Burkholderia pseudomallei secretion systems. BMC Bioinformatics, 2016, 17, 387.	1.2	4
13462	Multiple differential expression networks identify key genes in rectal cancer. Cancer Biomarkers, 2016, 16, 435-444.	0.8	3
13463	Ontology Reduction Based on Axiomatic Cognitive Model for Ontology Learning. , 2016, , .		0
13464	Not just a colourful metaphor: modelling the landscape of cellular development using Hopfield networks. Npj Systems Biology and Applications, 2016, 2, 16001.	1.4	30
13465	Semantic interrogation of a multi knowledge domain ontological model of tendinopathy identifies four strong candidate risk genes. Scientific Reports, 2016, 6, 19820.	1.6	14
13466	Gene set of chemosensory receptors in the polyembryonic endoparasitoid Macrocentrus cingulum. Scientific Reports, 2016, 6, 24078.	1.6	20
13467	Glucocorticoid receptor isoforms direct distinct mitochondrial programs to regulate ATP production. Scientific Reports, 2016, 6, 26419.	1.6	38
13468	Variation in serum biomarkers with sex and female hormonal status: implications for clinical tests. Scientific Reports, 2016, 6, 26947.	1.6	30
13469	Virus-induced gene silencing of the RPC5-like subunit of RNA polymerase III caused pleiotropic effects in Nicotiana benthamiana. Scientific Reports, 2016, 6, 27785.	1.6	7
13470	A new strategy for exploring the hierarchical structure of cancers by adaptively partitioning functional modules from gene expression network. Scientific Reports, 2016, 6, 28720.	1.6	13
13471	Antennal transcriptome and differential expression of olfactory genes in the yellow peach moth, Conogethes punctiferalis (Lepidoptera: Crambidae). Scientific Reports, 2016, 6, 29067.	1.6	50
13472	Obtaining Human Ischemic Stroke Gene Expression Biomarkers from Animal Models: A Cross-species Validation Study. Scientific Reports, 2016, 6, 29693.	1.6	17

#	ARTICLE	IF	CITATIONS
13473	Schistosome sex matters: a deep view into gonad-specific and pairing-dependent transcriptomes reveals a complex gender interplay. <i>Scientific Reports</i> , 2016, 6, 31150.	1.6	118
13474	OAHG: an integrated resource for annotating human genes with multi-level ontologies. <i>Scientific Reports</i> , 2016, 6, 34820.	1.6	106
13475	Integrating Information in Biological Ontologies and Molecular Networks to Infer Novel Terms. <i>Scientific Reports</i> , 2016, 6, 39237.	1.6	5
13476	Importance of metabolic rate to the relationship between the number of genes in a functional category and body size in Peto's paradox for cancer. <i>Royal Society Open Science</i> , 2016, 3, 160267.	1.1	5
13477	The Terroir Concept Interpreted through Grape Berry Metabolomics and Transcriptomics. <i>Journal of Visualized Experiments</i> , 2016, , .	0.2	9
13478	RE-RANKING FOR PRIORITIZATION OF DISEASE-RELATED GENES. <i>Biomedical Engineering - Applications, Basis and Communications</i> , 2016, 28, 1650027.	0.3	0
13479	MeSH-Informed Enrichment Analysis and MeSH-Guided Semantic Similarity Among Functional Terms and Gene Products in Chicken. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2447-2453.	0.8	10
13480	Metagenomics, Metatranscriptomics, and Metabolomics Approaches for Microbiome Analysis. <i>Evolutionary Bioinformatics</i> , 2016, 12s1, EBO.S36436.	0.6	227
13481	Representation of anatomy in online atlases and databases: a survey and collection of patterns for interface design. <i>BMC Developmental Biology</i> , 2016, 16, 18.	2.1	6
13482	Genetic analysis of variation in lifespan using a multiparental advanced intercross <i>Drosophila</i> mapping population. <i>BMC Genetics</i> , 2016, 17, 113.	2.7	22
13483	The cellular microscopy phenotype ontology. <i>Journal of Biomedical Semantics</i> , 2016, 7, 28.	0.9	24
13484	Generation of open biomedical datasets through ontology-driven transformation and integration processes. <i>Journal of Biomedical Semantics</i> , 2016, 7, 32.	0.9	24
13485	Functional coherence metrics in protein families. <i>Journal of Biomedical Semantics</i> , 2016, 7, 41.	0.9	0
13486	The Proteasix Ontology. <i>Journal of Biomedical Semantics</i> , 2016, 7, 33.	0.9	8
13487	COMODI: an ontology to characterise differences in versions of computational models in biology. <i>Journal of Biomedical Semantics</i> , 2016, 7, 46.	0.9	15
13488	Draft genome sequence of <i>Lampropedia cohaerens</i> strain CT6T isolated from arsenic rich microbial mats of a Himalayan hot water spring. <i>Standards in Genomic Sciences</i> , 2016, 11, 64.	1.5	8
13489	The complete genome sequence of the methanogenic archaeon ISO4-H5 provides insights into the methylotrophic lifestyle of a ruminal representative of the <i>Methanomassiliicoccales</i> . <i>Standards in Genomic Sciences</i> , 2016, 11, 59.	1.5	41
13490	Draft genome sequence of <i>Thermoactinomyces</i> sp. strain AS95 isolated from a Sebkhia in Thamelah, Algeria. <i>Standards in Genomic Sciences</i> , 2016, 11, 68.	1.5	4

#	ARTICLE	IF	CITATIONS
13491	Draft genome sequence of <i>Enterococcus faecium</i> strain LMG 8148. <i>Standards in Genomic Sciences</i> , 2016, 11, 63.	1.5	0
13492	High-quality draft genome sequence of <i>Sedimenticola selenatireducens</i> strain AK4OH1T, a gammaproteobacterium isolated from estuarine sediment. <i>Standards in Genomic Sciences</i> , 2016, 11, 66.	1.5	5
13493	An improved high-quality draft genome sequence of <i>Carnobacterium inhibens</i> subsp. <i>inhibens</i> strain K1T. <i>Standards in Genomic Sciences</i> , 2016, 11, 65.	1.5	2
13494	Complete genome sequence of the Antarctic <i>Halorubrum lacusprofundi</i> type strain ACAM 34. <i>Standards in Genomic Sciences</i> , 2016, 11, 70.	1.5	21
13495	High-quality permanent draft genome sequence of <i>Ensifer</i> sp. PC2, isolated from a nitrogen-fixing root nodule of the legume tree (Khejri) native to the Thar Desert of India. <i>Standards in Genomic Sciences</i> , 2016, 11, 43.	1.5	7
13496	Complete genome sequence of the haloalkaliphilic, obligately chemolithoautotrophic thiosulfate and sulfide-oxidizing β -proteobacterium <i>Thioalkalimicrobium cyclicum</i> type strain ALM 1 (DSM 14477T). <i>Standards in Genomic Sciences</i> , 2016, 11, 38.	1.5	6
13497	Comparing polysaccharide decomposition between the type strains <i>Gramella echinicola</i> KMM 6050T (DSM 19838T) and <i>Gramella portivictoriae</i> UST040801-001T (DSM 23547T), and emended description of <i>Gramella echinicola</i> Nedashkovskaya et al. 2005 emend. Shahina et al. 2014 and <i>Gramella portivictoriae</i> Lau et al. 2005. <i>Standards in Genomic Sciences</i> , 2016, 11, 37.	1.5	27
13498	Complete genome sequence of <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> KG16-1, isolated from vacuum-packaged vegetable sausages. <i>Standards in Genomic Sciences</i> , 2016, 11, 40.	1.5	28
13499	The complete genome sequence and analysis of vB_VorS-PVo5, a <i>Vibrio</i> phage infectious to the pathogenic bacterium <i>Vibrio ordalii</i> ATCC-33509. <i>Standards in Genomic Sciences</i> , 2016, 11, 45.	1.5	5
13500	Draft genomic sequence of a chromate- and sulfate-reducing <i>Alishewanella</i> strain with the ability to bioremediate Cr and Cd contamination. <i>Standards in Genomic Sciences</i> , 2016, 11, 48.	1.5	22
13501	The complete genome sequence of the rumen methanogen <i>Methanobrevibacter millerae</i> SM9. <i>Standards in Genomic Sciences</i> , 2016, 11, 49.	1.5	15
13502	Analysis on differentially expressed genes in watermelon rind color based on RNA-Seq. <i>Journal of Central South University</i> , 2016, 23, 2818-2826.	1.2	4
13503	Interactive visual analytics of molecular data in immersive environments via a semantic definition of the content and the context. , 2016, , .		12
13504	Loss of variation of state detected in soybean metabolic and human myelomonocytic leukaemia cell transcriptional networks under external stimuli. <i>Scientific Reports</i> , 2016, 6, 35946.	1.6	4
13505	PTIR: Predicted Tomato Interactome Resource. <i>Scientific Reports</i> , 2016, 6, 25047.	1.6	32
13506	A data science approach to candidate gene selection of pain regarded as a process of learning and neural plasticity. <i>Pain</i> , 2016, 157, 2747-2757.	2.0	35
13507	PARRoT- a homology-based strategy to quantify and compare RNA-sequencing from non-model organisms. <i>BMC Bioinformatics</i> , 2016, 17, 513.	1.2	6
13508	PROPER: global protein interaction network alignment through percolation matching. <i>BMC Bioinformatics</i> , 2016, 17, 527.	1.2	22

#	ARTICLE	IF	CITATIONS
13509	Robust multi-group gene set analysis with few replicates. BMC Bioinformatics, 2016, 17, 526.	1.2	4
13510	Differential variation patterns between hubs and bottlenecks in human protein-protein interaction networks. BMC Evolutionary Biology, 2016, 16, 260.	3.2	32
13511	Transcriptome analysis reveals the genetic basis underlying the seasonal development of keratinized nuptial spines in <i>Leptobranchium boringii</i> . BMC Genomics, 2016, 17, 978.	1.2	11
13512	Transcriptome analysis in switchgrass discloses ecotype difference in photosynthetic efficiency. BMC Genomics, 2016, 17, 1040.	1.2	9
13513	Bone morphogenetic protein-2-mediated pain and inflammation in a rat model of posterolateral arthrodesis. BMC Neuroscience, 2016, 17, 80.	0.8	12
13514	Tribbles ortholog NIPI-3 and bZIP transcription factor CEBP-1 regulate a <i>Caenorhabditis elegans</i> intestinal immune surveillance pathway. BMC Biology, 2016, 14, 105.	1.7	35
13515	An improved method for functional similarity analysis of genes based on Gene Ontology. BMC Systems Biology, 2016, 10, 119.	3.0	23
13516	Interspecies gene function prediction using semantic similarity. BMC Systems Biology, 2016, 10, 121.	3.0	13
13517	Mapping the membrane proteome of anaerobic gut fungi identifies a wealth of carbohydrate binding proteins and transporters. Microbial Cell Factories, 2016, 15, 212.	1.9	21
13518	msBiodat analysis tool, big data analysis for high-throughput experiments. BioData Mining, 2016, 9, 26.	2.2	1
13519	Germline APOBEC3B deletion is associated with breast cancer risk in an Asian multi-ethnic cohort and with immune cell presentation. Breast Cancer Research, 2016, 18, 56.	2.2	42
13520	XGR software for enhanced interpretation of genomic summary data, illustrated by application to immunological traits. Genome Medicine, 2016, 8, 129.	3.6	137
13521	Genome sequence and overview of <i>Oligoflexus tunisiensis</i> Shr3T in the eighth class Oligoflexia of the phylum Proteobacteria. Standards in Genomic Sciences, 2016, 11, 90.	1.5	12
13522	Complete genome sequence of new bacteriophage phiE142, which causes simultaneously lysis of multidrug-resistant <i>Escherichia coli</i> O157:H7 and <i>Salmonella enterica</i> . Standards in Genomic Sciences, 2016, 11, 89.	1.5	17
13523	Complete genome sequence of the actinomycete <i>Actinoalloteichus hymeniacidonis</i> type strain HPA 177T isolated from a marine sponge. Standards in Genomic Sciences, 2016, 11, 91.	1.5	11
13524	Protein expression data improves gene function prediction. , 2016, , .		0
13525	Effective comparative analysis of protein-protein interaction networks by measuring the steady-state network flow using a Markov model. BMC Bioinformatics, 2016, 17, 395.	1.2	14
13526	Prioritization, clustering and functional annotation of MicroRNAs using latent semantic indexing of MEDLINE abstracts. BMC Bioinformatics, 2016, 17, 350.	1.2	6

#	ARTICLE	IF	CITATIONS
13527	Potential molecular characteristics in situ in response to repetitive UVB irradiation. <i>Diagnostic Pathology</i> , 2016, 11, 129.	0.9	8
13528	A biologically informed method for detecting rare variant associations. <i>BioData Mining</i> , 2016, 9, 27.	2.2	16
13529	The Apollo Structured Vocabulary: an OWL2 ontology of phenomena in infectious disease epidemiology and population biology for use in epidemic simulation. <i>Journal of Biomedical Semantics</i> , 2016, 7, 50.	0.9	13
13530	Information and organization in public health institutes: an ontology-based modeling of the entities in the reception-analysis-report phases. <i>Journal of Biomedical Semantics</i> , 2016, 7, 51.	0.9	2
13531	The Ontology of Biological and Clinical Statistics (OBSC) for standardized and reproducible statistical analysis. <i>Journal of Biomedical Semantics</i> , 2016, 7, 53.	0.9	18
13532	A drug target slim: using gene ontology and gene ontology annotations to navigate protein-ligand target space in ChEMBL. <i>Journal of Biomedical Semantics</i> , 2016, 7, 59.	0.9	27
13533	Draft genome of the leopard gecko, <i>Eublepharis macularius</i> . <i>GigaScience</i> , 2016, 5, 47.	3.3	55
13534	Whole genome shotgun sequence of <i>Bacillus amyloliquefaciens</i> TF28, a biocontrol entophytic bacterium. <i>Standards in Genomic Sciences</i> , 2016, 11, 73.	1.5	6
13535	Complete genome sequence of <i>Methanoculleus bourgensis</i> strain MAB1, the syntrophic partner of mesophilic acetate-oxidising bacteria (SAOB). <i>Standards in Genomic Sciences</i> , 2016, 11, 80.	1.5	44
13536	Two draft genome sequences of <i>Pseudomonas jessenii</i> strains isolated from a copper contaminated site in Denmark. <i>Standards in Genomic Sciences</i> , 2016, 11, 86.	1.5	0
13537	Draft genome sequence of the marine Rhodobacteraceae strain O3.65, cultivated from oil-polluted seawater of the Deepwater Horizon oil spill. <i>Standards in Genomic Sciences</i> , 2016, 11, 81.	1.5	11
13538	Genome sequences and annotation of two urinary isolates of <i>E. coli</i> . <i>Standards in Genomic Sciences</i> , 2016, 11, 79.	1.5	10
13539	Draft genome of <i>Prochlorothrix hollandica</i> CCAP 1490/1T (CALU1027), the chlorophyll a/b-containing filamentous cyanobacterium. <i>Standards in Genomic Sciences</i> , 2016, 11, 82.	1.5	0
13540	Draft genome sequence of <i>Micromonospora</i> sp. DSW705 and distribution of biosynthetic gene clusters for depsipeptides bearing 4-amino-2,4-pentadienoate in actinomycetes. <i>Standards in Genomic Sciences</i> , 2016, 11, 84.	1.5	8
13541	Complete genome anatomy of the emerging potato pathogen <i>Dickeya solani</i> type strain IPO 2222T. <i>Standards in Genomic Sciences</i> , 2016, 11, 87.	1.5	44
13542	Coronary artery disease susceptibility gene <i>ADTRP</i> regulates cell cycle progression, proliferation, and apoptosis by global gene expression regulation. <i>Physiological Genomics</i> , 2016, 48, 554-564.	1.0	20
13543	An integrative data analysis platform for gene set analysis and knowledge discovery in a data warehouse framework. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw009.	1.4	34
13544	PGD: a pangolin genome hub for the research community. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw063.	1.4	5

#	ARTICLE	IF	CITATIONS
13545	Abasy Atlas: a comprehensive inventory of systems, global network properties and systems-level elements across bacteria. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw089.	1.4	19
13546	CoopTFD: a repository for predicted yeast cooperative transcription factor pairs. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw092.	1.4	3
13547	neXtA5: accelerating annotation of articles via automated approaches in neXtProt. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw098.	1.4	10
13548	SorghumFDB: sorghum functional genomics database with multidimensional network analysis. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw099.	1.4	47
13549	The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw100.	1.4	1,085
13550	HPIDB 2.0: a curated database for host-pathogen interactions. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw103.	1.4	202
13551	Automated detection of discourse segment and experimental types from the text of cancer pathway results sections. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw122.	1.4	15
13552	Modeling biochemical pathways in the gene ontology. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw126.	1.4	11
13553	IRNdb: the database of immunologically relevant non-coding RNAs. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw138.	1.4	12
13554	Complete Genome Sequence of <i>Bacillus pumilus</i> PDSLzg-1, a Hydrocarbon-Degrading Bacterium Isolated from Oil-Contaminated Soil in China. <i>Genome Announcements</i> , 2016, 4, .	0.8	17
13555	Ontology in Immunology. <i>Transplantation</i> , 2016, 100, 2014-2015.	0.5	0
13556	Lupus Nephritis IgG Induction of Calcium/Calmodulin-Dependent Protein Kinase IV Expression in Podocytes and Alteration of Their Function. <i>Arthritis and Rheumatology</i> , 2016, 68, 944-952.	2.9	50
13557	Comparative analysis of Cu (I)-catalyzed alkyne-azide cycloaddition (CuAAC) and strain-promoted alkyne-azide cycloaddition (SPAAC) in <i>GlcNAc</i> proteomics. <i>Electrophoresis</i> , 2016, 37, 1431-1436.	1.3	15
13558	GO annotation in InterPro: why stability does not indicate accuracy in a sea of changing annotations. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw027.	1.4	19
13559	The walnut (<i>Juglans regia</i>) genome sequence reveals diversity in genes coding for the biosynthesis of non-structural polyphenols. <i>Plant Journal</i> , 2016, 87, 507-532.	2.8	233
13560	Antimalarial Benzoxaboroles Target <i>Plasmodium falciparum</i> Leucyl-tRNA Synthetase. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 4886-4895.	1.4	58
13561	Tools for Predicting the Functional Impact of Nonsynonymous Genetic Variation. <i>Genetics</i> , 2016, 203, 635-647.	1.2	84
13562	Inter-laboratory study of human in vitro toxicogenomics-based tests as alternative methods for evaluating chemical carcinogenicity: a bioinformatics perspective. <i>Archives of Toxicology</i> , 2016, 90, 2215-2229.	1.9	16

#	ARTICLE	IF	CITATIONS
13563	Different evolutionary patterns of SNPs between domains and unassigned regions in human protein-coding sequences. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1127-1136.	1.0	2
13564	Dominance from the perspective of gene-gene and gene-chemical interactions. <i>Genetica</i> , 2016, 144, 23-36.	0.5	2
13565	The SBOL Stack: A Platform for Storing, Publishing, and Sharing Synthetic Biology Designs. <i>ACS Synthetic Biology</i> , 2016, 5, 487-497.	1.9	24
13566	Bioconductor's EnrichmentBrowser: seamless navigation through combined results of set- & network-based enrichment analysis. <i>BMC Bioinformatics</i> , 2016, 17, 45.	1.2	79
13567	Functional test of PCDHB11, the most human-specific neuronal surface protein. <i>BMC Evolutionary Biology</i> , 2016, 16, 75.	3.2	1
13568	The complete genome sequence and analysis of a plasmid-bearing myxobacterial strain <i>Myxococcus fulvus</i> 124B02 (M 206081). <i>Standards in Genomic Sciences</i> , 2016, 11, 1.	1.5	83
13569	Permanent draft genome sequence of <i>Desulfurococcus mobilis</i> type strain DSM 2161, a thermoacidophilic sulfur-reducing crenarchaeon isolated from acidic hot springs of Hveravellir, Iceland. <i>Standards in Genomic Sciences</i> , 2016, 11, 3.	1.5	2
13570	High-quality draft genome sequence and description of <i>Haemophilus massiliensis</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2016, 11, 31.	1.5	47
13571	Learning node labels with multi-category Hopfield networks. <i>Neural Computing and Applications</i> , 2016, 27, 1677-1692.	3.2	5
13572	Proteomic analysis of the plasma membrane-movement tubule complex of cowpea mosaic virus. <i>Archives of Virology</i> , 2016, 161, 1309-1314.	0.9	5
13573	Revisiting cobalt chloride preconditioning to prevent hypobaric hypoxia-induced damage: identification of global proteomic alteration and key networks. <i>Functional and Integrative Genomics</i> , 2016, 16, 281-295.	1.4	5
13574	Measuring similarity of individuals in description logics over the refinement space of conjunctive queries. <i>Journal of Intelligent Information Systems</i> , 2016, 47, 447-467.	2.8	1
13575	Comparative analysis of embryo surrounding region (Esr-6) genes in Turkish maize varieties: sequencing and modeling. <i>Revista Brasileira De Botanica</i> , 2016, 39, 287-293.	0.5	1
13576	Nanoparticles-cell association predicted by protein corona fingerprints. <i>Nanoscale</i> , 2016, 8, 12755-12763.	2.8	75
13577	Integrated transcriptomics and metabolomics reveal induction of hierarchies of resistance genes in potato against late blight. <i>Functional Plant Biology</i> , 2016, 43, 766.	1.1	24
13578	Slowed aging during reproductive dormancy is reflected in genome-wide transcriptome changes in <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2016, 17, 50.	1.2	95
13579	MicrO: an ontology of phenotypic and metabolic characters, assays, and culture media found in prokaryotic taxonomic descriptions. <i>Journal of Biomedical Semantics</i> , 2016, 7, 18.	0.9	12
13580	Complete genome sequence and genomic characterization of <i>Microcystis panniformis</i> FACHB 1757 by third-generation sequencing. <i>Standards in Genomic Sciences</i> , 2016, 11, 11.	1.5	19

#	ARTICLE	IF	CITATIONS
13581	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
13582	The Role of Transcription Factors at Antisense-Expressing Gene Pairs in Yeast. <i>Genome Biology and Evolution</i> , 2016, 8, 1748-1761.	1.1	6
13583	The Hsp70 homolog Ssb and the 14-3-3 protein Bmh1 jointly regulate transcription of glucose repressed genes in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2016, 44, 5629-5645.	6.5	25
13584	Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, W90-W97.	6.5	7,240
13585	Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. <i>Genome Biology</i> , 2016, 17, 111.	3.8	152
13586	Functional characterization of somatic mutations in cancer using network-based inference of protein activity. <i>Nature Genetics</i> , 2016, 48, 838-847.	9.4	703
13587	Toward reliable biomarker signatures in the age of liquid biopsies - how to standardize the small RNA-Seq workflow. <i>Nucleic Acids Research</i> , 2016, 44, 5995-6018.	6.5	97
13588	High-quality draft genome sequence of <i>Flavobacterium suncheonense</i> GH29-5T (DSM 17707T) isolated from greenhouse soil in South Korea, and emended description of <i>Flavobacterium suncheonense</i> GH29-5T. <i>Standards in Genomic Sciences</i> , 2016, 11, 42.	1.5	3
13589	Systematic Functional Annotation and Visualization of Biological Networks. <i>Cell Systems</i> , 2016, 2, 412-421.	2.9	142
13590	Evolution of domain-peptide interactions to coadapt specificity and affinity to functional diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3862-71.	3.3	36
13591	Transcriptional regulation of vascular cambium activity during the transition from juvenile to mature stages in <i>Cunninghamia lanceolata</i> . <i>Journal of Plant Physiology</i> , 2016, 200, 7-17.	1.6	19
13592	Comprehensive analysis of high-throughput screens with HiTSeekR. <i>Nucleic Acids Research</i> , 2016, 44, 6639-6648.	6.5	17
13593	Transcriptional signatures of influenza A/H1N1-specific IgG memory-like B cell response in older individuals. <i>Vaccine</i> , 2016, 34, 3993-4002.	1.7	39
13594	Mechanisms of transcription factor evolution in Metazoa. <i>Nucleic Acids Research</i> , 2016, 44, 6287-6297.	6.5	60
13595	Transcriptome sequences spanning key developmental states as a resource for the study of the cestode <i>Schistocephalus solidus</i> , a threespine stickleback parasite. <i>GigaScience</i> , 2016, 5, 24.	3.3	49
13596	NegGOA: negative GO annotations selection using ontology structure. <i>Bioinformatics</i> , 2016, 32, 2996-3004.	1.8	33
13597	Identification of genes and pathways associated with pancreatic ductal adenocarcinoma by bioinformatics analyses. <i>Oncology Letters</i> , 2016, 11, 1391-1397.	0.8	13
13598	Transcriptome, genetic editing, and microRNA divergence substantiate sympatric speciation of blind mole rat, <i>Spalax</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7584-7589.	3.3	25

#	ARTICLE	IF	CITATIONS
13599	CAGED-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs. <i>Bioinformatics</i> , 2016, 32, 2858-2860.	1.8	13
13600	Evolution of Gene Duplication in Plants. <i>Plant Physiology</i> , 2016, 171, 2294-2316.	2.3	1,094
13601	Salinity-induced changes in gene expression from anterior and posterior gills of <i>Callinectes sapidus</i> (Crustacea: Portunidae) with implications for crustacean ecological genomics. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2016, 19, 34-44.	0.4	22
13602	Plasma-derived Extracellular Vesicles Contain Predictive Biomarkers and Potential Therapeutic Targets for Myocardial Ischemic (MI) Injury. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2628-2640.	2.5	97
13603	Statistical Methods in Integrative Genomics. <i>Annual Review of Statistics and Its Application</i> , 2016, 3, 181-209.	4.1	75
13604	Identifying candidate genes for wood formation in poplar based on microarray network analysis and graph theory. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	7
13605	A systematic exploration of the associations between amino acid variants and post-translational modifications. <i>Neurocomputing</i> , 2016, 206, 13-18.	3.5	1
13606	Identification and tissue distribution of chemosensory protein and odorant binding protein genes in <i>Athetis dissimilis</i> (Lepidoptera: Noctuidae). <i>Applied Entomology and Zoology</i> , 2016, 51, 409-420.	0.6	28
13607	RNA-sequencing of <i>Cercospora beticola</i> DMI-sensitive and -resistant isolates after treatment with tetraconazole identifies common and contrasting pathway induction. <i>Fungal Genetics and Biology</i> , 2016, 92, 1-13.	0.9	30
13608	High-quality genome sequence and description of <i>Paenibacillus dakarensis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2016, 10, 132-141.	0.8	10
13609	OmniSearch: a semantic search system based on the Ontology for MicroRNA Target (OMIT) for microRNA-target gene interaction data. <i>Journal of Biomedical Semantics</i> , 2016, 7, 25.	0.9	27
13610	Structural adaption of extremophile proteins to the environments with special reference to hydrophobic networks. <i>Ecological Genetics and Genomics</i> , 2016, 1, 1-5.	0.3	7
13611	A semantic web based framework for the interoperability and exploitation of clinical models and EHR data. <i>Knowledge-Based Systems</i> , 2016, 105, 175-189.	4.0	40
13612	Genome sequence and description of <i>Anaerosalibacter massiliensis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2016, 10, 66-76.	0.8	125
13613	Next-Generation Sequencing and the Crustacean Immune System: The Need for Alternatives in Immune Gene Annotation. <i>Integrative and Comparative Biology</i> , 2016, 56, 1113-1130.	0.9	24
13614	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
13615	Data in support of the identification of neuronal and astrocyte proteins interacting with extracellularly applied oligomeric and fibrillar I \pm -synuclein assemblies by mass spectrometry. <i>Data in Brief</i> , 2016, 7, 221-228.	0.5	10
13616	A knowledgebase of the human Alu repetitive elements. <i>Journal of Biomedical Informatics</i> , 2016, 60, 77-83.	2.5	10

#	ARTICLE	IF	CITATIONS
13617	Systematic understanding the mechanisms of vitiligo pathogenesis and its treatment by Qubaibabuqi formula. <i>Journal of Ethnopharmacology</i> , 2016, 190, 272-287.	2.0	74
13618	Noncontiguous finished genome sequence and description of <i>Nocardioides massiliensis</i> sp. nov. GD13T. <i>New Microbes and New Infections</i> , 2016, 10, 47-57.	0.8	6
13619	Microarray-Based Phospho-Proteomic Profiling of Complex Biological Systems. <i>Translational Oncology</i> , 2016, 9, 124-129.	1.7	6
13620	Combinatorial Gene Regulatory Functions Underlie Ultraconserved Elements in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 2294-2306.	3.5	18
13621	Biomedical Ontology Quality Assurance Using a Big Data Approach. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2016, 10, 1-28.	2.5	16
13622	Analysis of transcriptome profiling from the brain at maturation and regression phases in starry flounder (<i>Platichthys stellatus</i>). <i>Gene Reports</i> , 2016, 4, 45-52.	0.4	1
13623	Autocrine effects of transgenic resistin reduce palmitate and glucose oxidation in brown adipose tissue. <i>Physiological Genomics</i> , 2016, 48, 420-427.	1.0	4
13624	Several type 2 diabetes-associated variants in genes annotated to WNT signaling interact with dietary fiber in relation to incidence of type 2 diabetes. <i>Genes and Nutrition</i> , 2016, 11, 6.	1.2	25
13625	Learning a hierarchical representation of the yeast transcriptomic machinery using an autoencoder model. <i>BMC Bioinformatics</i> , 2016, 17, 9.	1.2	76
13626	Missing value imputation for microRNA expression data by using a GO-based similarity measure. <i>BMC Bioinformatics</i> , 2016, 17, 10.	1.2	27
13627	Sparse regression models for unraveling group and individual associations in eQTL mapping. <i>BMC Bioinformatics</i> , 2016, 17, 136.	1.2	4
13628	ChemiRs: a web application for microRNAs and chemicals. <i>BMC Bioinformatics</i> , 2016, 17, 167.	1.2	29
13629	DrugGenEx-Net: a novel computational platform for systems pharmacology and gene expression-based drug repurposing. <i>BMC Bioinformatics</i> , 2016, 17, 202.	1.2	19
13630	Transcriptome sequencing based annotation and homologous evidence based scaffolding of <i>Anguilla japonica</i> draft genome. <i>BMC Genomics</i> , 2016, 17, 13.	1.2	9
13631	Comparative transcriptomics and proteomics of three different aphid species identifies core and diverse effector sets. <i>BMC Genomics</i> , 2016, 17, 172.	1.2	92
13632	Hologenome analysis of two marine sponges with different microbiomes. <i>BMC Genomics</i> , 2016, 17, 158.	1.2	60
13633	Long genes and genes with multiple splice variants are enriched in pathways linked to cancer and other multigenic diseases. <i>BMC Genomics</i> , 2016, 17, 225.	1.2	28
13634	A comparative gene analysis with rice identified orthologous group II HKT genes and their association with Na ⁺ concentration in bread wheat. <i>BMC Plant Biology</i> , 2016, 16, 21.	1.6	15

#	ARTICLE	IF	CITATIONS
13635	Genome-wide association study of antidepressant response: involvement of the inorganic cation transmembrane transporter activity pathway. <i>BMC Psychiatry</i> , 2016, 16, 106.	1.1	24
13636	Challenges in horizontal model integration. <i>BMC Systems Biology</i> , 2016, 10, 28.	3.0	0
13637	Identification of biological targets of therapeutic intervention for clear cell renal cell carcinoma based on bioinformatics approach. <i>Cancer Cell International</i> , 2016, 16, 16.	1.8	17
13638	LEAFDATA: a literature-curated database for Arabidopsis leaf development. <i>Plant Methods</i> , 2016, 12, 15.	1.9	6
13639	The link between orthology relations and gene trees: a correction perspective. <i>Algorithms for Molecular Biology</i> , 2016, 11, 4.	0.3	26
13640	A visual and curatorial approach to clinical variant prioritization and disease gene discovery in genome-wide diagnostics. <i>Genome Medicine</i> , 2016, 8, 13.	3.6	37
13641	Selectivity profiling of BCRP versus P-gp inhibition: from automated collection of polypharmacology data to multi-label learning. <i>Journal of Cheminformatics</i> , 2016, 8, 7.	2.8	26
13642	An ontology for major histocompatibility restriction. <i>Journal of Biomedical Semantics</i> , 2016, 7, 1.	0.9	43
13643	Linking rare and common disease: mapping clinical disease-phenotypes to ontologies in therapeutic target validation. <i>Journal of Biomedical Semantics</i> , 2016, 7, 8.	0.9	28
13644	Weblous and the Weblous Google Add-On - a web service and application for ontology building from templates. <i>Journal of Biomedical Semantics</i> , 2016, 7, 17.	0.9	6
13645	Extending gene ontology in the context of extracellular RNA and vesicle communication. <i>Journal of Biomedical Semantics</i> , 2016, 7, 19.	0.9	24
13646	Filtering large-scale event collections using a combination of supervised and unsupervised learning for event trigger classification. <i>Journal of Biomedical Semantics</i> , 2016, 7, 27.	0.9	1
13647	Permanent draft genome sequence of the probiotic strain <i>Propionibacterium freudenreichii</i> CIRM-BIA 129 (ITG P20). <i>Standards in Genomic Sciences</i> , 2016, 11, 6.	1.5	11
13648	Draft genome of the <i>Arabidopsis thaliana</i> phyllosphere bacterium, <i>Williamsia</i> sp. ARP1. <i>Standards in Genomic Sciences</i> , 2016, 11, 8.	1.5	10
13649	Complete genome sequence of <i>Methanospirillum hungatei</i> type strain JF1. <i>Standards in Genomic Sciences</i> , 2016, 11, 2.	1.5	33
13650	Complete genome sequence and characterization of avian pathogenic <i>Escherichia coli</i> field isolate ACN001. <i>Standards in Genomic Sciences</i> , 2016, 11, 13.	1.5	9
13651	Draft genome sequence for virulent and avirulent strains of <i>Xanthomonas arboricola</i> isolated from <i>Prunus</i> spp. in Spain. <i>Standards in Genomic Sciences</i> , 2016, 11, 12.	1.5	16
13652	Draft genome sequence of <i>Sphingomonas paucimobilis</i> strain LCT-SP1 isolated from the Shenzhou X spacecraft of China. <i>Standards in Genomic Sciences</i> , 2016, 11, 18.	1.5	6

#	ARTICLE	IF	CITATIONS
13653	Isolation and complete genome sequence of the thermophilic <i>Geobacillus</i> sp. 12AMOR1 from an Arctic deep-sea hydrothermal vent site. <i>Standards in Genomic Sciences</i> , 2016, 11, 16.	1.5	24
13654	Genome sequences of <i>Knoxdaviesia capensis</i> and <i>K. proteae</i> (Fungi: Ascomycota) from Protea trees in South Africa. <i>Standards in Genomic Sciences</i> , 2016, 11, 22.	1.5	6
13655	High-quality draft genome sequence of the <i>Thermus amyloliquefaciens</i> type strain YIM 77409T with an incomplete denitrification pathway. <i>Standards in Genomic Sciences</i> , 2016, 11, 20.	1.5	7
13656	Draft genomic sequence of <i>Nereida ignava</i> CECT 5292T, a marine bacterium of the family Rhodobacteraceae. <i>Standards in Genomic Sciences</i> , 2016, 11, 21.	1.5	11
13657	Draft genome sequence of chloride-tolerant <i>Leptospirillum ferriphilum</i> Sp-Cl from industrial bioleaching operations in northern Chile. <i>Standards in Genomic Sciences</i> , 2016, 11, 19.	1.5	29
13658	Genome sequence of <i>Shimia</i> str. SK013, a representative of the <i>Roseobacter</i> group isolated from marine sediment. <i>Standards in Genomic Sciences</i> , 2016, 11, 25.	1.5	11
13659	Insights into the single cell draft genome of <i>Candidatus Achromatium palustre</i> . <i>Standards in Genomic Sciences</i> , 2016, 11, 28.	1.5	13
13660	The complete genome sequence of <i>Eubacterium limosum</i> SA11, a metabolically versatile rumen acetogen. <i>Standards in Genomic Sciences</i> , 2016, 11, 26.	1.5	36
13661	Understanding the Systems Biology of Pathogen Virulence Using Semantic Methodologies. , 2016, , .		0
13662	Dimensions of Ontological Similarity. , 2016, , .		2
13663	Identification of S-phase DNA damage-response targets in fission yeast reveals conservation of damage-response networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3676-E3685.	3.3	13
13664	Antiinflammatory Effects of Budesonide in Human Fetal Lung. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2016, 55, 623-632.	1.4	33
13665	Compensation of Dosage-Sensitive Genes on the Chicken Z Chromosome. <i>Genome Biology and Evolution</i> , 2016, 8, 1233-1242.	1.1	57
13666	Metabolomics in epidemiology: from metabolite concentrations to integrative reaction networks. <i>International Journal of Epidemiology</i> , 2016, 45, 1319-1328.	0.9	40
13667	A Bayesian approach for estimating allele-specific expression from RNA-Seq data with diploid genomes. <i>BMC Genomics</i> , 2016, 17, 2.	1.2	22
13668	Topology based identification and comprehensive classification of four-transmembrane helix containing proteins (4TMs) in the human genome. <i>BMC Genomics</i> , 2016, 17, 268.	1.2	10
13669	A generic schema and data collection forms applicable to diverse entomological studies of mosquitoes. <i>Source Code for Biology and Medicine</i> , 2016, 11, 4.	1.7	15
13670	Draft genome sequence of <i>Paenibacillus</i> sp. strain A2. <i>Standards in Genomic Sciences</i> , 2016, 11, 9.	1.5	2

#	ARTICLE	IF	CITATIONS
13671	Genome sequence of <i>Shinella</i> sp. strain DD12, isolated from homogenized guts of starved <i>Daphnia magna</i> . <i>Standards in Genomic Sciences</i> , 2016, 11, 14.	1.5	3
13672	Draft genome sequence and overview of the purple non sulfur bacterium <i>Rhodopseudomonas palustris</i> 42OL. <i>Standards in Genomic Sciences</i> , 2016, 11, 24.	1.5	12
13673	Complete genome sequences of <i>Geobacillus</i> sp. WCH70, a thermophilic strain isolated from wood compost. <i>Standards in Genomic Sciences</i> , 2016, 11, 33.	1.5	11
13674	NSDF: Neuroscience Simulation Data Format. <i>Neuroinformatics</i> , 2016, 14, 147-167.	1.5	19
13675	Relationship between spatial organization and biological function, analyzed using gene ontology and chromosome conformation capture of human and fission yeast genomes. <i>Genes and Genomics</i> , 2016, 38, 693-705.	0.5	0
13676	BEACON: An Efficient SAT-Based Tool for Debugging $\{\mathcal{EL}\}^{\wedge+}$ Ontologies. <i>Lecture Notes in Computer Science</i> , 2016, , 521-530.	1.0	21
13677	Defining the consequences of genetic variation on a proteome-wide scale. <i>Nature</i> , 2016, 534, 500-505.	13.7	335
13678	An integer programming framework for inferring disease complexes from network data. <i>Bioinformatics</i> , 2016, 32, i271-i277.	1.8	44
13679	Next-generation profiling to identify the molecular etiology of Parkinson dementia. <i>Neurology: Genetics</i> , 2016, 2, e75.	0.9	25
13680	VariOtorator, a Software Tool for Variation Annotation with the Variation Ontology. <i>Human Mutation</i> , 2016, 37, 344-349.	1.1	4
13681	Malignant pheochromocytomas/paragangliomas harbor mutations in transport and cell adhesion genes. <i>International Journal of Cancer</i> , 2016, 138, 2201-2211.	2.3	24
13682	Protein substrates of the arginine methyltransferase Hmt1 identified by proteome arrays. <i>Proteomics</i> , 2016, 16, 465-476.	1.3	8
13683	Disordered nucleome: Abundance of intrinsic disorder in the DNA- and RNA-binding proteins in 1121 species from Eukaryota, Bacteria and Archaea. <i>Proteomics</i> , 2016, 16, 1486-1498.	1.3	92
13684	Proteomic profiling of eccrine sweat reveals its potential as a diagnostic biofluid for active tuberculosis. <i>Proteomics - Clinical Applications</i> , 2016, 10, 547-553.	0.8	45
13685	The impact of quality control in RNA-seq experiments. <i>Journal of Physics: Conference Series</i> , 2016, 705, 012003.	0.3	12
13686	A Symmetric Length-Aware Enrichment Test. <i>Journal of Computational Biology</i> , 2016, 23, 508-525.	0.8	1
13687	HNdb: an integrated database of gene and protein information on head and neck squamous cell carcinoma. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw026.	1.4	10
13688	BELTracker: evidence sentence retrieval for BEL statements. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw079.	1.4	12

#	ARTICLE	IF	CITATIONS
13689	Analyses of transcriptome sequences reveal multiple ancient large-scale duplication events in the ancestor of Sphagnopsida (Bryophyta). <i>New Phytologist</i> , 2016, 211, 300-318.	3.5	56
13690	ADAGE-Based Integration of Publicly Available <i>Pseudomonas aeruginosa</i> Gene Expression Data with Denoising Autoencoders Illuminates Microbe-Host Interactions. <i>MSystems</i> , 2016, 1, .	1.7	116
13691	Mechanistic underpinnings of dehydration stress in the American dog tick revealed through RNA-Seq and metabolomics. <i>Journal of Experimental Biology</i> , 2016, 219, 1808-1819.	0.8	41
13692	Predicting overlapping protein complexes from weighted protein interaction graphs by gradually expanding dense neighborhoods. <i>Artificial Intelligence in Medicine</i> , 2016, 71, 62-69.	3.8	8
13693	Alterations in gene expression during fasting-induced atresia of early secondary ovarian follicles of coho salmon, <i>Oncorhynchus kisutch</i> . <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2016, 201, 1-11.	0.8	7
13694	Bicluster detection using strength pareto front evolutionary algorithm. , 2016, , .		2
13695	Identification of the key regulating genes of diminished ovarian reserve (DOR) by network and gene ontology analysis. <i>Molecular Biology Reports</i> , 2016, 43, 923-937.	1.0	34
13696	The Exonuclease Trex2 Shapes Psoriatic Phenotype. <i>Journal of Investigative Dermatology</i> , 2016, 136, 2345-2355.	0.3	15
13697	Identification of novel biomarkers for preeclampsia on the basis of differential expression network analysis. <i>Experimental and Therapeutic Medicine</i> , 2016, 12, 201-207.	0.8	4
13698	MiRNA expression profile of ionizing radiation-induced liver injury in mouse using deep sequencing. <i>Cell Biology International</i> , 2016, 40, 873-886.	1.4	17
13699	IQSEC2 and X-linked syndromal intellectual disability. <i>Psychiatric Genetics</i> , 2016, 26, 101-108.	0.6	15
13700	Identification of candidate causal genes and their associated pathogenic mechanisms underlying teratozoospermia based on the spermatozoa transcript profiles. <i>Andrologia</i> , 2016, 48, 576-583.	1.0	10
13701	Hypothesis Test of Mediation Effect in Causal Mediation Model With High-Dimensional Continuous Mediators. <i>Biometrics</i> , 2016, 72, 402-413.	0.8	99
13702	Chitosan Degradation Products Promote Nerve Regeneration by Stimulating Schwann Cell Proliferation via miR-27a/FOXO1 Axis. <i>Molecular Neurobiology</i> , 2016, 53, 28-39.	1.9	79
13703	Microbial community dynamics during the early stages of plant polymer breakdown in paddy soil. <i>Environmental Microbiology</i> , 2016, 18, 2825-2842.	1.8	72
13704	Hippocampal Pruning as a New Theory of Schizophrenia Etiopathogenesis. <i>Molecular Neurobiology</i> , 2016, 53, 2065-2081.	1.9	28
13705	An in vivo molecular response analysis of colorectal cancer treated with <i>Astragalus membranaceus</i> extract. <i>Oncology Reports</i> , 2016, 35, 659-668.	1.2	25
13706	The Dynamics of Transcript Abundance during Cellularization of Developing Barley Endosperm. <i>Plant Physiology</i> , 2016, 170, 1549-1565.	2.3	47

#	ARTICLE	IF	CITATIONS
13707	Interaction between dietary lipids and gut microbiota regulates hepatic cholesterol metabolism. <i>Journal of Lipid Research</i> , 2016, 57, 474-481.	2.0	72
13708	Effect of single post-ovulatory administration of mifepristone (RU486) on transcript profile during the receptive period in human endometrium. <i>Reproduction</i> , 2016, 151, 331-349.	1.1	14
13709	Complete genome sequence of the potato pathogen <i>Ralstonia solanacearum</i> UY031. <i>Standards in Genomic Sciences</i> , 2016, 11, 7.	1.5	26
13710	Orphan Crops Browser: a bridge between model and orphan crops. <i>Molecular Breeding</i> , 2016, 36, 9.	1.0	18
13711	Human TNF- α induces differential protein phosphorylation in <i>Schistosoma mansoni</i> adult male worms. <i>Parasitology Research</i> , 2016, 115, 817-828.	0.6	18
13712	The Proteome of Filter-Grown Caco-2 Cells With a Focus on Proteins Involved in Drug Disposition. <i>Journal of Pharmaceutical Sciences</i> , 2016, 105, 817-827.	1.6	58
13713	Bottom-Up Proteomics Methods for Strain-Level Typing and Identification of Bacteria. , 2016, , 83-146.		2
13714	Identification of transcription factors and gene clusters in rabbit smooth muscle cells during high flow-induced vascular remodeling via microarray. <i>Gene</i> , 2016, 575, 407-414.	1.0	2
13715	MicroRNA Species in Follicular Fluid Associating With Polycystic Ovary Syndrome and Related Intermediary Phenotypes. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016, 101, 1579-1589.	1.8	58
13716	Enhancing protein function prediction with taxonomic constraints â€œ The Argot2.5 web server. <i>Methods</i> , 2016, 93, 15-23.	1.9	54
13717	Multi-omics enrichment analysis using the GeneTrail2 web service. <i>Bioinformatics</i> , 2016, 32, 1502-1508.	1.8	144
13718	Survival proteomes: the emerging proteotype of antimicrobial resistance. <i>FEMS Microbiology Reviews</i> , 2016, 40, 323-342.	3.9	40
13719	Consolidating and Exploring Antibiotic Resistance Gene Data Resources. <i>Journal of Clinical Microbiology</i> , 2016, 54, 851-859.	1.8	94
13720	Compendium of Immune Signatures Identifies Conserved and Species-Specific Biology in Response to Inflammation. <i>Immunity</i> , 2016, 44, 194-206.	6.6	238
13721	Repeated exposure to neurotoxic levels of chlorpyrifos alters hippocampal expression of neurotrophins and neuropeptides. <i>Toxicology</i> , 2016, 340, 53-62.	2.0	51
13722	Molecular systems evaluation of oligomerogenic APPE693Q and fibrillogenic APPKM670/671NL/PSEN1 ¹ exon9 mouse models identifies shared features with human Alzheimerâ€™s brain molecular pathology. <i>Molecular Psychiatry</i> , 2016, 21, 1099-1111.	4.1	18
13723	Synthetic cycle of the initiation module of a formylating nonribosomal peptide synthetase. <i>Nature</i> , 2016, 529, 239-242.	13.7	132
13724	Global transcriptome profiling analysis reveals insight into saliva-responsive genes in alfalfa. <i>Plant Cell Reports</i> , 2016, 35, 561-571.	2.8	29

#	ARTICLE	IF	CITATIONS
13725	A Proteome-wide Fission Yeast Interactome Reveals Network Evolution Principles from Yeasts to Human. <i>Cell</i> , 2016, 164, 310-323.	13.5	106
13726	Plant miRNA function prediction based on functional similarity network and transductive multi-label classification algorithm. <i>Neurocomputing</i> , 2016, 179, 283-289.	3.5	9
13727	Functional Alignment of Metabolic Networks. <i>Journal of Computational Biology</i> , 2016, 23, 390-399.	0.8	3
13728	RCSB Protein Data Bank: A Resource for Chemical, Biochemical, and Structural Explorations of Large and Small Biomolecules. <i>Journal of Chemical Education</i> , 2016, 93, 569-575.	1.1	66
13729	A quinazoline-based HDAC inhibitor affects gene expression pathways involved in cholesterol biosynthesis and mevalonate in prostate cancer cells. <i>Molecular BioSystems</i> , 2016, 12, 839-849.	2.9	7
13730	Label-Free, In-Solution Screening of Peptide Libraries for Binding to Protein Targets Using Hydrogen Exchange Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2016, 138, 1335-1343.	6.6	12
13731	Divergence and Functional Degradation of a Sex Chromosome-like Supergene. <i>Current Biology</i> , 2016, 26, 344-350.	1.8	266
13732	Identifying network-based biomarkers of complex diseases from high-throughput data. <i>Biomarkers in Medicine</i> , 2016, 10, 633-650.	0.6	35
13733	A transcriptional signature of hub connectivity in the mouse connectome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1435-1440.	3.3	197
13734	Mitochondrial electron transport chain identified as a novel molecular target of SPIO nanoparticles mediated cancer-specific cytotoxicity. <i>Biomaterials</i> , 2016, 83, 102-114.	5.7	77
13735	High quality permanent draft genome sequence of <i>Phaseolobacter flectens</i> ATCC 12775T, a plant pathogen of French bean pods. <i>Standards in Genomic Sciences</i> , 2016, 11, 4.	1.5	1
13736	Applications of Mass Spectrometry in Microbiology. , 2016, , .		9
13737	Exosomes decrease sensitivity of breast cancer cells to adriamycin by delivering microRNAs. <i>Tumor Biology</i> , 2016, 37, 5247-5256.	0.8	79
13738	Microarray analysis of di-n-butyl phthalate and 17 β -ethinyl-oestradiol responses in three-spined stickleback testes reveals novel candidate genes for endocrine disruption. <i>Ecotoxicology and Environmental Safety</i> , 2016, 124, 96-104.	2.9	10
13739	Identification and profiling of microRNAs in the ovaries of polytocous and monotocous goats during estrus. <i>Theriogenology</i> , 2016, 85, 769-780.	0.9	21
13740	Canine congenital portosystemic shunts: Disconnections dissected. <i>Veterinary Journal</i> , 2016, 211, 14-20.	0.6	12
13741	Bottom-Up Proteomics (2013-2015): Keeping up in the Era of Systems Biology. <i>Analytical Chemistry</i> , 2016, 88, 95-121.	3.2	52
13742	SynLethDB: synthetic lethality database toward discovery of selective and sensitive anticancer drug targets. <i>Nucleic Acids Research</i> , 2016, 44, D1011-D1017.	6.5	115

#	ARTICLE	IF	CITATIONS
13743	Bioinformatic tools for microRNA dissection. <i>Nucleic Acids Research</i> , 2016, 44, 24-44.	6.5	182
13744	Massively parallel <i>cis</i> -regulatory analysis in the mammalian central nervous system. <i>Genome Research</i> , 2016, 26, 238-255.	2.4	106
13745	Regulatory T Cells Orchestrate Similar Immune Evasion of Fetuses and Tumors in Mice. <i>Journal of Immunology</i> , 2016, 196, 678-690.	0.4	14
13746	Influence factors on the correlations between expression levels of neighboring pattern genes. <i>BioSystems</i> , 2016, 139, 23-28.	0.9	0
13747	Cancer Gene Profiling. <i>Methods in Molecular Biology</i> , 2016, , .	0.4	2
13748	Data standards can boost metabolomics research, and if there is a will, there is a way. <i>Metabolomics</i> , 2016, 12, 14.	1.4	97
13749	A novel topological centrality measure capturing biologically important proteins. <i>Molecular BioSystems</i> , 2016, 12, 666-673.	2.9	10
13750	Improving and Evaluating Topic Models and Other Models of Text. <i>Journal of the American Statistical Association</i> , 2016, 111, 1381-1403.	1.8	83
13752	ELM 2016 data update and new functionality of the eukaryotic linear motif resource. <i>Nucleic Acids Research</i> , 2016, 44, D294-D300.	6.5	289
13753	Rhinovirus Detection in Symptomatic and Asymptomatic Children: Value of Host Transcriptome Analysis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 193, 772-782.	2.5	98
13754	Analysis of Altered Micro RNA Expression Profiles in Focal Cortical Dysplasia IIB. <i>Journal of Child Neurology</i> , 2016, 31, 613-620.	0.7	6
13755	Recurrent Fusions in <i>MYB</i> and <i>MYBL1</i> Define a Common, Transcription Factor-Driven Oncogenic Pathway in Salivary Gland Adenoid Cystic Carcinoma. <i>Cancer Discovery</i> , 2016, 6, 176-187.	7.7	179
13756	Comparative transcriptome analysis of atrial septal defect identifies dysregulated genes during heart septum morphogenesis. <i>Gene</i> , 2016, 575, 303-312.	1.0	19
13757	A novel framework for inferring condition-specific TF and miRNA co-regulation of protein-protein interactions. <i>Gene</i> , 2016, 577, 55-64.	1.0	8
13758	MitoMiner v3.1, an update on the mitochondrial proteomics database. <i>Nucleic Acids Research</i> , 2016, 44, D1258-D1261.	6.5	182
13759	Orchestrated regulation of energy supply and energy expenditure: Transcriptional coexpression of metabolism, ion homeostasis, and sarcomeric genes in mammalian myocardium. <i>Heart Rhythm</i> , 2016, 13, 1131-1139.	0.3	6
13760	Genetic Evidence of Human Adaptation to a Cooked Diet. <i>Genome Biology and Evolution</i> , 2016, 8, 1091-1103.	1.1	29
13761	Systematic identification and correction of annotation errors in the genetic interaction map of <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2016, 44, e50-e50.	6.5	19

#	ARTICLE	IF	CITATIONS
13762	mRNA expression in different developmental stages of the chicken bursa of Fabricius. <i>Poultry Science</i> , 2016, 95, 1787-1794.	1.5	14
13763	New features of desiccation tolerance in the lichen photobiont <i>Trebouxia gelatinosa</i> are revealed by a transcriptomic approach. <i>Plant Molecular Biology</i> , 2016, 91, 319-339.	2.0	69
13764	Effect of chronic uremia on the transcriptional profile of the calcified aorta analyzed by RNA sequencing. <i>American Journal of Physiology - Renal Physiology</i> , 2016, 310, F477-F491.	1.3	45
13765	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
13766	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
13767	Health and population effects of rare gene knockouts in adult humans with related parents. <i>Science</i> , 2016, 352, 474-477.	6.0	272
13768	Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. <i>Science</i> , 2016, 352, 235-239.	6.0	391
13769	New day rising: state of the art in yeast functional genomics. <i>Briefings in Functional Genomics</i> , 2016, 15, 73-74.	1.3	0
13770	CLUSTERnGO: a user-defined modelling platform for two-stage clustering of time-series data. <i>Bioinformatics</i> , 2016, 32, 388-397.	1.8	7
13771	KMAD: knowledge-based multiple sequence alignment for intrinsically disordered proteins. <i>Bioinformatics</i> , 2016, 32, 932-936.	1.8	27
13772	Person-Oriented Modeling Methodology: A Case Study on Personal Credit Scoring. , 2016, , .		0
13773	Smokescreen: a targeted genotyping array for addiction research. <i>BMC Genomics</i> , 2016, 17, 145.	1.2	94
13774	Proteomic peptide phage display uncovers novel interactions of the PDZ1 ϵ 2 supramodule of syntenin. <i>FEBS Letters</i> , 2016, 590, 3-12.	1.3	24
13775	Phosphoproteomic analysis of induced resistance reveals activation of signal transduction processes by beneficial and pathogenic interaction in grapevine. <i>Journal of Plant Physiology</i> , 2016, 195, 59-72.	1.6	25
13776	Applications of Deep Learning in Biomedicine. <i>Molecular Pharmaceutics</i> , 2016, 13, 1445-1454.	2.3	535
13777	GOexpress: an R/Bioconductor package for the identification and visualisation of robust gene ontology signatures through supervised learning of gene expression data. <i>BMC Bioinformatics</i> , 2016, 17, 126.	1.2	40
13778	Predicting physiologically relevant SH3 domain mediated protein ϵ protein interactions in yeast. <i>Bioinformatics</i> , 2016, 32, 1865-1872.	1.8	6
13779	FlyBase: establishing a Gene Group resource for <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2016, 44, D786-D792.	6.5	284

#	ARTICLE	IF	CITATIONS
13780	Optimization of next-generation sequencing transcriptome annotation for species lacking sequenced genomes. <i>Molecular Ecology Resources</i> , 2016, 16, 446-458.	2.2	23
13781	The transcriptomic basis of tissue- and nutrition-dependent sexual dimorphism in the beetle <i>Onthophagus taurus</i> . <i>Ecology and Evolution</i> , 2016, 6, 1601-1613.	0.8	18
13782	kinMut-2: Identification and Interpretation of Pathogenic Variants in Human Protein Kinases. <i>Human Mutation</i> , 2016, 37, 36-42.	1.1	10
13783	<i>Microvirga massiliensis</i> sp. nov., the human commensal with the largest genome. <i>MicrobiologyOpen</i> , 2016, 5, 307-322.	1.2	27
13784	Effect of summer daylight exposure and genetic background on growth in growth hormone-deficient children. <i>Pharmacogenomics Journal</i> , 2016, 16, 540-550.	0.9	18
13785	BRG1/SMARCA4 is essential for neuroblastoma cell viability through modulation of cell death and survival pathways. <i>Oncogene</i> , 2016, 35, 5179-5190.	2.6	65
13786	Pharmacodynamics of Dimethyl Fumarate Are Tissue Specific and Involve NRF2-Dependent and -Independent Mechanisms. <i>Antioxidants and Redox Signaling</i> , 2016, 24, 1058-1071.	2.5	49
13787	MaizeGDB update: new tools, data and interface for the maize model organism database. <i>Nucleic Acids Research</i> , 2016, 44, D1195-D1201.	6.5	170
13788	Integrated microRNA-gene analysis of coronary artery disease based on miRNA and gene expression profiles. <i>Molecular Medicine Reports</i> , 2016, 13, 3063-3073.	1.1	7
13789	Expression Profiling of Macrophages Reveals Multiple Populations with Distinct Biological Roles in an Immunocompetent Orthotopic Model of Lung Cancer. <i>Journal of Immunology</i> , 2016, 196, 2847-2859.	0.4	86
13790	Comprehensive analysis of schizophrenia-associated loci highlights ion channel pathways and biologically plausible candidate causal genes. <i>Human Molecular Genetics</i> , 2016, 25, 1247-1254.	1.4	69
13791	Compound annotation with real time cellular activity profiles to improve drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2016, 11, 269-280.	2.5	3
13792	Deep-sequencing identification of differentially expressed miRNAs in decidua and villus of recurrent miscarriage patients. <i>Archives of Gynecology and Obstetrics</i> , 2016, 293, 1125-1135.	0.8	32
13793	Association of transcriptome-wide sequence variation with climate gradients in valley oak (<i>Quercus</i>) Tj ETQq1 1 0.784314 rgBT /Overbo 0.6 31	0.6	31
13794	Genome Reduction Uncovers a Large Dispensable Genome and Adaptive Role for Copy Number Variation in Asexually Propagated <i>Solanum tuberosum</i> . <i>Plant Cell</i> , 2016, 28, 388-405.	3.1	163
13795	Proteomics of terpenoid biosynthesis and secretion in trichomes of higher plant species. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1039-1049.	1.1	30
13796	Global Profiling of Huntingtin-associated protein E (HYPE)-Mediated AMPylation through a Chemical Proteomic Approach. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 715-725.	2.5	56
13797	A transcriptome study on <i>Macrobrachium rosenbergii</i> hepatopancreas experimentally challenged with white spot syndrome virus (WSSV). <i>Journal of Invertebrate Pathology</i> , 2016, 136, 10-22.	1.5	62

#	ARTICLE	IF	CITATIONS
13798	Spatially resolved proteomic mapping in living cells with the engineered peroxidase APEX2. <i>Nature Protocols</i> , 2016, 11, 456-475.	5.5	411
13799	Is the crowd better as an assistant or a replacement in ontology engineering? An exploration through the lens of the Gene Ontology. <i>Journal of Biomedical Informatics</i> , 2016, 60, 199-209.	2.5	10
13800	Functional screen identifies regulators of murine hematopoietic stem cell repopulation. <i>Journal of Experimental Medicine</i> , 2016, 213, 433-449.	4.2	78
13802	Quantitative proteomic analyses of mammary organoids reveals distinct signatures after exposure to environmental chemicals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1343-51.	3.3	45
13803	Integrating Publicly Available Data to Generate Computationally Predicted Adverse Outcome Pathways for Fatty Liver. <i>Toxicological Sciences</i> , 2016, 150, 510-520.	1.4	77
13804	A physiome interoperability roadmap for personalized drug development. <i>Interface Focus</i> , 2016, 6, 20150094.	1.5	8
13805	Network stratification analysis for identifying function-specific network layers. <i>Molecular BioSystems</i> , 2016, 12, 1232-1240.	2.9	1
13806	The Human Physiome: how standards, software and innovative service infrastructures are providing the building blocks to make it achievable. <i>Interface Focus</i> , 2016, 6, 20150103.	1.5	30
13807	Identification of protein complexes of microsomes in rat adipocytes by native gel coupled with LC-ESI-QTOF. <i>Molecular BioSystems</i> , 2016, 12, 1313-1323.	2.9	1
13808	A computational functional genomics based self-limiting self-concentration mechanism of cell specialization as a biological role of jumping genes. <i>Integrative Biology (United Kingdom)</i> , 2016, 8, 91-103.	0.6	2
13809	Predicting Protein Function via Semantic Integration of Multiple Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 220-232.	1.9	37
13810	Lack of tRNA-i6A modification causes mitochondrial-like metabolic deficiency in <i>S. pombe</i> by limiting activity of cytosolic tRNA ^{Tyr} , not mito-tRNA. <i>Rna</i> , 2016, 22, 583-596.	1.6	30
13811	Sperm proteomics: potential impact on male infertility treatment. <i>Expert Review of Proteomics</i> , 2016, 13, 285-296.	1.3	29
13812	Transcriptional response to heat shock in liver of snow trout (<i>Schizothorax richardsonii</i>) a vulnerable Himalayan Cyprinid fish. <i>Functional and Integrative Genomics</i> , 2016, 16, 203-213.	1.4	34
13813	A Proteomic Analysis of <i>Sarcoptes scabiei</i> (Acari: Sarcoptidae). <i>Journal of Medical Entomology</i> , 2016, 53, 553-561.	0.9	28
13814	Genome-wide transcriptional analysis of silica nanoparticle-induced toxicity in zebrafish embryos. <i>Toxicology Research</i> , 2016, 5, 609-620.	0.9	24
13815	Expression Profile of microRNAs and Their Targeted Pathways in Human Ovaries Detected by Next-Generation Small RNA Sequencing. <i>DNA and Cell Biology</i> , 2016, 35, 226-234.	0.9	9
13816	GiANT: gene set uncertainty in enrichment analysis. <i>Bioinformatics</i> , 2016, 32, 1891-1894.	1.8	7

#	ARTICLE	IF	CITATIONS
13817	A potential endophenotype for Alzheimer's disease: cerebrospinal fluid clusterin. <i>Neurobiology of Aging</i> , 2016, 37, 208.e1-208.e9.	1.5	44
13818	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
13819	Prime, Shock, and Kill: Priming CD4 T Cells from HIV Patients with a BCL-2 Antagonist before HIV Reactivation Reduces HIV Reservoir Size. <i>Journal of Virology</i> , 2016, 90, 4032-4048.	1.5	85
13820	Strategies in functional proteomics: Unveiling the pathways to precision oncology. <i>Cancer Letters</i> , 2016, 382, 86-94.	3.2	7
13821	High-throughput deep screening and identification of four peripheral leucocyte microRNAs as novel potential combination biomarkers for preeclampsia. <i>Journal of Perinatology</i> , 2016, 36, 263-267.	0.9	10
13822	Identification of differentially methylated regions in new genes associated with knee osteoarthritis. <i>Gene</i> , 2016, 576, 312-318.	1.0	28
13823	De novo transcriptome assembly of <i>Perkinsus olseni</i> trophozoite stimulated in vitro with Manila clam (<i>Ruditapes philippinarum</i>) plasma. <i>Journal of Invertebrate Pathology</i> , 2016, 135, 22-33.	1.5	14
13824	Screening of potential biomarkers for cholangiocarcinoma by integrated analysis of microarray data sets. <i>Cancer Gene Therapy</i> , 2016, 23, 48-53.	2.2	24
13825	Perturbation Detection Through Modeling of Gene Expression on a Latent Biological Pathway Network: A Bayesian Hierarchical Approach. <i>Journal of the American Statistical Association</i> , 2016, 111, 73-92.	1.8	7
13826	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13.	3.8	1,898
13827	An oncogenic MYB feedback loop drives alternate cell fates in adenoid cystic carcinoma. <i>Nature Genetics</i> , 2016, 48, 265-272.	9.4	216
13828	Incorporating biological knowledge for construction of fuzzy networks of gene associations. <i>Applied Soft Computing Journal</i> , 2016, 42, 144-155.	4.1	10
13829	An Adaptive Hybrid Algorithm for Global Network Alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 483-493.	1.9	11
13830	Analysis of copy number variations in Mexican Holstein cattle using axiom genome-wide Bos 1 array. <i>Genomics Data</i> , 2016, 7, 97-100.	1.3	6
13831	The challenge of identifying tuberculosis proteins in archaeological tissues. <i>Journal of Archaeological Science</i> , 2016, 66, 146-153.	1.2	37
13832	Epigenome-wide profiling of DNA methylation in paired samples of adipose tissue and blood. <i>Epigenetics</i> , 2016, 11, 227-236.	1.3	59
13833	Genomic Analyses Reveal Demographic History and Temperate Adaptation of the Newly Discovered Honey Bee Subspecies <i>Apis mellifera sinisxinyuan</i> n. ssp. <i>Molecular Biology and Evolution</i> , 2016, 33, 1337-1348.	3.5	125
13834	The tumor microenvironment and Immunoscore are critical determinants of dissemination to distant metastasis. <i>Science Translational Medicine</i> , 2016, 8, 327ra26.	5.8	360

#	ARTICLE	IF	CITATIONS
13835	Quality assurance of the gene ontology using abstraction networks. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1642001.	0.3	24
13836	Comparative transcriptome analysis of fruiting body and sporulating mycelia of <i>Villosiclava virens</i> reveals genes with putative functions in sexual reproduction. <i>Current Genetics</i> , 2016, 62, 575-584.	0.8	18
13837	Chronic TCDD exposure results in the dysregulation of gene expression in splenic B-lymphocytes and in the impairments in T-cell and B-cell differentiation in mouse model. <i>Journal of Environmental Sciences</i> , 2016, 39, 218-227.	3.2	7
13838	Genetic features of <i>Mycobacterium tuberculosis</i> modern Beijing sublineage. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-8.	3.0	35
13839	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
13840	Proteomic profiling of maize opaque endosperm mutants reveals selective accumulation of lysine-enriched proteins. <i>Journal of Experimental Botany</i> , 2016, 67, 1381-1396.	2.4	30
13841	Biofilms on Hospital Shower Hoses: Characterization and Implications for Nosocomial Infections. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2872-2883.	1.4	102
13842	Network-Based Identification and Prioritization of Key Regulators of Coronary Artery Disease Loci. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2016, 36, 928-941.	1.1	66
13843	Examining non-syndromic autosomal recessive intellectual disability (NS-ARID) genes for an enriched association with intelligence differences. <i>Intelligence</i> , 2016, 54, 80-89.	1.6	10
13844	Tissue-specific Proteogenomic Analysis of <i>Plutella xylostella</i> Larval Midgut Using a Multialgorithm Pipeline. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1791-1807.	2.5	19
13845	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
13846	Mutations in Subunits of the Activating Signal Cointegrator 1 Complex Are Associated with Prenatal Spinal Muscular Atrophy and Congenital Bone Fractures. <i>American Journal of Human Genetics</i> , 2016, 98, 473-489.	2.6	56
13847	Resuscitation with Valproic Acid Alters Inflammatory Genes in a Porcine Model of Combined Traumatic Brain Injury and Hemorrhagic Shock. <i>Journal of Neurotrauma</i> , 2016, 33, 1514-1521.	1.7	38
13848	Integrated system for extraction, purification, and digestion of membrane proteins. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 3495-3502.	1.9	3
13849	Extending gene ontology with gene association networks. <i>Bioinformatics</i> , 2016, 32, 1185-1194.	1.8	42
13850	Overexpression of mitochondrial uncoupling protein 1 (UCP1) induces a hypoxic response in <i>Nicotiana tabacum</i> leaves. <i>Journal of Experimental Botany</i> , 2016, 67, 301-313.	2.4	19
13851	Label-free proteomic methodology for the analysis of human kidney stone matrix composition. <i>Proteome Science</i> , 2016, 14, 4.	0.7	26
13852	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. <i>Biotechnology Advances</i> , 2016, 34, 663-686.	6.0	30

#	ARTICLE	IF	CITATIONS
13853	Orthogonal matrix factorization enables integrative analysis of multiple RNA binding proteins. <i>Bioinformatics</i> , 2016, 32, 1527-1535.	1.8	108
13854	SNaPP: Simplified Nanoproteomics Platform for Reproducible Global Proteomic Analysis of Nanogram Protein Quantities. <i>Endocrinology</i> , 2016, 157, 1307-1314.	1.4	48
13855	Integrated analysis of proteome and transcriptome changes in the mucopolysaccharidosis type VII mouse hippocampus. <i>Molecular Genetics and Metabolism</i> , 2016, 118, 41-54.	0.5	28
13856	Dendritic Cells Regulate GPR34 through Mitogenic Signals and Undergo Apoptosis in Its Absence. <i>Journal of Immunology</i> , 2016, 196, 2504-2513.	0.4	20
13857	Stable engineered vascular networks from human induced pluripotent stem cell-derived endothelial cells cultured in synthetic hydrogels. <i>Acta Biomaterialia</i> , 2016, 35, 32-41.	4.1	86
13858	High-quality genome sequencing and description of <i>Dermabacter indicis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2016, 11, 59-67.	0.8	6
13859	Link community detection based on line graphs with a novel link similarity measure. <i>International Journal of Modern Physics B</i> , 2016, 30, 1650023.	1.0	2
13860	Transcriptome analysis reveals key differentially expressed genes involved in wheat grain development. <i>Crop Journal</i> , 2016, 4, 92-106.	2.3	61
13861	WormExp: a web-based application for a <i>Caenorhabditis elegans</i> -specific gene expression enrichment analysis. <i>Bioinformatics</i> , 2016, 32, 943-945.	1.8	93
13862	Probiotic (<i>Enterococcus faecium</i>) induced responses of the hepatic proteome improves metabolic efficiency of broiler chickens (<i>Gallus gallus</i>). <i>BMC Genomics</i> , 2016, 17, 89.	1.2	57
13863	Labelling strategies for hierarchical multi-label classification techniques. <i>Pattern Recognition</i> , 2016, 56, 170-183.	5.1	33
13864	Enhanced uptake of antibiotic resistance genes in the presence of nanoalumina. <i>Nanotoxicology</i> , 2016, 10, 1051-1060.	1.6	61
13865	Complete genome sequence of a deeply branched marine Bacteroidia bacterium <i>Draconibacterium orientale</i> type strain FH5T. <i>Marine Genomics</i> , 2016, 26, 13-16.	0.4	6
13866	Medullary carcinoma of the colon: a distinct morphology reveals a distinctive immunoregulatory microenvironment. <i>Modern Pathology</i> , 2016, 29, 528-541.	2.9	60
13867	Illuminating drug action by network integration of disease genes: a case study of myocardial infarction. <i>Molecular BioSystems</i> , 2016, 12, 1653-1666.	2.9	21
13868	Identifying genetic modulators of the connectivity between transcription factors and their transcriptional targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1835-43.	3.3	9
13869	Comprehensive profiling of EBV gene expression in nasopharyngeal carcinoma through paired-end transcriptome sequencing. <i>Frontiers of Medicine</i> , 2016, 10, 61-75.	1.5	49
13870	iTRAQ proteomic analysis of salinity acclimation proteins in the gill of tropical marbled eel (<i>Anguilla</i>) Tj ETQq1 1 0.784314 rgBT ₁₂ /Overl	0.9	12

#	ARTICLE	IF	CITATIONS
13871	Computational Identification, Target Prediction, and Validation of Conserved miRNAs in Insulin Plant (<i>Costus pictus</i> D. Don). <i>Applied Biochemistry and Biotechnology</i> , 2016, 178, 513-526.	1.4	12
13872	TauCstF-64 Mediates Correct mRNA Polyadenylation and Splicing of Activator and Repressor Isoforms of the Cyclic AMP-Responsive Element Modulator (CREM) in Mouse Testis1. <i>Biology of Reproduction</i> , 2016, 94, 34.	1.2	16
13873	Ontology-Based Search of Genomic Metadata. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 233-247.	1.9	13
13874	CytoGEDEVOâ€”global alignment of biological networks with Cytoscape. <i>Bioinformatics</i> , 2016, 32, 1259-1261.	1.8	31
13875	Positive and negative forms of replicability in gene network analysis. <i>Bioinformatics</i> , 2016, 32, 1065-1073.	1.8	12
13876	Meta-analysis of Cancer Gene Profiling Data. <i>Methods in Molecular Biology</i> , 2016, 1381, 211-222.	0.4	3
13877	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. <i>Nature Genetics</i> , 2016, 48, 134-143.	9.4	1,167
13878	Systems genetics identifies a convergent gene network for cognition and neurodevelopmental disease. <i>Nature Neuroscience</i> , 2016, 19, 223-232.	7.1	131
13879	The differential expression of mRNAs and long noncoding RNAs between ectopic and eutopic endometria provides new insights into adenomyosis. <i>Molecular BioSystems</i> , 2016, 12, 362-370.	2.9	30
13880	Analysis of Text-Enriched Heterogeneous Information Networks. <i>Studies in Big Data</i> , 2016, , 115-139.	0.8	1
13881	Transcriptome analysis of the molting gland (Y-organ) from the blackback land crab, <i>Gecarcinus lateralis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2016, 17, 26-40.	0.4	21
13882	Photodynamic treatment with hexyl-aminolevulinatate mediates reversible thiol oxidation in core oxidative stress signaling proteins. <i>Molecular BioSystems</i> , 2016, 12, 796-805.	2.9	8
13883	Quantitative Proteomic Analysis Reveals Molecular Adaptations in the Hippocampal Synaptic Active Zone of Chronic Mild Stress-Unsusceptible Rats. <i>International Journal of Neuropsychopharmacology</i> , 2016, 19, pyv100.	1.0	27
13884	Genetic code expansion in stable cell lines enables encoded chromatin modification. <i>Nature Methods</i> , 2016, 13, 158-164.	9.0	133
13885	Overview of Plant Defence Systems: Lessons from <i>Arabidopsis-Botrytis cinerea</i> Systems Biology. , 2016, , 335-360.		3
13886	Introgression of Neandertal- and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. <i>American Journal of Human Genetics</i> , 2016, 98, 22-33.	2.6	226
13887	Long noncoding RNA expression profiles of hypoxic pulmonary hypertension rat model. <i>Gene</i> , 2016, 579, 23-28.	1.0	24
13888	traseR: an R package for performing trait-associated SNP enrichment analysis in genomic intervals. <i>Bioinformatics</i> , 2016, 32, 1214-1216.	1.8	23

#	ARTICLE	IF	CITATIONS
13889	simDEF: definition-based semantic similarity measure of gene ontology terms for functional similarity analysis of genes. <i>Bioinformatics</i> , 2016, 32, 1380-1387.	1.8	24
13890	C2-substituted aromatic cytokinin sugar conjugates delay the onset of senescence by maintaining the activity of the photosynthetic apparatus. <i>Phytochemistry</i> , 2016, 122, 22-33.	1.4	20
13891	Highly Charged Proteins: The Achilles' Heel of Aging Proteomes. <i>Structure</i> , 2016, 24, 329-336.	1.6	58
13892	Network-Assisted Disease Classification and Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2016, 1386, 353-374.	0.4	11
13893	Physiological and Molecular Alterations Promoted by <i>Schizotetranychus oryzae</i> Mite Infestation in Rice Leaves. <i>Journal of Proteome Research</i> , 2016, 15, 431-446.	1.8	22
13894	Identification and characterization of microRNAs in <i>Eucheuma denticulatum</i> by high-throughput sequencing and bioinformatics analysis. <i>RNA Biology</i> , 2016, 13, 343-352.	1.5	11
13895	Botrytis – the Fungus, the Pathogen and its Management in Agricultural Systems. , 2016, , .		167
13896	Transcriptome analysis of soiny mullet (<i>Liza haematocheila</i>) spleen in response to <i>Streptococcus dysgalactiae</i> . <i>Fish and Shellfish Immunology</i> , 2016, 49, 194-204.	1.6	49
13897	Postmortem human brain genomics in neuropsychiatric disorders – how far can we go?. <i>Current Opinion in Neurobiology</i> , 2016, 36, 107-111.	2.0	20
13898	Systematic Phenomics Analysis Deconvolutes Genes Mutated in Intellectual Disability into Biologically Coherent Modules. <i>American Journal of Human Genetics</i> , 2016, 98, 149-164.	2.6	270
13899	A proteogenomic approach to understand splice isoform functions through sequence and expression-based computational modeling. <i>Briefings in Bioinformatics</i> , 2016, 17, bbv109.	3.2	6
13900	Genomic Signatures of Selective Pressures and Introgression from Archaic Hominins at Human Innate Immunity Genes. <i>American Journal of Human Genetics</i> , 2016, 98, 5-21.	2.6	243
13901	Exome arrays capture polygenic rare variant contributions to schizophrenia. <i>Human Molecular Genetics</i> , 2016, 25, 1001-1007.	1.4	54
13902	Novel interactions of domain III from the envelope glycoprotein of dengue 2 virus with human plasma proteins. <i>Journal of Proteomics</i> , 2016, 131, 205-213.	1.2	16
13903	Harmonising and linking biomedical and clinical data across disparate data archives to enable integrative cross-biobank research. <i>European Journal of Human Genetics</i> , 2016, 24, 521-528.	1.4	27
13904	The inhibition of basal phosphoinositide-dependent phospholipase C activity in <i>Arabidopsis</i> suspension cells by abscisic or salicylic acid acts as a signalling hub accounting for an important overlap in transcriptome remodelling induced by these hormones. <i>Environmental and Experimental Botany</i> , 2016, 123, 37-49.	2.0	18
13905	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2016, 44, D7-D19.	6.5	1,417
13906	Umbilical cord gene expression reveals the molecular architecture of the fetal inflammatory response in extremely preterm newborns. <i>Pediatric Research</i> , 2016, 79, 473-481.	1.1	16

#	ARTICLE	IF	CITATIONS
13907	Emerging tools, concepts and ideas to track the modulator genes underlying plant drought adaptive traits: An overview. <i>Plant Signaling and Behavior</i> , 2016, 11, e1074370.	1.2	6
13908	PPIM: A Protein-Protein Interaction Database for Maize. <i>Plant Physiology</i> , 2016, 170, 618-626.	2.3	85
13909	Pathway-based variant enrichment analysis on the example of dilated cardiomyopathy. <i>Human Genetics</i> , 2016, 135, 31-40.	1.8	8
13910	The decrease in histone methyltransferase EZH2 in response to fluid shear stress alters endothelial gene expression and promotes quiescence. <i>Angiogenesis</i> , 2016, 19, 9-24.	3.7	62
13911	From Single Variants to Protein Cascades. <i>Journal of Biological Chemistry</i> , 2016, 291, 1582-1590.	1.6	2
13912	A magnetic protein biocompass. <i>Nature Materials</i> , 2016, 15, 217-226.	13.3	250
13913	Identification of Evening Complex Associated Proteins in Arabidopsis by Affinity Purification and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 201-217.	2.5	170
13914	Statistical mechanics of ontology based annotations. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2016, 442, 284-299.	1.2	3
13915	Whole-Exome Sequencing in Familial Parkinson Disease. <i>JAMA Neurology</i> , 2016, 73, 68.	4.5	71
13916	Multi-tissue transcriptome profiles for coho salmon (<i>Oncorhynchus kisutch</i>), a species undergoing rediploidization following whole-genome duplication. <i>Marine Genomics</i> , 2016, 25, 33-37.	0.4	19
13917	Label-Free Quantitative Proteomics Reveals Survival Mechanisms Developed by Hypertrophic Chondrocytes under ER Stress. <i>Journal of Proteome Research</i> , 2016, 15, 86-99.	1.8	14
13918	De-novo assembly and characterization of <i>Chlorella minutissima</i> UTEX2341 transcriptome by paired-end sequencing and the identification of genes related to the biosynthesis of lipids for biodiesel. <i>Marine Genomics</i> , 2016, 25, 69-74.	0.4	11
13919	Hierarchical multilabel classification based on path evaluation. <i>International Journal of Approximate Reasoning</i> , 2016, 68, 179-193.	1.9	21
13920	Pushing the annotation of cellular activities to a higher resolution: Predicting functions at the isoform level. <i>Methods</i> , 2016, 93, 110-118.	1.9	9
13921	Review: High-performance computing to detect epistasis in genome scale data sets. <i>Briefings in Bioinformatics</i> , 2016, 17, 368-379.	3.2	39
13922	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
13923	From Brain Maps to Cognitive Ontologies: Informatics and the Search for Mental Structure. <i>Annual Review of Psychology</i> , 2016, 67, 587-612.	9.9	258
13924	Recent Advances and Emerging Applications in Text and Data Mining for Biomedical Discovery. <i>Briefings in Bioinformatics</i> , 2016, 17, 33-42.	3.2	131

#	ARTICLE	IF	CITATIONS
13925	How computer science can help in understanding the 3D genome architecture. Briefings in Bioinformatics, 2016, 17, 733-744.	3.2	10
13926	Activation of the Nrf2 response by intrinsic hepatotoxic drugs correlates with suppression of NF- κ B activation and sensitizes toward TNF α -induced cytotoxicity. Archives of Toxicology, 2016, 90, 1163-1179.	1.9	54
13927	Non-monotonic doseâ€‘response effect of bisphenol A on rare minnow <i>Gobiocypris rarus</i> ovarian development. Chemosphere, 2016, 144, 304-311.	4.2	40
13928	Transcriptome analysis of <i>Solanum melongena</i> L. (eggplant) fruit to identify putative allergens and their epitopes. Gene, 2016, 576, 64-71.	1.0	16
13929	Global Alignment of Protein-Protein Interaction Networks: A Survey. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 689-705.	1.9	61
13930	Comparative analysis of molecular mechanism of spinal cord injury with time based on bioinformatics data. Spinal Cord, 2016, 54, 431-438.	0.9	13
13931	Transcriptomics and Gene Regulation. Translational Bioinformatics, 2016, , .	0.0	2
13932	Proteomic comparison of the EWS-FLI1 expressing cells EF with NIH-3T3 and actin remodeling effect of (R/W)9 cell-penetrating peptide. EuPA Open Proteomics, 2016, 10, 1-8.	2.5	4
13933	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomics Data. Methods in Molecular Biology, 2016, 1374, 115-140.	0.4	216
13934	PCSB/MIPS Plant Genome Information Resources and Concepts for the Analysis of Complex Grass Genomes. Methods in Molecular Biology, 2016, 1374, 165-186.	0.4	2
13935	Bayesian inference with historical data-based informative priors improves detection of differentially expressed genes. Bioinformatics, 2016, 32, 682-689.	1.8	11
13936	Differential expression profile of membrane proteins in L-02 cells exposed to trichloroethylene. Toxicology and Industrial Health, 2016, 32, 1774-1783.	0.6	1
13937	The Plant Ontology: A Tool for Plant Genomics. Methods in Molecular Biology, 2016, 1374, 89-114.	0.4	52
13938	Multiplex protein pattern unmixing using a non-linear variable-weighted support vector machine as optimized by a particle swarm optimization algorithm. Talanta, 2016, 147, 609-614.	2.9	14
13939	GM3 ganglioside and phosphatidylethanolamine-containing lipids are adipose tissue markers of insulin resistance in obese women. International Journal of Obesity, 2016, 40, 706-713.	1.6	28
13940	Bioengineering Human Myocardium on Native Extracellular Matrix. Circulation Research, 2016, 118, 56-72.	2.0	280
13941	Reconstruction and Analysis of the Evolution of Modular Transcriptional Regulatory Programs Using Arboretum. Methods in Molecular Biology, 2016, 1361, 375-389.	0.4	2
13942	Osteogenic Differentiation Gene Expression Profiling of hMSCs on Hydroxyapatite and Mineralized Collagen. Tissue Engineering - Part A, 2016, 22, 170-181.	1.6	59

#	ARTICLE	IF	CITATIONS
13943	Mapping the Transcriptome-Wide Landscape of RBP Binding Sites Using gPAR-CLIP-seq: Bioinformatic Analysis. <i>Methods in Molecular Biology</i> , 2016, 1361, 91-104.	0.4	3
13944	Different gene expression profiles between normal and thermally selected strains of rainbow trout, <i>Oncorhynchus mykiss</i> , as revealed by comprehensive transcriptome analysis. <i>Gene</i> , 2016, 576, 637-643.	1.0	20
13946	Comparative plasma proteomic studies of pulmonary TiO ₂ nanoparticle exposure in rats using liquid chromatography tandem mass spectrometry. <i>Journal of Proteomics</i> , 2016, 130, 85-93.	1.2	13
13947	DNA damage-induced ephrin-B2 reverse signaling promotes chemoresistance and drives EMT in colorectal carcinoma harboring mutant p53. <i>Cell Death and Differentiation</i> , 2016, 23, 707-722.	5.0	80
13948	Changes in Gene Expression of <i>Arabidopsis thaliana</i> Cell Cultures Upon Exposure to Real and Simulated Partial-g Forces. <i>Microgravity Science and Technology</i> , 2016, 28, 319-329.	0.7	17
13949	Integrated protein function prediction by mining function associations, sequences, and protein-protein and gene-gene interaction networks. <i>Methods</i> , 2016, 93, 84-91.	1.9	76
13950	Prediction of the engendering mechanism and specific genes of primary melanoma by bioinformatics analysis. <i>Dermatologica Sinica</i> , 2016, 34, 14-19.	0.2	7
13951	Transposition burst of mariner-like elements in the sequenced genome of <i>Rhodnius prolixus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 69, 14-24.	1.2	11
13952	Pathway Tools version 19.0 update: software for pathway/genome informatics and systems biology. <i>Briefings in Bioinformatics</i> , 2016, 17, 877-890.	3.2	250
13953	Protein function annotation using protein domain family resources. <i>Methods</i> , 2016, 93, 24-34.	1.9	32
13954	Protein Analysis of Sapienic Acid-Treated <i>Porphyromonas gingivalis</i> Suggests Differential Regulation of Multiple Metabolic Pathways. <i>Journal of Bacteriology</i> , 2016, 198, 157-167.	1.0	6
13955	Multiple Testing of Gene Sets from Gene Ontology: Possibilities and Pitfalls. <i>Briefings in Bioinformatics</i> , 2016, 17, 808-818.	3.2	26
13956	Excretory/secretory proteome of 14-day schistosomula, <i>Schistosoma japonicum</i> . <i>Journal of Proteomics</i> , 2016, 130, 221-230.	1.2	22
13957	Quantitative Proteomic Analysis of Differentially Expressed Proteins and Downstream Signaling Pathways in Chronic Bladder Ischemia. <i>Journal of Urology</i> , 2016, 195, 515-523.	0.2	14
13958	Common variants in <i>DRD2</i> are associated with sleep duration: the CARE consortium. <i>Human Molecular Genetics</i> , 2016, 25, 167-179.	1.4	40
13959	Identification of the transcriptional regulators by expression profiling infected with hepatitis B virus. <i>Clinics and Research in Hepatology and Gastroenterology</i> , 2016, 40, 57-72.	0.7	1
13960	Aberrant RNA splicing in cancer; expression changes and driver mutations of splicing factor genes. <i>Oncogene</i> , 2016, 35, 2413-2427.	2.6	426
13961	Using prior knowledge from cellular pathways and molecular networks for diagnostic specimen classification. <i>Briefings in Bioinformatics</i> , 2016, 17, 440-452.	3.2	25

#	ARTICLE	IF	CITATIONS
13962	Correspondence of DNA Methylation Between Blood and Brain Tissue and Its Application to Schizophrenia Research. <i>Schizophrenia Bulletin</i> , 2016, 42, 406-414.	2.3	227
13963	The EGF receptor ligand amphiregulin controls cell division via FoxM1. <i>Oncogene</i> , 2016, 35, 2075-2086.	2.6	29
13965	Bioinformatics methods in drug repurposing for Alzheimer's disease. <i>Briefings in Bioinformatics</i> , 2016, 17, 322-335.	3.2	78
13966	Long non-coding RNAs in innate and adaptive immunity. <i>Virus Research</i> , 2016, 212, 146-160.	1.1	79
13967	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. <i>Molecular Psychiatry</i> , 2016, 21, 189-197.	4.1	134
13968	A comprehensive comparative review of sequence-based predictors of DNA- and RNA-binding residues. <i>Briefings in Bioinformatics</i> , 2016, 17, 88-105.	3.2	88
13969	miRNAs as novel biomarkers in the management of prostate cancer. <i>Clinical Chemistry and Laboratory Medicine</i> , 2017, 55, 715-736.	1.4	89
13970	Improving Identification of Key Players in Aging via Network De-Noising and Core Inference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1056-1069.	1.9	5
13971	Identifying Spurious Interactions in the Protein-Protein Interaction Networks Using Local Similarity Preserving Embedding. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 345-352.	1.9	38
13972	Integrated Drug Expression Analysis for leukemia: an integrated in silico and in vivo approach to drug discovery. <i>Pharmacogenomics Journal</i> , 2017, 17, 351-359.	0.9	4
13973	Transcriptomic variation of pharmacogenes in multiple human tissues and lymphoblastoid cell lines. <i>Pharmacogenomics Journal</i> , 2017, 17, 137-145.	0.9	24
13974	Translational bioinformatics in the era of real-time biomedical, health care and wellness data streams. <i>Briefings in Bioinformatics</i> , 2017, 18, 105-124.	3.2	146
13975	Developing a Provenance Warehouse for the Systematic Brain Informatics Study. <i>International Journal of Information Technology and Decision Making</i> , 2017, 16, 1581-1609.	2.3	2
13976	Bridging semantics and syntax with graph algorithms—state-of-the-art of extracting biomedical relations. <i>Briefings in Bioinformatics</i> , 2017, 18, 160-178.	3.2	60
13977	Predicting Protein Functions by Using Unbalanced Random Walk Algorithm on Three Biological Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 360-369.	1.9	45
13978	<i>Campylobacter jejuni</i> in <i>Musca domestica</i> : An examination of survival and transmission potential in light of the innate immune responses of the house flies. <i>Insect Science</i> , 2017, 24, 584-598.	1.5	19
13979	Actin depolymerization-induced changes in proteome of Arabidopsis roots. <i>Journal of Proteomics</i> , 2017, 153, 89-99.	1.2	6
13980	A Survey of Visualization for Live Cell Imaging. <i>Computer Graphics Forum</i> , 2017, 36, 46-63.	1.8	14

#	ARTICLE	IF	CITATIONS
13981	Protein complex analysis: From raw protein lists to protein interaction networks. <i>Mass Spectrometry Reviews</i> , 2017, 36, 600-614.	2.8	22
13982	Transcriptome analysis reveals the accumulation mechanism of anthocyanins in 'Zijuan'™ tea (<i>Camellia</i>) Tj ETQo1 1 0.784314 rg8T 1.8 45	1.8	45
13983	Large-scale biological meta-database management. <i>Future Generation Computer Systems</i> , 2017, 67, 481-489.	4.9	7
13984	Genome-wide mapping of DNA methylation in Nile Tilapia. <i>Hydrobiologia</i> , 2017, 791, 247-257.	1.0	21
13985	Transcriptome of larvae representing the <i>Rhipicephalus sanguineus</i> complex. <i>Molecular and Cellular Probes</i> , 2017, 31, 85-90.	0.9	10
13986	COSNet: An R package for label prediction in unbalanced biological networks. <i>Neurocomputing</i> , 2017, 237, 397-400.	3.5	8
13987	High-resolution copy number variation analysis of schizophrenia in Japan. <i>Molecular Psychiatry</i> , 2017, 22, 430-440.	4.1	104
13988	Model-based contextualization of in vitro toxicity data quantitatively predicts in vivo drug response in patients. <i>Archives of Toxicology</i> , 2017, 91, 865-883.	1.9	16
13989	Genomic perspectives on the history and evolutionary ecology of tropical rainforest occupation by humans. <i>Quaternary International</i> , 2017, 448, 150-157.	0.7	13
13990	Transcription Factor Information System (TFIS): A Tool for Detection of Transcription Factor Binding Sites. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 378-391.	2.2	4
13991	An improved method for predicting interactions between virus and human proteins. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1650024.	0.3	23
13992	Glucose-mediated regulation of glycerol uptake in <i>Rhodosporidium toruloides</i> : Insights through transcriptomic analysis on dual substrate fermentation. <i>Engineering in Life Sciences</i> , 2017, 17, 282-291.	2.0	32
13993	Testis-specific RNA-Seq of <i>Calligrapha</i> (Chrysomelidae) as a transcriptomic resource for male-biased gene inquiry in Coleoptera. <i>Molecular Ecology Resources</i> , 2017, 17, 533-545.	2.2	1
13994	Dexmedetomidine increases acetylation level of histone through ERK1/2 pathway in dopamine neuron. <i>Human and Experimental Toxicology</i> , 2017, 36, 474-482.	1.1	10
13995	Endozoicomonas genomes reveal functional adaptation and plasticity in bacterial strains symbiotically associated with diverse marine hosts. <i>Scientific Reports</i> , 2017, 7, 40579.	1.6	207
13996	RNF43 germline and somatic mutation in serrated neoplasia pathway and its association with BRAF mutation. <i>Gut</i> , 2017, 66, 1645-1656.	6.1	157
13997	Comparative proteomic analysis of two pathogenic <i>Tritrichomonas foetus</i> genotypes: there is more to the proteome than meets the eye. <i>International Journal for Parasitology</i> , 2017, 47, 203-213.	1.3	16
13998	Analysis of genome instability biomarkers in children with non-syndromic orofacial clefts. <i>Mutagenesis</i> , 2017, 32, gew068.	1.0	8

#	ARTICLE	IF	CITATIONS
13999	Chronic drug-induced effects on contractile motion properties and cardiac biomarkers in human induced pluripotent stem cell-derived cardiomyocytes. <i>British Journal of Pharmacology</i> , 2017, 174, 3766-3779.	2.7	43
14000	An Efficient Semi-supervised Learning Approach to Predict SH2 Domain Mediated Interactions. <i>Methods in Molecular Biology</i> , 2017, 1555, 83-97.	0.4	0
14001	Pathogenicity Genes in <i>Ustilago virens</i> Revealed by a Predicted Protein-Protein Interaction Network. <i>Journal of Proteome Research</i> , 2017, 16, 1193-1206.	1.8	22
14002	Computational Methods for Annotation Transfers from Sequence. <i>Methods in Molecular Biology</i> , 2017, 1446, 55-67.	0.4	40
14003	The antineoplastic drug, trastuzumab, dysregulates metabolism in iPSC-derived cardiomyocytes. <i>Clinical and Translational Medicine</i> , 2017, 6, 5.	1.7	48
14004	Topologically inferring pathway activity for precise survival outcome prediction: breast cancer as a case. <i>Molecular BioSystems</i> , 2017, 13, 537-548.	2.9	11
14005	kME: Analyzing noisy and bidirectional transcriptional pathway responses in single subjects. <i>Journal of Biomedical Informatics</i> , 2017, 66, 32-41.	2.5	15
14006	WormBase ParaSite âˆ’ a comprehensive resource for helminth genomics. <i>Molecular and Biochemical Parasitology</i> , 2017, 215, 2-10.	0.5	527
14007	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
14008	Transcriptome profiling of sweetpotato tuberous roots during low temperature storage. <i>Plant Physiology and Biochemistry</i> , 2017, 112, 97-108.	2.8	37
14009	Age influences the olfactory profiles of the migratory oriental armyworm <i>mythimna separate</i> at the molecular level. <i>BMC Genomics</i> , 2017, 18, 32.	1.2	30
14010	Estradiol regulates expression of miRNAs associated with myogenesis in rainbow trout. <i>Molecular and Cellular Endocrinology</i> , 2017, 443, 1-14.	1.6	7
14011	Functional Transcriptomics in Diverse Intestinal Epithelial Cell Types Reveals Robust MicroRNA Sensitivity in Intestinal Stem Cells to Microbial Status. <i>Journal of Biological Chemistry</i> , 2017, 292, 2586-2600.	1.6	105
14012	Autophagy orchestrates adaptive responses to targeted therapy in endometrial cancer. <i>Autophagy</i> , 2017, 13, 608-624.	4.3	65
14013	PanViz: interactive visualization of the structure of functionally annotated pangenomes. <i>Bioinformatics</i> , 2017, 33, 1081-1082.	1.8	21
14014	Pharos: Collating protein information to shed light on the druggable genome. <i>Nucleic Acids Research</i> , 2017, 45, D995-D1002.	6.5	271
14015	Identification of highly connected hub genes in the protective response program of human macrophages and microglia activated by alpha B-crystallin. <i>Glia</i> , 2017, 65, 460-473.	2.5	16
14016	Genome sequencing and analysis of <i>Kloeckera apiculata</i> strain 34-9, a biocontrol agent against postharvest pathogens in citrus. <i>Genes and Genomics</i> , 2017, 39, 87-99.	0.5	6

#	ARTICLE	IF	CITATIONS
14017	Pathway analysis of complex diseases for GWAS, extending to consider rare variants, multi-omics and interactions. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 335-353.	1.1	54
14018	Maturation of conidia on conidiophores of <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2017, 98, 61-70.	0.9	43
14020	SemanticSCo: A platform to support the semantic composition of services for gene expression analysis. <i>Journal of Biomedical Informatics</i> , 2017, 66, 116-128.	2.5	5
14021	Sparse Simultaneous Signal Detection for Identifying Genetically Controlled Disease Genes. <i>Journal of the American Statistical Association</i> , 2017, 112, 1032-1046.	1.8	9
14022	Effects of selection for ethanol preference on gene expression in the nucleus accumbens of <i>HS</i> mice. <i>Genes, Brain and Behavior</i> , 2017, 16, 462-471.	1.1	24
14023	Immune adaptation to chronic intense exercise training: new microarray evidence. <i>BMC Genomics</i> , 2017, 18, 29.	1.2	40
14024	The DNA damage response of <i>C. elegans</i> affected by gravity sensing and radiosensitivity during the Shenzhou-8 spaceflight. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2017, 795, 15-26.	0.4	23
14025	Gene expression patterns regulating embryogenesis based on the integrated de novo transcriptome assembly of the Japanese flounder. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 22, 58-66.	0.4	3
14026	Hormonally Mediated Increases in Sex-Biased Gene Expression Accompany the Breakdown of Between-Sex Genetic Correlations in a Sexually Dimorphic Lizard. <i>American Naturalist</i> , 2017, 189, 315-332.	1.0	54
14027	Aberrant coordination geometries discovered in the most abundant metalloproteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 885-907.	1.5	8
14028	Left-Right Asymmetry of Maturation Rates in Human Embryonic Neural Development. <i>Biological Psychiatry</i> , 2017, 82, 204-212.	0.7	55
14029	Analysis of gene expression profiles between apical papilla tissues, stem cells from apical papilla and cell sheet to identify the key modulators in <i>MSC</i> 's niche. <i>Cell Proliferation</i> , 2017, 50, .	2.4	20
14030	Ontologies in Chemoinformatics. , 2017, , 2163-2181.		0
14031	Transcriptomic and hormone analyses reveal mechanisms underlying petal elongation in <i>Chrysanthemum morifolium</i> 'Jinba'. <i>Plant Molecular Biology</i> , 2017, 93, 593-606.	2.0	53
14032	Magnetic iron oxide nanoparticles accelerate osteogenic differentiation of mesenchymal stem cells via modulation of long noncoding RNA INZEB2. <i>Nano Research</i> , 2017, 10, 626-642.	5.8	71
14033	Deep Transcriptomic Profiling of M1 Macrophages Lacking <i>Trpc3</i> . <i>Scientific Reports</i> , 2017, 7, 39867.	1.6	8
14034	De novo assembly, annotation, and characterization of the whole brain transcriptome of male and female Syrian hamsters. <i>Scientific Reports</i> , 2017, 7, 40472.	1.6	18
14035	Dynamic community detection based on network structural perturbation and topological similarity. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2017, 2017, 013401.	0.9	31

#	ARTICLE	IF	CITATIONS
14036	A computational interactome for prioritizing genes associated with complex agronomic traits in rice (<i>Oryza sativa</i>). <i>Plant Journal</i> , 2017, 90, 177-188.	2.8	44
14037	A next-generation microarray further reveals stage-enriched gene expression pattern in the blood fluke <i>Schistosoma japonicum</i> . <i>Parasites and Vectors</i> , 2017, 10, 19.	1.0	16
14038	Temporal quantitative phosphoproteomics of ADP stimulation reveals novel central nodes in platelet activation and inhibition. <i>Blood</i> , 2017, 129, e1-e12.	0.6	97
14039	Differential function analysis: identifying structure and activation variations in dysregulated pathways. <i>Science China Information Sciences</i> , 2017, 60, 1.	2.7	3
14040	Whole-Genome Sequence of <i>Streptococcus parauberis</i> Strain SP-IIh, Isolated from Cows with Mastitis in Western China. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
14041	SH2 Domains. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	1
14042	Impairment of Host Liver Repopulation by Transplanted Hepatocytes in Aged Rats and the Release by Short-Term Growth Hormone Treatment. <i>American Journal of Pathology</i> , 2017, 187, 553-569.	1.9	2
14043	Genome Sequence of <i>Christensenella minuta</i> DSM 22607 ^T . <i>Genome Announcements</i> , 2017, 5, .	0.8	19
14044	Complete genome sequence of the salmonella enterica serovar enteritidis bacteriophages fSE1C and fSE4C isolated from food matrices. <i>Standards in Genomic Sciences</i> , 2017, 12, 1.	1.5	29
14045	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	13.7	332
14046	Inorganic nitrite modulates miRNA signatures in acute myocardial <i>in vivo</i> ischemia/reperfusion. <i>Free Radical Research</i> , 2017, 51, 91-102.	1.5	24
14047	DEIVA: a web application for interactive visual analysis of differential gene expression profiles. <i>BMC Genomics</i> , 2017, 18, 47.	1.2	41
14048	Complete genome sequence of the heavy metal resistant bacterium <i>Agromyces aureus</i> AR33T and comparison with related Actinobacteria. <i>Standards in Genomic Sciences</i> , 2017, 12, 2.	1.5	15
14049	Complete genome sequence of <i>Lutibacter profundus</i> LP1T isolated from an Arctic deep-sea hydrothermal vent system. <i>Standards in Genomic Sciences</i> , 2017, 12, 5.	1.5	11
14050	Comparative transcriptome analysis of vase life and carnation type in <i>Dianthus caryophyllus</i> L.. <i>Scientia Horticulturae</i> , 2017, 217, 61-72.	1.7	16
14051	Evolutionary Nonnegative Matrix Factorization Algorithms for Community Detection in Dynamic Networks. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2017, 29, 1045-1058.	4.0	121
14052	A systematic comparative evaluation of biclustering techniques. <i>BMC Bioinformatics</i> , 2017, 18, 55.	1.2	96
14053	Identification of the molecular mechanisms underlying dilated cardiomyopathy via bioinformatic analysis of gene expression profiles. <i>Experimental and Therapeutic Medicine</i> , 2017, 13, 273-279.	0.8	10

#	ARTICLE	IF	CITATIONS
14054	A Gibbs sampling method to determine biomarkers for asthma. <i>Computational Biology and Chemistry</i> , 2017, 67, 255-259.	1.1	1
14055	Differentially expressed immune-related genes in hemocytes of the pearl oyster <i>Pinctada fucata</i> against allograft identified by transcriptome analysis. <i>Fish and Shellfish Immunology</i> , 2017, 62, 247-256.	1.6	39
14056	Active Interaction Mapping Reveals the Hierarchical Organization of Autophagy. <i>Molecular Cell</i> , 2017, 65, 761-774.e5.	4.5	31
14057	Semantic Similarity in the Gene Ontology. <i>Methods in Molecular Biology</i> , 2017, 1446, 161-173.	0.4	42
14058	Systems Biology Approach in Hypertension Research. <i>Methods in Molecular Biology</i> , 2017, 1527, 69-79.	0.4	4
14059	Genome-Scale Networks Link Neurodegenerative Disease Genes to α -Synuclein through Specific Molecular Pathways. <i>Cell Systems</i> , 2017, 4, 157-170.e14.	2.9	102
14060	Multitask Matrix Completion for Learning Protein Interactions Across Diseases. <i>Journal of Computational Biology</i> , 2017, 24, 501-514.	0.8	9
14061	SCALEUS: Semantic Web Services Integration for Biomedical Applications. <i>Journal of Medical Systems</i> , 2017, 41, 54.	2.2	8
14062	The fire ant social chromosome supergene variant <i>Sb</i> shows low diversity but high divergence from <i>SB</i> . <i>Molecular Ecology</i> , 2017, 26, 2864-2879.	2.0	65
14063	Ulipristal acetate administration at mid-cycle changes gene expression profiling of endometrial biopsies taken during the receptive period of the human menstrual cycle. <i>Molecular and Cellular Endocrinology</i> , 2017, 447, 1-11.	1.6	21
14064	Comprehensive understanding of PM2.5 on gene and microRNA expression patterns in zebrafish (<i>Danio rerio</i>). <i>Journal of Environmental Health</i> , 2017, 138, 1-11.	3.9	38
14065	Plasticity in gene transcription explains the differential performance of two invasive fish species. <i>Evolutionary Applications</i> , 2017, 10, 563-576.	1.5	51
14066	Identification of core gene networks and hub genes associated with progression of non-alcoholic fatty liver disease by RNA sequencing. <i>Hepatology Research</i> , 2017, 47, 1445-1458.	1.8	23
14067	Predicting disease-related genes using integrated biomedical networks. <i>BMC Genomics</i> , 2017, 18, 1043.	1.2	46
14068	Hallmarks of Alzheimer's Disease in Stem-Cell-Derived Human Neurons Transplanted into Mouse Brain. <i>Neuron</i> , 2017, 93, 1066-1081.e8.	3.8	204
14069	Global Transcriptional Response of Human Liver Cells to Ethanol Stress of Different Strength Reveals Hormetic Behavior. <i>Alcoholism: Clinical and Experimental Research</i> , 2017, 41, 883-894.	1.4	4
14070	The complete genome sequence of the yogurt isolate <i>Streptococcus thermophilus</i> ACA-DC 2. <i>Standards in Genomic Sciences</i> , 2017, 12, 18.	1.5	31
14071	Mining Cancer Transcriptomes: Bioinformatic Tools and the Remaining Challenges. <i>Molecular Diagnosis and Therapy</i> , 2017, 21, 249-258.	1.6	13

#	ARTICLE	IF	CITATIONS
14072	Aberrant expression of cell cycle and material metabolism related genes contributes to hepatocellular carcinoma occurrence. <i>Pathology Research and Practice</i> , 2017, 213, 316-321.	1.0	64
14073	Candidate novel long noncoding RNAs, MicroRNAs and putative drugs for Parkinson's disease using a robust and efficient genome-wide association study. <i>Genomics</i> , 2017, 109, 158-164.	1.3	22
14074	Transcriptomic responses of the olive fruit fly <i>Bactrocera oleae</i> and its symbiont <i>Candidatus Erwinia dacicola</i> to olive feeding. <i>Scientific Reports</i> , 2017, 7, 42633.	1.6	58
14075	The Effects of LW-AFC on the Hippocampal Transcriptome in Senescence-Accelerated Mouse Prone 8 Strain, a Mouse Model of Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2017, 57, 227-240.	1.2	18
14076	Identification of miRNA-mRNA crosstalk in CD4+ T cells during HIV-1 infection by integrating transcriptome analyses. <i>Journal of Translational Medicine</i> , 2017, 15, 41.	1.8	10
14077	Anopheline salivary protein genes and gene families: an evolutionary overview after the whole genome sequence of sixteen <i>Anopheles</i> species. <i>BMC Genomics</i> , 2017, 18, 153.	1.2	59
14078	Potential probiotic-associated traits revealed from completed high quality genome sequence of <i>Lactobacillus fermentum</i> 3872. <i>Standards in Genomic Sciences</i> , 2017, 12, 19.	1.5	21
14079	The core regulatory network in human cells. <i>Biochemical and Biophysical Research Communications</i> , 2017, 484, 348-353.	1.0	4
14080	A familial study of azoospermic men identifies three novel causative mutations in three new human azoospermia genes. <i>Genetics in Medicine</i> , 2017, 19, 998-1006.	1.1	109
14081	Genetic analysis of impaired trimethylamine metabolism using whole exome sequencing. <i>BMC Medical Genetics</i> , 2017, 18, 11.	2.1	9
14082	The OncoPPi network of cancer-focused protein-protein interactions to inform biological insights and therapeutic strategies. <i>Nature Communications</i> , 2017, 8, 14356.	5.8	151
14083	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	3.8	417
14084	High quality draft genome sequence of <i>Janthinobacterium psychrotolerans</i> sp. nov., isolated from a frozen freshwater pond. <i>Standards in Genomic Sciences</i> , 2017, 12, 8.	1.5	28
14085	Microarray and gene co-expression analysis reveals that melatonin attenuates immune responses and modulates actin rearrangement in macrophages. <i>Biochemical and Biophysical Research Communications</i> , 2017, 485, 414-420.	1.0	18
14086	Genome Analysis of a Zygomycete Fungus <i>Choanephora cucurbitarum</i> Elucidates Necrotrophic Features Including Bacterial Genes Related to Plant Colonization. <i>Scientific Reports</i> , 2017, 7, 40432.	1.6	9
14087	Dynamic changes in the transcriptome of <i>Populus hopeiensis</i> in response to abscisic acid. <i>Scientific Reports</i> , 2017, 7, 42708.	1.6	11
14088	A Role of Metastable Regions and Their Connectivity in the Inactivation of a Redox-Regulated Chaperone and Its Inter-Chaperone Crosstalk. <i>Antioxidants and Redox Signaling</i> , 2017, 27, 1252-1267.	2.5	25
14089	gsSKAT: Rapid gene set analysis and multiple testing correction for rare variant association studies using weighted linear kernels. <i>Genetic Epidemiology</i> , 2017, 41, 297-308.	0.6	9

#	ARTICLE	IF	CITATIONS
14090	Regulatory network analysis of Epstein-Barr virus identifies functional modules and hub genes involved in infectious mononucleosis. <i>Archives of Virology</i> , 2017, 162, 1299-1309.	0.9	6
14091	Identification of potential therapeutic target genes, key miRNAs and mechanisms in oral lichen planus by bioinformatics analysis. <i>Archives of Oral Biology</i> , 2017, 78, 122-128.	0.8	5
14092	Genome-wide identification of direct HBx genomic targets. <i>BMC Genomics</i> , 2017, 18, 184.	1.2	52
14093	An atlas and analysis of bovine skeletal muscle long noncoding <sc>RNA</sc>s. <i>Animal Genetics</i> , 2017, 48, 278-286.	0.6	30
14094	MC4R-dependent suppression of appetite by bone-derived lipocalin 2. <i>Nature</i> , 2017, 543, 385-390.	13.7	299
14095	The Role of Lipid Droplets in <i>Mortierella alpina</i> Aging Revealed by Integrative Subcellular and Whole-Cell Proteome Analysis. <i>Scientific Reports</i> , 2017, 7, 43896.	1.6	19
14096	Transcriptomic insight into terpenoid and carbazole alkaloid biosynthesis, and functional characterization of two terpene synthases in curry tree (<i>Murraya koenigii</i>). <i>Scientific Reports</i> , 2017, 7, 44126.	1.6	34
14097	Loggerhead sea turtle embryos (<i>Caretta caretta</i>) regulate expression of stress response and developmental genes when exposed to a biologically realistic heat stress. <i>Molecular Ecology</i> , 2017, 26, 2978-2992.	2.0	39
14098	Analyzing structural changes in SNOMED CT's Bacterial infectious diseases using a visual semantic delta. <i>Journal of Biomedical Informatics</i> , 2017, 67, 101-116.	2.5	6
14099	Modelling plankton ecosystems in the meta-omics era. Are we ready?. <i>Marine Genomics</i> , 2017, 32, 1-17.	0.4	29
14100	Identification and characterization of differentially expressed miRNAs in subcutaneous adipose between Wagyu and Holstein cattle. <i>Scientific Reports</i> , 2017, 7, 44026.	1.6	54
14101	Prion-like proteins and their computational identification in proteomes. <i>Expert Review of Proteomics</i> , 2017, 14, 335-350.	1.3	24
14102	Gene expression metadata analysis reveals molecular mechanisms employed by <i>Phanerochaete chrysosporium</i> during lignin degradation and detoxification of plant extractives. <i>Current Genetics</i> , 2017, 63, 877-894.	0.8	34
14103	Transcriptome sequencing reveals abundant olfactory genes in the antennae of the rice leaf folder, <i>Cnaphalocrocis medinalis</i> (Lepidoptera: Pyralidae). <i>Entomological Science</i> , 2017, 20, 177-188.	0.3	25
14104	Proteome Analysis of Human Perilymph Using an Intraoperative Sampling Method. <i>Journal of Proteome Research</i> , 2017, 16, 1911-1923.	1.8	59
14105	Medium pH in submerged cultivation modulates differences in the intracellular protein profile of <i>Fusarium oxysporum</i> . <i>Preparative Biochemistry and Biotechnology</i> , 2017, 47, 664-672.	1.0	2
14106	Exploratory bioinformatics investigation reveals importance of <i>œjunk</i> -DNA in early embryo development. <i>BMC Genomics</i> , 2017, 18, 200.	1.2	55
14107	Ant colony optimization based hierarchical multi-label classification algorithm. <i>Applied Soft Computing Journal</i> , 2017, 55, 462-479.	4.1	14

#	ARTICLE	IF	CITATIONS
14108	Asymmetric interactions between doublesex and tissue- and sex-specific target genes mediate sexual dimorphism in beetles. <i>Nature Communications</i> , 2017, 8, 14593.	5.8	71
14109	Oocyte Developmental Competence: Insights from Cross-Species Differential Gene Expression and Human Oocyte-Specific Functional Gene Networks. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 156-168.	1.0	22
14110	An integrated analysis of cancer genes in clear cell renal cell carcinoma. <i>Future Oncology</i> , 2017, 13, 715-725.	1.1	7
14111	Dynamic gene expression analysis in a H1N1 influenza virus mouse pneumonia model. <i>Virus Genes</i> , 2017, 53, 357-366.	0.7	9
14113	Complete genome sequence of <i>Thermus brockianus</i> GE-1 reveals key enzymes of xylan/xylose metabolism. <i>Standards in Genomic Sciences</i> , 2017, 12, 22.	1.5	4
14114	Genetic loci associated with chronic obstructive pulmonary disease overlap with loci for lung function and pulmonary fibrosis. <i>Nature Genetics</i> , 2017, 49, 426-432.	9.4	306
14115	De novo transcriptome assemblies of four accessions of the metal hyperaccumulator plant <i>Noccaea caerulescens</i> . <i>Scientific Data</i> , 2017, 4, 160131.	2.4	38
14116	Whole-exome sequencing of 228 patients with sporadic Parkinson's disease. <i>Scientific Reports</i> , 2017, 7, 41188.	1.6	27
14117	Genome features of moderately halophilic polyhydroxyalkanoate-producing <i>Yangia</i> sp. CCB-MM3. <i>Standards in Genomic Sciences</i> , 2017, 12, 12.	1.5	12
14118	A statistical framework for pathway and gene identification from integrative analysis. <i>Journal of Multivariate Analysis</i> , 2017, 156, 1-17.	0.5	1
14119	Synthetic vulnerabilities of mesenchymal subpopulations in pancreatic cancer. <i>Nature</i> , 2017, 542, 362-366.	13.7	105
14121	Canalization Leads to Similar Whole Bone Mechanical Function at Maturity in Two Inbred Strains of Mice. <i>Journal of Bone and Mineral Research</i> , 2017, 32, 1002-1013.	3.1	8
14122	Comparative transcriptome analysis of two contrasting watermelon genotypes during fruit development and ripening. <i>BMC Genomics</i> , 2017, 18, 3.	1.2	72
14123	Multiple effects of ellagic acid on human colorectal carcinoma cells identified by gene expression profile analysis. <i>International Journal of Oncology</i> , 2017, 50, 613-621.	1.4	30
14124	Identifying the optimal gene and gene set in hepatocellular carcinoma based on differential expression and differential co-expression algorithm. <i>Oncology Reports</i> , 2017, 37, 1066-1074.	1.2	6
14125	The Plasma Proteome Is Associated with Anthropometric Status of Undernourished Nepalese School-Aged Children. <i>Journal of Nutrition</i> , 2017, 147, jn243014.	1.3	15
14126	Expression of β -globin by cancer cells promotes cell survival during blood-borne dissemination. <i>Nature Communications</i> , 2017, 8, 14344.	5.8	96
14127	The <i>Echinococcus canadensis</i> (G7) genome: a key knowledge of parasitic plathyhelminth human diseases. <i>BMC Genomics</i> , 2017, 18, 204.	1.2	42

#	ARTICLE	IF	CITATIONS
14128	Genome sequence of a high agarase-producing strain <i>Flammeovirga</i> sp. SJP92. <i>Standards in Genomic Sciences</i> , 2017, 12, 13.	1.5	20
14129	Semantic Data Integration. , 2017, , 263-305.		11
14130	Quantifying the Importance of the Rare Biosphere for Microbial Community Response to Organic Pollutants in a Freshwater Ecosystem. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	60
14131	Resequencing and annotation of the <i>Nostoc punctiforme</i> ATCC 29133 genome: facilitating biofuel and high-value chemical production. <i>AMB Express</i> , 2017, 7, 42.	1.4	12
14132	ATGC transcriptomics: a web-based application to integrate, explore and analyze de novo transcriptomic data. <i>BMC Bioinformatics</i> , 2017, 18, 121.	1.2	6
14133	The maternal plasma proteome changes as a function of gestational age in normal pregnancy: a longitudinal study. <i>American Journal of Obstetrics and Gynecology</i> , 2017, 217, 67.e1-67.e21.	0.7	66
14134	Systemic QSAR and phenotypic virtual screening: chasing butterflies in drug discovery. <i>Drug Discovery Today</i> , 2017, 22, 994-1007.	3.2	28
14135	Whole-genome sequencing identifies common-to-rare variants associated with human blood metabolites. <i>Nature Genetics</i> , 2017, 49, 568-578.	9.4	341
14136	Social network architecture of human immune cells unveiled by quantitative proteomics. <i>Nature Immunology</i> , 2017, 18, 583-593.	7.0	296
14137	De novo transcriptome and expression profile analyses of the Asian corn borer (<i>Ostrinia furnacalis</i>) reveals relevant flubendiamide response genes. <i>BMC Genomics</i> , 2017, 18, 20.	1.2	33
14138	Transcriptome analysis of <i>Ruditapes philippinarum</i> hepatopancreas provides insights into immune signaling pathways under <i>Vibrio anguillarum</i> infection. <i>Fish and Shellfish Immunology</i> , 2017, 64, 14-23.	1.6	35
14139	Correction: Retraction: Ectopic expression of the histone methyltransferase <i>Ezh2</i> in haematopoietic stem cells causes myeloproliferative disease. <i>Nature Communications</i> , 2017, 8, 14005.	5.8	43
14140	Functional constraints on adaptive evolution of protein ubiquitination sites. <i>Scientific Reports</i> , 2017, 7, 39949.	1.6	6
14141	Chamomile Flower, Myrrh, and Coffee Charcoal, Components of a Traditional Herbal Medicinal Product, Diminish Proinflammatory Activation in Human Macrophages. <i>Planta Medica</i> , 2017, 83, 846-854.	0.7	20
14142	A Precision Medicine Initiative for Alzheimer's disease: the road ahead to biomarker-guided integrative disease modeling. <i>Climacteric</i> , 2017, 20, 107-118.	1.1	112
14143	Complete genome sequence of <i>Jiangella gansuensis</i> strain YIM 002T (DSM 44835T), the type species of the genus <i>Jiangella</i> and source of new antibiotic compounds. <i>Standards in Genomic Sciences</i> , 2017, 12, 21.	1.5	9
14144	SWATH label-free proteomics analyses revealed the roles of oxidative stress and antioxidant defending system in sclerotia formation of <i>Polyporus umbellatus</i> . <i>Scientific Reports</i> , 2017, 7, 41283.	1.6	9
14147	Dimethylsulfoniopropionate biosynthesis in marine bacteria and identification of the key gene in this process. <i>Nature Microbiology</i> , 2017, 2, 17009.	5.9	222

#	ARTICLE	IF	CITATIONS
14148	Colostrum and milk protein rankings and ratios of importance to neonatal calf health using a proteomics approach. <i>Journal of Dairy Science</i> , 2017, 100, 2711-2728.	1.4	32
14149	Identification of potential drug targets based on a computational biology algorithm for venous thromboembolism. <i>International Journal of Molecular Medicine</i> , 2017, 39, 463-471.	1.8	1
14150	Systematic analysis of the achaete-scute complex-like gene signature in clinical cancer patients. <i>Molecular and Clinical Oncology</i> , 2017, 6, 7-18.	0.4	23
14151	Rare copy number variants in patients with congenital conotruncal heart defects. <i>Birth Defects Research</i> , 2017, 109, 271-295.	0.8	15
14152	Expression profiling-based clustering of healthy subjects recapitulates classifications defined by clinical observation in Chinese medicine. <i>Journal of Genetics and Genomics</i> , 2017, 44, 191-197.	1.7	22
14153	Proteome scale identification, classification and structural analysis of iron-binding proteins in bread wheat. <i>Journal of Inorganic Biochemistry</i> , 2017, 170, 63-74.	1.5	12
14154	Comparative transcriptome analysis provides insight into differentially expressed genes related to cytoplasmic male sterility in broccoli (<i>Brassica oleracea</i> var. <i>italica</i>). <i>Scientia Horticulturae</i> , 2017, 217, 234-242.	1.7	18
14155	Opportunities and challenges of whole-genome and -exome sequencing. <i>BMC Genetics</i> , 2017, 18, 14.	2.7	160
14156	Draft genome sequence of <i>Lactobacillus plantarum</i> strains E2C2 and E2C5 isolated from human stool culture. <i>Standards in Genomic Sciences</i> , 2017, 12, 15.	1.5	15
14157	De Novo Assembly and Characterization of Transcriptome in Somatic Muscles of the Polychaete <i>Perinereis aibuhitensis</i> . <i>Journal of Coastal Research</i> , 2017, 33, 931.	0.1	1
14158	Genomic Comparison of Indigenous African and Northern European Chickens Reveals Putative Mechanisms of Stress Tolerance Related to Environmental Selection Pressure. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1525-1537.	0.8	38
14159	Identification of genes associated with the effect of inflammation on the neurotransmission of vascular smooth muscle cell. <i>Experimental and Therapeutic Medicine</i> , 2017, 13, 1303-1312.	0.8	5
14160	Asbestos and Mesothelioma. <i>Current Cancer Research</i> , 2017, , .	0.2	5
14161	Identification of Key Gene Modules in Human Osteosarcoma by Co-Expression Analysis Weighted Gene Co-Expression Network Analysis (WGCNA). <i>Journal of Cellular Biochemistry</i> , 2017, 118, 3953-3959.	1.2	99
14162	Genetic architecture of gene expression underlying variation in host response to porcine reproductive and respiratory syndrome virus infection. <i>Scientific Reports</i> , 2017, 7, 46203.	1.6	32
14163	Protease-Inhibitor Interaction Predictions: Lessons on the Complexity of Protein-Protein Interactions. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1038-1051.	2.5	16
14164	Triangular Alignment (TAME): A Tensor-Based Approach for Higher-Order Network Alignment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1446-1458.	1.9	25
14165	Bioinformatics from a Big Data Perspective: Meeting the Challenge. <i>Lecture Notes in Computer Science</i> , 2017, , 349-359.	1.0	0

#	ARTICLE	IF	CITATIONS
14166	Gene co-expression network reconstruction: a review on computational methods for inferring functional information from plant-based expression data. <i>Plant Biotechnology Reports</i> , 2017, 11, 71-86.	0.9	34
14167	Systemic evaluation of cellular reprogramming processes exploiting a novel R-tool: <i><i>eegc</i></i> . <i>Bioinformatics</i> , 2017, 33, 2532-2538.	1.8	4
14168	Identification of protein complexes by integrating multiple alignment of protein interaction networks. <i>Bioinformatics</i> , 2017, 33, 1681-1688.	1.8	72
14169	Prediction of optimal gene functions for osteosarcoma using gene ontology and microarray profiles. <i>Journal of Bone Oncology</i> , 2017, 7, 18-22.	1.0	6
14170	Transcriptional Dependencies in Diffuse Intrinsic Pontine Glioma. <i>Cancer Cell</i> , 2017, 31, 635-652.e6.	7.7	290
14171	Master Transcriptional Regulators in Cancer: Discovery via Reverse Engineering Approaches and Subsequent Validation. <i>Cancer Research</i> , 2017, 77, 2186-2190.	0.4	11
14172	Comparative Transcriptome Sequence Analysis of Sporulation-Related Genes of <i>Aspergillus cristatus</i> in Response to Low and High Osmolarity. <i>Current Microbiology</i> , 2017, 74, 806-814.	1.0	12
14173	Accumulation, elimination, sequestration, and genetic variation of lead (Pb ²⁺) loads within and between generations of <i>Drosophila melanogaster</i> . <i>Chemosphere</i> , 2017, 181, 368-375.	4.2	28
14174	Integrating personalized gene expression profiles into predictive disease-associated gene pools. <i>Npj Systems Biology and Applications</i> , 2017, 3, 10.	1.4	54
14175	Identification of potential biomarkers of sepsis using bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2017, 13, 1689-1696.	0.8	16
14176	Comprehensive Analysis of MILE Gene Expression Data Set Advances Discovery of Leukaemia Type and Subtype Biomarkers. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 24-35.	2.2	8
14177	A mouse tissue transcription factor atlas. <i>Nature Communications</i> , 2017, 8, 15089.	5.8	90
14178	Systematic Synergy of Glucose and GLP-1 to Stimulate Insulin Secretion Revealed by Quantitative Phosphoproteomics. <i>Scientific Reports</i> , 2017, 7, 1018.	1.6	6
14179	Unified Alignment of Protein-Protein Interaction Networks. <i>Scientific Reports</i> , 2017, 7, 953.	1.6	40
14180	Mapping genes for calcium signaling and their associated human genetic disorders. <i>Bioinformatics</i> , 2017, 33, 2547-2554.	1.8	16
14181	A microRNA-mRNA expression network during oral siphon regeneration in <i>Ciona</i> . <i>Development (Cambridge)</i> , 2017, 144, 1787-1797.	1.2	16
14182	Transcriptome Analyses of Two Citrus Cultivars (Shiranuhi and Huangguogan) in Seedling Etiolation. <i>Scientific Reports</i> , 2017, 7, 46245.	1.6	15
14183	NSSRF: global network similarity search with subgraph signatures and its applications. <i>Bioinformatics</i> , 2017, 33, 1696-1702.	1.8	6

#	ARTICLE	IF	CITATIONS
14184	Atrial electrophysiological and molecular remodelling induced by obstructive sleep apnoea. <i>Journal of Cellular and Molecular Medicine</i> , 2017, 21, 2223-2235.	1.6	28
14185	Knowledge management of eco-industrial park for efficient energy utilization through ontology-based approach. <i>Applied Energy</i> , 2017, 204, 1412-1421.	5.1	49
14186	Comprehensive comparison of two protein family of P-ATPases (13A1 and 13A3) in insects. <i>Computational Biology and Chemistry</i> , 2017, 68, 266-281.	1.1	5
14187	Differential lactate and cholesterol synthetic activities in XY and XX Sertoli cells. <i>Scientific Reports</i> , 2017, 7, 41912.	1.6	4
14188	Signals of selection in conditionally expressed genes in the diversification of three horned beetle species. <i>Journal of Evolutionary Biology</i> , 2017, 30, 1644-1657.	0.8	10
14189	Summarizing Biological Networks. <i>Computational Biology</i> , 2017, , .	0.1	0
14191	Novel mononuclear Cu (II) terpyridine complexes: Impact of fused ring thiophene and thiazole head groups towards DNA/BSA interaction, cleavage and antiproliferative activity on HepG2 and triple negative CAL-51 cell line. <i>European Journal of Medicinal Chemistry</i> , 2017, 135, 434-446.	2.6	48
14192	The E. coli molecular phenotype under different growth conditions. <i>Scientific Reports</i> , 2017, 7, 45303.	1.6	46
14193	goSTAG: gene ontology subtrees to tag and annotate genes within a set. <i>Source Code for Biology and Medicine</i> , 2017, 12, 6.	1.7	10
14194	Bioinformatics Approaches to the Structure and Function of Intrinsically Disordered Proteins. , 2017, , 167-203.		5
14195	RNA Editing During Sexual Development Occurs in Distantly Related Filamentous Ascomycetes. <i>Genome Biology and Evolution</i> , 2017, 9, 855-868.	1.1	44
14196	The histone demethylase PHF8 is a molecular safeguard of the IFN γ response. <i>Nucleic Acids Research</i> , 2017, 45, gkw1346.	6.5	12
14197	Genome-wide identification of physically clustered genes suggests chromatin-level co-regulation in male reproductive development in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2017, 45, 3253-3265.	6.5	35
14198	Transcriptional signatures of connectomic subregions of the human striatum. <i>Genes, Brain and Behavior</i> , 2017, 16, 647-663.	1.1	36
14199	Epigenome-wide association study of DNA methylation in panic disorder. <i>Clinical Epigenetics</i> , 2017, 9, 6.	1.8	47
14200	Substrates and oxygen dependent citric acid production by <i>Yarrowia lipolytica</i> : insights through transcriptome and fluxome analyses. <i>Microbial Cell Factories</i> , 2017, 16, 78.	1.9	80
14201	Microarray profiling of long non-coding RNAs associated with idiopathic pulmonary arterial hypertension. <i>Experimental and Therapeutic Medicine</i> , 2017, 13, 2657-2666.	0.8	13
14202	Microarray-based screening of differentially expressed genes in glucocorticoid-induced avascular necrosis. <i>Molecular Medicine Reports</i> , 2017, 15, 3583-3590.	1.1	4

#	ARTICLE	IF	CITATIONS
14203	Cytoplasmic overexpression of RNA-binding protein HuR is a marker of poor prognosis in meningioma, and HuR knockdown decreases meningioma cell growth and resistance to hypoxia. <i>Journal of Pathology</i> , 2017, 242, 421-434.	2.1	27
14204	Analysis of Informative Features for Negative Selection in Protein Function Prediction. <i>Lecture Notes in Computer Science</i> , 2017, , 267-276.	1.0	2
14205	Effects of dietary physical or nutritional factors on morphology of rumen papillae and transcriptome changes in lactating dairy cows based on three different forage-based diets. <i>BMC Genomics</i> , 2017, 18, 353.	1.2	55
14206	Functional annotation of a novel toxin-antitoxin system Xn-RelT of <i>Xenorhabdus nematophila</i> ; a combined in silico and in vitro approach. <i>Journal of Molecular Modeling</i> , 2017, 23, 189.	0.8	4
14207	Transcriptomic and macroevolutionary evidence for phenotypic uncoupling between frog life history phases. <i>Nature Communications</i> , 2017, 8, 15213.	5.8	40
14208	Expansion of the redox-sensitive proteome coincides with the plastid endosymbiosis. <i>Nature Plants</i> , 2017, 3, 17066.	4.7	26
14209	Transposable Element Misregulation Is Linked to the Divergence between Parental piRNA Pathways in <i>Drosophila</i> Hybrids. <i>Genome Biology and Evolution</i> , 2017, 9, 1450-1470.	1.1	26
14210	Comparative transcriptome analysis of shortened fruit mutant in woodland strawberry (<i>Fragaria</i>) Tj ETQq1 1 0.784314 rgBT /Overloc	1.7	12
14211	What is a cognitive ontology, anyway?. <i>Philosophical Explorations</i> , 2017, 20, 123-128.	0.4	14
14212	Peptidomic Analysis of Cultured Cardiomyocytes Exposed to Acute Ischemic-Hypoxia. <i>Cellular Physiology and Biochemistry</i> , 2017, 41, 358-368.	1.1	15
14213	Navigating through the Jungle of Allergens: Features and Applications of Allergen Databases. <i>International Archives of Allergy and Immunology</i> , 2017, 173, 1-11.	0.9	16
14214	TheCellMap.org: A Web-Accessible Database for Visualizing and Mining the Global Yeast Genetic Interaction Network. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1539-1549.	0.8	114
14215	Identification of the zinc, copper and cadmium metalloproteome of the protozoan <i>Tetrahymena thermophila</i> by systematic bioinformatics. <i>Archives of Microbiology</i> , 2017, 199, 1141-1149.	1.0	24
14216	Tradict enables accurate prediction of eukaryotic transcriptional states from 100 marker genes. <i>Nature Communications</i> , 2017, 8, 15309.	5.8	18
14217	Proteomic analysis of aged microglia: shifts in transcription, bioenergetics, and nutrient response. <i>Journal of Neuroinflammation</i> , 2017, 14, 96.	3.1	89
14218	Integrated clinicopathological features and gene microarray analysis of pancreatic neuroendocrine tumors. <i>Gene</i> , 2017, 625, 72-77.	1.0	9
14219	Neuroserpin polymers cause oxidative stress in a neuronal model of the dementia FENIB. <i>Neurobiology of Disease</i> , 2017, 103, 32-44.	2.1	25
14220	Identification of a target protein of Hydra actinoporin-like toxin-1 (HALT-1) using GST affinity purification and SILAC-based quantitative proteomics. <i>Toxicon</i> , 2017, 133, 153-161.	0.8	6

#	ARTICLE	IF	CITATIONS
14221	Exosomes in mammals with greater habitat variability contain more proteins and RNAs. <i>Royal Society Open Science</i> , 2017, 4, 170162.	1.1	3
14222	Identification of molecular characteristics induced by radiotherapy in rectal cancer based on microarray data. <i>Oncology Letters</i> , 2017, 13, 2777-2783.	0.8	6
14223	Cascading Effects of Nanoparticle Coatings: Surface Functionalization Dictates the Assemblage of Complexed Proteins and Subsequent Interaction with Model Cell Membranes. <i>ACS Nano</i> , 2017, 11, 5489-5499.	7.3	57
14224	Comparative transcriptomic analysis of <i>Gardnerella vaginalis</i> biofilms vs. planktonic cultures using RNA-seq. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 3.	2.9	66
14225	Altered interactions between unicellular and multicellular genes drive hallmarks of transformation in a diverse range of solid tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6406-6411.	3.3	159
14226	Assessment of Whole-Exome Sequence Data in Attempted Suicide within a Bipolar Disorder Cohort. <i>Molecular Neuropsychiatry</i> , 2017, 3, 1-11.	3.0	13
14227	Identification of Key Gene Modules of Neuropathic Pain by Co-Expression Analysis. <i>Journal of Cellular Biochemistry</i> , 2017, 118, 4436-4443.	1.2	9
14228	Exploring Protein Function Using the <i>Saccharomyces</i> Genome Database. <i>Methods in Molecular Biology</i> , 2017, 1611, 169-182.	0.4	2
14229	Ortholog Identification and Comparative Analysis of Microbial Genomes Using MBLD and RECOG. <i>Methods in Molecular Biology</i> , 2017, 1611, 147-168.	0.4	4
14230	Protein and Sugar Export and Assembly in Gram-positive Bacteria. <i>Current Topics in Microbiology and Immunology</i> , 2017, , .	0.7	5
14231	A large-scale benchmark of gene prioritization methods. <i>Scientific Reports</i> , 2017, 7, 46598.	1.6	44
14232	Deciphering Pancreatic Islet β Cell and δ Cell Maturation Pathways and Characteristic Features at the Single-Cell Level. <i>Cell Metabolism</i> , 2017, 25, 1194-1205.e4.	7.2	130
14233	Modeling gene-wise dependencies improves the identification of drug response biomarkers in cancer studies. <i>Bioinformatics</i> , 2017, 33, 1362-1369.	1.8	10
14234	Potential roles of microRNAs and their target genes in human multiple myeloma. <i>European Journal of Haematology</i> , 2017, 99, 178-185.	1.1	8
14235	Vitamin A-Retinoic Acid Signaling Regulates Hematopoietic Stem Cell Dormancy. <i>Cell</i> , 2017, 169, 807-823.e19.	13.5	339
14236	Altered protein glycosylation predicts Alzheimer's disease and modulates its pathology in disease model <i>Drosophila</i> . <i>Neurobiology of Aging</i> , 2017, 56, 159-171.	1.5	18
14237	Using hyperLOPIT to perform high-resolution mapping of the spatial proteome. <i>Nature Protocols</i> , 2017, 12, 1110-1135.	5.5	113
14238	Oxidation of protein-bound methionine in Photofrin-photodynamic therapy-treated human tumor cells explored by methionine-containing peptide enrichment and quantitative proteomics approach. <i>Scientific Reports</i> , 2017, 7, 1370.	1.6	13

#	ARTICLE	IF	CITATIONS
14239	Annotating function to differentially expressed LincRNAs in myelodysplastic syndrome using a network-based method. <i>Bioinformatics</i> , 2017, 33, 2622-2630.	1.8	14
14240	Exploratory analysis of <i>Symbiodinium</i> transcriptomes reveals potential latent infection by large dsDNA viruses. <i>Environmental Microbiology</i> , 2017, 19, 3909-3919.	1.8	25
14241	Impacts of temperature and lunar day on gene expression profiles during a monthly reproductive cycle in the brooding coral <i>Pocillopora damicornis</i> . <i>Molecular Ecology</i> , 2017, 26, 3913-3925.	2.0	15
14242	Associating Gene Ontology Terms with Pfam Protein Domains. <i>Lecture Notes in Computer Science</i> , 2017, , 127-138.	1.0	1
14243	Gene co-expression network analysis identifies porcine genes associated with variation in metabolizing fenbendazole and flunixin meglumine in the liver. <i>Scientific Reports</i> , 2017, 7, 1357.	1.6	10
14244	The accessible chromatin landscape during conversion of human embryonic stem cells to trophoblast by bone morphogenetic protein 4. <i>Biology of Reproduction</i> , 2017, 96, 1267-1278.	1.2	16
14245	Next-generation DNA sequencing identifies novel gene variants and pathways involved in specific language impairment. <i>Scientific Reports</i> , 2017, 7, 46105.	1.6	79
14246	Aberrantly expressed long noncoding RNAs in recurrent implantation failure: A microarray related study. <i>Systems Biology in Reproductive Medicine</i> , 2017, 63, 269-278.	1.0	25
14247	Using closure tables to enable cross-querying of ontologies in database-driven applications. , 2017, 2017, 493-496.		0
14248	Discovering relationships between nuclear receptor signaling pathways, genes, and tissues in Transcriptome. <i>Science Signaling</i> , 2017, 10, .	1.6	35
14249	Protein Function Prediction. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	15
14250	PARP3 is a promoter of chromosomal rearrangements and limits G4 DNA. <i>Nature Communications</i> , 2017, 8, 15110.	5.8	32
14251	IGF2BP3 functions as a potential oncogene and is a crucial target of miR-34a in gastric carcinogenesis. <i>Molecular Cancer</i> , 2017, 16, 77.	7.9	115
14252	Neuro-symbolic representation learning on biological knowledge graphs. <i>Bioinformatics</i> , 2017, 33, 2723-2730.	1.8	92
14253	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, 45040.	1.6	98
14254	Little Cigars are More Toxic than Cigarettes and Uniquely Change the Airway Gene and Protein Expression. <i>Scientific Reports</i> , 2017, 7, 46239.	1.6	29
14255	Exploring a causal role of DNA methylation in the relationship between maternal vitamin B12 during pregnancy and child's IQ at age 8, cognitive performance and educational attainment: a two-step Mendelian randomization study. <i>Human Molecular Genetics</i> , 2017, 26, 3001-3013.	1.4	50
14256	Permanent draft genome of <i>Thiobacillus thioparus</i> DSM 505T, an obligately chemolithoautotrophic member of the Betaproteobacteria. <i>Standards in Genomic Sciences</i> , 2017, 12, 10.	1.5	34

#	ARTICLE	IF	CITATIONS
14257	Construction of Functional Gene Networks Using Phylogenetic Profiles. <i>Methods in Molecular Biology</i> , 2017, 1526, 87-98.	0.4	10
14258	An RNA-seq analysis from non-small cell lung cancer biopsies suggests an important role for aberrant alternative splicing in its pathophysiology. <i>Health and Technology</i> , 2017, 7, 133-140.	2.1	2
14259	E2f11 is a meiosis-specific transcription factor in the protist <i>Tetrahymena thermophila</i> . <i>Cell Cycle</i> , 2017, 16, 123-135.	1.3	9
14260	Inferring Function from Homology. <i>Methods in Molecular Biology</i> , 2017, 1526, 23-40.	0.4	5
14261	Brain transcriptome atlases: a computational perspective. <i>Brain Structure and Function</i> , 2017, 222, 1557-1580.	1.2	19
14262	TROM: A Testing-Based Method for Finding Transcriptomic Similarity of Biological Samples. <i>Statistics in Biosciences</i> , 2017, 9, 105-136.	0.6	16
14263	PROSNET: INTEGRATING HOMOLOGY WITH MOLECULAR NETWORKS FOR PROTEIN FUNCTION PREDICTION. , 2017, 22, 27-38.		10
14265	Working with Ontologies. <i>Methods in Molecular Biology</i> , 2017, 1525, 123-135.	0.4	6
14266	Transcriptomic response of the insect vector, <i>Peregrinus maidis</i> , to Maize mosaic rhabdovirus and identification of conserved responses to propagative viruses in hopper vectors. <i>Virology</i> , 2017, 509, 71-81.	1.1	24
14267	Integrated gene expression profiling and chromatin immunoprecipitation followed by sequencing: Analysis of the C-terminal binding protein in breast cancer. <i>Journal of Obstetrics and Gynaecology Research</i> , 2017, 43, 1472-1480.	0.6	2
14268	Genomewide transcriptional reprogramming in the seagrass <i>Cymodocea nodosa</i> under experimental ocean acidification. <i>Molecular Ecology</i> , 2017, 26, 4241-4259.	2.0	27
14269	Long noncoding RNA expression profile in HLE B-3 cells during TGF- β 2-induced epithelial-mesenchymal transition. <i>BMC Ophthalmology</i> , 2017, 17, 69.	0.6	10
14270	Methods to analyze big data in pharmacogenomics research. <i>Pharmacogenomics</i> , 2017, 18, 807-820.	0.6	10
14271	Bioinformatics analyses of the differences between lung adenocarcinoma and squamous cell carcinoma using The Cancer Genome Atlas expression data. <i>Molecular Medicine Reports</i> , 2017, 16, 609-616.	1.1	19
14272	JDINAC: joint density-based non-parametric differential interaction network analysis and classification using high-dimensional sparse omics data. <i>Bioinformatics</i> , 2017, 33, 3080-3087.	1.8	24
14273	The Zebrafish Model Organism Database: new support for human disease models, mutation details, gene expression phenotypes and searching. <i>Nucleic Acids Research</i> , 2017, 45, D758-D768.	6.5	71
14274	High quality draft genome of <i>Nakamurella lactea</i> type strain, a rock actinobacterium, and emended description of <i>Nakamurella lactea</i> . <i>Standards in Genomic Sciences</i> , 2017, 12, 4.	1.5	14
14275	High resolution time-course mapping of early transcriptomic, molecular and cellular phenotypes in Huntington's disease CAG knock-in mice across multiple genetic backgrounds. <i>Human Molecular Genetics</i> , 2017, 26, 913-922.	1.4	37

#	ARTICLE	IF	CITATIONS
14276	Drug repurposing for aging research using model organisms. <i>Aging Cell</i> , 2017, 16, 1006-1015.	3.0	34
14277	Reconstructing cell cycle pseudo time-series via single-cell transcriptome data. <i>Nature Communications</i> , 2017, 8, 22.	5.8	121
14278	Differential effects of a post-anthesis heat stress on wheat (<i>Triticum aestivum</i> L.) grain proteome determined by iTRAQ. <i>Scientific Reports</i> , 2017, 7, 3468.	1.6	44
14279	Integrated Servers for Structure-Informed Function Prediction. , 2017, , 427-448.		0
14280	Architecture of the human interactome defines protein communities and disease networks. <i>Nature</i> , 2017, 545, 505-509.	13.7	1,190
14281	Global gene expression analysis provides insight into local adaptation to geothermal streams in tadpoles of the Andean toad <i>Rhinella spinulosa</i> . <i>Scientific Reports</i> , 2017, 7, 1966.	1.6	10
14282	Characteristics and Expression Profile of <i>KRT71</i> Screened by Suppression Subtractive Hybridization cDNA Library in Curly Fleece Chinese Tan Sheep. <i>DNA and Cell Biology</i> , 2017, 36, 552-564.	0.9	11
14283	GeMSTONE: orchestrated prioritization of human germline mutations in the cloud. <i>Nucleic Acids Research</i> , 2017, 45, W207-W214.	6.5	2
14284	Comparative membrane proteomics analyses of breast cancer cell lines to understand the molecular mechanism of breast cancer brain metastasis. <i>Electrophoresis</i> , 2017, 38, 2124-2134.	1.3	21
14285	Developing transcriptional profiles in <i>Orbicella franksi</i> exposed to copper: Characterizing responses associated with a spectrum of laboratory-controlled environmental conditions. <i>Aquatic Toxicology</i> , 2017, 189, 60-76.	1.9	1
14286	Genomic and phenotypic analyses of <i>Pseudomonas psychrotolerans</i> PRS08-11306 reveal a turnerbactin biosynthesis gene cluster that contributes to nitrogen fixation. <i>Journal of Biotechnology</i> , 2017, 253, 10-13.	1.9	12
14287	A computational framework for distinguishing direct versus indirect interactions in human functional protein-protein interaction networks. <i>Integrative Biology (United Kingdom)</i> , 2017, 9, 595-606.	0.6	7
14288	Macroanalysis in the Arts and Sciences. , 2017, , 87-100.		0
14289	GLANET: genomic loci annotation and enrichment tool. <i>Bioinformatics</i> , 2017, 33, 2818-2828.	1.8	15
14290	APRICOT: an integrated computational pipeline for the sequence-based identification and characterization of RNA-binding proteins. <i>Nucleic Acids Research</i> , 2017, 45, e96-e96.	6.5	22
14291	Grain subproteome responses to nitrogen and sulfur supply in diploid wheat <i>Triticum monococcum</i> ssp. <i>monococcum</i> . <i>Plant Journal</i> , 2017, 91, 894-910.	2.8	54
14292	Genome-scale transcriptional study of hybrid effects and regulatory divergence in an F1 hybrid <i>Ruellia</i> (Wild Petunias: Acanthaceae) and its parents. <i>BMC Plant Biology</i> , 2017, 17, 15.	1.6	13
14293	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2017, 38, 1182-1192.	1.1	39

#	ARTICLE	IF	CITATIONS
14294	Exposure of Induced Pluripotent Stem Cell-Derived Vascular Endothelial and Smooth Muscle Cells in Coculture to Hemodynamics Induces Primary Vascular Cell-Like Phenotypes. <i>Stem Cells Translational Medicine</i> , 2017, 6, 1673-1683.	1.6	32
14295	Identification of genetic variants associated with Huntington's disease progression: a genome-wide association study. <i>Lancet Neurology</i> , The, 2017, 16, 701-711.	4.9	248
14296	Identification and characterization of the leaf specific networks of inner and rosette leaves in <i>Brassica rapa</i> . <i>Biochemical and Biophysical Research Communications</i> , 2017, 490, 821-826.	1.0	4
14297	Cholinergic neuron gene expression differences captured by translational profiling in a mouse model of Alzheimer's disease. <i>Neurobiology of Aging</i> , 2017, 57, 104-119.	1.5	24
14298	Autophagy gene FIP200 in neural progenitors non- cell autonomously controls differentiation by regulating microglia. <i>Journal of Cell Biology</i> , 2017, 216, 2581-2596.	2.3	32
14299	Gene co-expression network analysis for identifying modules and functionally enriched pathways in SCA2. <i>Human Molecular Genetics</i> , 2017, 26, 3069-3080.	1.4	40
14300	Contrasting gene expression programs correspond with predator-induced phenotypic plasticity within and across generations in <i>Daphnia</i> . <i>Molecular Ecology</i> , 2017, 26, 5003-5015.	2.0	39
14301	Statistical contributions to bioinformatics: Design, modelling, structure learning and integration. <i>Statistical Modelling</i> , 2017, 17, 245-289.	0.5	15
14302	Antagonistic regulation of spermatogonial differentiation in zebrafish (<i>Danio rerio</i>) by <i>Igf3</i> and <i>Amh</i> . <i>Molecular and Cellular Endocrinology</i> , 2017, 454, 112-124.	1.6	55
14303	Transcriptome of <i>Pterospermum kingtungense</i> provides implications on the mechanism underlying its rapid vegetative growth and limestone adaptation. <i>Scientific Reports</i> , 2017, 7, 3198.	1.6	5
14304	Functional dissection of human targets for KSHV-encoded miRNAs using network analysis. <i>Scientific Reports</i> , 2017, 7, 3159.	1.6	4
14305	Sex-Specific Transcript Diversity in the Fly Head Is Established during Pupal Stages and Adulthood and Is Largely Independent of the Mating Process and the Germline. <i>Sexual Development</i> , 2017, 11, 94-108.	1.1	0
14306	Integration of transcriptomic and metabolic data reveals hub transcription factors involved in drought stress response in sunflower (<i>Helianthus annuus</i> L.). <i>Plant Molecular Biology</i> , 2017, 94, 549-564.	2.0	51
14307	The Sequences of 1504 Mutants in the Model Rice Variety Kitaake Facilitate Rapid Functional Genomic Studies. <i>Plant Cell</i> , 2017, 29, 1218-1231.	3.1	138
14308	Uncovering the pathogenesis of microtia using bioinformatics approach. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2017, 99, 30-35.	0.4	3
14309	Co-expression analysis among microRNAs, long non-coding RNAs, and messenger RNAs to understand the pathogenesis and progression of diabetic kidney disease at the genetic level. <i>Methods</i> , 2017, 124, 46-56.	1.9	11
14310	Predicting protein function via multi-label supervised topic model on gene ontology. <i>Biotechnology and Biotechnological Equipment</i> , 2017, 31, 630-638.	0.5	11
14311	Bioinformatics analysis of gene expression profiles of esophageal squamous cell carcinoma. <i>Ecological Management and Restoration</i> , 2017, 30, 1-8.	0.2	20

#	ARTICLE	IF	CITATIONS
14312	Sequencing, de novo assembling, and annotating the genome of the endangered Chinese crocodile lizard <i>Shinisaurus crocodilurus</i> . <i>GigaScience</i> , 2017, 6, 1-6.	3.3	23
14313	Long-lasting antinociceptive effects of green light in acute and chronic pain in rats. <i>Pain</i> , 2017, 158, 347-360.	2.0	81
14314	Chromatin module inference on cellular trajectories identifies key transition points and poised epigenetic states in diverse developmental processes. <i>Genome Research</i> , 2017, 27, 1250-1262.	2.4	14
14315	Inferring miRNA sponge co-regulation of protein-protein interactions in human breast cancer. <i>BMC Bioinformatics</i> , 2017, 18, 243.	1.2	20
14316	Gene expression and adaptive noncoding changes during human evolution. <i>BMC Genomics</i> , 2017, 18, 435.	1.2	13
14317	Comparative transcriptome profiling and morphology provide insights into endocarp cleaving of apricot cultivar (<i>Prunus armeniaca</i> L.). <i>BMC Plant Biology</i> , 2017, 17, 72.	1.6	40
14318	Optimizing complex phenotypes through model-guided multiplex genome engineering. <i>Genome Biology</i> , 2017, 18, 100.	3.8	23
14319	CaMELS: <i>in silico</i> prediction of calmodulin binding proteins and their binding sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1724-1740.	1.5	24
14320	Integration of over 9,000 mass spectrometry experiments builds a global map of human protein complexes. <i>Molecular Systems Biology</i> , 2017, 13, 932.	3.2	177
14321	Data management and data enrichment for systems biology projects. <i>Journal of Biotechnology</i> , 2017, 261, 229-237.	1.9	23
14322	Genome-wide association meta-analysis of 78,308 individuals identifies new loci and genes influencing human intelligence. <i>Nature Genetics</i> , 2017, 49, 1107-1112.	9.4	425
14323	The draft genome of blunt snout bream (<i>Megalobrama amblycephala</i>) reveals the development of intermuscular bone and adaptation to herbivorous diet. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	95
14324	HGVA: the Human Genome Variation Archive. <i>Nucleic Acids Research</i> , 2017, 45, W189-W194.	6.5	6
14325	Comprehensive discovery of subsample gene expression components by information explanation: therapeutic implications in cancer. <i>BMC Medical Genomics</i> , 2017, 10, 12.	0.7	18
14327	Predicting potential gene ontology from cellular response data. , 2017, , .		1
14328	Dynamic regulation of VEGF-inducible genes by an ERK-ERG-p300 transcriptional network. <i>Development (Cambridge)</i> , 2017, 144, 2428-2444.	1.2	68
14329	Biallelic Mutations in CFAP43 and CFAP44 Cause Male Infertility with Multiple Morphological Abnormalities of the Sperm Flagella. <i>American Journal of Human Genetics</i> , 2017, 100, 854-864.	2.6	220
14330	De novo assembly and analysis of the <i>Pugionium cornutum</i> (L.) Gaertn. transcriptome and identification of genes involved in the drought response. <i>Gene</i> , 2017, 626, 290-297.	1.0	16

#	ARTICLE	IF	CITATIONS
14331	The genome sequence of sweet cherry (<i>Prunus avium</i>) for use in genomics-assisted breeding. DNA Research, 2017, 24, 499-508.	1.5	212
14332	A resource of potential drug targets and strategic decision-making for obstructive sleep apnoea pharmacotherapy. Respiriology, 2017, 22, 861-873.	1.3	50
14333	Absence of juvenile hormone signalling regulates the dynamic expression profiles of nutritional metabolism genes during diapause preparation in the cabbage beetle <i>Colaphellus bowringi</i> . Insect Molecular Biology, 2017, 26, 530-542.	1.0	33
14334	Genomic Analysis of Genotype-by-Social Environment Interaction for <i>Drosophila melanogaster</i> Aggressive Behavior. Genetics, 2017, 206, 1969-1984.	1.2	21
14335	Complete genome sequence of a denitrifying bacterium, <i>Pseudomonas</i> sp. CC6-YY-74, isolated from Arctic Ocean sediment. Marine Genomics, 2017, 35, 47-49.	0.4	10
14336	Huanglongbing pathogen <i>Candidatus Liberibacter asiaticus</i> exploits the energy metabolism and host defence responses of its vector <i>Diptera diaphorina citri</i> . Physiological Entomology, 2017, 42, 319-335.	0.6	18
14337	Mass spectrometric detection combined with bioinformatic analysis identified possible protein markers and key pathways associated with bladder cancer. Gene, 2017, 626, 407-413.	1.0	14
14338	<i>In vitro</i> expansion of mouse primordial germ cell-like cells recapitulates an epigenetic blank slate. EMBO Journal, 2017, 36, 1888-1907.	3.5	92
14339	The ProFunc Function Prediction Server. Methods in Molecular Biology, 2017, 1611, 75-95.	0.4	22
14340	Phylogenomics. , 2017, , .		47
14341	Catch and Release of Cytokines Mediated by Tumor Phosphatidylserine Converts Transient Exposure into Long-Lived Inflammation. Molecular Cell, 2017, 66, 635-647.e7.	4.5	34
14342	Systematic discovery of mutation-specific synthetic lethals by mining pan-cancer human primary tumor data. Nature Communications, 2017, 8, 15580.	5.8	77
14343	EST-SSR marker development and transcriptome sequencing analysis of different tissues of Korean pine (<i>Pinus koraiensis</i> Sieb. et Zucc.). Biotechnology and Biotechnological Equipment, 0, , 1-11.	0.5	10
14344	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. Journal of Experimental Medicine, 2017, 214, 2073-2088.	4.2	30
14345	Identification of key genes and pathways for peri-implantitis through the analysis of gene expression data. Experimental and Therapeutic Medicine, 2017, 13, 1832-1840.	0.8	14
14346	RNA-based ovarian cancer research from a gene to systems biomedicine™ perspective. Systems Biology in Reproductive Medicine, 2017, 63, 219-238.	1.0	18
14347	Type of gonadotropin used during controlled ovarian stimulation induces differential gene expression in human cumulus cells: A randomized study. European Journal of Obstetrics, Gynecology and Reproductive Biology, 2017, 215, 124-133.	0.5	6
14348	Polymer-coated cardiopulmonary bypass circuit attenuates upregulation of both proteases/protease inhibitors and platelet degranulation in pigs. Perfusion (United Kingdom), 2017, 32, 645-655.	0.5	6

#	ARTICLE	IF	CITATIONS
14349	Uniform neural tissue models produced on synthetic hydrogels using standard culture techniques. <i>Experimental Biology and Medicine</i> , 2017, 242, 1679-1689.	1.1	31
14350	High quality permanent draft genome sequence of <i>Chryseobacterium bovis</i> DSM 19482T, isolated from raw cow milk. <i>Standards in Genomic Sciences</i> , 2017, 12, 31.	1.5	2
14351	Omics Data Complementarity Underlines Functional Cross-Communication in Yeast. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.0	0
14352	Bacterial and Viral Products Affect Differential Pattern Recognition Receptor Activation of Chicken Thrombocytes Evidenced through RNA Sequencing. <i>Journal of Immunology</i> , 2017, 199, 774-781.	0.4	13
14353	Upregulation of cyclin B1 plays potential roles in the invasiveness of pituitary adenomas. <i>Journal of Clinical Neuroscience</i> , 2017, 43, 267-273.	0.8	20
14354	Transcriptome analysis of the immune reaction of the pearl oyster <i>Pinctada fucata</i> to xenograft from <i>Pinctada maxima</i> . <i>Fish and Shellfish Immunology</i> , 2017, 67, 331-345.	1.6	29
14355	Multilineage communication regulates human liver bud development from pluripotency. <i>Nature</i> , 2017, 546, 533-538.	13.7	458
14356	Transcriptional responses of detoxification genes to four plant allelochemicals in <i>Aphis gossypii</i> . <i>Journal of Economic Entomology</i> , 2017, 110, 624-631.	0.8	24
14357	A structural perspective on the interactions of TRAF6 and β asigin during the onset of melanoma: A molecular dynamics simulation study. <i>Journal of Molecular Recognition</i> , 2017, 30, e2643.	1.1	6
14358	De novo assembly, gene annotation, and molecular marker development using Illumina paired-end transcriptome sequencing in the clam <i>Saxidomus purpuratus</i> . <i>Genes and Genomics</i> , 2017, 39, 675-685.	0.5	7
14359	Systems biology of facial development: contributions of ectoderm and mesenchyme. <i>Developmental Biology</i> , 2017, 426, 97-114.	0.9	49
14360	Lipidome determinants of maximal lifespan in mammals. <i>Scientific Reports</i> , 2017, 7, 5.	1.6	60
14361	Comparative network stratification analysis for identifying functional interpretable network biomarkers. <i>BMC Bioinformatics</i> , 2017, 18, 48.	1.2	7
14362	HESML: A scalable ontology-based semantic similarity measures library with a set of reproducible experiments and a replication dataset. <i>Information Systems</i> , 2017, 66, 97-118.	2.4	42
14363	Novel <i>trans</i> -Ferulic Acid Derivatives Containing a Chalcone Moiety as Potential Activator for Plant Resistance Induction. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 4367-4377.	2.4	82
14364	Comparative analysis of MBD-seq and MeDIP-seq and estimation of gene expression changes in a rodent model of schizophrenia. <i>Genomics</i> , 2017, 109, 204-213.	1.3	21
14365	Scallop genome provides insights into evolution of bilaterian karyotype and development. <i>Nature Ecology and Evolution</i> , 2017, 1, 120.	3.4	353
14366	Protein-coding genes in B chromosomes of the grasshopper <i>Eyprepocnemis plorans</i> . <i>Scientific Reports</i> , 2017, 7, 45200.	1.6	53

#	ARTICLE	IF	CITATIONS
14367	Proteomic signature of muscle fibre hyperplasia in response to faba bean intake in grass carp. <i>Scientific Reports</i> , 2017, 7, 45950.	1.6	51
14368	Stress-dependent opposing roles for mitophagy in aging of the ascomycete <i>Podospora anserina</i> . <i>Autophagy</i> , 2017, 13, 1037-1052.	4.3	38
14369	SANA: simulated annealing far outperforms many other search algorithms for biological network alignment. <i>Bioinformatics</i> , 2017, 33, 2156-2164.	1.8	78
14370	RefBool: a reference-based algorithm for discretizing gene expression data. <i>Bioinformatics</i> , 2017, 33, 1953-1962.	1.8	7
14371	Genome-wide sequencing of longan (<i>Dimocarpus longan</i> Lour.) provides insights into molecular basis of its polyphenol-rich characteristics. <i>GigaScience</i> , 2017, 6, 1-14.	3.3	103
14372	InterPro in 2017—beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
14373	Tracking the evolution of 3D gene organization demonstrates its connection to phenotypic divergence. <i>Nucleic Acids Research</i> , 2017, 45, 4330-4343.	6.5	7
14374	A New Natural Product Analog of Blasticidin S Reveals Cellular Uptake Facilitated by the NorA Multidrug Transporter. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	10
14375	Gene expression profiling during the embryo-to-larva transition in the giant red sea urchin <i>Mesocentrotus franciscanus</i> . <i>Ecology and Evolution</i> , 2017, 7, 2798-2811.	0.8	11
14376	Methods for Microbiome Analysis. <i>Translational Medicine Research</i> , 2017, , 269-298.	0.0	1
14377	Draft genome analysis of <i>Dietzia</i> sp. 111N12-1, isolated from the South China Sea with bioremediation activity. <i>Brazilian Journal of Microbiology</i> , 2017, 48, 393-394.	0.8	10
14378	An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. <i>Cell</i> , 2017, 169, 350-360.e12.	13.5	322
14379	Ontology-based automatic identification of public health-related Turkish tweets. <i>Computers in Biology and Medicine</i> , 2017, 83, 1-9.	3.9	10
14380	The effects of shared information on semantic calculations in the gene ontology. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 195-211.	1.9	3
14381	Characterization of Leaf Transcriptome in <i>Banksia hookeriana</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 49-56.	3.0	14
14382	Systematic expression profiling analysis mines dys-regulated modules in active tuberculosis based on re-weighted protein-protein interaction network and attract algorithm. <i>Microbial Pathogenesis</i> , 2017, 107, 48-53.	1.3	2
14383	Large-Scale Profiling Reveals the Influence of Genetic Variation on Gene Expression in Human Induced Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 533-546.e7.	5.2	157
14384	Identification of key genes and pathways associated with spinal cord injury. <i>Molecular Medicine Reports</i> , 2017, 15, 1577-1584.	1.1	11

#	ARTICLE	IF	CITATIONS
14385	Behavioral, transcriptomic and epigenetic responses to social challenge in honey bees. <i>Genes, Brain and Behavior</i> , 2017, 16, 579-591.	1.1	57
14386	<i>Hugonella massiliensis</i> gen. nov., sp. nov., genome sequence, and description of a new strictly anaerobic bacterium isolated from the human gut. <i>MicrobiologyOpen</i> , 2017, 6, e00458.	1.2	18
14387	Hybrid ontology-learning materials engineering system for pharmaceutical products: Multi-label entity recognition and concept detection. <i>Computers and Chemical Engineering</i> , 2017, 107, 49-60.	2.0	13
14388	Global analysis of canola genes targeted by SHORT HYPOCOTYL UNDER BLUE 1 during endosperm and embryo development. <i>Plant Journal</i> , 2017, 91, 158-171.	2.8	5
14389	A meta-analysis testing eusocial co-option theories in termite gut physiology and symbiosis. <i>Communicative and Integrative Biology</i> , 2017, 10, e1295187.	0.6	9
14391	Ovarian Cancer Differential Interactome and Network Entropy Analysis Reveal New Candidate Biomarkers. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 285-294.	1.0	15
14392	<i>Fuente</i> : functional enrichment for bioinformatics. <i>Bioinformatics</i> , 2017, 33, 2604-2606.	1.8	8
14393	Light influences cytokinin biosynthesis and sensing in <i>Nostoc</i> (cyanobacteria). <i>Journal of Phycology</i> , 2017, 53, 703-714.	1.0	19
14394	Characterization of siRNAs derived from cucumber mosaic virus in infected tobacco plants. <i>Archives of Virology</i> , 2017, 162, 2077-2082.	0.9	10
14395	The functional genomic studies of curcumin. <i>Seminars in Cancer Biology</i> , 2017, 46, 107-118.	4.3	61
14396	Glucocorticoid receptor binding to chromatin is selectively controlled by the coregulator Hic-5 and chromatin remodeling enzymes. <i>Journal of Biological Chemistry</i> , 2017, 292, 9320-9334.	1.6	17
14397	EXPath tool—a system for comprehensively analyzing regulatory pathways and coexpression networks from high-throughput transcriptome data. <i>DNA Research</i> , 2017, 24, 371-375.	1.5	12
14398	Genome-wide identification of microRNA targets in the neglected disease pathogens of the genus <i>Echinococcus</i> . <i>Molecular and Biochemical Parasitology</i> , 2017, 214, 91-100.	0.5	22
14399	Identification of prognostic genes and gene sets for early-stage non-small cell lung cancer using bi-level selection methods. <i>Scientific Reports</i> , 2017, 7, 46164.	1.6	9
14400	Whole-transcriptome RNA-seq, gene set enrichment pathway analysis, and exon coverage analysis of two plastid RNA editing mutants. <i>Plant Signaling and Behavior</i> , 2017, 12, e1312242.	1.2	5
14401	The Transcriptome of <i>Leishmania major</i> Developmental Stages in Their Natural Sand Fly Vector. <i>MBio</i> , 2017, 8, .	1.8	86
14402	Genome sequence of lung pathogenic <i>Escherichia coli</i> O78, a chimeric strain isolated from pneumonia forest musk deer. <i>Genes and Genomics</i> , 2017, 39, 805-815.	0.5	5
14403	eTumorType, An Algorithm of Discriminating Cancer Types for Circulating Tumor Cells or Cell-free DNAs in Blood. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 130-140.	3.0	15

#	ARTICLE	IF	CITATIONS
14404	Case-control analysis of truncating mutations in DNA damage response genes connects TEX15 and FANCD2 with hereditary breast cancer susceptibility. <i>Scientific Reports</i> , 2017, 7, 681.	1.6	20
14405	Transcriptomic analysis of two <i>Beauveria bassiana</i> strains grown on cuticle extracts of the silkworm uncovers their different metabolic response at early infection stage. <i>Journal of Invertebrate Pathology</i> , 2017, 145, 45-54.	1.5	23
14406	A Genome-wide Analysis of Human Pluripotent Stem Cell-Derived Endothelial Cells in 2D or 3D Culture. <i>Stem Cell Reports</i> , 2017, 8, 907-918.	2.3	41
14407	PML protein organizes heterochromatin domains where it regulates histone H3.3 deposition by ATRX/DAXX. <i>Genome Research</i> , 2017, 27, 913-921.	2.4	52
14408	Blood transcriptomes and de novo identification of candidate loci for mating success in lekking great snipe (<i>Gallinago media</i>). <i>Molecular Ecology</i> , 2017, 26, 3458-3471.	2.0	8
14409	Identification of novel cancer therapeutic targets using a designed and pooled shRNA library screen. <i>Scientific Reports</i> , 2017, 7, 43023.	1.6	33
14410	The druggable genome and support for target identification and validation in drug development. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	437
14411	Comparative transcriptome analyses of flower development in four species of <i>Achimenes</i> (Gesneriaceae). <i>BMC Genomics</i> , 2017, 18, 240.	1.2	41
14412	Differential proteomic analysis revealing the ovule abortion in the female-sterile line of <i>Pinus tabulaeformis</i> Carr.. <i>Plant Science</i> , 2017, 260, 31-49.	1.7	8
14413	Transcriptomic profiling of 39 commonly-used neuroblastoma cell lines. <i>Scientific Data</i> , 2017, 4, 170033.	2.4	113
14414	A comprehensive analysis of cancer-driving mutations and genes in kidney cancer. <i>Oncology Letters</i> , 2017, 13, 2151-2160.	0.8	4
14415	Community-Wide Evaluation of Computational Function Prediction. <i>Methods in Molecular Biology</i> , 2017, 1446, 133-146.	0.4	17
14417	Gene Expression Profiling with Cre-Conditional Pseudorabies Virus Reveals a Subset of Midbrain Neurons That Participate in Reward Circuitry. <i>Journal of Neuroscience</i> , 2017, 37, 4128-4144.	1.7	47
14418	Mitochondrial chaperone HSP60 regulates anti-bacterial immunity via p38 MAP kinase signaling. <i>EMBO Journal</i> , 2017, 36, 1046-1065.	3.5	66
14419	Proteome-Scale Human Interactomics. <i>Trends in Biochemical Sciences</i> , 2017, 42, 342-354.	3.7	129
14420	GFD-Net: A novel semantic similarity methodology for the analysis of gene networks. <i>Journal of Biomedical Informatics</i> , 2017, 68, 71-82.	2.5	7
14421	A reductionist approach to extract robust molecular markers from microarray data series – Isolating markers to track osseointegration. <i>Journal of Biomedical Informatics</i> , 2017, 68, 104-111.	2.5	4
14422	Functional proteomic analysis of corticosteroid pharmacodynamics in rat liver: Relationship to hepatic stress, signaling, energy regulation, and drug metabolism. <i>Journal of Proteomics</i> , 2017, 160, 84-105.	1.2	22

#	ARTICLE	IF	CITATIONS
14423	Three-Dimensional Encapsulation of <i>Saccharomyces cerevisiae</i> in Silicate Matrices Creates Distinct Metabolic States as Revealed by Gene Chip Analysis. <i>ACS Nano</i> , 2017, 11, 3560-3575.	7.3	17
14424	Autism gene Ube3a and seizures impair sociability by repressing VTA Cbln1. <i>Nature</i> , 2017, 543, 507-512.	13.7	125
14425	Extracting Genes Involved in Disease from a Connected Network of Perturbed Biological Processes. <i>Journal of Computational Biology</i> , 2017, 24, 460-469.	0.8	1
14426	Modeling anorexia nervosa: transcriptional insights from human iPSC-derived neurons. <i>Translational Psychiatry</i> , 2017, 7, e1060-e1060.	2.4	22
14427	Systems Biology of Metabolism. <i>Annual Review of Biochemistry</i> , 2017, 86, 245-275.	5.0	173
14428	Draft genome sequence of <i>Arthrobacter</i> sp. strain B6 isolated from the high-arsenic sediments in Datong Basin, China. <i>Standards in Genomic Sciences</i> , 2017, 12, 11.	1.5	13
14429	Changes in microRNA abundance may regulate diapause in the flesh fly, <i>Sarcophaga bullata</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2017, 84, 1-14.	1.2	70
14430	Systematic protein-protein interaction mapping for clinically relevant human GPCRs. <i>Molecular Systems Biology</i> , 2017, 13, 918.	3.2	63
14431	Copy number variation in 19 Italian multiplex families with autism spectrum disorder: Importance of synaptic and neurite elongation genes. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 547-556.	1.1	7
14432	Outlier analyses to test for local adaptation to breeding grounds in a migratory arctic seabird. <i>Ecology and Evolution</i> , 2017, 7, 2370-2381.	0.8	30
14433	Genetic diversity of disease resistance genes in foxtail millet (<i>Setaria italica</i> L.). <i>Plant Gene</i> , 2017, 10, 8-16.	1.4	23
14434	Deciphering the Acute Cellular Phosphoproteome Response to Irradiation with X-rays, Protons and Carbon Ions. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 855-872.	2.5	27
14435	Genome-wide identification of heat stress-responsive small RNAs in tall fescue (<i>Festuca arundinacea</i>) by high-throughput sequencing. <i>Journal of Plant Physiology</i> , 2017, 213, 157-165.	1.6	17
14436	Systems-level understanding of ethanol-induced stresses and adaptation in <i>E. coli</i> . <i>Scientific Reports</i> , 2017, 7, 44150.	1.6	43
14437	Complete genome sequence of <i>Pseudomonas stutzeri</i> strain RCH2 isolated from a Hexavalent Chromium [Cr(VI)] contaminated site. <i>Standards in Genomic Sciences</i> , 2017, 12, 23.	1.5	12
14438	Screening of potential gene markers for predicting carotid atheroma plaque formation using bioinformatics approaches. <i>Molecular Medicine Reports</i> , 2017, 15, 2039-2048.	1.1	5
14439	The histone demethylase KDM3A, and its downstream target MCAM, promote Ewing Sarcoma cell migration and metastasis. <i>Oncogene</i> , 2017, 36, 4150-4160.	2.6	56
14440	Complete genome sequencing and antibiotics biosynthesis pathways analysis of <i>Streptomyces lydicus</i> 103. <i>Scientific Reports</i> , 2017, 7, 44786.	1.6	15

#	ARTICLE	IF	CITATIONS
14441	SWIM: a computational tool to unveiling crucial nodes in complex biological networks. <i>Scientific Reports</i> , 2017, 7, 44797.	1.6	50
14442	Does an increased body mass index affect endometrial gene expression patterns in infertile patients? A functional genomics analysis. <i>Fertility and Sterility</i> , 2017, 107, 740-748.e2.	0.5	60
14443	Molecular mechanisms underlying the positive role of treadmill training in locomotor recovery after spinal cord injury. <i>Spinal Cord</i> , 2017, 55, 441-446.	0.9	10
14444	The Genomic Architecture of Interactions Between Natural Genetic Polymorphisms and Environments in Yeast Growth. <i>Genetics</i> , 2017, 205, 925-937.	1.2	19
14445	PGSB/MIPS PlantsDB Database Framework for the Integration and Analysis of Plant Genome Data. <i>Methods in Molecular Biology</i> , 2017, 1533, 33-44.	0.4	8
14446	The Bio-Analytic Resource for Plant Biology. <i>Methods in Molecular Biology</i> , 2017, 1533, 119-148.	0.4	36
14447	An Optimized Chromatographic Strategy for Multiplexing In Parallel Reaction Monitoring Mass Spectrometry: Insights from Quantitation of Activated Kinases. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 265-277.	2.5	42
14448	Discovery of short linear motif-mediated interactions through phage display of intrinsically disordered regions of the human proteome. <i>FEBS Journal</i> , 2017, 284, 485-498.	2.2	81
14449	Stable Binding of the Conserved Transcription Factor Grainy Head to its Target Genes Throughout <i>Drosophila melanogaster</i> Development. <i>Genetics</i> , 2017, 205, 605-620.	1.2	50
14450	Evolution of plant conducting cells: perspectives from key regulators of vascular cell differentiation. <i>Journal of Experimental Botany</i> , 2017, 68, 17-26.	2.4	48
14451	Genome-wide assessment of sequence-intrinsic enhancer responsiveness at single-base-pair resolution. <i>Nature Biotechnology</i> , 2017, 35, 136-144.	9.4	78
14452	Long-term propagation of tree shrew spermatogonial stem cells in culture and successful generation of transgenic offspring. <i>Cell Research</i> , 2017, 27, 241-252.	5.7	63
14453	Screening of potential biomarkers for prenatal diagnosis of trisomy 21. <i>Journal of Obstetrics and Gynaecology</i> , 2017, 37, 435-440.	0.4	3
14454	Comprehensive analysis of differently expressed genes and proteins in albino and green plantlets from a wheat anther culture. <i>Biologia Plantarum</i> , 2017, 61, 255-265.	1.9	11
14455	Developing the Quantitative Histopathology Image Ontology (QHIO): A case study using the hot spot detection problem. <i>Journal of Biomedical Informatics</i> , 2017, 66, 129-135.	2.5	16
14456	Predictive Outcomes for HER2-enriched Cancer Using Growth and Metastasis Signatures Driven By SPARC. <i>Molecular Cancer Research</i> , 2017, 15, 304-316.	1.5	21
14457	Gene expression profile changes in rat dorsal horn after sciatic nerve injury. <i>Neurological Research</i> , 2017, 39, 176-182.	0.6	14
14458	Transcriptome Analysis of Sugarcane Response to the Infection by Sugarcane Steak Mosaic Virus (SCSMV). <i>Tropical Plant Biology</i> , 2017, 10, 45-55.	1.0	21

#	ARTICLE	IF	CITATIONS
14459	Gene-based analyses reveal novel genetic overlap and allelic heterogeneity across five major psychiatric disorders. <i>Human Genetics</i> , 2017, 136, 263-274.	1.8	55
14460	A Genome-wide Association Study Identifies Risk Alleles in Plasminogen and P4HA2 Associated with Giant Cell Arteritis. <i>American Journal of Human Genetics</i> , 2017, 100, 64-74.	2.6	78
14461	Learning the Structural Vocabulary of a Network. <i>Neural Computation</i> , 2017, 29, 287-312.	1.3	2
14462	A Multi-step Transcriptional and Chromatin State Cascade Underlies Motor Neuron Programming from Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2017, 20, 205-217.e8.	5.2	86
14463	Evaluating Functional Annotations of Enzymes Using the Gene Ontology. <i>Methods in Molecular Biology</i> , 2017, 1446, 111-132.	0.4	14
14464	Functional Analysis of miRNAs Using the DIANA Tools Online Suite. <i>Methods in Molecular Biology</i> , 2017, 1517, 25-50.	0.4	66
14465	Stem Cell Transcriptome Responses and Corresponding Biomarkers That Indicate the Transition from Adaptive Responses to Cytotoxicity. <i>Chemical Research in Toxicology</i> , 2017, 30, 905-922.	1.7	37
14466	Long noncoding RNA HIT000218960 promotes papillary thyroid cancer oncogenesis and tumor progression by upregulating the expression of high mobility group AT-hook 2 (HMGA2) gene. <i>Cell Cycle</i> , 2017, 16, 224-231.	1.3	47
14467	Global transcriptional response of solvent-sensitive and solvent-tolerant <i>Pseudomonas putida</i> strains exposed to toluene. <i>Environmental Microbiology</i> , 2017, 19, 645-658.	1.8	36
14468	The evolution of function within the Nudix homology clan. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 775-811.	1.5	53
14469	A Practical Guide to Using Glycomics Databases. , 2017, , .		6
14470	Digital gene expression profiling analysis of DNA repair pathways in colon cancer stem population of HT29 cells. <i>Acta Biochimica Et Biophysica Sinica</i> , 2017, 49, 90-100.	0.9	4
14471	Modellierung und Simulation von Protein-Interaktionen am Beispiel von Wirts-Pathogen-Interaktionen. , 2017, , .		0
14472	Novel boronate material affords efficient enrichment of glycopeptides by synergized hydrophilic and affinity interactions. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 519-528.	1.9	18
14473	Drug-drug interaction discovery and demystification using Semantic Web technologies. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2017, 24, 556-564.	2.2	28
14474	Environmental factor and inflammation-driven alteration of the total peripheral T-cell compartment in granulomatosis with polyangiitis. <i>Journal of Autoimmunity</i> , 2017, 78, 79-91.	3.0	34
14475	Identification and characterization of microRNAs expressed in antennae of <i>Holotrichia parallela</i> Motschulsky and their possible roles in olfactory regulation. <i>Archives of Insect Biochemistry and Physiology</i> , 2017, 94, e21369.	0.6	8
14476	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomic Data. <i>Methods in Molecular Biology</i> , 2017, 1533, 1-31.	0.4	189

#	ARTICLE	IF	CITATIONS
14477	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
14478	Integrated analysis reveals candidate mRNA and their potential roles in uterine leiomyomas. <i>Journal of Obstetrics and Gynaecology Research</i> , 2017, 43, 149-156.	0.6	8
14479	Proteomic investigation of human cystic echinococcosis in the liver. <i>Molecular and Biochemical Parasitology</i> , 2017, 211, 9-14.	0.5	17
14480	Impaired liver regeneration in aged mice can be rescued by silencing Hippo core kinases MST1 and MST2. <i>EMBO Molecular Medicine</i> , 2017, 9, 46-60.	3.3	98
14481	Pathway-based genome-wide association analysis of milk coagulation properties, curd firmness, cheese yield, and curd nutrient recovery in dairy cattle. <i>Journal of Dairy Science</i> , 2017, 100, 1223-1231.	1.4	32
14482	Co-expression changes of lncRNAs and mRNAs in the cervical sympathetic ganglia in diabetic cardiac autonomic neuropathic rats. <i>Journal of Neuroscience Research</i> , 2017, 95, 1690-1699.	1.3	13
14483	Multistage feature selection approach for high-dimensional cancer data. <i>Soft Computing</i> , 2017, 21, 6895-6906.	2.1	26
14484	FLAGdb++: A Bioinformatic Environment to Study and Compare Plant Genomes. <i>Methods in Molecular Biology</i> , 2017, 1533, 79-101.	0.4	0
14485	Comparative interactomics for virus-human protein-protein interactions: DNA viruses versus RNA viruses. <i>FEBS Open Bio</i> , 2017, 7, 96-107.	1.0	42
14486	Distinct Molecular Signature of Murine Fetal Liver and Adult Hematopoietic Stem Cells Identify Novel Regulators of Hematopoietic Stem Cell Function. <i>Stem Cells and Development</i> , 2017, 26, 573-584.	1.1	15
14488	Overexpression of protein kinase STK25 in mice exacerbates ectopic lipid accumulation, mitochondrial dysfunction and insulin resistance in skeletal muscle. <i>Diabetologia</i> , 2017, 60, 553-567.	2.9	37
14489	A systematic analysis of term reuse and term overlap across biomedical ontologies. <i>Semantic Web</i> , 2017, 8, 853-871.	1.1	49
14490	Comparative analysis of tree peony petal development by transcriptome sequencing. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	10
14491	Ontology-based systematical representation and drug class effect analysis of package insert-reported adverse events associated with cardiovascular drugs used in China. <i>Scientific Reports</i> , 2017, 7, 13819.	1.6	15
14492	Review of computational methods for virus-host protein interaction prediction: a case study on novel Ebola-human interactions. <i>Briefings in Functional Genomics</i> , 2018, 17, 381-391.	1.3	19
14493	Modelling pyruvate dehydrogenase under hypoxia and its role in cancer metabolism. <i>Royal Society Open Science</i> , 2017, 4, 170360.	1.1	19
14494	A novel method to measure the semantic similarity of HPO terms. <i>International Journal of Data Mining and Bioinformatics</i> , 2017, 17, 173.	0.1	51
14495	RNA-sequencing predicts three novel genes in response to drought in electron beam irradiation treated tobacco. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	0

#	ARTICLE	IF	CITATIONS
14496	Enzyme function and its evolution. <i>Current Opinion in Structural Biology</i> , 2017, 47, 151-156.	2.6	13
14497	The maternal-zygotic transition and zygotic activation of the <i>Mnemiopsis leidyi</i> genome occurs within the first three cleavage cycles. <i>Molecular Reproduction and Development</i> , 2017, 84, 1218-1229.	1.0	8
14498	PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. <i>Nature Communications</i> , 2017, 8, 1167.	5.8	40
14499	Depletion of Myofibril-Associated Proteins Using Selective Protein Extraction as a Tool in Cardiac Proteomics. <i>Methods in Molecular Biology</i> , 2017, 1788, 1-9.	0.4	0
14500	Identification of key genes for diabetic kidney disease using biological informatics methods. <i>Molecular Medicine Reports</i> , 2017, 16, 7931-7938.	1.1	7
14501	MARK3-mediated phosphorylation of ARHGEF2 couples microtubules to the actin cytoskeleton to establish cell polarity. <i>Science Signaling</i> , 2017, 10, .	1.6	52
14504	A knowledge-based system for generating interaction networks from ecological data. <i>Data and Knowledge Engineering</i> , 2017, 112, 55-78.	2.1	3
14505	Adenovirus E1A TRRAP-targeting domain-mediated enhancement of MYC association with the NuA4 complex activates a panel of MYC target genes enriched for gene expression and ribosome biogenesis. <i>Virology</i> , 2017, 512, 172-179.	1.1	2
14506	Transcriptome analysis uncovers <i>Arabidopsis</i> F-BOX STRESS INDUCED 1 as a regulator of jasmonic acid and abscisic acid stress gene expression. <i>BMC Genomics</i> , 2017, 18, 533.	1.2	30
14507	Caspase-1 cleaves PPAR β for potentiating the pro-tumor action of TAMs. <i>Nature Communications</i> , 2017, 8, 766.	5.8	129
14508	Genetic diversity and structure of wild and cultivated <i>Amorphophallus paeoniifolius</i> populations in southwestern China as revealed by RAD-seq. <i>Scientific Reports</i> , 2017, 7, 14183.	1.6	22
14509	Physiological and transcriptome response to cadmium in cosmos (<i>Cosmos bipinnatus</i> Cav.) seedlings. <i>Scientific Reports</i> , 2017, 7, 14691.	1.6	25
14510	Network analysis reveals a causal role of mitochondrial gene activity in atherosclerotic lesion formation. <i>Atherosclerosis</i> , 2017, 267, 39-48.	0.4	26
14511	Predicting bull fertility using genomic data and biological information. <i>Journal of Dairy Science</i> , 2017, 100, 9656-9666.	1.4	55
14512	Circular RNAs of the nucleophosmin (NPM1) gene in acute myeloid leukemia. <i>Haematologica</i> , 2017, 102, 2039-2047.	1.7	72
14513	Identifying Gene Interaction Networks. <i>Methods in Molecular Biology</i> , 2017, 1666, 539-556.	0.4	11
14515	RNA Function Prediction. <i>Methods in Molecular Biology</i> , 2017, 1654, 17-28.	0.4	17
14516	The Compressed Vocabulary of the Proteins of Archaea. , 2017, , 147-174.		7

#	ARTICLE	IF	CITATIONS
14517	An Evaluation of Gene Set Analysis for Biomarker Discovery with Applications to Myeloma Research. , 2017, , 413-434.		2
14518	Screening and identification of key biomarkers in hepatocellular carcinoma: Evidence from bioinformatic analysis. <i>Oncology Reports</i> , 2017, 38, 2607-2618.	1.2	187
14519	Protein Function Prediction. <i>Methods in Molecular Biology</i> , 2017, 1654, 55-75.	0.4	28
14520	Isolation and complete genome sequence of <i>Halorientalis hydrocarbonoclasticus</i> sp. nov., a hydrocarbon-degrading haloarchaeon. <i>Extremophiles</i> , 2017, 21, 1081-1090.	0.9	23
14521	Ant-infecting <i>Ophiocordyceps</i> genomes reveal a high diversity of potential behavioral manipulation genes and a possible major role for enterotoxins. <i>Scientific Reports</i> , 2017, 7, 12508.	1.6	52
14523	Clustergrammer, a web-based heatmap visualization and analysis tool for high-dimensional biological data. <i>Scientific Data</i> , 2017, 4, 170151.	2.4	176
14524	Computational Approaches to Identify Genetic Interactions for Cancer Therapeutics. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.0	5
14525	Genomic adaptation to polyphagy and insecticides in a major East Asian noctuid pest. <i>Nature Ecology and Evolution</i> , 2017, 1, 1747-1756.	3.4	269
14526	SoyBase: A Comprehensive Database for Soybean Genetic and Genomic Data. <i>Compendium of Plant Genomes</i> , 2017, , 193-211.	0.3	2
14528	Constrained vertebrate evolution by pleiotropic genes. <i>Nature Ecology and Evolution</i> , 2017, 1, 1722-1730.	3.4	72
14529	Monitoring storage induced changes in the platelet proteome employing label free quantitative mass spectrometry. <i>Scientific Reports</i> , 2017, 7, 11045.	1.6	27
14530	Gene ontology-based analysis of time series gene expression data using support vector machines. , 2017, , 22-52.		0
14531	Knowledge Rich Natural Language Queries over Structured Biological Databases. , 2017, , .		3
14532	Gene expression analysis: Regulation of key genes associated with mycophenolate mofetil treatment of symptomatic carotid artery stenosis. <i>Molecular Medicine Reports</i> , 2017, 16, 7450-7458.	1.1	1
14533	Exploring the key genes and pathways of osteosarcoma with pulmonary metastasis using a gene expression microarray. <i>Molecular Medicine Reports</i> , 2017, 16, 7423-7431.	1.1	28
14534	Inflammasome-driven catecholamine catabolism in macrophages blunts lipolysis during ageing. <i>Nature</i> , 2017, 550, 119-123.	13.7	329
14535	A computational method using differential gene expression to predict altered metabolism of multicellular organisms. <i>Molecular BioSystems</i> , 2017, 13, 2418-2427.	2.9	4
14536	Exploring differentially expressed genes associated with fertility instability of S-type cytoplasmic male-sterility in maize by RNA-seq. <i>Journal of Integrative Agriculture</i> , 2017, 16, 1689-1699.	1.7	6

#	ARTICLE	IF	CITATIONS
14537	HashGO: hashing gene ontology for protein function prediction. <i>Computational Biology and Chemistry</i> , 2017, 71, 264-273.	1.1	15
14538	Differential carbonylation of proteins in end-stage human fatty and nonfatty NASH. <i>Free Radical Biology and Medicine</i> , 2017, 113, 280-290.	1.3	7
14539	Gene co-opening network deciphers gene functional relationships. <i>Molecular BioSystems</i> , 2017, 13, 2428-2439.	2.9	11
14540	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome Research</i> , 2017, 27, 1843-1858.	2.4	139
14541	Long non-coding RNA expression profiles in different severity EV71-infected hand foot and mouth disease patients. <i>Biochemical and Biophysical Research Communications</i> , 2017, 493, 1594-1600.	1.0	11
14542	Annotation of nerve cord transcriptome in earthworm <i>Eisenia fetida</i> . <i>Genomics Data</i> , 2017, 14, 91-105.	1.3	17
14543	Transcriptomic Analysis of Octanoic Acid Response in <i>Drosophila sechellia</i> Using RNA-Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3867-3873.	0.8	21
14544	RNA-Seq Analysis of Differentiated Keratinocytes Reveals a Massive Response to Late Events during Human Papillomavirus 16 Infection, Including Loss of Epithelial Barrier Function. <i>Journal of Virology</i> , 2017, 91, .	1.5	47
14545	Regulation of m6A Transcripts by the 3'5' RNA Helicase YTHDC2 Is Essential for a Successful Meiotic Program in the Mammalian Germline. <i>Molecular Cell</i> , 2017, 68, 374-387.e12.	4.5	370
14546	Trichostatin A and 5-Aza-2-Deoxycytidine influence the expression of cold-induced genes in <i>Arabidopsis</i> . <i>Plant Signaling and Behavior</i> , 2017, 12, e1389828.	1.2	12
14547	Transcriptomic Characterization of the Human Cell Cycle in Individual Unsynchronized Cells. <i>Journal of Molecular Biology</i> , 2017, 429, 3909-3924.	2.0	11
14548	Enriching Nanomaterials Omics Data: An Integration Technique to Generate Biological Descriptors. <i>Small Methods</i> , 2017, 1, 1700139.	4.6	10
14549	Early Transcriptional Divergence Marks Virus-Specific Primary Human CD8+ T Cells in Chronic versus Acute Infection. <i>Immunity</i> , 2017, 47, 648-663.e8.	6.6	50
14550	Unwavering Pathobiology of Volumetric Muscle Loss Injury. <i>Scientific Reports</i> , 2017, 7, 13179.	1.6	95
14551	MicroRNA Signature of Cigarette Smoking and Evidence for a Putative Causal Role of MicroRNAs in Smoking-Related Inflammation and Target Organ Damage. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	45
14552	MicroRNA expression changes following synthesis of three full-sib <i>Populus</i> triploid populations with different heterozygosities. <i>Plant Molecular Biology</i> , 2017, 95, 215-225.	2.0	7
14553	Widespread Post-transcriptional Attenuation of Genomic Copy-Number Variation in Cancer. <i>Cell Systems</i> , 2017, 5, 386-398.e4.	2.9	102
14554	A genome-scale analysis of mRNA targeting to plant mitochondria: upstream AUGs in 5' untranslated regions reduce mitochondrial association. <i>Plant Journal</i> , 2017, 92, 1132-1142.	2.8	26

#	ARTICLE	IF	CITATIONS
14555	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. <i>Cell Systems</i> , 2017, 5, 485-497.e3.	2.9	19
14556	Identification of SNP markers associated with milk and fat yields in multibreed dairy cattle using two genetic group structures. <i>Livestock Science</i> , 2017, 206, 95-104.	0.6	2
14557	Identification of prostate cancer hub genes and therapeutic agents using bioinformatics approach. <i>Cancer Biomarkers</i> , 2017, 20, 553-561.	0.8	20
14558	Hemodynamic Forces Sculpt Developing Heart Valves through a KLF2-WNT9B Paracrine Signaling Axis. <i>Developmental Cell</i> , 2017, 43, 274-289.e5.	3.1	114
14559	iPhemap: an atlas of phenotype to genotype relationships of human iPSC models of neurological diseases. <i>EMBO Molecular Medicine</i> , 2017, 9, 1742-1762.	3.3	24
14560	Analysis of protein targets in pathogen-host interaction in infectious diseases: a case study on <i>Plasmodium falciparum</i> and <i>Homo sapiens</i> interaction network. <i>Briefings in Functional Genomics</i> , 2018, 17, 441-450.	1.3	25
14561	<i>Panax ginseng</i> genome examination for ginsenoside biosynthesis. <i>GigaScience</i> , 2017, 6, 1-15.	3.3	150
14562	Comparative transcriptomic analysis of high and low egg-producing duck ovaries. <i>Poultry Science</i> , 2017, 96, 4378-4388.	1.5	48
14563	Alterations in the long non-coding RNA transcriptome in mesangial cells treated with aldosterone in vitro. <i>Molecular Medicine Reports</i> , 2017, 16, 6004-6012.	1.1	2
14564	A Problem-Driven Approach for Building a Bioinformatics GraphDB. <i>Lecture Notes in Computer Science</i> , 2017, , 134-144.	1.0	0
14565	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
14566	Evaluating phenotype-driven approaches for genetic diagnoses from exomes in a clinical setting. <i>Scientific Reports</i> , 2017, 7, 13509.	1.6	26
14567	Comprehensive characterization of differentially expressed genes in thyroid cancer. <i>Future Oncology</i> , 2017, 13, 2159-2169.	1.1	9
14568	Congenic mice demonstrate the presence of QTLs conferring obesity and hypercholesterolemia on chromosome 1 in the TALLYHO mouse. <i>Mammalian Genome</i> , 2017, 28, 487-497.	1.0	9
14569	Transcriptome profiling of red swamp crayfish (<i>Procambarus clarkii</i>) hepatopancreas in response to lipopolysaccharide (LPS) infection. <i>Fish and Shellfish Immunology</i> , 2017, 71, 423-433.	1.6	33
14570	DNA N6-methyladenine is dynamically regulated in the mouse brain following environmental stress. <i>Nature Communications</i> , 2017, 8, 1122.	5.8	182
14571	Role of the luxS gene in bacteriocin biosynthesis by <i>Lactobacillus plantarum</i> KLDS1.0391: A proteomic analysis. <i>Scientific Reports</i> , 2017, 7, 13871.	1.6	24
14572	<i>Leishmania tropica</i> infected human lesions: Whole genome transcription profiling. <i>Acta Tropica</i> , 2017, 176, 236-241.	0.9	26

#	ARTICLE	IF	CITATIONS
14573	Single-Nucleotide Polymorphisms in Vitamin D-Related Genes May Modify Vitamin D-Breast Cancer Associations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1761-1771.	1.1	15
14574	Rapid functional and evolutionary changes follow gene duplication in yeast. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171393.	1.2	41
14575	Mouse Genome Informatics (MGI) Resource: Genetic, Genomic, and Biological Knowledgebase for the Laboratory Mouse. <i>ILAR Journal</i> , 2017, 58, 17-41.	1.8	77
14576	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
14577	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017, 3, e1700299.	4.7	142
14578	Membrane Proteomics of Impaired Energetics and Cytoskeletal Disorganization in Elderly Diet-Induced Diabetic Mice. <i>Journal of Proteome Research</i> , 2017, 16, 3504-3513.	1.8	6
14579	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
14580	A genome-by-environment interaction classifier for precision medicine: personal transcriptome response to rhinovirus identifies children prone to asthma exacerbations. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2017, 24, 1116-1126.	2.2	23
14581	HTLV-1-infected thymic epithelial cells convey the virus to CD4 + T lymphocytes. <i>Immunobiology</i> , 2017, 222, 1053-1063.	0.8	6
14582	High Expression of AHSP, EPB42, GYPC and HEMGN Predicts Favorable Prognosis in FLT3-ITD-Negative Acute Myeloid Leukemia. <i>Cellular Physiology and Biochemistry</i> , 2017, 42, 1973-1984.	1.1	27
14583	Genome-wide association and pathway-based analysis using latent variables related to milk protein composition and cheesemaking traits in dairy cattle. <i>Journal of Dairy Science</i> , 2017, 100, 9085-9102.	1.4	18
14584	The high-quality genome of <i>Brassica napus</i> cultivar 'ZS11'™ reveals the introgression history in semi-winter morphotype. <i>Plant Journal</i> , 2017, 92, 452-468.	2.8	233
14585	The genomic basis of cichlid fish adaptation within the deepwater twilight zone of Lake Malawi. <i>Evolution Letters</i> , 2017, 1, 184-198.	1.6	21
14586	Genome-Wide Analysis and Expression Profiles of the MYB Genes in <i>Brachypodium distachyon</i> . <i>Plant and Cell Physiology</i> , 2017, 58, 1777-1788.	1.5	41
14587	Molecular mechanisms of breast cancer metastasis by gene expression profile analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 4671-4677.	1.1	31
14588	Identification of prognostic markers of high grade prostate cancer through an integrated bioinformatics approach. <i>Journal of Cancer Research and Clinical Oncology</i> , 2017, 143, 2571-2579.	1.2	34
14589	Multiplexed quantification of proteins and transcripts in single cells. <i>Nature Biotechnology</i> , 2017, 35, 936-939.	9.4	684
14590	RefEx, a reference gene expression dataset as a web tool for the functional analysis of genes. <i>Scientific Data</i> , 2017, 4, 170105.	2.4	55

#	ARTICLE	IF	CITATIONS
14591	A survey on Ebola genome and current trends in computational research on the Ebola virus. Briefings in Functional Genomics, 2018, 17, 374-380.	1.3	4
14592	New Genes and Functional Innovation in Mammals. Genome Biology and Evolution, 2017, 9, 1886-1900.	1.1	50
14593	The draft genome assembly of <i>Rhododendron delavayi</i> Franch. var. <i>delavayi</i> . GigaScience, 2017, 6, 1-11.	3.3	64
14594	Identification of pivotal genes and pathways for spinal cord injury via bioinformatics analysis. Molecular Medicine Reports, 2017, 16, 3929-3937.	1.1	6
14595	The effect of Bu Zhong Yi Qi decoction on simulated weightlessness-induced muscle atrophy and its mechanisms. Molecular Medicine Reports, 2017, 16, 5165-5174.	1.1	14
14596	Exploring regulation in tissues with eQTL networks. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7841-E7850.	3.3	82
14597	Identifying consistent disease subnetworks using DNet. Methods, 2017, 131, 104-110.	1.9	16
14598	Features of the Chaperone Cellular Network Revealed through Systematic Interaction Mapping. Cell Reports, 2017, 20, 2735-2748.	2.9	47
14599	Logic programming reveals alteration of key transcription factors in multiple myeloma. Scientific Reports, 2017, 7, 9257.	1.6	20
14600	Deconvolution of DNA methylation identifies differentially methylated gene regions on 1p36 across breast cancer subtypes. Scientific Reports, 2017, 7, 11594.	1.6	20
14601	Gene expression profiling of calcifications in breast cancer. Scientific Reports, 2017, 7, 11427.	1.6	21
14602	Transcriptome characterization of HPG axis from Chinese sea perch <i>Lateolabrax maculatus</i> . Journal of Fish Biology, 2017, 91, 1407-1418.	0.7	7
14603	Aberrant expression of epithelial leucine-rich repeat containing G protein-coupled receptor 5α-positive cells in the eutopic endometrium in endometriosis and implications in deep-infiltrating endometriosis. Fertility and Sterility, 2017, 108, 858-867.e2.	0.5	9
14604	Identification of circular RNA in the <i>Bombyx mori</i> silk gland. Insect Biochemistry and Molecular Biology, 2017, 89, 97-106.	1.2	39
14605	Evolutionary shifts in gene expression decoupled from gene duplication across functionally distinct spider silk glands. Scientific Reports, 2017, 7, 8393.	1.6	26
14606	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. Nature Biotechnology, 2017, 35, 969-976.	9.4	356
14607	N ¹ - and O-Acetylation in <i>Mycobacterium tuberculosis</i> Lineage 7 and Lineage 4 Strains: Proteins Involved in Bioenergetics, Virulence, and Antimicrobial Resistance Are Acetylated. Journal of Proteome Research, 2017, 16, 4045-4059.	1.8	37
14608	Protein complexes, big data, machine learning and integrative proteomics: lessons learned over a decade of systematic analysis of protein interaction networks. Expert Review of Proteomics, 2017, 14, 845-855.	1.3	19

#	ARTICLE	IF	CITATIONS
14609	Draft Genome Sequence of <i>Methylocaldum</i> sp. Strain 14B, an Obligate Hydrogen Sulfide-Tolerant Methanotrophic Strain That Can Convert Biogas to Methanol. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
14610	An individualized gene expression signature for prediction of lung adenocarcinoma metastases. <i>Molecular Oncology</i> , 2017, 11, 1630-1645.	2.1	28
14611	Comparative study of the leaf transcriptomes and ionoms of <i>Juglans regia</i> and its wild relative species <i>Juglans cathayensis</i> . <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	6
14612	Expression in rice of an autoactive variant of <i>Medicago truncatula</i> DMI3, the Ca ²⁺ /calmodulin-dependent protein kinase from the common symbiotic pathway modifies root transcriptome and improves mycorrhizal colonization. <i>Plant Biotechnology Reports</i> , 2017, 11, 271-287.	0.9	13
14613	Differential gene expression profiling analysis in <i>Pleurotus ostreatus</i> during interspecific antagonistic interactions with <i>Dichomitus squalens</i> and <i>Trametes versicolor</i> . <i>Fungal Biology</i> , 2017, 121, 1025-1036.	1.1	11
14614	Identification of pathogenic genes related to rheumatoid arthritis through integrated analysis of DNA methylation and gene expression profiling. <i>Gene</i> , 2017, 634, 62-67.	1.0	3
14615	Profiling of Single-Cell Transcriptomes. <i>Current Protocols in Mouse Biology</i> , 2017, 7, 145-175.	1.2	16
14616	Intracellular spectral recompositioning of light enhances algal photosynthetic efficiency. <i>Science Advances</i> , 2017, 3, e1603096.	4.7	42
14617	Transcriptome Analysis of Induced Pluripotent Stem Cell (iPSC)-derived Pancreatic β -like Cell Differentiation. <i>Cell Transplantation</i> , 2017, 26, 1380-1391.	1.2	11
14618	Surgical data science for next-generation interventions. <i>Nature Biomedical Engineering</i> , 2017, 1, 691-696.	11.6	283
14619	Combined transcriptomic and proteomic analysis constructs a new model for light-induced anthocyanin biosynthesis in eggplant (<i>Solanum melongena</i> L.). <i>Plant, Cell and Environment</i> , 2017, 40, 3069-3087.	2.8	72
14620	Screening of candidate key genes associated with human osteosarcoma using bioinformatics analysis. <i>Oncology Letters</i> , 2017, 14, 2887-2893.	0.8	12
14621	Integrated analysis of microRNA and mRNA expression profiles during the sex-differentiation sensitive period in oriental river prawn, <i>Macrobrachium nipponense</i> . <i>Scientific Reports</i> , 2017, 7, 12011.	1.6	22
14622	CODA: Integrating multi-level context-oriented directed associations for analysis of drug effects. <i>Scientific Reports</i> , 2017, 7, 7519.	1.6	16
14623	Joint inflammation related citrullination of functional arginines in extracellular proteins. <i>Scientific Reports</i> , 2017, 7, 8246.	1.6	18
14624	Discovering Condition-Specific Gene Co-Expression Patterns Using Gaussian Mixture Models: A Cancer Case Study. <i>Scientific Reports</i> , 2017, 7, 8617.	1.6	44
14625	Effects of short indels on protein structure and function in human genomes. <i>Scientific Reports</i> , 2017, 7, 9313.	1.6	58
14626	FunctionAnnotator, a versatile and efficient web tool for non-model organism annotation. <i>Scientific Reports</i> , 2017, 7, 10430.	1.6	29

#	ARTICLE	IF	CITATIONS
14627	Genomic and transcriptomic analyses reveal differential regulation of diverse terpenoid and polyketides secondary metabolites in <i>Herichium erinaceus</i> . <i>Scientific Reports</i> , 2017, 7, 10151.	1.6	33
14628	Small molecule-based lineage switch of human adipose-derived stem cells into neural stem cells and functional GABAergic neurons. <i>Scientific Reports</i> , 2017, 7, 10166.	1.6	31
14629	The developmental transcriptome landscape of receptive endometrium during embryo implantation in dairy goats. <i>Gene</i> , 2017, 633, 82-95.	1.0	16
14630	Bioinformatics analyses of pathways and gene predictions in IL-1 β and IL-1 γ knockout mice with spinal cord injury. <i>Acta Histochemica</i> , 2017, 119, 663-670.	0.9	10
14631	Effect of fluoride treatment on gene expression in tea plant (<i>Camellia sinensis</i>). <i>Scientific Reports</i> , 2017, 7, 9847.	1.6	31
14632	Whole-Genome Sequences of <i>Brucella melitensis</i> Strain QY1, Isolated from Sheep in Gansu, China. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
14633	Gene2DisCo: Gene to disease using disease commonalities. <i>Artificial Intelligence in Medicine</i> , 2017, 82, 34-46.	3.8	6
14634	Gene Ontology-Based Analysis of Zebrafish Omics Data Using the Web Tool Comparative Gene Ontology. <i>Zebrafish</i> , 2017, 14, 492-494.	0.5	26
14635	Discovering Inconsistencies in PubMed Abstracts through Ontology-Based Information Extraction. , 2017, , .		11
14636	An overview of posttraumatic stress disorder genetic studies by analyzing and integrating genetic data into genetic database PTSDgene. <i>Neuroscience and Biobehavioral Reviews</i> , 2017, 83, 647-656.	2.9	17
14637	Lessons from the Hamster: <i>Cricetulus griseus</i> Tissue and CHO Cell Line Proteome Comparison. <i>Journal of Proteome Research</i> , 2017, 16, 3672-3687.	1.8	11
14638	Efficient Mitochondrial Glutamine Targeting Prevails Over Glioblastoma Metabolic Plasticity. <i>Clinical Cancer Research</i> , 2017, 23, 6292-6304.	3.2	69
14639	Mutation intolerant genes and targets of FMRP are enriched for nonsynonymous alleles in schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 724-731.	1.1	19
14640	Transcriptome analysis of yellow catfish (<i>Pelteobagrus fulvidraco</i>) liver challenged with polyriboinosinic polyribocytidylic acid (poly I:C). <i>Fish and Shellfish Immunology</i> , 2017, 68, 395-403.	1.6	25
14641	The viable but nonculturable state induction and genomic analyses of <i>Lactobacillus casei</i> BM ϵ LC14617, a beer ϵ spoilage bacterium. <i>MicrobiologyOpen</i> , 2017, 6, e00506.	1.2	37
14642	Using the hierarchy of biological ontologies to identify mechanisms in flat networks. <i>Biology and Philosophy</i> , 2017, 32, 627-649.	0.7	9
14643	Activating transcription factor 3 promotes loss of the acinar cell phenotype in response to cerulein-induced pancreatitis in mice. <i>Molecular Biology of the Cell</i> , 2017, 28, 2347-2359.	0.9	21
14644	MYC and hsa-miRNA-423-5p as biomarkers in nasopharyngeal carcinoma revealed by miRNA-mRNA-pathway network integrated analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 1039-1046.	1.1	6

#	ARTICLE	IF	CITATIONS
14645	Gene expression profile data for mouse facial development. <i>Data in Brief</i> , 2017, 13, 242-247.	0.5	5
14647	Seed desiccation mechanisms co ϵ opted for vegetative desiccation in the resurrection grass <i>Oropetium thomaeum</i> . <i>Plant, Cell and Environment</i> , 2017, 40, 2292-2306.	2.8	49
14648	Disease genes prioritizing mechanisms: a comprehensive and systematic literature review. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2017, 6, 1.	1.2	16
14649	Transcriptome landscape of human primary monocytes at different sequencing depth. <i>Genomics</i> , 2017, 109, 463-470.	1.3	9
14650	Spike and slab biclustering. <i>Pattern Recognition</i> , 2017, 72, 186-195.	5.1	7
14651	\langle sc \rangle RNA sequencing in post ϵ mortem human brains of neuropsychiatric disorders. <i>Psychiatry and Clinical Neurosciences</i> , 2017, 71, 663-672.	1.0	14
14652	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	1.3	123
14653	The evolution of duplicate gene expression in mammalian organs. <i>Genome Research</i> , 2017, 27, 1461-1474.	2.4	85
14654	Effect of electroacupuncture on gene expression in calcium signaling pathway in hippocampal cells in mice with cerebral ischemia reperfusion. <i>Journal of Traditional Chinese Medicine = Chung I Tsa Chih Ying Wen Pan / Sponsored By All-China Association of Traditional Chinese Medicine, Academy of Traditional Chinese Medicine</i> , 2017, 37, 252-260.	0.4	5
14655	Temporal and spatial transcriptomic and micro \langle sc \rangle RNA dynamics of \langle sc \rangle CAM photosynthesis in pineapple. <i>Plant Journal</i> , 2017, 92, 19-30.	2.8	78
14656	Unsupervised Extraction of Stable Expression Signatures from Public Compendia with an Ensemble of Neural Networks. <i>Cell Systems</i> , 2017, 5, 63-71.e6.	2.9	84
14657	Data on the genome-wide identification of CNL R-genes in <i>Setaria italica</i> (L.) P. Beauv.. <i>Data in Brief</i> , 2017, 13, 259-273.	0.5	3
14658	Towards Intelligent Thermal Energy Management of Eco-industrial Park through Ontology-based Approach. <i>Energy Procedia</i> , 2017, 105, 3295-3300.	1.8	2
14659	An empirical analysis of ontology reuse in BioPortal. <i>Journal of Biomedical Informatics</i> , 2017, 71, 165-177.	2.5	29
14660	Encoding of coordination complexes with XML. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 76, 242-259.	1.3	2
14661	Full Characterization of Localization Diversity in the Human Protein Interactome. <i>Journal of Proteome Research</i> , 2017, 16, 3019-3029.	1.8	22
14662	A statistical framework for biomedical literature mining. <i>Statistics in Medicine</i> , 2017, 36, 3461-3474.	0.8	7
14663	De novo transcriptome sequencing and analysis of <i>Euphorbia pekinensis</i> Rupr. and identification of genes involved in diterpenoid biosynthesis. <i>Plant Gene</i> , 2017, 12, 33-42.	1.4	5

#	ARTICLE	IF	CITATIONS
14664	Metabolic modeling to identify engineering targets for <i>Komagataella phaffii</i> : The effect of biomass composition on gene target identification. <i>Biotechnology and Bioengineering</i> , 2017, 114, 2605-2615.	1.7	16
14665	KrÄppel-like factor 4 acts as a potential therapeutic target of Sijunzi decoction for treatment of colorectal cancer. <i>Cancer Gene Therapy</i> , 2017, 24, 361-366.	2.2	20
14666	T-GOWler: Discovering Generalized Process Models Within Texts. <i>Journal of Computational Biology</i> , 2017, 24, 799-808.	0.8	0
14667	Improvement of biomass and lipid yield under stress conditions by using diploid strains of <i>Chlamydomonas reinhardtii</i> . <i>Algal Research</i> , 2017, 26, 180-189.	2.4	41
14668	Rapid evolution of female-biased genes among four species of <i>Anopheles</i> malaria mosquitoes. <i>Genome Research</i> , 2017, 27, 1536-1548.	2.4	60
14669	Quantitative Temporal in Vivo Proteomics Deciphers the Transition of Virus-Driven Myeloid Cells into M2 Macrophages. <i>Journal of Proteome Research</i> , 2017, 16, 3391-3406.	1.8	15
14670	Exploring Approaches for Detecting Protein Functional Similarity within an Orthology-based Framework. <i>Scientific Reports</i> , 2017, 7, 381.	1.6	6
14671	Leveraging multiple genomic data to prioritize disease-causing indels from exome sequencing data. <i>Scientific Reports</i> , 2017, 7, 1804.	1.6	3
14672	Multiple Trait Covariance Association Test Identifies Gene Ontology Categories Associated with Chill Coma Recovery Time in <i>Drosophila melanogaster</i> . <i>Scientific Reports</i> , 2017, 7, 2413.	1.6	25
14673	Auxin regulates functional gene groups in a fold-change-specific manner in <i>Arabidopsis thaliana</i> roots. <i>Scientific Reports</i> , 2017, 7, 2489.	1.6	42
14674	Transcriptomes and expression profiling of deep-sea corals from the Red Sea provide insight into the biology of azooxanthellate corals. <i>Scientific Reports</i> , 2017, 7, 6442.	1.6	21
14675	iTRAQ-based quantitative proteomic analysis reveals alterations in the metabolism of <i>Actinidia arguta</i> . <i>Scientific Reports</i> , 2017, 7, 5670.	1.6	11
14676	Active nuclear transcriptome analysis reveals inflammasome-dependent mechanism for early neutrophil response to <i>Mycobacterium marinum</i> . <i>Scientific Reports</i> , 2017, 7, 6505.	1.6	26
14677	Transcriptome profiling of monocytes from XLA patients revealed the innate immune function dysregulation due to the BTK gene expression deficiency. <i>Scientific Reports</i> , 2017, 7, 6836.	1.6	19
14678	PhosphoPredict: A bioinformatics tool for prediction of human kinase-specific phosphorylation substrates and sites by integrating heterogeneous feature selection. <i>Scientific Reports</i> , 2017, 7, 6862.	1.6	72
14679	In silico analyses of conservational, functional and phylogenetic distribution of the LuxI and LuxR homologs in Gram-positive bacteria. <i>Scientific Reports</i> , 2017, 7, 6969.	1.6	32
14680	Enriching Traditional Protein-protein Interaction Networks with Alternative Conformations of Proteins. <i>Scientific Reports</i> , 2017, 7, 7180.	1.6	15
14681	Gene microarray analysis of expression profiles in liver ischemia and reperfusion. <i>Molecular Medicine Reports</i> , 2017, 16, 3299-3307.	1.1	6

#	ARTICLE	IF	CITATIONS
14682	Quality assurance of chemical ingredient classification for the National Drug File “ Reference Terminology. <i>Journal of Biomedical Informatics</i> , 2017, 73, 30-42.	2.5	6
14683	Protein microarray analysis identifies key cytokines associated with malignant middle cerebral artery infarction. <i>Brain and Behavior</i> , 2017, 7, e00746.	1.0	12
14684	Locally adapted populations of a copepod can evolve different gene expression patterns under the same environmental pressures. <i>Ecology and Evolution</i> , 2017, 7, 4312-4325.	0.8	19
14685	Comparative transcriptome analysis of tube feet of different colors in the sea urchin <i>Strongylocentrotus intermedius</i> . <i>Genes and Genomics</i> , 2017, 39, 1215-1225.	0.5	13
14686	Predicting multicellular function through multi-layer tissue networks. <i>Bioinformatics</i> , 2017, 33, i190-i198.	1.8	304
14687	Interval-Valued Rank in Finite Ordered Sets. <i>Order</i> , 2017, 34, 491-512.	0.3	0
14688	Differential immune responses of <i>Monochamus alternatus</i> against symbiotic and entomopathogenic fungi. <i>Science China Life Sciences</i> , 2017, 60, 902-910.	2.3	12
14689	Commensal microbiota maintains alveolar macrophages with a low level of CCL24 production to generate anti-metastatic tumor activity. <i>Scientific Reports</i> , 2017, 7, 7471.	1.6	24
14690	BELMiner: adapting a rule-based relation extraction system to extract biological expression language statements from bio-medical literature evidence sentences. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	38
14691	FirebrowserR: an R client to the Broad Institute’s Firehose Pipeline. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, baw160.	1.4	144
14692	Workflow and web application for annotating NCBI BioProject transcriptome data. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	6
14693	Better living through ontologies at the Immune Epitope Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	8
14694	CHOMine: an integrated data warehouse for CHO systems biology and modeling. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	2
14695	In silico characterization of tandem repeats in <i>Trichophyton rubrum</i> and related dermatophytes provides new insights into their role in pathogenesis. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	4
14696	Triage by ranking to support the curation of protein interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	10
14697	Role of 108 schizophrenia-associated loci in modulating psychopathological dimensions in schizophrenia and bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 757-764.	1.1	38
14698	Implicating candidate genes at GWAS signals by leveraging topologically associating domains. <i>European Journal of Human Genetics</i> , 2017, 25, 1286-1289.	1.4	18
14699	The draft genome sequence of a desert tree <i>Populus pruinosa</i> . <i>GigaScience</i> , 2017, 6, 1-7.	3.3	61

#	ARTICLE	IF	CITATIONS
14700	From <i>Saccharomyces cerevisiae</i> to human: The important gene co-expression modules. <i>Biomedical Reports</i> , 2017, 7, 153-158.	0.9	29
14701	Identification of potential key genes associated with glioblastoma based on the gene expression profile. <i>Oncology Letters</i> , 2017, 14, 2045-2052.	0.8	12
14702	Strategies and tools to improve crop productivity by targeting photosynthesis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160377.	1.8	19
14703	Functional Annotation of Human Protein Coding Isoforms via Non-convex Multi-Instance Learning. , 2017, , .		10
14704	Identification of key genes and pathways associated with obesity in children. <i>Experimental and Therapeutic Medicine</i> , 2017, 14, 1065-1073.	0.8	38
14705	Bioinformatics Resources for Interpreting Proteomics Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2017, 1647, 267-295.	0.4	1
14706	Neural Precursor-Derived Pleiotrophin Mediates Subventricular Zone Invasion by Glioma. <i>Cell</i> , 2017, 170, 845-859.e19.	13.5	159
14707	InÂvitro expression of Sec-dependent pathway and type 4B secretion system in <i>Piscirickettsia salmonis</i> . <i>Microbial Pathogenesis</i> , 2017, 110, 586-593.	1.3	21
14708	Machine Learningâ€‘Based Gene Prioritization Identifies Novel Candidate Risk Genes for Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2017, 23, 1516-1523.	0.9	49
14709	The differentially expressed genes identification in dwarf mutant of <i>Gossypium hirsutum</i> by RNA-Seq approach. <i>Agri Gene</i> , 2017, 5, 37-44.	1.9	2
14710	A transcriptomic insight into the impacts of mast cells in lung, breast, and colon cancers. <i>Oncolmmunology</i> , 2017, 6, e1360457.	2.1	16
14711	Large Scale Medical Data Mining for Accurate Diagnosis: A Blueprint. <i>Scalable Computing and Communications</i> , 2017, , 157-176.	0.5	16
14712	Towards Building a Knowledge Base of Monetary Transactions from a News Collection. , 2017, , .		3
14713	Molecular and Cellular Events During Infection of Potato by PVY. , 2017, , 21-42.		1
14714	Pregnancy-induced changes in metabolome and proteome in ovine uterine flushingsâ€. <i>Biology of Reproduction</i> , 2017, 97, 273-287.	1.2	22
14715	Gene expression reversal toward pre-adult levels in the aging human brain and age-related loss of cellular identity. <i>Scientific Reports</i> , 2017, 7, 5894.	1.6	35
14716	Microarray gene-expression study in fibroblast and lymphoblastoid cell lines from antipsychotic-naÃ‘ve first-episode schizophrenia patients. <i>Journal of Psychiatric Research</i> , 2017, 95, 91-101.	1.5	12
14717	PCPPI: a comprehensive database for the prediction of <i>Penicillium</i> â€‘crop proteinâ€‘protein interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	10

#	ARTICLE	IF	CITATIONS
14718	Prediction of cassava protein interactome based on interolog method. <i>Scientific Reports</i> , 2017, 7, 17206.	1.6	18
14719	Human hair follicle transcriptome profiling: a minimally invasive tool to assess molecular adaptations upon low-volume, high-intensity interval training. <i>Physiological Reports</i> , 2017, 5, e13534.	0.7	9
14720	Gene expression profile analysis of the bone microenvironment in patients with spinal metastases. <i>Oncology Letters</i> , 2017, 15, 61-68.	0.8	3
14721	Ensemble Modeling Approach Targeting Heterogeneous RNA-Seq data: Application to Melanoma Pseudogenes. <i>Scientific Reports</i> , 2017, 7, 17344.	1.6	2
14722	SNP co-association and network analyses identify E2F3, KDM5A and BACH2 as key regulators of the bovine milk fatty acid profile. <i>Scientific Reports</i> , 2017, 7, 17317.	1.6	21
14723	Highly expressed genes evolve under strong epistasis from a proteome-wide scan in <i>E. coli</i> . <i>Scientific Reports</i> , 2017, 7, 15844.	1.6	4
14724	Mountain hare transcriptome and diagnostic markers as resources to monitor hybridization with European hares. <i>Scientific Data</i> , 2017, 4, 170178.	2.4	11
14725	Identifying microRNA targets in epithelial-mesenchymal transition using joint-intervention causal inference. , 2017, , .		2
14726	Upregulation of long noncoding RNA APO03419.16 predicts high risk of aging-associated idiopathic pulmonary fibrosis. <i>Molecular Medicine Reports</i> , 2017, 16, 8085-8091.	1.1	17
14727	Severe riboflavin deficiency induces alterations in the hepatic proteome of starter Pekin ducks. <i>British Journal of Nutrition</i> , 2017, 118, 641-650.	1.2	17
14728	Identification of molecular mechanisms of glutamine in pancreatic cancer. <i>Oncology Letters</i> , 2017, 14, 6395-6402.	0.8	4
14730	Functional Genomic Approaches to Psychophysiology. , 0, , 354-376.		1
14731	Whole Exome Sequencing reveals new candidate genes in host genomic susceptibility to Respiratory Syncytial Virus Disease. <i>Scientific Reports</i> , 2017, 7, 15888.	1.6	29
14732	Genome-wide identification and differential analysis of translational initiation. <i>Nature Communications</i> , 2017, 8, 1749.	5.8	100
14733	Whole-Genome Sequence of the 1,4-Dioxane-Degrading Bacterium <i>Mycobacterium dioxanotrophicus</i> PH-06. <i>Genome Announcements</i> , 2017, 5, .	0.8	19
14735	IMA: Identifying disease-related genes using MeSH terms and association rules. <i>Journal of Biomedical Informatics</i> , 2017, 76, 110-123.	2.5	8
14736	Exome array analysis identifies GPR35 as a novel susceptibility gene for anthracycline-induced cardiotoxicity in childhood cancer. <i>Pharmacogenetics and Genomics</i> , 2017, 27, 445-453.	0.7	22
14737	Bacterial endosymbionts influence host sexuality and reveal reproductive genes of early divergent fungi. <i>Nature Communications</i> , 2017, 8, 1843.	5.8	85

#	ARTICLE	IF	CITATIONS
14738	Comparison of different approaches for identifying subnetworks in metabolic networks. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1750025.	0.3	4
14739	Comparative ecological transcriptomics and the contribution of gene expression to the evolutionary potential of a threatened fish. <i>Molecular Ecology</i> , 2017, 26, 6841-6856.	2.0	30
14740	Genome-wide DNA methylome alterations in acute coronary syndrome. <i>International Journal of Molecular Medicine</i> , 2017, 41, 220-232.	1.8	11
14741	Proteome-wide identification of lysine 2-hydroxyisobutyrylation reveals conserved and novel histone modifications in <i>Physcomitrella patens</i> . <i>Scientific Reports</i> , 2017, 7, 15553.	1.6	38
14742	Migrainomics – identifying brain and genetic markers of migraine. <i>Nature Reviews Neurology</i> , 2017, 13, 725-741.	4.9	37
14743	Chemical Similarity Enrichment Analysis (ChemRICH) as alternative to biochemical pathway mapping for metabolomic datasets. <i>Scientific Reports</i> , 2017, 7, 14567.	1.6	257
14744	Use of Biomedical Ontologies for Integration of Biological Knowledge for Learning and Prediction of Adverse Drug Reactions. <i>Gene Regulation and Systems Biology</i> , 2017, 11, 117762501769607.	2.3	14
14745	Integrative Analysis of Proteomics Data to Obtain Clinically Relevant Markers. <i>Methods in Molecular Biology</i> , 2017, 1788, 89-111.	0.4	1
14746	Accessing biological data as Prolog facts. , 2017, , .		1
14747	Global gene expression analysis combined with a genomics approach for the identification of signal transduction networks involved in postnatal mouse myocardial proliferation and development. <i>International Journal of Molecular Medicine</i> , 2017, 41, 311-321.	1.8	13
14748	Prokineticin receptor-1-dependent paracrine and autocrine pathways control cardiac tcf21+ fibroblast progenitor cell transformation into adipocytes and vascular cells. <i>Scientific Reports</i> , 2017, 7, 12804.	1.6	19
14749	Insights into gene expression profiles induced by Socs3 depletion in keratinocytes. <i>Scientific Reports</i> , 2017, 7, 15830.	1.6	6
14750	Plant Bioinformatics: Next Generation Sequencing Approaches. , 2017, , 1-106.		1
14751	Systems-Based Approach to the Analyses of Plant Functions: Conceptual Understanding, Implementation, and Analysis. , 2017, , 107-133.		3
14752	Common mechanism of pathogenesis in various types of metastatic osteosarcoma. <i>Oncology Letters</i> , 2017, 14, 6307-6313.	0.8	6
14753	Draft Genome Sequence of the Polysaccharide-Degrading Marine Bacterium <i>Pseudoalteromonas</i> sp. Strain A601. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
14754	Deep sequencing and comprehensive expression analysis identifies several molecules potentially related to human poorly differentiated hepatocellular carcinoma. <i>FEBS Open Bio</i> , 2017, 7, 1696-1706.	1.0	17
14755	De novo sequencing of seed transcriptome and development of genic-SSR markers in common buckwheat (<i>Fagopyrum esculentum</i>). <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	15

#	ARTICLE	IF	CITATIONS
14756	iTRAQ-Based Proteomic Analysis of Neonatal Kidney from Offspring of Protein Restricted Rats Reveals Abnormalities in Intraflagellar Transport Proteins. <i>Cellular Physiology and Biochemistry</i> , 2017, 44, 185-199.	1.1	32
14757	MicroRNA-146a promotes IgE class switch in B cells via upregulating 14-3-3 β expression. <i>Molecular Immunology</i> , 2017, 92, 180-189.	1.0	26
14758	Contribution of epigenetic landscapes and transcription factors to X-chromosome reactivation in the inner cell mass. <i>Nature Communications</i> , 2017, 8, 1297.	5.8	52
14759	Preliminary identification of key miRNAs, signaling pathways, and genes associated with Hirschsprung's disease by analysis of tissue microRNA expression profiles. <i>World Journal of Pediatrics</i> , 2017, 13, 489-495.	0.8	11
14760	GRAFENE: Graphlet-based alignment-free network approach integrates 3D structural and sequence (residue order) data to improve protein structural comparison. <i>Scientific Reports</i> , 2017, 7, 14890.	1.6	21
14761	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
14762	Genome-wide analysis and prediction of functional long noncoding RNAs in osteoblast differentiation under simulated microgravity. <i>Molecular Medicine Reports</i> , 2017, 16, 8180-8188.	1.1	10
14763	Identification of differentially expressed molecular functions associated with breast cancer using Gibbs sampling. <i>Oncology Letters</i> , 2017, 14, 7489-7494.	0.8	6
14764	Multidimensional knowledge-based framework is an essential step in the categorization of gene sets in complex disorders. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1750022.	0.3	5
14765	A Long Noncoding RNA Signature That Predicts Pathological Complete Remission Rate Sensitive in Neoadjuvant Treatment of Breast Cancer. <i>Translational Oncology</i> , 2017, 10, 988-997.	1.7	16
14766	Genome-wide discovery of long intergenic noncoding RNAs and their epigenetic signatures in the rat. <i>Scientific Reports</i> , 2017, 7, 14817.	1.6	3
14767	Signatures of adaptation and symbiosis in genomes and transcriptomes of <i>Symbiodinium</i> . <i>Scientific Reports</i> , 2017, 7, 15021.	1.6	35
14768	Functional Genomics in Wine Yeast: DNA Arrays and Next Generation Sequencing. , 2017, , 573-604.		1
14770	Differentially expressed genes in the caecal and colonic mucosa of Landrace finishing pigs with high and low food conversion ratios. <i>Scientific Reports</i> , 2017, 7, 14886.	1.6	14
14771	Comparative transcriptome analysis reveals potentially novel roles of Homeobox genes in adipose deposition in fat-tailed sheep. <i>Scientific Reports</i> , 2017, 7, 14491.	1.6	50
14772	Microarray-Based Gene Expression Analysis for Veterinary Pathologists: A Review. <i>Veterinary Pathology</i> , 2017, 54, 734-755.	0.8	13
14773	Circular RNAs play an important role in late-stage gastric cancer: Circular RNA expression profiles and bioinformatics analyses. <i>Tumor Biology</i> , 2017, 39, 101042831770585.	0.8	22
14774	Transcriptome profiling and expression analysis of immune responsive genes in the liver of Golden mahseer (<i>Tor putitora</i>) challenged with <i>Aeromonas hydrophila</i> . <i>Fish and Shellfish Immunology</i> , 2017, 67, 655-666.	1.6	36

#	ARTICLE	IF	CITATIONS
14775	Characterisation of Plasmodium falciparum populations selected on the human endothelial receptors P-selectin, E-selectin, CD9 and CD151. <i>Scientific Reports</i> , 2017, 7, 4069.	1.6	13
14776	Ontology-based support for taxonomic functions. <i>Ecological Informatics</i> , 2017, 41, 11-23.	2.3	2
14777	Effective biomedical document classification for identifying publications relevant to the mouse Gene Expression Database (GXD). <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	12
14778	Proteomic-Biostatistic Integrated Approach for Finding the Underlying Molecular Determinants of Hypertension in Human Plasma. <i>Hypertension</i> , 2017, 70, 412-419.	1.3	19
14779	Time-matched analysis of DNA adduct formation and early gene expression as predictive tool for renal carcinogenesis in methylazoxymethanol acetate treated Eker rats. <i>Archives of Toxicology</i> , 2017, 91, 3427-3438.	1.9	8
14780	Alterations of expression of inflammation/immune-related genes in the dorsal and ventral striatum of adult C57BL/6J mice following chronic oxycodone self-administration: a RNA sequencing study. <i>Psychopharmacology</i> , 2017, 234, 2259-2275.	1.5	54
14781	Network analysis of mitonuclear GWAS reveals functional networks and tissue expression profiles of disease-associated genes. <i>Human Genetics</i> , 2017, 136, 55-65.	1.8	14
14782	Prognostic medication: for predicting premonition and recovery. <i>Artificial Life and Robotics</i> , 2017, 22, 449-456.	0.7	2
14783	Physiological characteristics of <i>Magnetospirillum gryphiswaldense</i> MSR-1 that control cell growth under high-iron and low-oxygen conditions. <i>Scientific Reports</i> , 2017, 7, 2800.	1.6	19
14784	Transcriptional consequences of XPA disruption in human cell lines. <i>DNA Repair</i> , 2017, 57, 76-90.	1.3	19
14785	Identification of Jak-STAT signaling involvement in sarcoidosis severity via a novel microRNA-regulated peripheral blood mononuclear cell gene signature. <i>Scientific Reports</i> , 2017, 7, 4237.	1.6	67
14786	Bioinformatics analysis of transcription profiling of solid pseudopapillary neoplasm of the pancreas. <i>Molecular Medicine Reports</i> , 2017, 16, 1635-1642.	1.1	9
14787	Assessing glycolytic flux alterations resulting from genetic perturbations in <i>E. coli</i> using a biosensor. <i>Metabolic Engineering</i> , 2017, 42, 194-202.	3.6	22
14788	How Ontologies Can Help in Software Engineering. <i>Lecture Notes in Computer Science</i> , 2017, , 26-44.	1.0	8
14789	SPOWL, , 2017, , .		8
14790	RNA-Seq reveals differential expression patterns of genes associated with carotenoid accumulation in loquat. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	3
14791	Genome-wide differential mRNA expression profiles in follicles of two breeds and at two stages of estrus cycle of gilts. <i>Scientific Reports</i> , 2017, 7, 5052.	1.6	23
14792	HDNetDB: A Molecular Interaction Database for Network-Oriented Investigations into Huntingtonâ€™s Disease. <i>Scientific Reports</i> , 2017, 7, 5216.	1.6	20

#	ARTICLE	IF	CITATIONS
14793	Long noncoding RNA expression profile changes associated with dietary energy in the sheep testis during sexual maturation. <i>Scientific Reports</i> , 2017, 7, 5180.	1.6	51
14794	Systematic discovery of novel eukaryotic transcriptional regulators using sequence homology independent prediction. <i>BMC Genomics</i> , 2017, 18, 480.	1.2	12
14795	Complete genome sequence and whole-genome phylogeny of <i>Kosmotoga pacifica</i> type strain SLHJ1T from an East Pacific hydrothermal sediment. <i>Standards in Genomic Sciences</i> , 2017, 12, 3.	1.5	4
14796	In-depth genome characterization of a Brazilian common bean core collection using DArTseq high-density SNP genotyping. <i>BMC Genomics</i> , 2017, 18, 423.	1.2	81
14797	Protein Sorting Prediction. <i>Methods in Molecular Biology</i> , 2017, 1615, 23-57.	0.4	6
14798	mTFkb: a knowledgebase for fundamental annotation of mouse transcription factors. <i>Scientific Reports</i> , 2017, 7, 3022.	1.6	21
14799	Reactome enhanced pathway visualization. <i>Bioinformatics</i> , 2017, 33, 3461-3467.	1.8	140
14800	Transcriptomic profiling of <i>Melilotus albus</i> near-isogenic lines contrasting for coumarin content. <i>Scientific Reports</i> , 2017, 7, 4577.	1.6	21
14801	Best Practices in Manual Annotation with the Gene Ontology. <i>Methods in Molecular Biology</i> , 2017, 1446, 41-54.	0.4	21
14802	How Does the Scientific Community Contribute to Gene Ontology?. <i>Methods in Molecular Biology</i> , 2017, 1446, 85-93.	0.4	9
14803	Proteomic analysis reveals large amounts of decomposition enzymes and major metabolic pathways involved in algicidal process of <i>Trametes versicolor</i> F21a. <i>Scientific Reports</i> , 2017, 7, 3907.	1.6	25
14804	MicroRNA profiling in the dentate gyrus in epileptic rats. <i>Medicine (United States)</i> , 2017, 96, e6744.	0.4	8
14805	Microarray expression profile of circular RNAs in chronic thromboembolic pulmonary hypertension. <i>Medicine (United States)</i> , 2017, 96, e7354.	0.4	56
14806	Identification and functional analysis of the risk microRNAs associated with cerebral low-grade glioma prognosis. <i>Molecular Medicine Reports</i> , 2017, 16, 1173-1179.	1.1	12
14807	Transcriptome and metabolome analysis of <i>Ferula gummosa</i> Boiss. to reveal major biosynthetic pathways of galbanum compounds. <i>Functional and Integrative Genomics</i> , 2017, 17, 725-737.	1.4	17
14808	Salivary gland transcripts of the kissing bug, <i>Panstrongylus chinai</i> , a vector of Chagas disease. <i>Acta Tropica</i> , 2017, 174, 122-129.	0.9	12
14809	Transcriptome analysis of the Antarctic psychrotrophic bacterium <i>Psychrobacter</i> sp. G in response to temperature stress. <i>Acta Oceanologica Sinica</i> , 2017, 36, 78-87.	0.4	10
14810	Bactericidal potential of silver nanoparticles synthesized using cell-free extract of <i>Comamonas acidovorans</i> : in vitro and in silico approaches. <i>3 Biotech</i> , 2017, 7, 92.	1.1	36

#	ARTICLE	IF	CITATIONS
14811	Complex detection from PPI data using ensemble method. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2017, 6, 1.	1.2	2
14812	Parallel biclustering detection using strength Pareto front evolutionary algorithm. <i>Information Sciences</i> , 2017, 415-416, 283-297.	4.0	16
14813	Challenges and perspectives of metaproteomic data analysis. <i>Journal of Biotechnology</i> , 2017, 261, 24-36.	1.9	195
14814	Identification of regulators of germ stem cell enwrapment by its niche in <i>C. elegans</i> . <i>Developmental Biology</i> , 2017, 429, 271-284.	0.9	23
14815	Expression profiling indicating low selenium-sensitive microRNA levels linked to cell cycle and cell stress response pathways in the CaCo-2 cell line. <i>British Journal of Nutrition</i> , 2017, 117, 1212-1221.	1.2	17
14816	Improving the detection of pathways in genome-wide association studies by combined effects of SNPs from Linkage Disequilibrium blocks. <i>Scientific Reports</i> , 2017, 7, 3512.	1.6	9
14817	Altered microRNA and Piwi-interacting RNA profiles in cumulus cells from patients with diminished ovarian reserve. <i>Biology of Reproduction</i> , 2017, 97, 91-103.	1.2	16
14818	Plasma and White Blood Cells Show Different miRNA Expression Profiles in Parkinson's Disease. <i>Journal of Molecular Neuroscience</i> , 2017, 62, 244-254.	1.1	49
14819	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
14820	Classification of effects of drug combinations with support vector machines. , 2017, , .		0
14821	Improved methods and resources for paramecium genomics: transcription units, gene annotation and gene expression. <i>BMC Genomics</i> , 2017, 18, 483.	1.2	54
14822	DIGNiFI: Discovering causative genes for orphan diseases using protein-protein interaction networks. <i>BMC Systems Biology</i> , 2017, 11, 23.	3.0	12
14823	SEQUOIA: significance enhanced network querying through context-sensitive random walk and minimization of network conductance. <i>BMC Systems Biology</i> , 2017, 11, 20.	3.0	6
14824	Evaluating the effect of annotation size on measures of semantic similarity. <i>Journal of Biomedical Semantics</i> , 2017, 8, 7.	0.9	26
14825	Data- and expert-driven rule induction and filtering framework for functional interpretation and description of gene sets. <i>Journal of Biomedical Semantics</i> , 2017, 8, 23.	0.9	3
14826	FlyExpress 7: An Integrated Discovery Platform To Study Coexpressed Genes Using <i>in Situ</i> Hybridization Images in <i>Drosophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2791-2797.	0.8	4
14827	Automated detection of records in biological sequence databases that are inconsistent with the literature. <i>Journal of Biomedical Informatics</i> , 2017, 71, 229-240.	2.5	12
14828	The IDA-LIKE peptides IDL6 and IDL7 are negative modulators of stress responses in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2017, 68, 3557-3571.	2.4	34

#	ARTICLE	IF	CITATIONS
14829	The pomegranate (<i>Punica granatum</i> L.) genome and the genomics of punicalagin biosynthesis. <i>Plant Journal</i> , 2017, 91, 1108-1128.	2.8	109
14830	Detection of QTL for traits related to adaptation to sub-optimal climatic conditions in chickens. <i>Genetics Selection Evolution</i> , 2017, 49, 39.	1.2	11
14831	Structure alignment-based classification of RNA-binding pockets reveals regional RNA recognition motifs on protein surfaces. <i>BMC Bioinformatics</i> , 2017, 18, 27.	1.2	7
14832	Identifying miRNA sponge modules using biclustering and regulatory scores. <i>BMC Bioinformatics</i> , 2017, 18, 44.	1.2	25
14833	Multiple network algorithm for epigenetic modules via the integration of genome-wide DNA methylation and gene expression data. <i>BMC Bioinformatics</i> , 2017, 18, 72.	1.2	52
14834	How can functional annotations be derived from profiles of phenotypic annotations?. <i>BMC Bioinformatics</i> , 2017, 18, 96.	1.2	5
14835	NEArender: an R package for functional interpretation of "omics" data via network enrichment analysis. <i>BMC Bioinformatics</i> , 2017, 18, 118.	1.2	16
14836	In silico prediction of lncRNA function using tissue specific and evolutionary conserved expression. <i>BMC Bioinformatics</i> , 2017, 18, 144.	1.2	42
14837	Avoiding the pitfalls of gene set enrichment analysis with SetRank. <i>BMC Bioinformatics</i> , 2017, 18, 151.	1.2	93
14838	NaviGO: interactive tool for visualization and functional similarity and coherence analysis with gene ontology. <i>BMC Bioinformatics</i> , 2017, 18, 177.	1.2	53
14839	Comparison of different cell type correction methods for genome-scale epigenetics studies. <i>BMC Bioinformatics</i> , 2017, 18, 216.	1.2	80
14840	In silico re-identification of properties of drug target proteins. <i>BMC Bioinformatics</i> , 2017, 18, 248.	1.2	26
14841	QueryOR: a comprehensive web platform for genetic variant analysis and prioritization. <i>BMC Bioinformatics</i> , 2017, 18, 225.	1.2	20
14842	Across-proteome modeling of dimer structures for the bottom-up assembly of protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2017, 18, 257.	1.2	9
14843	Integration of quantitated expression estimates from polyA-selected and rRNA-depleted RNA-seq libraries. <i>BMC Bioinformatics</i> , 2017, 18, 301.	1.2	40
14844	Transcriptomic evidence for the control of soybean root isoflavonoid content by regulation of overlapping phenylpropanoid pathways. <i>BMC Genomics</i> , 2017, 18, 70.	1.2	19
14845	A machine learning classifier trained on cancer transcriptomes detects NF1 inactivation signal in glioblastoma. <i>BMC Genomics</i> , 2017, 18, 127.	1.2	30
14846	Chronic nicotine differentially affects murine transcriptome profiling in isolated cortical interneurons and pyramidal neurons. <i>BMC Genomics</i> , 2017, 18, 194.	1.2	7

#	ARTICLE	IF	CITATIONS
14847	Genome evolutionary dynamics followed by diversifying selection explains the complexity of the <i>Sesamum indicum</i> genome. <i>BMC Genomics</i> , 2017, 18, 257.	1.2	17
14848	Sex-specific differences in transcriptome profiles of brain and muscle tissue of the tropical gar. <i>BMC Genomics</i> , 2017, 18, 283.	1.2	13
14849	Poplar stem transcriptome is massively remodelled in response to single or repeated mechanical stimuli. <i>BMC Genomics</i> , 2017, 18, 300.	1.2	24
14850	The predictive nature of transcript expression levels on protein expression in adult human brain. <i>BMC Genomics</i> , 2017, 18, 322.	1.2	51
14851	Pan genome and CRISPR analyses of the bacterial fish pathogen <i>Moritella viscosa</i> . <i>BMC Genomics</i> , 2017, 18, 313.	1.2	10
14852	Statistical analysis of fractionation resistance by functional category and expression. <i>BMC Genomics</i> , 2017, 18, 366.	1.2	1
14853	<i>Drosophila melanogaster</i> positive transcriptional elongation factors regulate metabolic and sex-biased expression in adults. <i>BMC Genomics</i> , 2017, 18, 384.	1.2	3
14854	Genome-wide characterization and expression analyses of superoxide dismutase (SOD) genes in <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2017, 18, 376.	1.2	101
14855	Genomic adaptation to agricultural environments: cabbage white butterflies (<i>Pieris rapae</i>) as a case study. <i>BMC Genomics</i> , 2017, 18, 412.	1.2	13
14856	RNA sequencing and transcriptome arrays analyses show opposing results for alternative splicing in patient derived samples. <i>BMC Genomics</i> , 2017, 18, 443.	1.2	74
14857	Gene expression of <i>Vibrio parahaemolyticus</i> growing in laboratory isolation conditions compared to those common in its natural ocean environment. <i>BMC Microbiology</i> , 2017, 17, 118.	1.3	6
14858	An integrated RNAseq-1H NMR metabolomics approach to understand soybean primary metabolism regulation in response to <i>Rhizoctonia foliar</i> blight disease. <i>BMC Plant Biology</i> , 2017, 17, 84.	1.6	68
14859	Finding low-conductance sets with dense interactions (FLCD) for better protein complex prediction. <i>BMC Systems Biology</i> , 2017, 11, 22.	3.0	8
14860	Network reconstruction of the mouse secretory pathway applied on CHO cell transcriptome data. <i>BMC Systems Biology</i> , 2017, 11, 37.	3.0	14
14861	HGPEC: a Cytoscape app for prediction of novel disease-gene and disease-disease associations and evidence collection based on a random walk on heterogeneous network. <i>BMC Systems Biology</i> , 2017, 11, 61.	3.0	29
14862	N-of-1-pathways MixEnrich: advancing precision medicine via single-subject analysis in discovering dynamic changes of transcriptomes. <i>BMC Medical Genomics</i> , 2017, 10, 27.	0.7	29
14863	Plasmobase: a comparative database of predicted domain architectures for <i>Plasmodium</i> genomes. <i>Malaria Journal</i> , 2017, 16, 241.	0.8	5
14864	Exploring the FGFR3-related oncogenic mechanism in bladder cancer using bioinformatics strategy. <i>World Journal of Surgical Oncology</i> , 2017, 15, 66.	0.8	13

#	ARTICLE	IF	CITATIONS
14865	Medical Subject Heading (MeSH) annotations illuminate maize genetics and evolution. <i>Plant Methods</i> , 2017, 13, 8.	1.9	7
14866	Approximating the correction of weighted and unweighted orthology and paralogy relations. <i>Algorithms for Molecular Biology</i> , 2017, 12, 4.	0.3	16
14867	Gene set analysis controlling for length bias in RNA-seq experiments. <i>BioData Mining</i> , 2017, 10, 5.	2.2	7
14868	Gene Set Enrichment Analyses: lessons learned from the heart failure phenotype. <i>BioData Mining</i> , 2017, 10, 18.	2.2	4
14869	Mining a differential sialotranscriptome of <i>Rhipicephalus microplus</i> guides antigen discovery to formulate a vaccine that reduces tick infestations. <i>Parasites and Vectors</i> , 2017, 10, 206.	1.0	46
14870	Type 2 diabetes and obesity induce similar transcriptional reprogramming in human myocytes. <i>Genome Medicine</i> , 2017, 9, 47.	3.6	37
14871	Modulated evaluation metrics for drug-based ontologies. <i>Journal of Biomedical Semantics</i> , 2017, 8, 17.	0.9	10
14872	NCBO Ontology Recommender 2.0: an enhanced approach for biomedical ontology recommendation. <i>Journal of Biomedical Semantics</i> , 2017, 8, 21.	0.9	59
14873	Priming increases the anti-tumor effect and therapeutic window of ¹⁷⁷ Lu-octreotate in nude mice bearing human small intestine neuroendocrine tumor GOT1. <i>EJNMMI Research</i> , 2017, 7, 6.	1.1	16
14874	High-quality draft genome sequence of <i>Rhizobium mesoamericanum</i> strain STM6155, a <i>Mimosa pudica</i> microsymbiont from New Caledonia. <i>Standards in Genomic Sciences</i> , 2017, 12, 7.	1.5	2
14875	Complete genome sequence of <i>Pseudomonas brassicacearum</i> strain L13-6-12, a biological control agent from the rhizosphere of potato. <i>Standards in Genomic Sciences</i> , 2017, 12, 6.	1.5	19
14876	Draft genome sequence of type strain HBR26T and description of <i>Rhizobium aethiopicum</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2017, 12, 14.	1.5	26
14877	Draft genome sequences of eight bacteria isolated from the indoor environment: <i>Staphylococcus capitis</i> strain H36, <i>S. capitis</i> strain H65, <i>S. cohnii</i> strain H62, <i>S. hominis</i> strain H69, <i>Microbacterium</i> sp. strain H83, <i>Mycobacterium iranicum</i> strain H39, <i>Plantibacter</i> sp. strain H53, and <i>Pseudomonas oryzihabitans</i> strain H72. <i>Standards in Genomic Sciences</i> , 2017, 12, 17.	1.5	9
14878	Complete genome sequence of <i>Pseudoalteromonas</i> phage vB_PspS-H40/1 (formerly H40/1) that infects <i>Pseudoalteromonas</i> sp. strain H40 and is used as biological tracer in hydrological transport studies. <i>Standards in Genomic Sciences</i> , 2017, 12, 20.	1.5	8
14879	High-quality-draft genome sequence of the fermenting bacterium <i>Anaerobium acetethylicum</i> type strain GluBS11T (DSM 29698). <i>Standards in Genomic Sciences</i> , 2017, 12, 24.	1.5	6
14880	High quality draft genome sequence of an extremely halophilic archaeon <i>Natrinema altunense</i> strain AJ2T. <i>Standards in Genomic Sciences</i> , 2017, 12, 25.	1.5	1
14881	High-quality permanent draft genome sequence of the <i>Bradyrhizobium elkanii</i> type strain USDA 76T, isolated from <i>Glycine max</i> (L.) Merr. <i>Standards in Genomic Sciences</i> , 2017, 12, 26.	1.5	11
14882	Complete genome sequence of <i>Kosakonia oryzae</i> type strain Ola 51T. <i>Standards in Genomic Sciences</i> , 2017, 12, 28.	1.5	12

#	ARTICLE	IF	CITATIONS
14883	Genome sequencing and analysis of <i>Ralstonia solanacearum</i> phylotype I strains FJAT-91, FJAT-452 and FJAT-462 isolated from tomato, eggplant, and chili pepper in China. <i>Standards in Genomic Sciences</i> , 2017, 12, 29.	1.5	1
14884	Genome sequencing and description of <i>Oerskovia enterophila</i> VJag, an agar- and cellulose-degrading bacterium. <i>Standards in Genomic Sciences</i> , 2017, 12, 30.	1.5	2
14885	Chromosomal features of <i>Escherichia coli</i> serotype O2:K2, an avian pathogenic <i>E. coli</i> . <i>Standards in Genomic Sciences</i> , 2017, 12, 33.	1.5	5
14886	Genomics insights into production of 2-methylisoborneol and a putative cyanobactin by <i>Planktothricoides</i> sp. SR001. <i>Standards in Genomic Sciences</i> , 2017, 12, 35.	1.5	8
14888	Downregulation of PKC ζ /Pard3/Pard6b is responsible for lung adenocarcinoma cell EMT and invasion. <i>Cellular Signalling</i> , 2017, 38, 49-59.	1.7	34
14889	Ten-eleven translocation 2 interacts with forkhead box O3 and regulates adult neurogenesis. <i>Nature Communications</i> , 2017, 8, 15903.	5.8	82
14890	DNA methylation in schizophrenia in different patient-derived cell types. <i>NPJ Schizophrenia</i> , 2017, 3, 6.	2.0	25
14891	A molecular hypothesis to explain direct and inverse co-morbidities between Alzheimer's Disease, Glioblastoma and Lung cancer. <i>Scientific Reports</i> , 2017, 7, 4474.	1.6	85
14892	Characterization of 2 Novel Ependymoma Cell Lines With Chromosome 1q Gain Derived From Posterior Fossa Tumors of Childhood. <i>Journal of Neuropathology and Experimental Neurology</i> , 2017, 76, 595-604.	0.9	19
14893	Shaping functional gut microbiota using dietary bioactives to reduce colon cancer risk. <i>Seminars in Cancer Biology</i> , 2017, 46, 191-204.	4.3	45
14894	Genome-wide copy number variation in the bovine genome detected using low coverage sequence of popular beef breeds. <i>Animal Genetics</i> , 2017, 48, 141-150.	0.6	39
14895	The Gene Ontology Handbook. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	63
14896	Analysis of the interplay between methylation and expression reveals its potential role in cancer aetiology. <i>Functional and Integrative Genomics</i> , 2017, 17, 53-68.	1.4	14
14897	Proteomic analysis of transgenic rice overexpressing a calmodulin calcium sensor reveals its effects on redox signaling and homeostasis. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2017, 26, 235-245.	0.9	3
14898	Functional architecture and global properties of the <i>Corynebacterium glutamicum</i> regulatory network: Novel insights from a dataset with a high genomic coverage. <i>Journal of Biotechnology</i> , 2017, 257, 199-210.	1.9	16
14899	Sequencing and de novo assembly of visceral mass transcriptome of the critically endangered land snail <i>Satsuma myomphala</i> : Annotation and SSR discovery. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 21, 77-89.	0.4	10
14900	Proteomic analysis of peel browning of 'Nanguo' pears after low temperature storage. <i>Journal of the Science of Food and Agriculture</i> , 2017, 97, 2460-2467.	1.7	28
14901	Weighted Epistatic Analysis of NSAIDs Hypersensitivity Data. <i>Engineering Applications of Artificial Intelligence</i> , 2017, 62, 312-319.	4.3	0

#	ARTICLE	IF	CITATIONS
14902	Gene expression, signal transduction pathways and functional networks associated with growth of sporadic vestibular schwannomas. <i>Journal of Neuro-Oncology</i> , 2017, 131, 283-292.	1.4	15
14903	Computational approaches for the identification of cancer genes and pathways. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2017, 9, e1364.	6.6	65
14904	<i>Cancer Genomics.</i> , 2017, , 43-63.		0
14905	Characterization of genes and pathways that respond to heat stress in Holstein calves through transcriptome analysis. <i>Cell Stress and Chaperones</i> , 2017, 22, 29-42.	1.2	67
14906	The Comparative Toxicogenomics Database: update 2017. <i>Nucleic Acids Research</i> , 2017, 45, D972-D978.	6.5	526
14907	Limitations of Transâ€Species Inferences: The Case of Spatialâ€Numerical Associations in Chicks and Humans. <i>Cognitive Science</i> , 2017, 41, 2267-2274.	0.8	6
14908	Evaluation of the genetic basis of primary hypoadrenocorticism in Standard Poodles using SNP array genotyping and whole-genome sequencing. <i>Mammalian Genome</i> , 2017, 28, 56-65.	1.0	9
14909	Comparative transcriptomic analyses of male and female adult <i>Toxocara canis</i> . <i>Gene</i> , 2017, 600, 85-89.	1.0	12
14910	miRPathDB: a new dictionary on microRNAs and target pathways. <i>Nucleic Acids Research</i> , 2017, 45, D90-D96.	6.5	102
14911	Introducing the Big Knowledge to Use (BK2U) challenge. <i>Annals of the New York Academy of Sciences</i> , 2017, 1387, 12-24.	1.8	5
14912	Comparison of miRNA profiling during airway epithelial repair in undifferentiated and differentiated cells in vitro. <i>Journal of Applied Genetics</i> , 2017, 58, 205-212.	1.0	4
14913	Biological effect of aqueous C60 aggregates on <i>Scenedesmus obliquus</i> revealed by transcriptomics and non-targeted metabolomics. <i>Journal of Hazardous Materials</i> , 2017, 324, 221-229.	6.5	58
14914	Primer on Ontologies. <i>Methods in Molecular Biology</i> , 2017, 1446, 3-13.	0.4	44
14915	Visualizing GO Annotations. <i>Methods in Molecular Biology</i> , 2017, 1446, 207-220.	0.4	12
14916	The Evidence and Conclusion Ontology (ECO): Supporting GO Annotations. <i>Methods in Molecular Biology</i> , 2017, 1446, 245-259.	0.4	33
14917	The Gene Ontology and the Meaning of Biological Function. <i>Methods in Molecular Biology</i> , 2017, 1446, 15-24.	0.4	156
14918	Primer on the Gene Ontology. <i>Methods in Molecular Biology</i> , 2017, 1446, 25-37.	0.4	63
14919	Gene expression plasticity as a mechanism of coral adaptation to a variable environment. <i>Nature Ecology and Evolution</i> , 2017, 1, 14.	3.4	306

#	ARTICLE	IF	CITATIONS
14920	Evaluating Computational Gene Ontology Annotations. <i>Methods in Molecular Biology</i> , 2017, 1446, 97-109.	0.4	10
14921	Genome-wide analysis of gene expression to distinguish photoperiod-dependent and -independent flowering in Brassicaceae. <i>Genes and Genomics</i> , 2017, 39, 207-223.	0.5	2
14922	Changes in mammary histology and transcriptome profiles by low-dose exposure to environmental phenols at critical windows of development. <i>Environmental Research</i> , 2017, 152, 233-243.	3.7	26
14923	Quantitative telomeric chromatin isolation protocol for human cells. <i>Methods</i> , 2017, 114, 28-38.	1.9	8
14924	Proteome analysis of acute kidney injury – Discovery of new predominantly renal candidates for biomarker of kidney disease. <i>Journal of Proteomics</i> , 2017, 151, 66-73.	1.2	18
14925	Human CD40 ligand deficiency dysregulates the macrophage transcriptome causing functional defects that are improved by exogenous IFN- β . <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 900-912.e7.	1.5	27
14926	A comprehensive draft genome sequence for lupin (<i>Lupinus angustifolius</i>), an emerging health food: insights into plant-microbe interactions and legume evolution. <i>Plant Biotechnology Journal</i> , 2017, 15, 318-330.	4.1	153
14927	RNA-seq analysis of <i>Brachypodium distachyon</i> responses to Barley stripe mosaic virus infection. <i>Crop Journal</i> , 2017, 5, 1-10.	2.3	4
14928	Protein-Induced Pluripotent Stem Cells Ameliorate Cognitive Dysfunction and Reduce A β 2 Deposition in a Mouse Model of Alzheimer's Disease. <i>Stem Cells Translational Medicine</i> , 2017, 6, 293-305.	1.6	58
14929	Restriction site associated DNA (RAD) for de novo sequencing and marker discovery in sugarcane borer, <i>Diatraea saccharalis</i> Fab. (Lepidoptera: Crambidae). <i>Molecular Ecology Resources</i> , 2017, 17, 454-465.	2.2	5
14930	Peak-Finding Algorithms. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.top093179.	0.2	0
14931	Quantitative proteomic analysis of the <i>Saccharomyces cerevisiae</i> industrial strains CAT-1 and PE-2. <i>Journal of Proteomics</i> , 2017, 151, 114-121.	1.2	18
14932	Distributional logic programming for Bayesian knowledge representation. <i>International Journal of Approximate Reasoning</i> , 2017, 80, 52-66.	1.9	5
14933	Analyzing Microarray Data. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot093112.	0.2	5
14934	The effects of levonorgestrel on FSH-stimulated primary rat granulosa cell cultures through gene expression profiling are associated to hormone and folliculogenesis processes. <i>Molecular and Cellular Endocrinology</i> , 2017, 439, 337-345.	1.6	8
14935	RNA-seq analysis reveals the role of secondary metabolism in the response of URS 21, a race-nonspecific resistant cultivar, to crown rust. <i>Plant Pathology</i> , 2017, 66, 702-712.	1.2	1
14936	Genome-wide analysis and characterization of molecular evolution of the HCT gene family in pear (<i>Pyrus bretschneideri</i>). <i>Plant Systematics and Evolution</i> , 2017, 303, 71-90.	0.3	23
14937	Trinitrobenzene sulfonic acid-induced intestinal injury in neonatal mice activates transcriptional networks similar to those seen in human necrotizing enterocolitis. <i>Pediatric Research</i> , 2017, 81, 99-112.	1.1	33

#	ARTICLE	IF	CITATIONS
14938	Comparative transcriptome analysis of barley (<i>Hordeum vulgare</i> L.) glossy mutant using RNA-Seq. <i>Revista Brasileira De Botanica</i> , 2017, 40, 247-256.	0.5	7
14939	The Bayesian Ontology Language \mathcal{BEL} . <i>BEL Journal of Automated Reasoning</i> , 2017, 58, 67-95.	1.1	19
14940	Immunoproteomic analysis of house dust mite antigens reveals distinct classes of dominant T cell antigens according to function and serological reactivity. <i>Clinical and Experimental Allergy</i> , 2017, 47, 577-592.	1.4	26
14941	Transcriptomic profile of Manila clam (<i>Ruditapes philippinarum</i>) haemocytes in response to <i>Perkinsus olseni</i> infection. <i>Aquaculture</i> , 2017, 467, 170-181.	1.7	15
14942	De novo transcriptome sequencing of marine-derived <i>Aspergillus glaucus</i> and comparative analysis of metabolic and developmental variations in response to salt stress. <i>Genes and Genomics</i> , 2017, 39, 317-329.	0.5	10
14943	Deep sequencing of the transcriptome reveals distinct flavonoid metabolism features of black tartary buckwheat (<i>Fagopyrum tataricum</i> Gaertn.). <i>Progress in Biophysics and Molecular Biology</i> , 2017, 124, 49-60.	1.4	34
14944	Identification of transcripts involved in digestion, detoxification and immune response from transcriptome of <i>Empoasca vitis</i> (Hemiptera: Cicadellidae) nymphs. <i>Genomics</i> , 2017, 109, 58-66.	1.3	14
14946	Loss of <i>ppr3</i> , <i>ppr4</i> , <i>ppr6</i> , or <i>ppr10</i> perturbs iron homeostasis and leads to apoptotic cell death in <i>Schizosaccharomyces pombe</i> . <i>FEBS Journal</i> , 2017, 284, 324-337.	2.2	20
14947	Systematic Characterization and Prediction of Human Hypertension Genes. <i>Hypertension</i> , 2017, 69, 349-355.	1.3	9
14948	Global transcriptomic response of <i>Anoxybacillus</i> sp. SK 3-4 to aluminum exposure. <i>Journal of Basic Microbiology</i> , 2017, 57, 151-161.	1.8	7
14949	Integrating Bio-ontologies and Controlled Clinical Terminologies: From Base Pairs to Bedside Phenotypes. <i>Methods in Molecular Biology</i> , 2017, 1446, 275-287.	0.4	1
14950	Immune competence assessment in marine medaka (<i>Orzias melastigma</i>) – a holistic approach for immunotoxicology. <i>Environmental Science and Pollution Research</i> , 2017, 24, 27687-27701.	2.7	13
14951	Novel biomarkers of nasopharyngeal carcinoma metastasis risk identified by reverse phase protein array based tumor profiling with consideration of plasma Epstein-Barr virus DNA load. <i>Proteomics - Clinical Applications</i> , 2017, 11, 1600090.	0.8	7
14952	Insights into specificity, redundancy and new cellular functions of C/EBP α and C/EBP β transcription factors through interactome network analysis. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 467-476.	1.1	19
14953	Gene expression profiling of granule cells and Purkinje cells in the zebrafish cerebellum. <i>Journal of Comparative Neurology</i> , 2017, 525, 1558-1585.	0.9	34
14954	Proteomic maps of subcellular protein fractions of the Asian citrus psyllid <i>Diaphorina citri</i> , the vector of citrus huanglongbing. <i>Physiological Entomology</i> , 2017, 42, 36-64.	0.6	8
14955	Translational Advances in the Field of Pulmonary Hypertension. It Will Take More Than ϵ miRNAs. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 195, 167-178.	2.5	70
14956	The PathoYeast database: an information system for the analysis of gene and genomic transcription regulation in pathogenic yeasts. <i>Nucleic Acids Research</i> , 2017, 45, D597-D603.	6.5	35

#	ARTICLE	IF	CITATIONS
14957	Comparative analysis of human and mouse CpG islands using dbCGI. , 2017, , .		1
14958	Dataflow representation of data analyses: Toward a platform for collaborative data science. IBM Journal of Research and Development, 2017, 61, 9:1-9:13.	3.2	9
14959	Comprehensive characterization of cancer genes in hepatocellular carcinoma genomes. Oncology Letters, 2017, 15, 1503-1510.	0.8	12
14960	A proteome view of structural, functional, and taxonomic characteristics of major protein domain clusters. Scientific Reports, 2017, 7, 14210.	1.6	1
14961	Bioinformatics analysis of differentially expressed gene profiles associated with systemic lupus erythematosus. Molecular Medicine Reports, 2018, 17, 3591-3598.	1.1	9
14962	Associating Genomics and Clinical Information by Means of Semantic Based Ranking. , 2017, , .		0
14963	Identifying hub genes and potential mechanisms associated with senescence in human annulus cells by gene expression profiling and bioinformatics analysis. Molecular Medicine Reports, 2018, 17, 3465-3472.	1.1	4
14964	Identification of key genes associated with bladder cancer using gene expression profiles. Oncology Letters, 2018, 15, 297-303.	0.8	17
14965	Bioinformatic analysis of gene expression profiling of intracranial aneurysm. Molecular Medicine Reports, 2018, 17, 3473-3480.	1.1	13
14966	Decellularization and Solubilization of Porcine Liver for Use as a Substrate for Porcine Hepatocyte Culture. Cell Transplantation, 2017, 26, 1840-1854.	1.2	69
14967	p27Kip1, PCAF and PAX5 cooperate in the transcriptional regulation of specific target genes. Nucleic Acids Research, 2017, 45, 5086-5099.	6.5	14
14968	eTRIKS analytical environment: A modular high performance framework for medical data analysis. , 2017, , .		6
14969	Downregulated miRNAâ€™1269a variant (rs73239138) decreases the susceptibility to gastric cancer via targeting ZNF70. Oncology Letters, 2017, 14, 6345-6354.	0.8	11
14970	The Complete Genome Sequence of the Phytopathogenic Fungus Sclerotinia sclerotiorum Reveals Insights into the Genome Architecture of Broad Host Range Pathogens. Genome Biology and Evolution, 2017, 9, 593-618.	1.1	187
14971	IMAP: An iterative method for aligning protein-protein interaction networks. , 2017, , .		1
14972	Genome expression profiling predicts the molecular mechanism of peripheral myelination. International Journal of Molecular Medicine, 2017, 41, 1500-1508.	1.8	8
14973	MeSH term-based semantic analysis of microRNA regulation on glucocorticoid resistance in pediatric acute lymphoblastic leukemia. , 2017, , .		1
14974	Surgical data science, an emerging field of medicine. , 2017, , .		7

#	ARTICLE	IF	CITATIONS
14975	Identification of regulatory role of DNA methylation in colon cancer gene expression via systematic bioinformatics analysis. <i>Medicine (United States)</i> , 2017, 96, e8487.	0.4	18
14976	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
14977	Gene expression profiles and protein-protein interaction networks during tongue carcinogenesis in the tumor microenvironment. <i>Molecular Medicine Reports</i> , 2017, 17, 165-171.	1.1	8
14978	Proteomic Analysis Shows Constitutive Secretion of MIF and p53-associated Activity of COX-2 in Lung Fibroblasts. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 339-351.	3.0	5
14979	Biotoxicity of Cry1Ab protein on wolf spider <i>Pardosa pseudoannulata</i> . <i>Ecotoxicology</i> , 2017, 26, 1336-1343.	1.1	4
14980	Transcriptome of wax apple (<i>Syzygium samarangense</i>) provides insights into nitric oxide-induced delays of postharvest cottony softening. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	18
14981	A flexible ontology for inference of emergent whole cell function from relationships between subcellular processes. <i>Scientific Reports</i> , 2017, 7, 17689.	1.6	25
14982	A hypothesis-driven approach to assessing significance of differences in RNA expression levels among specific groups of genes. <i>Current Plant Biology</i> , 2017, 11-12, 46-51.	2.3	4
14983	LncRNA profiling of skeletal muscles in Large White pigs and Mashen pigs during development ^{1,2} . <i>Journal of Animal Science</i> , 2017, 95, 4239-4250.	0.2	47
14984	A parallel algorithm for mining maximal frequent subgraphs. , 2017, , .		1
14985	Transcriptome analysis of peripheral blood mononuclear cells from chronic hepatitis B and hepatocellular carcinoma patients: a network-based attitude. <i>Future Virology</i> , 2017, 12, 729-737.	0.9	1
14986	Long-read sequence assembly of the firefly <i>Pyrocoelia pectoralis</i> genome. <i>GigaScience</i> , 2017, 6, 1-7.	3.3	32
14987	Draft genome of the lined seahorse, <i>Hippocampus erectus</i> . <i>GigaScience</i> , 2017, 6, 1-6.	3.3	38
14988	The muscle development transcriptome landscape of ovariectomized goat. <i>Royal Society Open Science</i> , 2017, 4, 171415.	1.1	13
14989	Phosphoproteomics of cAMP signaling of <i>Bordetella</i> adenylate cyclase toxin in mouse dendritic cells. <i>Scientific Reports</i> , 2017, 7, 16298.	1.6	7
14990	Enhanced Desiccation Tolerance in Mature Cultures of the Streptophytic Green Alga <i>Zygnema circumcarinatum</i> Revealed by Transcriptomics. <i>Plant and Cell Physiology</i> , 2017, 58, 2067-2084.	1.5	95
14991	Learning Knowledge Embeddings by Combining Limit-based Scoring Loss. , 2017, , .		22
14992	Abnormal DNA methylation may contribute to the progression of osteosarcoma. <i>Molecular Medicine Reports</i> , 2017, 17, 193-199.	1.1	12

#	ARTICLE	IF	CITATIONS
14993	A polygenic score for schizophrenia predicts glycemic control. <i>Translational Psychiatry</i> , 2017, 7, 1295.	2.4	16
14994	Ontobee: A linked ontology data server to support ontology term dereferencing, linkage, query and integration. <i>Nucleic Acids Research</i> , 2017, 45, D347-D352.	6.5	110
14995	Novel phosphate deficiency-responsive long non-coding RNAs in the legume model plant <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2017, 68, 5937-5948.	2.4	77
14996	OGEE v2: an update of the online gene essentiality database with special focus on differentially essential genes in human cancer cell lines. <i>Nucleic Acids Research</i> , 2017, 45, D940-D944.	6.5	153
14997	Proteomic Analysis Reveals Grb2 as a Key Regulator of Periodic Mechanical Stress Transduction in Chondrocytes. <i>Cellular Physiology and Biochemistry</i> , 2017, 44, 1509-1525.	1.1	5
14998	Subchronic olanzapine exposure leads to increased expression of myelination-related genes in rat fronto-medial cortex. <i>Translational Psychiatry</i> , 2017, 7, 1262.	2.4	16
14999	On the Ontological Modelling of Co-medication and Drug Interactions in Medical Cancer Therapy Regimens for a Clinical Decision Support System. , 2017, , .		2
15000	Bayesian functional enrichment analysis for the Reactome database. <i>Statistical Theory and Related Fields</i> , 2017, 1, 185-193.	0.2	1
15001	Quantitative Proteomics of the E. coli Membranome. <i>Methods in Enzymology</i> , 2017, 586, 15-36.	0.4	24
15002	First draft genome sequence of a strain from the genus <i>Fusibacter</i> isolated from Salar de AscotÃ¡n in Northern Chile. <i>Standards in Genomic Sciences</i> , 2017, 12, 43.	1.5	21
15003	The Ontology of Biological and Clinical Statistics (OBCS)â€based statistical method standardization and metaâ€analysis of host responses to yellow fever vaccines. <i>Quantitative Biology</i> , 2017, 5, 291-301.	0.3	4
15004	Ancestral Genome Estimation Reveals the History of Ecological Diversification in <i>Agrobacterium</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 3413-3431.	1.1	31
15005	Towards enhanced and interpretable clustering/classification in integrative genomics. <i>Nucleic Acids Research</i> , 2017, 45, e169-e169.	6.5	1
15006	Experimental Evaluation of Crowdsourcing on the Characterization of Data Visualization Techniques. , 2017, , .		1
15007	Towards a framework for tensor ontologies over Neo4j: Representations and operations. , 2017, , .		12
15008	Identification of candidate genes for Rituximab response in rheumatoid arthritis with weighted gene co-expression network analysis. , 2017, , .		0
15009	Multi-layer Big Knowledge Visualization Scheme for Comprehending Neoplasm Ontology Content. , 2017, , .		2
15010	An effective approach to detecting both small and large complexes from protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2017, 18, 419.	1.2	18

#	ARTICLE	IF	CITATIONS
15011	Epistasis analysis of microRNAs on pathological stages in colon cancer based on an Empirical Bayesian Elastic Net method. <i>BMC Genomics</i> , 2017, 18, 756.	1.2	4
15012	Principles for the regulation of multiple developmental pathways by a versatile transcriptional factor, BLIMP1. <i>Nucleic Acids Research</i> , 2017, 45, 12152-12169.	6.5	12
15013	Draft genome sequence of the cellulolytic endophyte <i>Chitinophaga costaii</i> A37T2T. <i>Standards in Genomic Sciences</i> , 2017, 12, 53.	1.5	13
15014	Insights from the draft genome into the pathogenicity of a clinical isolate of <i>Elizabethkingia meningoseptica</i> Em3. <i>Standards in Genomic Sciences</i> , 2017, 12, 56.	1.5	13
15015	Data Science and symbolic AI: Synergies, challenges and opportunities. <i>Data Science</i> , 2017, 1, 27-38.	0.7	21
15016	High-quality draft genome sequence of <i>Aquidulcibacter paucihalophilus</i> TH12T isolated from cyanobacterial aggregates in a eutrophic lake. <i>Standards in Genomic Sciences</i> , 2017, 12, 69.	1.5	1
15017	The complete genome sequence of <i>Ensifer meliloti</i> strain CCMM B554 (FSM-MA), a highly effective nitrogen-fixing microsymbiont of <i>Medicago truncatula</i> Gaertn. <i>Standards in Genomic Sciences</i> , 2017, 12, 75.	1.5	3
15018	Orchidstra 2.0 A Transcriptomics Resource for the Orchid Family. <i>Plant and Cell Physiology</i> , 2017, 58, pcw220.	1.5	72
15019	The improvement of the parallel algorithm for randomization-based enrichment analysis. , 2017, , .		0
15020	Auditing subtype inconsistencies among gene ontology concepts. , 2017, , .		7
15021	Classifying gene coexpression networks using state subnetworks. , 2017, , .		0
15022	Mining quasi frequent coexpression subnetworks. , 2017, , .		0
15023	Self-defense of <i>Escherichia coli</i> against damages caused by nanoalumina. <i>Environmental Toxicology and Pharmacology</i> , 2017, 55, 110-117.	2.0	15
15024	Selective Constraints on Coding Sequences of Nervous System Genes Are a Major Determinant of Duplicate Gene Retention in Vertebrates. <i>Molecular Biology and Evolution</i> , 2017, 34, 2773-2791.	3.5	43
15025	Comparative Genome Analysis Reveals Adaptation to the Ectophytic Lifestyle of Sooty Blotch and Flyspeck Fungi. <i>Genome Biology and Evolution</i> , 2017, 9, 3137-3151.	1.1	11
15026	Changes in microRNA expression in the brachial plexus avulsion model of neuropathic pain. <i>International Journal of Molecular Medicine</i> , 2017, 41, 1509-1517.	1.8	13
15027	Computational Methods to Predict Protein Functions from Protein-Protein Interaction Networks. <i>Current Protein and Peptide Science</i> , 2017, 18, 1120-1131.	0.7	8
15028	Bioinformatic analysis of gene expression profiles of pituitary gonadotroph adenomas. <i>Oncology Letters</i> , 2017, 15, 1655-1663.	0.8	10

#	ARTICLE	IF	CITATIONS
15029	Combining ATAC-seq with nuclei sorting for discovery of cis-regulatory regions in plant genomes. <i>Nucleic Acids Research</i> , 2017, 45, e41-e41.	6.5	231
15030	DeepText2Go: Improving large-scale protein function prediction with deep semantic text representation. , 2017, , .		4
15031	Co-expression networks between protein encoding mitochondrial genes and all the remaining genes in human tissues. , 2017, , .		0
15032	Bioinformatical analysis of gene expression signatures of different glioma subtypes. <i>Oncology Letters</i> , 2017, 15, 2807-2814.	0.8	7
15033	A deep learning model for predicting tumor suppressor genes and oncogenes from PDB structure. , 2017, , .		8
15034	Multiple network-constrained regressions expand insights into influenza vaccination responses. <i>Bioinformatics</i> , 2017, 33, i208-i216.	1.8	9
15035	Prevalent function of genome loci associated with development of multiple sclerosis as revealed by GWAS and eQTL analysis. <i>Russian Journal of Genetics</i> , 2017, 53, 982-987.	0.2	0
15036	Enterobacteria virulence factor prediction server. <i>International Journal of Engineering and Technology(UAE)</i> , 2017, 7, 435.	0.2	0
15037	A molecular signature of lung cancer: potential biomarkers for adenocarcinoma and squamous cell carcinoma. <i>Oncotarget</i> , 2017, 8, 105492-105509.	0.8	23
15038	Orchestrating a Network of Mereo(topo)logical Theories. , 2017, , .		6
15039	Transcriptional response profiles of paired tumor-normal samples offer novel perspectives in pan-cancer analysis. <i>Oncotarget</i> , 2017, 8, 41334-41347.	0.8	22
15040	Tree Structure for Expressive MapReduce Framework. , 2017, , .		0
15041	Identification of laryngeal cancer prognostic biomarkers using an inflammatory gene-related, competitive endogenous RNA network. <i>Oncotarget</i> , 2017, 8, 9525-9534.	0.8	19
15043	Gold-standard ontology-based anatomical annotation in the CRAFT Corpus. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	4
15044	Leveraging word embeddings and medical entity extraction for biomedical dataset retrieval using unstructured texts. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	16
15045	Wegweiser durch den Allergendschungel: Allergendatenbanken, ihre Merkmale und Anwendungsgebiete. <i>Karger Kompass Pneumologie</i> , 2017, 5, 138-148.	0.0	0
15047	MiRFFS: a functional group-based feature selection method for the identification of microRNA biomarkers. <i>International Journal of Data Mining and Bioinformatics</i> , 2017, 18, 40.	0.1	4
15048	RDF, the Semantic Web, Jordan, Jordan and Jordan. , 0, , 35-70.		0

#	ARTICLE	IF	CITATIONS
15049	A Transcriptomic Analysis of Physiological Significance of Hypoxia-inducible Factor-1 α in Myogenesis and Carbohydrate Metabolism of Genioglossus in Mice. Chinese Medical Journal, 2017, 130, 1570-1577.	0.9	3
15050	Selected Reaction Monitoring: A Valid Tool for Targeted Quantitation of Protein Biomarker Discovery. Journal of Analytical & Bioanalytical Techniques, 2017, 08, .	0.6	0
15051	Evolution and genome specialization of <i>Brucella suis</i> biovar 2 Iberian lineages. BMC Genomics, 2017, 18, 726.	1.2	11
15052	Transcriptome Profiling in Systems Vascular Medicine. Frontiers in Pharmacology, 2017, 8, 563.	1.6	22
15053	Lower Expression of SLC27A1 Enhances Intramuscular Fat Deposition in Chicken via Down-Regulated Fatty Acid Oxidation Mediated by CPT1A. Frontiers in Physiology, 2017, 8, 449.	1.3	58
15054	Identification and Expression Profiling of Chemosensory Genes in <i>Dendrolimus punctatus</i> Walker. Frontiers in Physiology, 2017, 8, 471.	1.3	37
15055	Update on 13 Syndromes Affecting Craniofacial and Dental Structures. Frontiers in Physiology, 2017, 8, 1038.	1.3	32
15056	An Integrated Analysis of miRNAs and Methylated Genes Encoding mRNAs and lncRNAs in Sheep Breeds with Different Fecundity. Frontiers in Physiology, 2017, 8, 1049.	1.3	30
15057	Heat Stress Regulates the Expression of Genes at Transcriptional and Post-Transcriptional Levels, Revealed by RNA-seq in <i>Brachypodium distachyon</i> . Frontiers in Plant Science, 2016, 7, 2067.	1.7	38
15058	RNA-Seq of Guar (<i>Cyamopsis tetragonoloba</i> , L. Taub.) Leaves: De novo Transcriptome Assembly, Functional Annotation and Development of Genomic Resources. Frontiers in Plant Science, 2017, 8, 91.	1.7	54
15059	Differential Transcriptional Regulation in Roots of Tomato Near-Isogenic Lines in Response to Rapid-Onset Water Stress. Frontiers in Plant Science, 2017, 8, 166.	1.7	4
15060	Global Transcriptome Analysis and Identification of Differentially Expressed Genes in Strawberry after Preharvest Application of Benzothiadiazole and Chitosan. Frontiers in Plant Science, 2017, 8, 235.	1.7	59
15061	Transcriptomic Analysis Reveals Mechanisms of Sterile and Fertile Flower Differentiation and Development in <i>Viburnum macrocephalum</i> f. <i>keteleeri</i> . Frontiers in Plant Science, 2017, 8, 261.	1.7	30
15062	Comparative Analysis of Expression Profiles of Panicle Development among Tolerant and Sensitive Rice in Response to Drought Stress. Frontiers in Plant Science, 2017, 08, 437.	1.7	19
15063	Identification of Candidate Genes and Biosynthesis Pathways Related to Fertility Conversion by Wheat KTM3315A Transcriptome Profiling. Frontiers in Plant Science, 2017, 8, 449.	1.7	31
15064	Transcriptome Analysis of a Female-sterile Mutant (<i>fsm</i>) in Chinese Cabbage (<i>Brassica campestris</i> ssp.) Tj ETQq1 1 0.784314 μ gBT /Over	1.7	16
15065	Insights into the Mechanism of Proliferation on the Special Microbes Mediated by Phenolic Acids in the <i>Radix pseudostellariae</i> Rhizosphere under Continuous Monoculture Regimes. Frontiers in Plant Science, 2017, 8, 659.	1.7	29
15066	Molecular Mechanisms behind the Physiological Resistance to Intense Transient Warming in an Iconic Marine Plant. Frontiers in Plant Science, 2017, 8, 1142.	1.7	59

#	ARTICLE	IF	CITATIONS
15067	Phenotypic and Comparative Transcriptome Analysis of Different Ploidy Plants in <i>Dendrocalamus latiflorus</i> Munro. <i>Frontiers in Plant Science</i> , 2017, 8, 1371.	1.7	14
15068	Identification of Genes under Positive Selection Reveals Differences in Evolutionary Adaptation between Brown-Algal Species. <i>Frontiers in Plant Science</i> , 2017, 8, 1429.	1.7	17
15069	Molecular Resources from Transcriptomes in the Brassicaceae Family. <i>Frontiers in Plant Science</i> , 2017, 8, 1488.	1.7	11
15070	Comparative Genomics of <i>Ralstonia solanacearum</i> Identifies Candidate Genes Associated with Cool Virulence. <i>Frontiers in Plant Science</i> , 2017, 8, 1565.	1.7	25
15071	Novel Insights into miRNA Regulation of Storage Protein Biosynthesis during Wheat Caryopsis Development under Drought Stress. <i>Frontiers in Plant Science</i> , 2017, 8, 1707.	1.7	32
15072	Global Analysis of Small RNA Dynamics during Seed Development of <i>Picea glauca</i> and <i>Arabidopsis thaliana</i> Populations Reveals Insights on their Evolutionary Trajectories. <i>Frontiers in Plant Science</i> , 2017, 8, 1719.	1.7	8
15073	Identification of MsHsp20 Gene Family in <i>Malus sieversii</i> and Functional Characterization of MsHsp16.9 in Heat Tolerance. <i>Frontiers in Plant Science</i> , 2017, 8, 1761.	1.7	31
15074	The Functional Genetics of Handedness and Language Lateralization: Insights from Gene Ontology, Pathway and Disease Association Analyses. <i>Frontiers in Psychology</i> , 2017, 8, 1144.	1.1	28
15075	Big Regeneration Mechanisms via Systems Biology and Big Database Mining Methods. , 2017, , 373-430.		0
15076	<i>Apophysomyces variabilis</i> : draft genome sequence and comparison of predictive virulence determinants with other medically important Mucorales. <i>BMC Genomics</i> , 2017, 18, 736.	1.2	20
15077	Aberrant promoter methylation profiles and association with survival in patients with hepatocellular carcinoma. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 2501-2509.	1.0	10
15078	iTRAQ-based Proteomic Analysis of APPSw,Ind Mice Provides Insights into the Early Changes in Alzheimer's Disease. <i>Current Alzheimer Research</i> , 2017, 14, 1109-1122.	0.7	8
15079	Evaluation of shared genetic aetiology between osteoarthritis and bone mineral density identifies SMAD3 as a novel osteoarthritis risk locus. <i>Human Molecular Genetics</i> , 2017, 26, 3850-3858.	1.4	56
15080	Transcriptome analysis of endometrial tissues following GnRH agonist treatment in a mouse adenomyosis model. <i>Drug Design, Development and Therapy</i> , 2017, Volume11, 695-704.	2.0	7
15081	Characterization of amylolytic enzyme overproducing mutant of <i>Aspergillus luchuensis</i> ; obtained by ion beam mutagenesis. <i>Journal of General and Applied Microbiology</i> , 2017, 63, 339-346.	0.4	5
15082	Leveraging network analytics to infer patient syndrome and identify causal genes in rare disease cases. <i>BMC Genomics</i> , 2017, 18, 551.	1.2	11
15083	Global gene expression reveals stress-responsive genes in <i>Aspergillus fumigatus</i> mycelia. <i>BMC Genomics</i> , 2017, 18, 942.	1.2	25
15084	The impact of RNA sequence library construction protocols on transcriptomic profiling of leukemia. <i>BMC Genomics</i> , 2017, 18, 629.	1.2	42

#	ARTICLE	IF	CITATIONS
15085	Using Next-Generation Sequencing to Detect Differential Expression Genes in <i>Bradysia odoriphaga</i> after Exposure to Insecticides. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2445.	1.8	12
15086	Interpreting whole genome and exome sequencing data of individual gastric cancer samples. <i>BMC Genomics</i> , 2017, 18, 517.	1.2	11
15087	The purplish bifurcate mussel <i>Mytilisepta virgata</i> gene expression atlas reveals a remarkable tissue functional specialization. <i>BMC Genomics</i> , 2017, 18, 590.	1.2	32
15088	Single-cell RNA-Seq analysis reveals dynamic trajectories during mouse liver development. <i>BMC Genomics</i> , 2017, 18, 946.	1.2	70
15089	Genomewide association mapping and pathway analysis of meat tenderness in Polled Nellore cattle ¹ . <i>Journal of Animal Science</i> , 2017, 95, 1945-1956.	0.2	6
15090	Whole-transcriptome analysis delineates the human placenta gene network and its associations with fetal growth. <i>BMC Genomics</i> , 2017, 18, 520.	1.2	53
15091	Systematic Selection of Reference Genes for the Normalization of Circulating RNA Transcripts in Pregnant Women Based on RNA-Seq Data. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1709.	1.8	26
15092	De Novo Assembly and Analysis of <i>Polygonatum sibiricum</i> Transcriptome and Identification of Genes Involved in Polysaccharide Biosynthesis. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1950.	1.8	36
15093	Genome Sequence of <i>Pseudomonas stutzeri</i> 273 and Identification of the Exopolysaccharide EPS273 Biosynthesis Locus. <i>Marine Drugs</i> , 2017, 15, 218.	2.2	16
15094	Using Network Extracted Ontologies to Identify Novel Genes with Roles in Appressorium Development in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Microorganisms</i> , 2017, 5, 3.	1.6	12
15095	ProLanGO: Protein Function Prediction Using Neural Machine Translation Based on a Recurrent Neural Network. <i>Molecules</i> , 2017, 22, 1732.	1.7	151
15096	Biochemical, Physiological and Transcriptomic Comparison between Burley and Flue-Cured Tobacco Seedlings in Relation to Carbohydrates and Nitrate Content. <i>Molecules</i> , 2017, 22, 2126.	1.7	17
15097	Detecting Disease Specific Pathway Substructures through an Integrated Systems Biology Approach. <i>Non-coding RNA</i> , 2017, 3, 20.	1.3	25
15098	Ontology-Based Big Data Management. <i>Systems</i> , 2017, 5, 45.	1.2	24
15099	Label-Free Quantitative Proteomic Analysis of Chitosan Oligosaccharide-Treated Rice Infected with Southern Rice Black-Streaked Dwarf Virus. <i>Viruses</i> , 2017, 9, 115.	1.5	71
15100	Bacterial Virus Ontology; Coordinating across Databases. <i>Viruses</i> , 2017, 9, 126.	1.5	3
15101	Differential regulation of miRNA and mRNA expression in the myocardium of Nrf2 knockout mice. <i>BMC Genomics</i> , 2017, 18, 509.	1.2	16
15102	Cutaneous transcriptome analysis in NIH hairless mice. <i>PLoS ONE</i> , 2017, 12, e0182463.	1.1	25

#	ARTICLE	IF	CITATIONS
15103	Genome sequence of the ectophytic fungus <i>Ramichloridium luteum</i> reveals unique evolutionary adaptations to plant surface niche. <i>BMC Genomics</i> , 2017, 18, 729.	1.2	12
15104	Proteomic mapping of cytosol-facing outer mitochondrial and ER membranes in living human cells by proximity biotinylation. <i>ELife</i> , 2017, 6, .	2.8	276
15105	Handling Big Data in Precision Medicine. , 2017, , 251-268.		3
15106	Advanced Toxicological Risk Assessment by Implementation of Ontologies Operationalized in Computational Models. <i>Applied in Vitro Toxicology</i> , 2017, 3, 325-332.	0.6	8
15107	Equine skeletal muscle adaptations to exercise and training: evidence of differential regulation of autophagosomal and mitochondrial components. <i>BMC Genomics</i> , 2017, 18, 595.	1.2	33
15108	Weighted Gene Co-expression Network Analysis of the Dioscin Rich Medicinal Plant <i>Dioscorea nipponica</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 789.	1.7	21
15109	Melatonin Suppresses Neuropathic Pain via MT2-Dependent and -Independent Pathways in Dorsal Root Ganglia Neurons of Mice. <i>Theranostics</i> , 2017, 7, 2015-2032.	4.6	40
15110	Data Sharing and Reuse. , 2017, , 211-225.		0
15111	CATH: an expanded resource to predict protein function through structure and sequence. <i>Nucleic Acids Research</i> , 2017, 45, D289-D295.	6.5	344
15112	Seven Recommendations to Make Your Invasive Alien Species Data More Useful. <i>Frontiers in Applied Mathematics and Statistics</i> , 2017, 3, .	0.7	29
15113	Navigating the Functional Landscape of Transcription Factors via Non-Negative Tensor Factorization Analysis of MEDLINE Abstracts. <i>Frontiers in Bioengineering and Biotechnology</i> , 2017, 5, 48.	2.0	5
15114	A Hierarchical Multi-Label Classification Algorithm for Gene Function Prediction. <i>Algorithms</i> , 2017, 10, 138.	1.2	13
15115	Simplified Swarm Optimization-Based Function Module Detection in Protein-Protein Interaction Networks. <i>Applied Sciences (Switzerland)</i> , 2017, 7, 412.	1.3	6
15116	Integrative Bioinformatic Analysis of Transcriptomic Data Identifies Conserved Molecular Pathways Underlying Ionizing Radiation-Induced Bystander Effects (RIBE). <i>Cancers</i> , 2017, 9, 160.	1.7	5
15117	Saliva as a Blood Alternative for Genome-Wide DNA Methylation Profiling by Methylated DNA Immunoprecipitation (MeDIP) Sequencing. <i>Epigenomes</i> , 2017, 1, 14.	0.8	8
15118	Expression Profiling in <i>Pinus pinaster</i> in Response to Infection with the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> . <i>Forests</i> , 2017, 8, 279.	0.9	22
15119	Transcriptome Characterization of the Chinese Fir (<i>Cunninghamia lanceolata</i> (Lamb.) Hook.) and Expression Analysis of Candidate Phosphate Transporter Genes. <i>Forests</i> , 2017, 8, 420.	0.9	6
15120	Non-Coding RNAs in Lung Cancer: Contribution of Bioinformatics Analysis to the Development of Non-Invasive Diagnostic Tools. <i>Genes</i> , 2017, 8, 8.	1.0	28

#	ARTICLE	IF	CITATIONS
15121	Fine Mapping and Transcriptome Analysis Reveal Candidate Genes Associated with Hybrid Lethality in Cabbage (<i>Brassica Oleracea</i>). <i>Genes</i> , 2017, 8, 147.	1.0	15
15122	Viral Infection Identifies Micropeptides Differentially Regulated in smORF-Containing lncRNAs. <i>Genes</i> , 2017, 8, 206.	1.0	50
15123	Transcription Factors Responding to Pb Stress in Maize. <i>Genes</i> , 2017, 8, 231.	1.0	35
15124	Hybrid Sequencing of Full-Length cDNA Transcripts of Stems and Leaves in <i>Dendrobium officinale</i> . <i>Genes</i> , 2017, 8, 257.	1.0	20
15125	The Plasticizer Bisphenol A Perturbs the Hepatic Epigenome: A Systems Level Analysis of the miRNome. <i>Genes</i> , 2017, 8, 269.	1.0	28
15126	Differential Expression of Serum MicroRNAs Supports CD4+ T Cell Differentiation into Th2/Th17 Cells in Severe Equine Asthma. <i>Genes</i> , 2017, 8, 383.	1.0	39
15127	Identification of Key Candidate Genes and Pathways in Colorectal Cancer by Integrated Bioinformatical Analysis. <i>International Journal of Molecular Sciences</i> , 2017, 18, 722.	1.8	132
15128	Delineating the Common Biological Pathways Perturbed by ASD's Genetic Etiology: Lessons from Network-Based Studies. <i>International Journal of Molecular Sciences</i> , 2017, 18, 828.	1.8	25
15129	In-Depth Proteomic Analysis of the Hippocampus in a Rat Model after Cerebral Ischaemic Injury and Repair by Danhong Injection (DHI). <i>International Journal of Molecular Sciences</i> , 2017, 18, 1355.	1.8	25
15130	Methylated cis-regulatory elements mediate KLF4-dependent gene transactivation and cell migration. <i>ELife</i> , 2017, 6, .	2.8	39
15131	Systematic integration of biomedical knowledge prioritizes drugs for repurposing. <i>ELife</i> , 2017, 6, .	2.8	333
15132	Empirical Comparison of Visualization Tools for Larger-Scale Network Analysis. <i>Advances in Bioinformatics</i> , 2017, 2017, 1-8.	5.7	44
15133	The Distinct Transcriptional Response of the Midgut of <i>Amblyomma sculptum</i> and <i>Amblyomma aureolatum</i> Ticks to <i>Rickettsia rickettsii</i> Correlates to Their Differences in Susceptibility to Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 129.	1.8	23
15134	The Proteome of Biologically Active Membrane Vesicles from <i>Piscirickettsia salmonis</i> LF-89 Type Strain Identifies Plasmid-Encoded Putative Toxins. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 420.	1.8	22
15135	Systemic Responses of Multidrug-Resistant <i>Pseudomonas aeruginosa</i> and <i>Acinetobacter baumannii</i> Following Exposure to the Antimicrobial Peptide Cathelicidin-BF Imply Multiple Intracellular Targets. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 466.	1.8	17
15136	Analysis of the Salivary Gland Transcriptome of Unfed and Partially Fed <i>Amblyomma sculptum</i> Ticks and Descriptive Proteome of the Saliva. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 476.	1.8	79
15137	Disease Risk Assessment Using a Voronoi-Based Network Analysis of Genes and Variants Scores. <i>Frontiers in Genetics</i> , 2017, 8, 29.	1.1	0
15138	Deletion Extents Are Not the Cause of Clinical Variability in 22q11.2 Deletion Syndrome: Does the Interaction between DGCR8 and miRNA-CNVs Play a Major Role?. <i>Frontiers in Genetics</i> , 2017, 8, 47.	1.1	13

#	ARTICLE	IF	CITATIONS
15139	A Preliminary List of Horizontally Transferred Genes in Prokaryotes Determined by Tree Reconstruction and Reconciliation. <i>Frontiers in Genetics</i> , 2017, 8, 112.	1.1	11
15140	<i>Triportheus albus</i> Cope, 1872 in the Blackwater, Clearwater, and Whitewater of the Amazon: A Case of Phenotypic Plasticity?. <i>Frontiers in Genetics</i> , 2017, 8, 114.	1.1	16
15141	Identification and Characterization of MicroRNAs in the Goat (<i>Capra hircus</i>) Rumen during Embryonic Development. <i>Frontiers in Genetics</i> , 2017, 8, 163.	1.1	14
15142	Co-Inflammatory Roles of TGF β 1 in the Presence of TNF α Drive a Pro-inflammatory Fate in Mesenchymal Stem Cells. <i>Frontiers in Immunology</i> , 2017, 8, 479.	2.2	27
15143	<i>Mycobacterium bovis</i> Bacillus Calmette-Guérin Alters Melanoma Microenvironment Favoring Antitumor T Cell Responses and Improving M2 Macrophage Function. <i>Frontiers in Immunology</i> , 2017, 8, 965.	2.2	32
15144	Microarray Analysis Identifies the Potential Role of Long Non-Coding RNA in Regulating Neuroinflammation during Japanese Encephalitis Virus Infection. <i>Frontiers in Immunology</i> , 2017, 8, 1237.	2.2	22
15145	Robust Inference of Genetic Exchange Communities from Microbial Genomes Using TF-IDF. <i>Frontiers in Microbiology</i> , 2017, 8, 21.	1.5	14
15146	Distribution of Secretion Systems in the Genus <i>Legionella</i> and Its Correlation with Pathogenicity. <i>Frontiers in Microbiology</i> , 2017, 08, 388.	1.5	18
15147	Comparative Genomics Analysis of a New Exiguobacterium Strain from Salar de Huasco Reveals a Repertoire of Stress-Related Genes and Arsenic Resistance. <i>Frontiers in Microbiology</i> , 2017, 8, 456.	1.5	55
15148	Genome Sequencing Reveals the Complex Polysaccharide-Degrading Ability of Novel Deep-Sea Bacterium <i>Flammeovirga pacifica</i> WPAGA1. <i>Frontiers in Microbiology</i> , 2017, 8, 600.	1.5	40
15149	Transcriptome Analysis of <i>Arabidopsis thaliana</i> in Response to <i>Plasmodiophora brassicae</i> during Early Infection. <i>Frontiers in Microbiology</i> , 2017, 8, 673.	1.5	60
15150	Computational Exploration of Putative LuxR Solos in Archaea and Their Functional Implications in Quorum Sensing. <i>Frontiers in Microbiology</i> , 2017, 8, 798.	1.5	22
15151	Food Safety in the Age of Next Generation Sequencing, Bioinformatics, and Open Data Access. <i>Frontiers in Microbiology</i> , 2017, 8, 909.	1.5	87
15152	Genome-Wide Mapping of Transcriptional Regulation and Metabolism Describes Information-Processing Units in <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1466.	1.5	17
15153	Protein-Protein Interactions in Virus-Host Systems. <i>Frontiers in Microbiology</i> , 2017, 8, 1557.	1.5	113
15154	Metatranscriptomics Reveals the Functions and Enzyme Profiles of the Microbial Community in Chinese Nong-Flavor Liquor Starter. <i>Frontiers in Microbiology</i> , 2017, 8, 1747.	1.5	68
15155	iTRAQ Proteomic Analysis Reveals That Metabolic Pathways Involving Energy Metabolism Are Affected by Tea Tree Oil in <i>Botrytis cinerea</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1989.	1.5	23
15156	pH Stress-Induced Cooperation between <i>Rhodococcus ruber</i> YYL and <i>Bacillus cereus</i> MLY1 in Biodegradation of Tetrahydrofuran. <i>Frontiers in Microbiology</i> , 2017, 8, 2297.	1.5	25

#	ARTICLE	IF	CITATIONS
15157	A Comprehensive Overview of Online Resources to Identify and Predict Bacterial Essential Genes. <i>Frontiers in Microbiology</i> , 2017, 8, 2331.	1.5	44
15158	Reduced Circulating Levels of miR-433 and miR-133b Are Potential Biomarkers for Parkinson's Disease. <i>Frontiers in Cellular Neuroscience</i> , 2017, 11, 170.	1.8	54
15159	Computer-Aided Experiment Planning toward Causal Discovery in Neuroscience. <i>Frontiers in Neuroinformatics</i> , 2017, 11, 12.	1.3	6
15160	Extending XNAT Platform with an Incremental Semantic Framework. <i>Frontiers in Neuroinformatics</i> , 2017, 11, 57.	1.3	5
15161	Exosomes and Homeostatic Synaptic Plasticity Are Linked to Each other and to Huntington's, Parkinson's, and Other Neurodegenerative Diseases by Database-Enabled Analyses of Comprehensively Curated Datasets. <i>Frontiers in Neuroscience</i> , 2017, 11, 149.	1.4	50
15162	The Biological Function of the Prion Protein: A Cell Surface Scaffold of Signaling Modules. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 77.	1.4	105
15163	Integrated Computational Analysis of Genes Associated with Human Hereditary Insensitivity to Pain. A Drug Repurposing Perspective. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 252.	1.4	10
15164	Dorsal and Ventral Hippocampus Differentiate in Functional Pathways and Differentially Associate with Neurological Disease-Related Genes during Postnatal Development. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 331.	1.4	57
15165	Gene Set Analysis: As Applied to Public Health and Biomedical Studies. <i>Handbook of Statistics</i> , 2017, 36, 205-227.	0.4	0
15166	An Integrative Genomics Approach for Associating Genome-Wide Association Studies Information With Localized and Metastatic Prostate Cancer Phenotypes. <i>Biomarker Insights</i> , 2017, 12, 117727191769581.	1.0	4
15167	PAIRS: Prediction of Activation/Inhibition Regulation Signaling Pathway. <i>Computational Intelligence and Neuroscience</i> , 2017, 2017, 1-5.	1.1	5
15168	Protein Function Prediction Using Deep Restricted Boltzmann Machines. <i>BioMed Research International</i> , 2017, 2017, 1-9.	0.9	10
15169	Microarray Analysis and Detection of MicroRNAs Associated with Chronic Thromboembolic Pulmonary Hypertension. <i>BioMed Research International</i> , 2017, 2017, 1-9.	0.9	17
15170	Bacterial colonization stimulates a complex physiological response in the immature human intestinal epithelium. <i>ELife</i> , 2017, 6, .	2.8	132
15171	Identification of Transcriptional Modules and Key Genes in Chickens Infected with <i>Salmonella enterica</i> Serovar Pullorum Using Integrated Coexpression Analyses. <i>BioMed Research International</i> , 2017, 2017, 1-12.	0.9	8
15172	Native KCC2 interactome reveals PACSIN1 as a critical regulator of synaptic inhibition. <i>ELife</i> , 2017, 6, .	2.8	44
15173	The ESRP1-GPR137 axis contributes to intestinal pathogenesis. <i>ELife</i> , 2017, 6, .	2.8	24
15174	A comparative transcriptomic analysis of replicating and dormant liver stages of the relapsing malaria parasite <i>Plasmodium cynomolgi</i> . <i>ELife</i> , 2017, 6, .	2.8	56

#	ARTICLE	IF	CITATIONS
15175	LPS-induced modules of co-expressed genes in equine peripheral blood mononuclear cells. <i>BMC Genomics</i> , 2017, 18, 34.	1.2	12
15176	The Effect of the Human Peptide GHK on Gene Expression Relevant to Nervous System Function and Cognitive Decline. <i>Brain Sciences</i> , 2017, 7, 20.	1.1	35
15177	Differently expressed long noncoding RNAs and mRNAs in TK6 cells exposed to low dose hydroquinone. <i>Oncotarget</i> , 2017, 8, 95554-95567.	0.8	9
15178	SFMetaDB: a comprehensive annotation of mouse RNA splicing factor RNA-Seq datasets. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	12
15179	Genome-wide imaging association study implicates functional activity and glial homeostasis of the caudate in smoking addiction. <i>BMC Genomics</i> , 2017, 18, 740.	1.2	7
15180	Reduced expression of miR-205-5p promotes apoptosis and inhibits proliferation and invasion in lung cancer A549 cells by upregulation of ZEB2 and downregulation of erbB3. <i>Molecular Medicine Reports</i> , 2017, 15, 3231-3238.	1.1	27
15181	Comparative transcriptomic analysis identifies reprogramming and differentiation genes differentially expressed in UiPSCs and ESCs. <i>BioScience Trends</i> , 2017, 11, 355-359.	1.1	1
15182	Weighted gene co-expression network analysis of expression data of monozygotic twins identifies specific modules and hub genes related to BMI. <i>BMC Genomics</i> , 2017, 18, 872.	1.2	53
15183	Expression profile of mitochondrial voltage-dependent anion channel-1 (VDAC1) influenced genes is associated with pulmonary hypertension. <i>Korean Journal of Physiology and Pharmacology</i> , 2017, 21, 353.	0.6	3
15184	Automatic identification of informative regions with epigenomic changes associated to hematopoiesis. <i>Nucleic Acids Research</i> , 2017, 45, 9244-9259.	6.5	19
15185	Use of biological priors enhances understanding of genetic architecture and genomic prediction of complex traits within and between dairy cattle breeds. <i>BMC Genomics</i> , 2017, 18, 604.	1.2	43
15186	Assisted clustering of gene expression data using ANCut. <i>BMC Genomics</i> , 2017, 18, 623.	1.2	10
15187	miRNA alteration is an important mechanism in sugarcane response to low-temperature environment. <i>BMC Genomics</i> , 2017, 18, 833.	1.2	61
15188	Specific MicroRNA Pattern in Colon Tissue of Young Children with Eosinophilic Colitis. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1050.	1.8	2
15189	EUCANEXT: an integrated database for the exploration of genomic and transcriptomic data from Eucalyptus species. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	12
15190	De novo transcriptome analysis shows differential expression of genes in salivary glands of edible bird's nest producing swiftlets. <i>BMC Genomics</i> , 2017, 18, 504.	1.2	9
15191	Gene and miRNA expression profiles in PBMCs from patients with severe and mild emphysema and PiZZ alpha1-antitrypsin deficiency. <i>International Journal of COPD</i> , 2017, Volume 12, 3381-3390.	0.9	21
15192	Linking Hematopoietic Differentiation to Co-Expressed Sets of Pluripotency-Associated and Imprinted Genes and to Regulatory microRNA-Transcription Factor Motifs. <i>PLoS ONE</i> , 2017, 12, e0166852.	1.1	7

#	ARTICLE	IF	CITATIONS
15193	Integration of MicroRNA, mRNA, and Protein Expression Data for the Identification of Cancer-Related MicroRNAs. PLoS ONE, 2017, 12, e0168412.	1.1	40
15194	Network Centrality Analysis in Fungi Reveals Complex Regulation of Lost and Gained Genes. PLoS ONE, 2017, 12, e0169459.	1.1	12
15195	Underexpression of Specific Interferon Genes Is Associated with Poor Prognosis of Melanoma. PLoS ONE, 2017, 12, e0170025.	1.1	12
15196	The ins and outs of eukaryotic viruses: Knowledge base and ontology of a viral infection. PLoS ONE, 2017, 12, e0171746.	1.1	7
15197	The essential and downstream common proteins of amyotrophic lateral sclerosis: A protein-protein interaction network analysis. PLoS ONE, 2017, 12, e0172246.	1.1	14
15198	De novo assembly of the sea trout (<i>Salmo trutta m. trutta</i>) skin transcriptome to identify putative genes involved in the immune response and epidermal mucus secretion. PLoS ONE, 2017, 12, e0172282.	1.1	34
15199	The amyloid interactome: Exploring protein aggregation. PLoS ONE, 2017, 12, e0173163.	1.1	25
15200	Olfactory effects of a hypervariable multicomponent pheromone in the red-legged salamander, <i>Plethodon shermani</i> . PLoS ONE, 2017, 12, e0174370.	1.1	7
15201	Computational identifying and characterizing circular RNAs and their associated genes in hepatocellular carcinoma. PLoS ONE, 2017, 12, e0174436.	1.1	18
15202	Constructing a biodiversity terminological inventory. PLoS ONE, 2017, 12, e0175277.	1.1	12
15203	Transcriptome and proteome responses in RNAlater preserved tissue of <i>Arabidopsis thaliana</i> . PLoS ONE, 2017, 12, e0175943.	1.1	38
15204	The natural history of molecular functions inferred from an extensive phylogenomic analysis of gene ontology data. PLoS ONE, 2017, 12, e0176129.	1.1	12
15205	Tracking disease progression by searching paths in a temporal network of biological processes. PLoS ONE, 2017, 12, e0176172.	1.1	6
15206	De novo assembly and comparative transcriptome analysis of the foot from Chinese green mussel (<i>Perna viridis</i>) in response to cadmium stimulation. PLoS ONE, 2017, 12, e0176677.	1.1	18
15207	A new two-stage method for revealing missing parts of edges in protein-protein interaction networks. PLoS ONE, 2017, 12, e0177029.	1.1	1
15208	De novo transcriptome assembly and quantification reveal differentially expressed genes between soft-seed and hard-seed pomegranate (<i>Punica granatum L.</i>). PLoS ONE, 2017, 12, e0178809.	1.1	34
15209	Predicting human protein subcellular localization by heterogeneous and comprehensive approaches. PLoS ONE, 2017, 12, e0178832.	1.1	10
15210	A sorghum (<i>Sorghum bicolor</i>) mutant with altered carbon isotope ratio. PLoS ONE, 2017, 12, e0179567.	1.1	5

#	ARTICLE	IF	CITATIONS
15211	WetA bridges cellular and chemical development in <i>Aspergillus flavus</i> . PLoS ONE, 2017, 12, e0179571.	1.1	48
15212	Prediction of novel target genes and pathways involved in irinotecan-resistant colorectal cancer. PLoS ONE, 2017, 12, e0180616.	1.1	22
15213	De novo assembly of a transcriptome from the eggs and early embryos of <i>Astropecten aranciatus</i> . PLoS ONE, 2017, 12, e0184090.	1.1	9
15214	The mouse <i>Jhy</i> gene regulates ependymal cell differentiation and ciliogenesis. PLoS ONE, 2017, 12, e0184957.	1.1	15
15215	Transcriptome analysis of Callery pear (<i>Pyrus calleryana</i>) reveals a comprehensive signalling network in response to <i>Alternaria alternata</i> . PLoS ONE, 2017, 12, e0184988.	1.1	16
15216	Meta-analysis of peripheral blood gene expression modules for COPD phenotypes. PLoS ONE, 2017, 12, e0185682.	1.1	17
15217	Transcriptome analysis of mRNA and microRNAs in intramuscular fat tissues of castrated and intact male Chinese Qinchuan cattle. PLoS ONE, 2017, 12, e0185961.	1.1	31
15218	Post-weaning epiphyseolysis causes distal femur dysplasia and foreshortened hindlimbs in fetuin-A-deficient mice. PLoS ONE, 2017, 12, e0187030.	1.1	20
15219	ChIP-Seq analysis identifies p27(Kip1)-target genes involved in cell adhesion and cell signalling in mouse embryonic fibroblasts. PLoS ONE, 2017, 12, e0187891.	1.1	11
15220	Mechanisms of action of <i>Coxiella burnetii</i> effectors inferred from host-pathogen protein interactions. PLoS ONE, 2017, 12, e0188071.	1.1	12
15221	The integration of weighted gene association networks based on information entropy. PLoS ONE, 2017, 12, e0190029.	1.1	6
15222	Opposing roles of Toll-like receptor and cytosolic DNA-STING signaling pathways for <i>Staphylococcus aureus</i> cutaneous host defense. PLoS Pathogens, 2017, 13, e1006496.	2.1	61
15223	A conserved maternal-specific repressive domain in <i>Zelda</i> revealed by Cas9-mediated mutagenesis in <i>Drosophila melanogaster</i> . PLoS Genetics, 2017, 13, e1007120.	1.5	36
15224	A high resolution atlas of gene expression in the domestic sheep (<i>Ovis aries</i>). PLoS Genetics, 2017, 13, e1006997.	1.5	210
15225	Identification of shared risk loci and pathways for bipolar disorder and schizophrenia. PLoS ONE, 2017, 12, e0171595.	1.1	77
15226	Transcriptome analysis of muskrat scented glands degeneration mechanism. PLoS ONE, 2017, 12, e0176935.	1.1	7
15227	A density-based approach for detecting complexes in weighted PPI networks by semantic similarity. PLoS ONE, 2017, 12, e0180570.	1.1	10
15228	Semantic prioritization of novel causative genomic variants. PLoS Computational Biology, 2017, 13, e1005500.	1.5	28

#	ARTICLE	IF	CITATIONS
15229	Analysis of temporal transcription expression profiles reveal links between protein function and developmental stages of <i>Drosophila melanogaster</i> . <i>PLoS Computational Biology</i> , 2017, 13, e1005791.	1.5	12
15230	Diverse type 2 diabetes genetic risk factors functionally converge in a phenotype-focused gene network. <i>PLoS Computational Biology</i> , 2017, 13, e1005816.	1.5	15
15231	The highly buffered <i>Arabidopsis</i> immune signaling network conceals the functions of its components. <i>PLoS Genetics</i> , 2017, 13, e1006639.	1.5	138
15232	High rate of adaptation of mammalian proteins that interact with <i>Plasmodium</i> and related parasites. <i>PLoS Genetics</i> , 2017, 13, e1007023.	1.5	37
15233	The combinatorial control of alternative splicing in <i>C. elegans</i> . <i>PLoS Genetics</i> , 2017, 13, e1007033.	1.5	10
15234	Transcriptomic responses of <i>Biomphalaria pfeifferi</i> to <i>Schistosoma mansoni</i> : Investigation of a neglected African snail that supports more <i>S. mansoni</i> transmission than any other snail species. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005984.	1.3	30
15235	Draft Genome Sequence of <i>Lactobacillus brevis</i> Strain 3M004, a Probiotic with Potential Quorum-Sensing Regulation. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
15236	Strength of functional signature correlates with effect size in autism. <i>Genome Medicine</i> , 2017, 9, 64.	3.6	12
15237	Complete genome of a novel virulent phage ST0 lysing <i>Escherichia coli</i> H8. <i>Standards in Genomic Sciences</i> , 2017, 12, 85.	1.5	2
15238	First gene-ontology enrichment analysis based on bacterial coregenome variants: insights into adaptations of <i>Salmonella</i> serovars to mammalian- and avian-hosts. <i>BMC Microbiology</i> , 2017, 17, 222.	1.3	41
15239	Genome-wide trait-trait dynamics correlation study dissects the gene regulation pattern in maize kernels. <i>BMC Plant Biology</i> , 2017, 17, 163.	1.6	5
15240	A post-gene silencing bioinformatics protocol for plant-defence gene validation and underlying process identification: case study of the <i>Arabidopsis thaliana</i> NPR1. <i>BMC Plant Biology</i> , 2017, 17, 218.	1.6	5
15241	Hedgehog inhibitor sonidegib potentiates 177Lu-octreotate therapy of GOT1 human small intestine neuroendocrine tumors in nude mice. <i>BMC Cancer</i> , 2017, 17, 528.	1.1	24
15242	Guanylate-binding protein-1 is a potential new therapeutic target for triple-negative breast cancer. <i>BMC Cancer</i> , 2017, 17, 727.	1.1	34
15243	Lightweight predicate extraction for patient-level cancer information and ontology development. <i>BMC Medical Informatics and Decision Making</i> , 2017, 17, 73.	1.5	8
15244	Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive <i>Helicoverpa</i> pest species. <i>BMC Biology</i> , 2017, 15, 63.	1.7	238
15245	Whole transcriptome RNA-Seq analysis reveals extensive cell type-specific compartmentalization in <i>Volvox carteri</i> . <i>BMC Biology</i> , 2017, 15, 111.	1.7	19
15246	NetGen: a novel network-based probabilistic generative model for gene set functional enrichment analysis. <i>BMC Systems Biology</i> , 2017, 11, 75.	3.0	3

#	ARTICLE	IF	CITATIONS
15247	Reconstructing cancer drug response networks using multitask learning. <i>BMC Systems Biology</i> , 2017, 11, 96.	3.0	5
15248	Graph-theoretical comparison of normal and tumor networks in identifying BRCA genes. <i>BMC Systems Biology</i> , 2017, 11, 110.	3.0	14
15249	RNA sequencing identifies novel non-coding RNA and exon-specific effects associated with cigarette smoking. <i>BMC Medical Genomics</i> , 2017, 10, 58.	0.7	48
15250	Measuring disease similarity and predicting disease-related ncRNAs by a novel method. <i>BMC Medical Genomics</i> , 2017, 10, 71.	0.7	49
15251	Platform-independent gene expression signature differentiates sessile serrated adenomas/polyps and hyperplastic polyps of the colon. <i>BMC Medical Genomics</i> , 2017, 10, 81.	0.7	14
15252	Integrated genomic characterization of cancer genes in glioma. <i>Cancer Cell International</i> , 2017, 17, 90.	1.8	47
15253	Identification of genes and pathways potentially related to PHF20 by gene expression profile analysis of glioblastoma U87 cell line. <i>Cancer Cell International</i> , 2017, 17, 87.	1.8	9
15254	Identification of differential genomic DNA Methylation in the hypothalamus of pubertal rat using reduced representation Bisulfite sequencing. <i>Reproductive Biology and Endocrinology</i> , 2017, 15, 81.	1.4	18
15255	The Human Behaviour-Change Project: harnessing the power of artificial intelligence and machine learning for evidence synthesis and interpretation. <i>Implementation Science</i> , 2017, 12, 121.	2.5	216
15256	A time-course microarray data analysis reveals consistent dysregulated genes and upstream microRNAs in autoantibody-mediated arthritis. <i>Journal of Orthopaedic Surgery and Research</i> , 2017, 12, 186.	0.9	1
15257	Dissecting the role of non-coding RNAs in the accumulation of amyloid and tau neuropathologies in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2017, 12, 51.	4.4	70
15258	Time-resolved transcriptome analysis and lipid pathway reconstruction of the oleaginous green microalga <i>Monoraphidium neglectum</i> reveal a model for triacylglycerol and lipid hyperaccumulation. <i>Biotechnology for Biofuels</i> , 2017, 10, 197.	6.2	35
15259	Transcriptomic characterization of <i>Caecomyces churrovis</i> : a novel, non-rhizoid-forming lignocellulolytic anaerobic fungus. <i>Biotechnology for Biofuels</i> , 2017, 10, 305.	6.2	70
15260	β -Carboxymuconolactone decarboxylase: a novel cell cycle-related basal body protein in the early branching eukaryote <i>Trichomonas vaginalis</i> . <i>Parasites and Vectors</i> , 2017, 10, 443.	1.0	2
15261	Genome-wide profiling of transcribed enhancers during macrophage activation. <i>Epigenetics and Chromatin</i> , 2017, 10, 50.	1.8	41
15262	Granatum: a graphical single-cell RNA-Seq analysis pipeline for genomics scientists. <i>Genome Medicine</i> , 2017, 9, 108.	3.6	63
15263	Complete genome sequence of the <i>Vibrio vulnificus</i> strain VV2014DJH, a human-pathogenic bacterium isolated from a death case in China. <i>Gut Pathogens</i> , 2017, 9, 67.	1.6	4
15264	DisSetSim: an online system for calculating similarity between disease sets. <i>Journal of Biomedical Semantics</i> , 2017, 8, 28.	0.9	17

#	ARTICLE	IF	CITATIONS
15265	Investigations on factors influencing HPO-based semantic similarity calculation. <i>Journal of Biomedical Semantics</i> , 2017, 8, 34.	0.9	3
15266	Entity recognition in the biomedical domain using a hybrid approach. <i>Journal of Biomedical Semantics</i> , 2017, 8, 51.	0.9	34
15267	Integrating phenotype ontologies with PhenomeNET. <i>Journal of Biomedical Semantics</i> , 2017, 8, 58.	0.9	28
15268	Production of poly- β -glutamic acid by a thermotolerant glutamate-independent strain and comparative analysis of the glutamate dependent difference. <i>AMB Express</i> , 2017, 7, 213.	1.4	16
15269	The Gene Ontology of eukaryotic cilia and flagella. <i>Cilia</i> , 2017, 6, 10.	1.8	6
15270	Deciphering Gene Sets Annotations with Ontology Based Visualization. , 2017, , .		1
15271	CellNetVis: a web tool for visualization of biological networks using force-directed layout constrained by cellular components. <i>BMC Bioinformatics</i> , 2017, 18, 395.	1.2	20
15272	Mimvec: a deep learning approach for analyzing the human phenome. <i>BMC Systems Biology</i> , 2017, 11, 76.	3.0	5
15273	Comparison of multiple transcriptomes exposes unified and divergent features of quiescent and activated skeletal muscle stem cells. <i>Skeletal Muscle</i> , 2017, 7, 28.	1.9	29
15274	Genome of Russian wheat aphid an economically important cereal aphid. <i>Standards in Genomic Sciences</i> , 2017, 12, 90.	1.5	25
15275	Integrative biological simulation praxis: Considerations from physics, philosophy, and data/model curation practices. <i>Cellular Logistics</i> , 2017, 7, e1392400.	0.9	5
15276	Complete genome sequence of <i>Microbulbifer</i> sp. CCB-MM1, a halophile isolated from Matang Mangrove Forest, Malaysia. <i>Standards in Genomic Sciences</i> , 2017, 12, 36.	1.5	11
15277	The genome of the cotton bacterial blight pathogen <i>Xanthomonas citri</i> pv. <i>malvacearum</i> strain MSCT1. <i>Standards in Genomic Sciences</i> , 2017, 12, 42.	1.5	7
15278	Insights into <i>Cedecea neteri</i> strain M006 through complete genome sequence, a rare bacterium from aquatic environment. <i>Standards in Genomic Sciences</i> , 2017, 12, 40.	1.5	24
15279	Complete genome sequence of the sand-sediment actinobacterium <i>Nocardioides dokdonensis</i> FR1436T. <i>Standards in Genomic Sciences</i> , 2017, 12, 44.	1.5	4
15280	High-quality genome sequence of the radioresistant bacterium <i>Deinococcus ficus</i> KS 0460. <i>Standards in Genomic Sciences</i> , 2017, 12, 46.	1.5	10
15281	Draft genome sequences of two opportunistic pathogenic strains of <i>Staphylococcus cohnii</i> isolated from human patients. <i>Standards in Genomic Sciences</i> , 2017, 12, 49.	1.5	11
15282	Genome sequence of the sulfur-oxidizing <i>Bathymodiolus thermophilus</i> gill endosymbiont. <i>Standards in Genomic Sciences</i> , 2017, 12, 50.	1.5	32

#	ARTICLE	IF	CITATIONS
15283	Genome sequence of the white-rot fungus <i>Irpex lacteus</i> F17, a type strain of lignin degrader fungus. Standards in Genomic Sciences, 2017, 12, 55.	1.5	15
15284	High-quality draft genome sequence of <i>Ensifer meliloti</i> Mlalz-1, a microsymbiont of <i>Medicago laciniata</i> (L.) miller collected in Lanzarote, Canary Islands, Spain. Standards in Genomic Sciences, 2017, 12, 58.	1.5	0
15285	Complete genome sequence of <i>Thermotoga</i> sp. strain RQ7. Standards in Genomic Sciences, 2017, 12, 62.	1.5	9
15286	Draft genome sequence and characterization of commensal <i>Escherichia coli</i> strain BG1 isolated from bovine gastro-intestinal tract. Standards in Genomic Sciences, 2017, 12, 61.	1.5	9
15287	High-quality-draft genomic sequence of <i>Paenibacillus ferrarius</i> CY1T with the potential to bioremediate Cd, Cr and Se contamination. Standards in Genomic Sciences, 2017, 12, 60.	1.5	4
15288	First draft genome sequence of a strain belonging to the <i>Zoogloea</i> genus and its gene expression in situ. Standards in Genomic Sciences, 2017, 12, 64.	1.5	8
15289	Draft genome sequence of <i>Marinobacterium rhizophilum</i> CL-YJ9T (DSM 18822T), isolated from the rhizosphere of the coastal tidal-flat plant <i>Suaeda japonica</i> . Standards in Genomic Sciences, 2017, 12, 65.	1.5	1
15290	Genomic insights into the thiamin metabolism of <i>Paenibacillus thiaminolyticus</i> NRRL B-4156 and <i>P. apiarius</i> NRRL B-23460. Standards in Genomic Sciences, 2017, 12, 59.	1.5	5
15291	Complete genome sequence of <i>Paenibacillus yonginensis</i> DCY84T, a novel plant Symbiont that promotes growth via induced systemic resistance. Standards in Genomic Sciences, 2017, 12, 63.	1.5	13
15292	Complete genome sequence of <i>Pseudomonas corrugata</i> strain RM1-1-4, a stress protecting agent from the rhizosphere of an oilseed rape bait plant. Standards in Genomic Sciences, 2017, 12, 66.	1.5	4
15293	Draft genome sequence of <i>Venturia carpophila</i> , the causal agent of peach scab. Standards in Genomic Sciences, 2017, 12, 68.	1.5	22
15294	Genome overview of eight <i>Candida boidinii</i> strains isolated from human activities and wild environments. Standards in Genomic Sciences, 2017, 12, 70.	1.5	13
15295	Draft genome sequence of the type strain of the sulfur-oxidizing acidophile, <i>Acidithiobacillus albertensis</i> (DSM 14366). Standards in Genomic Sciences, 2017, 12, 77.	1.5	17
15296	Draft genome sequences of <i>Bradyrhizobium shewense</i> sp. nov. ERR11T and <i>Bradyrhizobium yuanmingense</i> CCBAU 10071T. Standards in Genomic Sciences, 2017, 12, 74.	1.5	29
15297	The complete genome sequence of the rumen bacterium <i>Butyrivibrio hungatei</i> MB2003. Standards in Genomic Sciences, 2017, 12, 72.	1.5	29
15298	The genomic study of an environmental isolate of <i>Scedosporium apiospermum</i> shows its metabolic potential to degrade hydrocarbons. Standards in Genomic Sciences, 2017, 12, 71.	1.5	25
15299	Draft genome sequence of <i>Bacillus velezensis</i> 2A-2B strain: a rhizospheric inhabitant of <i>Sporobolus airoides</i> (Torr.) Torr., with antifungal activity against root rot causing phytopathogens. Standards in Genomic Sciences, 2017, 12, 73.	1.5	26
15300	Draft genome sequence of <i>Pseudomonas extremaustralis</i> strain USBA-GBX 515 isolated from Superparamo soil samples in Colombian Andes. Standards in Genomic Sciences, 2017, 12, 78.	1.5	7

#	ARTICLE	IF	CITATIONS
15301	Draft genome of <i>Paraburkholderia caballeronis</i> TNe-841T, a free-living, nitrogen-fixing, tomato plant-associated bacterium. <i>Standards in Genomic Sciences</i> , 2017, 12, 80.	1.5	7
15302	Genome sequence of <i>Acuticoccus yangtzensis</i> JL1095T (DSM 28604T) isolated from the Yangtze Estuary. <i>Standards in Genomic Sciences</i> , 2017, 12, 91.	1.5	4
15303	Complete genome sequence analysis of <i>Archaeoglobus fulgidus</i> strain 7324 (DSM 8774), a hyperthermophilic archaeal sulfate reducer from a North Sea oil field. <i>Standards in Genomic Sciences</i> , 2017, 12, 79.	1.5	19
15304	Complete genome sequence of esterase-producing bacterium <i>Croceicoccus marinus</i> E4A9T. <i>Standards in Genomic Sciences</i> , 2017, 12, 88.	1.5	4
15305	Genome sequence of the model plant pathogen <i>Pectobacterium carotovorum</i> SCC1. <i>Standards in Genomic Sciences</i> , 2017, 12, 87.	1.5	16
15306	Draft genome sequence of <i>Dethiosulfovibrio salsuginis</i> DSM 21565T an anaerobic, slightly halophilic bacterium isolated from a Colombian saline spring. <i>Standards in Genomic Sciences</i> , 2017, 12, 86.	1.5	0
15307	Draft genome sequence of <i>Acidithiobacillus thiooxidans</i> CLST isolated from the acidic hypersaline Gorbea salt flat in northern Chile. <i>Standards in Genomic Sciences</i> , 2017, 12, 84.	1.5	20
15308	Differentially expressed miRNAs in hepatocellular carcinoma cells under hypoxic conditions are associated with transcription and phosphorylation. <i>Oncology Letters</i> , 2017, 15, 467-474.	0.8	11
15309	Assessment of genome annotation using gene function similarity within the gene neighborhood. <i>BMC Bioinformatics</i> , 2017, 18, 345.	1.2	5
15310	NoGOA: predicting noisy GO annotations using evidences and sparse representation. <i>BMC Bioinformatics</i> , 2017, 18, 350.	1.2	13
15311	ODG: Omics database generator - a tool for generating, querying, and analyzing multi-omics comparative databases to facilitate biological understanding. <i>BMC Bioinformatics</i> , 2017, 18, 367.	1.2	13
15312	BUFET: boosting the unbiased miRNA functional enrichment analysis using bitsets. <i>BMC Bioinformatics</i> , 2017, 18, 399.	1.2	9
15313	Prediction of Human Phenotype Ontology terms by means of hierarchical ensemble methods. <i>BMC Bioinformatics</i> , 2017, 18, 449.	1.2	22
15314	A rapid and accurate approach for prediction of interactomes from co-elution data (PrInCE). <i>BMC Bioinformatics</i> , 2017, 18, 457.	1.2	54
15315	A multi-network clustering method for detecting protein complexes from multiple heterogeneous networks. <i>BMC Bioinformatics</i> , 2017, 18, 463.	1.2	21
15316	ADAGE signature analysis: differential expression analysis with data-defined gene sets. <i>BMC Bioinformatics</i> , 2017, 18, 512.	1.2	17
15317	LiverWiki: a wiki-based database for human liver. <i>BMC Bioinformatics</i> , 2017, 18, 452.	1.2	4
15318	Complete genome sequence of the sulfur-oxidizing chemolithoautotrophic <i>Sulfurovum lithotrophicum</i> 42BKTT. <i>Standards in Genomic Sciences</i> , 2017, 12, 54.	1.5	17

#	ARTICLE	IF	CITATIONS
15319	Genome-wide meta-analysis in Japanese populations identifies novel variants at the TMC6â€“TMC8 and SIX3â€“SIX2 loci associated with HbA1c. <i>Scientific Reports</i> , 2017, 7, 16147.	1.6	28
15320	A practical guide to filtering and prioritizing genetic variants. <i>BioTechniques</i> , 2017, 62, 18-30.	0.8	57
15321	The Grass Carp Genome Database (GCGD): an online platform for genome features and annotations. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	14
15322	GOstruct 2.0. , 2017, , .		8
15323	Leveraging Online Resources to Prioritize Candidate Genes for Functional Analyses: Using the Fetal Testis as a Test Case. <i>Sexual Development</i> , 2017, 11, 1-20.	1.1	4
15324	<i>miR-9a</i> mediates the role of Lethal giant larvae as an epithelial growth inhibitor in <i>Drosophila</i>. <i>Biology Open</i> , 2018, 7, .	0.6	6
15325	Landscape of fluid sets of hairpin-derived 21-/24-nt-long small RNAs at seed set uncovers special epigenetic features in <i>Picea glauca</i>. <i>Genome Biology and Evolution</i> , 2017, 9, evw283.	1.1	34
15326	Long non-coding RNA associated-competing endogenous RNAs are induced by clusterin in retinal pigment epithelial cells. <i>Molecular Medicine Reports</i> , 2017, 16, 8399-8405.	1.1	10
15327	Proposal of application method of Inductive Logic Programming to microarray data. , 2017, , .		0
15328	Exploring the key genes and pathways in enchondromas using a gene expression microarray. <i>Oncotarget</i> , 2017, 8, 43967-43977.	0.8	7
15329	Characterization of the <i>Rosellinia necatrix</i> Transcriptome and Genes Related to Pathogenesis by Single-Molecule mRNA Sequencing. <i>Plant Pathology Journal</i> , 2017, 33, 362-369.	0.7	5
15330	Integrated analysis reveals candidate genes and transcription factors in lung adenocarcinoma. <i>Molecular Medicine Reports</i> , 2017, 16, 8371-8379.	1.1	4
15331	High expression of long nonâ€“coding HOTAIR correlated with hepatocarcinogenesis and metastasis. <i>Molecular Medicine Reports</i> , 2017, 17, 1148-1156.	1.1	20
15332	Comprehensive microRNA-sequencing of exosomes derived from head and neck carcinoma cells<i> in vitro</i> reveals common secretion profiles and potential utility as salivary biomarkers. <i>Oncotarget</i> , 2017, 8, 82459-82474.	0.8	80
15333	Screening and validation of differentially expressed extracellular miRNAs in acute pancreatitis. <i>Molecular Medicine Reports</i> , 2017, 16, 6412-6418.	1.1	11
15334	Genome-wide DNA methylation analysis in permanent atrial fibrillation. <i>Molecular Medicine Reports</i> , 2017, 16, 5505-5514.	1.1	23
15335	Extracting compact representation of knowledge from gene expression data for protein-protein interaction. <i>International Journal of Data Mining and Bioinformatics</i> , 2017, 17, 279.	0.1	1
15336	The Plani Plant Animation Framework. <i>International Journal of Computer Graphics & Animation</i> , 2017, 7, 1-20.	0.3	0

#	ARTICLE	IF	CITATIONS
15337	Isocitrate dehydrogenase mutations suppress STAT1 and CD8+ T cell accumulation in gliomas. <i>Journal of Clinical Investigation</i> , 2017, 127, 1425-1437.	3.9	334
15338	A dual-strategy expression screen for candidate connectivity labels in the developing thalamus. <i>PLoS ONE</i> , 2017, 12, e0177977.	1.1	11
15339	Structural Chemogenomics Databases to Navigate Protein-Ligand Interaction Space. , 2017, , 444-471.		1
15340	Genenames.org: the HGNC and VGNC resources in 2017. <i>Nucleic Acids Research</i> , 2017, 45, D619-D625.	6.5	308
15341	Transcriptome (ESTs) of Avocado -Native-Mexicano Early Seed Development Shows Abundance of Regulatory, Antioxidant and Defense Genes. , 0, , .		0
15342	Computational Challenges and -omics Approaches for the Identification of microRNAs and Targets. , 2017, , 39-59.		1
15343	Mouse Genome Database (MGD)-2017: community knowledge resource for the laboratory mouse. <i>Nucleic Acids Research</i> , 2017, 45, D723-D729.	6.5	255
15344	Bioinformatic analysis of computational identified differentially expressed genes in tumor stoma of pregnancy-associated breast cancer. <i>Molecular Medicine Reports</i> , 2017, 16, 3345-3350.	1.1	5
15345	Transcriptomic profiling of genes in matured dimorphic seeds of euhalophyte Suaeda salsa. <i>BMC Genomics</i> , 2017, 18, 727.	1.2	27
15346	Identification of the anticancer effects of a novel proteasome inhibitor, ixazomib, on colorectal cancer using a combined method of microarray and bioinformatics analysis. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 3591-3606.	1.0	13
15347	Auditing National Cancer Institute thesaurus neoplasm concepts in groups of high error concentration. <i>Applied Ontology</i> , 2017, 12, 113-130.	1.0	3
15348	Bioinformatics analysis of key genes and signaling pathways associated with myocardial infarction following telomerase activation. <i>Molecular Medicine Reports</i> , 2017, 16, 2915-2924.	1.1	2
15349	Proteomic analysis of lung metastases in a murine breast cancer model reveals divergent influence of CTSB and CTSL overexpression. <i>Journal of Cancer</i> , 2017, 8, 4065-4074.	1.2	10
15350	Peripheral leukocyte microRNAs as novel biomarkers for COPD. <i>International Journal of COPD</i> , 2017, Volume 12, 1101-1112.	0.9	18
15351	Identification of the Sex-Biased Gene Expression and Putative Sex-Associated Genes in <i>Eucommia ulmoides</i> Oliver Using Comparative Transcriptome Analyses. <i>Molecules</i> , 2017, 22, 2255.	1.7	16
15352	Genes Interacting with Occupational Exposures to Low Molecular Weight Agents and Irritants on Adult-Onset Asthma in Three European Studies. <i>Environmental Health Perspectives</i> , 2017, 125, 207-214.	2.8	23
15353	Association of 15-hydroxyprostaglandin dehydrogenase and poor prognosis of obese breast cancer patients. <i>Oncotarget</i> , 2017, 8, 22842-22853.	0.8	8
15354	Identification of novel genetic etiology and key molecular pathways for seminoma via network-based studies. <i>International Journal of Oncology</i> , 2017, 51, 1280-1290.	1.4	13

#	ARTICLE	IF	CITATIONS
15355	Mapping the function of neuronal ion channels in model and experiment. <i>ELife</i> , 2017, 6, .	2.8	33
15356	Detecting the genetic link between Alzheimer's disease and obesity using bioinformatics analysis of GWAS data. <i>Oncotarget</i> , 2017, 8, 55915-55919.	0.8	14
15357	Understanding protein-protein interaction networks from conserved patterns to conserved controllability. <i>International Journal of Data Mining and Bioinformatics</i> , 2017, 19, 168.	0.1	0
15358	cFLIP critically modulates apoptotic resistance in epithelial-to-mesenchymal transition. <i>Oncotarget</i> , 2017, 8, 101072-101086.	0.8	6
15359	Identification of core genes and outcome in gastric cancer using bioinformatics analysis. <i>Oncotarget</i> , 2017, 8, 70271-70280.	0.8	118
15360	A 16-gene signature predicting prognosis of patients with oral tongue squamous cell carcinoma. <i>PeerJ</i> , 2017, 5, e4062.	0.9	23
15361	Differential expression of circulating biomarkers of tumor phenotype and outcomes in previously treated non-small cell lung cancer patients receiving erlotinib vs. cytotoxic chemotherapy. <i>Oncotarget</i> , 2017, 8, 58108-58121.	0.8	7
15362	Identification of crucial genes associated with Parkinson's disease using microarray data. <i>Molecular Medicine Reports</i> , 2017, 17, 3775-3782.	1.1	4
15363	Bioinformatics analysis of the CDK2 functions in neuroblastoma. <i>Molecular Medicine Reports</i> , 2017, 17, 3951-3959.	1.1	9
15364	Fish Ontology framework for taxonomy-based fish recognition. <i>PeerJ</i> , 2017, 5, e3811.	0.9	8
15365	Pupylation sites prediction with ensemble classification model. <i>International Journal of Data Mining and Bioinformatics</i> , 2017, 18, 91.	0.1	46
15366	Functional 5â€™ UTR motif discovery with LESMoN: Local Enrichment of Sequence Motifs in biological Networks. <i>Nucleic Acids Research</i> , 2017, 45, 10415-10427.	6.5	9
15367	Pathway crosstalk analysis in prostate cancer based on protein-protein network data. <i>Neoplasma</i> , 2017, 64, 22-31.	0.7	17
15368	A comprehensive analysis of candidate gene signatures in oral squamous cell carcinoma. <i>Neoplasma</i> , 2017, 64, 167-174.	0.7	4
15369	Screening key miRNAs for human hepatocellular carcinoma based on miRNA-mRNA functional synergistic network. <i>Neoplasma</i> , 2017, 64, 816-823.	0.7	14
15370	Identification of potential key genes associated with diffuse large B-cell lymphoma based on microarray gene expression profiling. <i>Neoplasma</i> , 2017, 64, 824-833.	0.7	4
15371	Genome Sequencing Revealed Chromium and Other Heavy Metal Resistance Genes in <i>E. cloacae</i> B2-Dha. <i>Journal of Microbial & Biochemical Technology</i> , 2017, 9, .	0.2	2
15372	BRWLDA: bi-random walks for predicting lncRNA-disease associations. <i>Oncotarget</i> , 2017, 8, 60429-60446.	0.8	67

#	ARTICLE	IF	CITATIONS
15373	Big Drug Design Mechanisms via Systems Biology and Big Database Mining. , 2017, , 737-845.		1
15374	Nucleosome Positioning of Intronless Genes in the Human Genome. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1111-1121.	1.9	3
15375	Investigating the impact human protein-protein interaction networks have on disease-gene analysis. <i>International Journal of Machine Learning and Cybernetics</i> , 2018, 9, 455-464.	2.3	10
15376	hsa-mir183/EGR1-mediated regulation of E2F1 is required for CML stem/progenitor cell survival. <i>Blood</i> , 2018, 131, 1532-1544.	0.6	40
15377	Inflammatory Cytokines Induce Podoplanin Expression at the Tumor Invasive Front. <i>American Journal of Pathology</i> , 2018, 188, 1276-1288.	1.9	28
15378	Improved genomic resources and new bioinformatic workflow for the carcinogenic parasite <i>Clonorchis sinensis</i> : Biotechnological implications. <i>Biotechnology Advances</i> , 2018, 36, 894-904.	6.0	20
15379	mRNA chip-based analysis on transcription factor regulatory network central nodes of protection targets of Deproteinized Extract of Calf Blood on acute liver injury in mice. <i>International Immunopharmacology</i> , 2018, 56, 212-216.	1.7	1
15380	Exploring autophagy with Gene Ontology. <i>Autophagy</i> , 2018, 14, 419-436.	4.3	64
15381	Cystic Fibrosis, Cystic Fibrosis Transmembrane Conductance Regulator and Drugs: Insights from Cellular Trafficking. <i>Handbook of Experimental Pharmacology</i> , 2018, 245, 385-425.	0.9	10
15382	Complete genome sequence of the marine <i>Rhodococcus</i> sp. H-CA8f isolated from Comau fjord in Northern Patagonia, Chile. <i>Marine Genomics</i> , 2018, 40, 13-17.	0.4	9
15383	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 317-332.	21.5	263
15384	Mendelian Disease Associations Reveal Novel Insights into Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 471-481.	0.9	5
15385	Mutational Pleiotropy and the Strength of Stabilizing Selection Within and Between Functional Modules of Gene Expression. <i>Genetics</i> , 2018, 208, 1601-1616.	1.2	14
15386	Gene expression in retinal ischemic post-conditioning. <i>Graefe's Archive for Clinical and Experimental Ophthalmology</i> , 2018, 256, 935-949.	1.0	8
15387	Transcriptome analysis of wheat seedling and spike tissues in the hybrid Jingmai 8 uncovered genes involved in heterosis. <i>Planta</i> , 2018, 247, 1307-1321.	1.6	32
15388	The Immunome of Colon Cancer: Functional In Silico Analysis of Antigenic Proteins Deduced from IgG Microarray Profiling. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 73-84.	3.0	21
15389	Identification of functional modules induced by bare-metal stents and paclitaxel-eluting stents in coronary heart disease. <i>Experimental and Therapeutic Medicine</i> , 2018, 15, 3801-3808.	0.8	2
15390	Transcriptomic studies in tolerance: Lessons learned and the path forward. <i>Human Immunology</i> , 2018, 79, 395-401.	1.2	6

#	ARTICLE	IF	CITATIONS
15391	GOLabeler: improving sequence-based large-scale protein function prediction by learning to rank. <i>Bioinformatics</i> , 2018, 34, 2465-2473.	1.8	136
15392	Brain-specific functional relationship networks inform autism spectrum disorder gene prediction. <i>Translational Psychiatry</i> , 2018, 8, 56.	2.4	61
15393	A multi-omic analysis reveals the regulatory role of CD180 during the response of macrophages to <i>Borrelia burgdorferi</i> . <i>Emerging Microbes and Infections</i> , 2018, 7, 1-13.	3.0	9
15394	Gene expression of indoor fungal communities under damp building conditions: Implications for human health. <i>Indoor Air</i> , 2018, 28, 548-558.	2.0	34
15395	Primate fetal hepatic responses to maternal obesity: epigenetic signalling pathways and lipid accumulation. <i>Journal of Physiology</i> , 2018, 596, 5823-5837.	1.3	51
15396	Toward an integrated map of genetic interactions in cancer cells. <i>Molecular Systems Biology</i> , 2018, 14, e7656.	3.2	64
15397	Discovering Fuzzy Structural Patterns for Graph Analytics. <i>IEEE Transactions on Fuzzy Systems</i> , 2018, 26, 2785-2796.	6.5	31
15398	Brick : Metadata schema for portable smart building applications. <i>Applied Energy</i> , 2018, 226, 1273-1292.	5.1	129
15399	Revealing <i>Mytilus galloprovincialis</i> transcriptomic profiles during ontogeny. <i>Developmental and Comparative Immunology</i> , 2018, 84, 292-306.	1.0	18
15400	A Novel Computational Approach for Global Alignment for Multiple Biological Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 2060-2066.	1.9	13
15401	Quantitative Models for Microscopic to Macroscopic Biological Macromolecules and Tissues. , 2018, , .		3
15402	Evolution, functional differentiation, and co-expression of the RLK gene family revealed in Jilin ginseng, <i>Panax ginseng</i> C.A. Meyer. <i>Molecular Genetics and Genomics</i> , 2018, 293, 845-859.	1.0	14
15403	De novo transcriptome analysis of abiotic stress-responsive transcripts of <i>Hevea brasiliensis</i> . <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	15
15404	Convergent downstream candidate mechanisms of independent intergenic polymorphisms between co-classified diseases implicate epistasis among noncoding elements. , 2018, , .		1
15405	Analysis of the miRNA-mRNA-lncRNA network in human estrogen receptor-positive and estrogen receptor-negative breast cancer based on TCGA data. <i>Gene</i> , 2018, 658, 28-35.	1.0	67
15406	Gene expression network regulated by DNA methylation and microRNA during microcystin-leucine arginine induced malignant transformation in human hepatocyte L02 cells. <i>Toxicology Letters</i> , 2018, 289, 42-53.	0.4	37
15407	Spatiotemporal compartmentalization of hepatic NADH and NADPH metabolism. <i>Journal of Biological Chemistry</i> , 2018, 293, 7508-7516.	1.6	81
15408	A Novel Five-Node Feed-Forward Loop Unravels miRNA-Gene-TF Regulatory Relationships in Ischemic Stroke. <i>Molecular Neurobiology</i> , 2018, 55, 8251-8262.	1.9	12

#	ARTICLE	IF	CITATIONS
15409	Association study between copy number variation and beef fatty acid profile of Nellore cattle. <i>Journal of Applied Genetics</i> , 2018, 59, 203-223.	1.0	29
15410	MetaGO: Predicting Gene Ontology of Non-homologous Proteins Through Low-Resolution Protein Structure Prediction and Protein-Protein Network Mapping. <i>Journal of Molecular Biology</i> , 2018, 430, 2256-2265.	2.0	58
15411	Genome-wide transcriptome analysis identifies alternative splicing regulatory network and key splicing factors in mouse and human psoriasis. <i>Scientific Reports</i> , 2018, 8, 4124.	1.6	20
15412	Gene expression differs in susceptible and resistant amphibians exposed to <i>Batrachochytrium dendrobatidis</i> . <i>Royal Society Open Science</i> , 2018, 5, 170910.	1.1	37
15413	From systems biology to P4 medicine: applications in respiratory medicine. <i>European Respiratory Review</i> , 2018, 27, 170110.	3.0	35
15414	MicroRNAs, Gene's Regulator in Prostate Cancer. , 2018, , 21-36.		0
15415	β^2 -adrenergic receptor-mediated negative regulation of group 2 innate lymphoid cell responses. <i>Science</i> , 2018, 359, 1056-1061.	6.0	262
15416	Photoperiodic control of the <i>Arabidopsis</i> proteome reveals a translational coincidence mechanism. <i>Molecular Systems Biology</i> , 2018, 14, e7962.	3.2	74
15417	The genome sequence of 'Kurodagosun', a major carrot variety in Japan and China, reveals insights into biological research and carrot breeding. <i>Molecular Genetics and Genomics</i> , 2018, 293, 861-871.	1.0	27
15418	Comparative proteomic analysis of ovaries from Huoyan geese between pre-laying and laying periods using an iTRAQ-based approach. <i>Poultry Science</i> , 2018, 97, 2170-2182.	1.5	8
15419	Gene expression profile analysis of the progression of carotid atherosclerotic plaques. <i>Molecular Medicine Reports</i> , 2018, 17, 5789-5795.	1.1	11
15420	Genetic variants in two pathways influence serum urate levels and gout risk: a systematic pathway analysis. <i>Scientific Reports</i> , 2018, 8, 3848.	1.6	5
15421	SABIO-RK: an updated resource for manually curated biochemical reaction kinetics. <i>Nucleic Acids Research</i> , 2018, 46, D656-D660.	6.5	92
15422	Pretreatment with cholesterol-loaded cyclodextrins prevents loss of motility associated proteins during cryopreservation of addra gazelle (<i>Nanger dama ruficollis</i>) spermatozoa. <i>Cryobiology</i> , 2018, 81, 74-80.	0.3	14
15423	Interleukins and their signaling pathways in the Reactome biological pathway database. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1411-1416.	1.5	11
15424	Managing big RDF data in clouds: Challenges, opportunities, and solutions. <i>Sustainable Cities and Society</i> , 2018, 39, 375-386.	5.1	29
15425	Landscape of the spliced leader trans-splicing mechanism in <i>Schistosoma mansoni</i> . <i>Scientific Reports</i> , 2018, 8, 3877.	1.6	20
15426	Identification of genomic differences among peripheral arterial beds in atherosclerotic and healthy arteries. <i>Scientific Reports</i> , 2018, 8, 3940.	1.6	78

#	ARTICLE	IF	CITATIONS
15427	Quantitative proteomic and phosphoproteomic comparison of human colon cancer DLD-1 cells differing in ploidy and chromosome stability. <i>Molecular Biology of the Cell</i> , 2018, 29, 1031-1047.	0.9	41
15428	Transcriptome analysis of flax (<i>Linum usitatissimum</i> L.) undergoing osmotic stress. <i>Industrial Crops and Products</i> , 2018, 116, 215-223.	2.5	22
15429	Complete genomic analysis of multidrug-resistance <i>Pseudomonas aeruginosa</i> Guangzhou-Pae617, the host of megaplasmid pBM413. <i>Microbial Pathogenesis</i> , 2018, 117, 265-269.	1.3	9
15430	The Differentially Expressed Genes of Human Sporadic Cerebral Cavernous Malformations. <i>World Neurosurgery</i> , 2018, 113, e247-e270.	0.7	4
15431	Comprehensive analysis of long noncoding RNA and mRNA expression patterns in sheep testicular maturation. <i>Biology of Reproduction</i> , 2018, 99, 650-661.	1.2	47
15432	Menin regulates the serine biosynthetic pathway in Ewing sarcoma. <i>Journal of Pathology</i> , 2018, 245, 324-336.	2.1	35
15433	Transcriptome profiling of genes involved in photosynthesis in <i>Elaeagnus angustifolia</i> L. under salt stress. <i>Photosynthetica</i> , 2018, 56, 998-1009.	0.9	56
15434	Proteome-wide analysis of cysteine oxidation reveals metabolic sensitivity to redox stress. <i>Nature Communications</i> , 2018, 9, 1581.	5.8	178
15435	Starvation during pregnancy impairs fetal oogenesis and folliculogenesis in offspring in the mouse. <i>Cell Death and Disease</i> , 2018, 9, 452.	2.7	17
15436	Network-Based Approaches for Pathway Level Analysis. <i>Current Protocols in Bioinformatics</i> , 2018, 61, 8.25.1-8.25.24.	25.8	33
15437	Clustering of multi-domain protein sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 759-776.	1.5	2
15438	Switch of Mitochondrial Superoxide Dismutase into a Prooxidant Peroxidase in Manganese-Deficient Cells and Mice. <i>Cell Chemical Biology</i> , 2018, 25, 413-425.e6.	2.5	36
15439	Transcriptomic Analysis of Xylan Oligosaccharide Utilization Systems in <i>Pediococcus acidilactici</i> Strain BCC-1. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 4725-4733.	2.4	21
15440	Proteomic Analysis of Cancer-Associated Fibroblasts Reveals a Paracrine Role for MFAP5 in Human Oral Tongue Squamous Cell Carcinoma. <i>Journal of Proteome Research</i> , 2018, 17, 2045-2059.	1.8	65
15441	Implications of publicly available genomic data resources in searching for therapeutic targets of obesity and type 2 diabetes. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-13.	3.2	2
15442	Gene Expression Analysis in Human Peripheral Blood Cells after 900 MHz RF-EMF Short-Term Exposure. <i>Radiation Research</i> , 2018, 189, 529-540.	0.7	6
15443	A B-ARR-mediated cytokinin transcriptional network directs hormone cross-regulation and shoot development. <i>Nature Communications</i> , 2018, 9, 1604.	5.8	130
15444	Cardiac recovery via extended cell-free delivery of extracellular vesicles secreted by cardiomyocytes derived from induced pluripotent stem cells. <i>Nature Biomedical Engineering</i> , 2018, 2, 293-303.	11.6	249

#	ARTICLE	IF	CITATIONS
15445	Systemic surfaceome profiling identifies target antigens for immune-based therapy in subtypes of advanced prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4473-E4482.	3.3	96
15446	EMUDRA: Ensemble of Multiple Drug Repositioning Approaches to improve prediction accuracy. Bioinformatics, 2018, 34, 3151-3159.	1.8	30
15447	Novel sequencing technologies to support industrial biotechnology. FEMS Microbiology Letters, 2018, 365, .	0.7	15
15448	Chromosome-scale assembly of the Monopterus genome. GigaScience, 2018, 7, .	3.3	30
15449	Targeting of RNA Polymerase II by a nuclear <i>Legionella pneumophila</i> Dot/Icm effector SnpL. Cellular Microbiology, 2018, 20, e12852.	1.1	21
15450	Molecular cloning, expression, and functional characterization of the $\hat{2}$ -agarase AgaB-4 from <i>Paenibacillus agarexedens</i> . AMB Express, 2018, 8, 49.	1.4	11
15451	K-means Clustering: An Efficient Algorithm for Protein Complex Detection. Advances in Intelligent Systems and Computing, 2018, , 449-459.	0.5	1
15452	Transcriptomics reveals a cross-modulatory effect between riboflavin and iron and outlines responses to riboflavin biosynthesis and uptake in <i>Vibrio cholerae</i> . Scientific Reports, 2018, 8, 3149.	1.6	17
15453	Detecting signatures of positive selection in non-model species using genomic data. Zoological Journal of the Linnean Society, 2018, 184, 528-583.	1.0	67
15454	Transcriptome characterization and screening of molecular markers in ecologically important Himalayan species (<i>Rhododendron arboreum</i>). Genome, 2018, 61, 417-428.	0.9	18
15455	Characterization of the complete mitochondrial genome of <i>Metastrongylus salmi</i> (<i>M. salmi</i>) derived from Tibetan pigs in Tibet, China. Acta Parasitologica, 2018, 63, 280-286.	0.4	3
15456	Analysis of potential genes and pathways associated with the colorectal normal mucosa-adenoma-carcinoma sequence. Cancer Medicine, 2018, 7, 2555-2566.	1.3	42
15457	Fish red blood cells express immune genes and responses. Aquaculture and Fisheries, 2018, 3, 14-21.	1.2	63
15458	Transcriptome of the bivalve <i>Limecola balthica</i> L. from Western Pacific: A new resource for studies of European populations. Marine Genomics, 2018, 40, 58-63.	0.4	4
15459	The non-human primate kidney transcriptome in fetal development. Journal of Medical Primatology, 2018, 47, 157-171.	0.3	3
15460	TGF- $\hat{2}$ 1 resulting in differential microRNA expression in bovine granulosa cells. Gene, 2018, 663, 88-100.	1.0	15
15461	Predicting protein submitochondrial locations by incorporating the pseudo-position specific scoring matrix into the general Chou's pseudo-amino acid composition. Journal of Theoretical Biology, 2018, 450, 86-103.	0.8	72
15462	Multiscale analysis of a regenerative therapy for treatment of volumetric muscle loss injury. Cell Death Discovery, 2018, 4, 33.	2.0	93

#	ARTICLE	IF	CITATIONS
15463	Whole Genome Sequence of an Edible and Potential Medicinal Fungus, <i>Cordyceps guangdongensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1863-1870.	0.8	23
15464	Expression of scavenger receptor <i>MARCO</i> defines a targetable tumor-associated macrophage subset in non-small cell lung cancer. <i>International Journal of Cancer</i> , 2018, 143, 1741-1752.	2.3	65
15465	Whole-genome sequence and genome annotation of <i>Xanthomonas citri</i> pv. <i>mangiferae</i> indicae, causal agent of bacterial black spot on <i>Mangifera indica</i> . <i>Archives of Microbiology</i> , 2018, 200, 835-840.	1.0	4
15466	Genomic prediction applied to high-biomass sorghum for bioenergy production. <i>Molecular Breeding</i> , 2018, 38, 49.	1.0	28
15467	Comparative proteomics analysis of human and ruminant milk serum reveals variation in protection and nutrition. <i>Food Chemistry</i> , 2018, 261, 274-282.	4.2	46
15468	A postprocessing method in the HMC framework for predicting gene function based on biological instrumental data. <i>Review of Scientific Instruments</i> , 2018, 89, 034302.	0.6	0
15469	Searching and Extracting Data from the EMBL-EBI Complex Portal. <i>Methods in Molecular Biology</i> , 2018, 1764, 377-390.	0.4	7
15470	Cancer drug target identification and node-level analysis of the network of MAPK pathways. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2018, 7, 1.	1.2	2
15471	Key gene co-expression modules and functional pathways involved in the pathogenesis of Graves' disease. <i>Molecular and Cellular Endocrinology</i> , 2018, 474, 252-259.	1.6	12
15472	The latent geometry of the human protein interaction network. <i>Bioinformatics</i> , 2018, 34, 2826-2834.	1.8	24
15473	MTGO: PPI Network Analysis Via Topological and Functional Module Identification. <i>Scientific Reports</i> , 2018, 8, 5499.	1.6	103
15474	De novo draft assembly of the <i>Botryllodes leachii</i> genome provides further insight into tunicate evolution. <i>Scientific Reports</i> , 2018, 8, 5518.	1.6	36
15475	Prognostic Significance of LncRNA PVT1 and Its Potential Target Gene Network in Human Cancers: a Comprehensive Inquiry Based Upon 21 Cancer Types and 9972 Cases. <i>Cellular Physiology and Biochemistry</i> , 2018, 46, 591-608.	1.1	16
15476	Understanding antidepressant discontinuation syndrome (ADS) through preclinical experimental models. <i>European Journal of Pharmacology</i> , 2018, 829, 129-140.	1.7	12
15477	A Beginner's Guide to Analysis of RNA Sequencing Data. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 59, 145-157.	1.4	78
15478	A comprehensive analysis of the predicted targets of miR-642b-3p associated with the long non-coding RNA HOXA11-AS in NSCLC cells. <i>Oncology Letters</i> , 2018, 15, 6147-6160.	0.8	17
15479	Global and gene-specific DNA methylation effects of different asbestos fibres on human bronchial epithelial cells. <i>Environment International</i> , 2018, 115, 301-311.	4.8	10
15480	Circular RNA expression profiles of mouse ovaries during postnatal development and the function of circular RNA epidermal growth factor receptor in granulosa cells. <i>Metabolism: Clinical and Experimental</i> , 2018, 85, 192-204.	1.5	47

#	ARTICLE	IF	CITATIONS
15481	Protein CoAlation and antioxidant function of coenzyme A in prokaryotic cells. <i>Biochemical Journal</i> , 2018, 475, 1909-1937.	1.7	60
15482	Insect symbionts as valuable grist for the biotechnological mill: an alkaliphilic silkworm gut bacterium for efficient lactic acid production. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 4951-4962.	1.7	33
15483	Human Sertoli cells support high levels of Zika virus replication and persistence. <i>Scientific Reports</i> , 2018, 8, 5477.	1.6	75
15484	Experimental validation of predicted cancer genes using FRET. <i>Methods and Applications in Fluorescence</i> , 2018, 6, 035007.	1.1	2
15485	Open chromatin dynamics reveals stage-specific transcriptional networks in hiPSC-based neurodevelopmental model. <i>Stem Cell Research</i> , 2018, 29, 88-98.	0.3	18
15486	Massive mining of publicly available RNA-seq data from human and mouse. <i>Nature Communications</i> , 2018, 9, 1366.	5.8	507
15487	Profiling expression of coding genes, long noncoding <scp>RNA</scp>, and circular <scp>RNA</scp> in lung adenocarcinoma by ribosomal <scp>RNA</scp>-depleted <scp>RNA</scp> sequencing. <i>FEBS Open Bio</i> , 2018, 8, 544-555.	1.0	54
15488	A resource for sustainable management: De novo assembly and annotation of the liver transcriptome of the Atlantic chub mackerel, <i>Scomber colias</i> . <i>Data in Brief</i> , 2018, 18, 276-284.	0.5	7
15489	Genomic signatures of parasite-driven natural selection in north European Atlantic salmon (<i>Salmo</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.4	15
15490	Peripherally derived macrophages can engraft the brain independent of irradiation and maintain an identity distinct from microglia. <i>Journal of Experimental Medicine</i> , 2018, 215, 1627-1647.	4.2	281
15491	Biological signaling pathways and potential mathematical network representations: biological discovery through optimization. <i>Cancer Medicine</i> , 2018, 7, 1875-1895.	1.3	4
15492	Molecular Correlates of In Vitro Responses to Dacomitinib and Afatinib in Bladder Cancer. <i>Bladder Cancer</i> , 2018, 4, 77-90.	0.2	19
15493	Ranked Gene Ontology Based Protein Function Prediction by Analysis of Protein-Protein Interactions. <i>Advances in Intelligent Systems and Computing</i> , 2018, , 419-427.	0.5	3
15494	Lymphatic exosomes promote dendritic cell migration along guidance cues. <i>Journal of Cell Biology</i> , 2018, 217, 2205-2221.	2.3	57
15495	De novo transcriptome assembly and analysis of differential gene expression following peptidoglycan (PGN) challenge in <i>Antheraea pernyi</i> . <i>International Journal of Biological Macromolecules</i> , 2018, 112, 1199-1207.	3.6	8
15496	The R2R3 transcription factor HIMYB8 and its role in flavonoid biosynthesis in hop (<i>Humulus lupulus</i>) Tj ETQq1 1 0.784314 rgBT/Over to	1.7	24
15497	Comparative analysis of low complexity regions in Plasmodia. <i>Scientific Reports</i> , 2018, 8, 335.	1.6	20
15498	In vitro RNA-seq-based toxicogenomics assessment shows reduced biological effect of tobacco heating products when compared to cigarette smoke. <i>Scientific Reports</i> , 2018, 8, 1145.	1.6	31

#	ARTICLE	IF	CITATIONS
15499	GO FEAT: a rapid web-based functional annotation tool for genomic and transcriptomic data. <i>Scientific Reports</i> , 2018, 8, 1794.	1.6	99
15500	High-throughput sequencing analysis revealed the regulation patterns of small RNAs on the development of <i>A. comosus</i> var. <i>bracteatus</i> leaves. <i>Scientific Reports</i> , 2018, 8, 1947.	1.6	11
15501	Quantification of glioblastoma mass effect by lateral ventricle displacement. <i>Scientific Reports</i> , 2018, 8, 2827.	1.6	23
15502	Inhibition of Endothelial NOTCH1 Signaling Attenuates Inflammation by Reducing Cytokine-Mediated Histone Acetylation at Inflammatory Enhancers. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, 854-869.	1.1	37
15503	AOP-DB: A database resource for the exploration of Adverse Outcome Pathways through integrated association networks. <i>Toxicology and Applied Pharmacology</i> , 2018, 343, 71-83.	1.3	59
15504	Draft genomes of two blister beetles <i>Hycleus cichorii</i> and <i>Hycleus phaleratus</i> . <i>GigaScience</i> , 2018, 7, 1-7.	3.3	30
15505	Increased proteomic complexity in <i>Drosophila</i> hybrids during development. <i>Science Advances</i> , 2018, 4, eaao3424.	4.7	12
15506	New insight into sludge reduction induced by different substrate allocation strategy between oxygen and nitrate/nitrite as terminal electron acceptor. <i>Bioresource Technology</i> , 2018, 257, 7-16.	4.8	16
15507	Dual transcriptomics reveals co-evolutionary mechanisms of intestinal parasite infections in blue mussels <i>Mytilus edulis</i> . <i>Molecular Ecology</i> , 2018, 27, 1505-1519.	2.0	15
15508	QTLs for susceptibility to <i>Stemphylium vesicarium</i> in pear. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	7
15509	CrosstalkNet: A Visualization Tool for Differential Co-expression Networks and Communities. <i>Cancer Research</i> , 2018, 78, 2140-2143.	0.4	1
15510	Integrated analysis of gene expression signatures associated with colon cancer from three datasets. <i>Gene</i> , 2018, 654, 95-102.	1.0	26
15511	Effects of Qijian mixture on type 2 diabetes assessed by metabonomics, gut microbiota and network pharmacology. <i>Pharmacological Research</i> , 2018, 130, 93-109.	3.1	83
15512	A meta-analytic approach to genes that are associated with impaired and elevated spatial memory performance. <i>Psychiatry Research</i> , 2018, 261, 508-516.	1.7	8
15513	SMRT sequencing of full-length transcriptome of flea beetle <i>Agasicles hygrophila</i> (Selman and Vogt). <i>Scientific Reports</i> , 2018, 8, 2197.	1.6	49
15514	Big data and precision medicine: challenges and strategies with healthcare data. <i>International Journal of Data Science and Analytics</i> , 2018, 6, 241-249.	2.4	24
15515	Systematic Gene-to-Phenotype Arrays: A High-Throughput Technique for Molecular Phenotyping. <i>Molecular Cell</i> , 2018, 69, 321-333.e3.	4.5	7
15516	Chromatin Modification and Global Transcriptional Silencing in the Oocyte Mediated by the mRNA Decay Activator ZFP36L2. <i>Developmental Cell</i> , 2018, 44, 392-402.e7.	3.1	65

#	ARTICLE	IF	CITATIONS
15517	Genomic resequencing combined with quantitative proteomic analyses elucidate the survival mechanisms of <i>Lactobacillus plantarum</i> P-8 in a long-term glucose-limited experiment. <i>Journal of Proteomics</i> , 2018, 176, 37-45.	1.2	9
15518	ComClus: A Self-Grouping Framework for Multi-Network Clustering. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2018, 30, 435-448.	4.0	14
15521	Oxygen drives hepatocyte differentiation and phenotype stability in liver cell lines. <i>Journal of Cell Communication and Signaling</i> , 2018, 12, 575-588.	1.8	30
15522	Comparative proteomic profiling of human dental pulp stem cells and periodontal ligament stem cells under in vitro osteogenic induction. <i>Archives of Oral Biology</i> , 2018, 89, 9-19.	0.8	15
15523	Network Analysis of UBE3A/E6AP-Associated Proteins Provides Connections to Several Distinct Cellular Processes. <i>Journal of Molecular Biology</i> , 2018, 430, 1024-1050.	2.0	32
15524	Gene annotation bias impedes biomedical research. <i>Scientific Reports</i> , 2018, 8, 1362.	1.6	125
15525	Co-complex protein membership evaluation using Maximum Entropy on GO ontology and InterPro annotation. <i>Bioinformatics</i> , 2018, 34, 1884-1892.	1.8	18
15526	Investigation into the underlying molecular mechanisms of hypertensive nephrosclerosis using bioinformatics analyses. <i>Molecular Medicine Reports</i> , 2018, 17, 4440-4448.	1.1	5
15527	Assessing the quality of domain ontologies: Metrics and an automated ranking system. <i>Data and Knowledge Engineering</i> , 2018, 115, 32-47.	2.1	25
15528	Neuregulin 1 discovered as a cleavage target for the HCV NS3/4A protease by a microfluidic membrane protein array. <i>New Biotechnology</i> , 2018, 45, 113-122.	2.4	1
15529	Molecular characterization of the vitamin D receptor (VDR) gene in Holstein cows. <i>Research in Veterinary Science</i> , 2018, 118, 146-150.	0.9	1
15530	Proteome Data Improves Protein Function Prediction in the Interactome of <i>Helicobacter pylori</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 961-973.	2.5	8
15531	Osmoadaptation of wine yeast (<i>Saccharomyces cerevisiae</i>) during Icewine fermentation leads to high levels of acetic acid. <i>Journal of Applied Microbiology</i> , 2018, 124, 1506-1520.	1.4	21
15532	Exploring the Antimicrobial Action of Quaternary Amines against <i>Acinetobacter baumannii</i> . <i>MBio</i> , 2018, 9, .	1.8	41
15533	Dysregulated genes and their functional pathways in luteinized granulosa cells from PCOS patients after cabergoline treatment. <i>Reproduction</i> , 2018, 155, 373-381.	1.1	16
15534	Transcriptome analysis in tissue sectors with contrasting crocins accumulation provides novel insights into apocarotenoid biosynthesis and regulation during chromoplast biogenesis. <i>Scientific Reports</i> , 2018, 8, 2843.	1.6	41
15535	Asynchronous and pathological windows of implantation: two causes of recurrent implantation failure. <i>Human Reproduction</i> , 2018, 33, 626-635.	0.4	76
15536	Quantitative genetic methods depending on the nature of the phenotypic trait. <i>Annals of the New York Academy of Sciences</i> , 2018, 1422, 29-47.	1.8	56

#	ARTICLE	IF	CITATIONS
15537	The Biotrophic Development of <i>Ustilago maydis</i> Studied by RNA-Seq Analysis. <i>Plant Cell</i> , 2018, 30, 300-323.	3.1	186
15538	TOXsIgN: a cross-species repository for toxicogenomic signatures. <i>Bioinformatics</i> , 2018, 34, 2116-2122.	1.8	22
15539	The Planteome database: an integrated resource for reference ontologies, plant genomics and phenomics. <i>Nucleic Acids Research</i> , 2018, 46, D1168-D1180.	6.5	133
15540	Potential prognostic biomarkers identified by DNA methylation profiling analysis for patients with lung adenocarcinoma. <i>Oncology Letters</i> , 2018, 15, 3552-3557.	0.8	10
15541	Ultra-low input transcriptomics reveal the spore functional content and phylogenetic affiliations of poorly studied arbuscular mycorrhizal fungi. <i>DNA Research</i> , 2018, 25, 217-227.	1.5	33
15542	Highly Efficient Exosome Isolation and Protein Analysis by an Integrated Nanomaterial-Based Platform. <i>Analytical Chemistry</i> , 2018, 90, 2787-2795.	3.2	65
15543	Transcriptomic alterations during ageing reflect the shift from cancer to degenerative diseases in the elderly. <i>Nature Communications</i> , 2018, 9, 327.	5.8	94
15544	<i>Arabidopsis</i> mRNA decay landscape arises from specialized RNA decay substrates, decapping-mediated feedback, and redundancy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1485-E1494.	3.3	102
15545	Integrated analysis of the genetic basis of suicidal behavior. <i>Psychiatric Genetics</i> , 2018, 28, 31-37.	0.6	10
15546	Deciphering genetic factors that determine melon fruit quality traits using RNA-seq-based high-resolution QTL and eQTL mapping. <i>Plant Journal</i> , 2018, 94, 169-191.	2.8	133
15547	Ubiquitin C decrement plays a pivotal role in replicative senescence of bone marrow mesenchymal stromal cells. <i>Cell Death and Disease</i> , 2018, 9, 139.	2.7	14
15548	Comparative Analysis of Sequence Clustering Methods for Deduplication of Biological Databases. <i>Journal of Data and Information Quality</i> , 2018, 9, 1-27.	1.5	6
15549	<i>DMC1</i> mutation that causes human non-obstructive azoospermia and premature ovarian insufficiency identified by whole-exome sequencing. <i>Journal of Medical Genetics</i> , 2018, 55, 198-204.	1.5	91
15550	Large-scale Meta-analysis Suggests Low Regional Modularity in Lateral Frontal Cortex. <i>Cerebral Cortex</i> , 2018, 28, 3414-3428.	1.6	28
15551	Cancer Systems Biology. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	8
15552	The OncoPPi Portal: an integrative resource to explore and prioritize protein-protein interactions for cancer target discovery. <i>Bioinformatics</i> , 2018, 34, 1183-1191.	1.8	41
15553	Developmental control of hypoxia during bud burst in grapevine. <i>Plant, Cell and Environment</i> , 2018, 41, 1154-1170.	2.8	43
15554	Whole-Genome Sequences of <i>Brucella melitensis</i> Strain QH61, Isolated from Yak in Qinghai, China. <i>Genome Announcements</i> , 2018, 6, .	0.8	0

#	ARTICLE	IF	CITATIONS
15555	The protective role of DOT1L in UV-induced melanomagenesis. <i>Nature Communications</i> , 2018, 9, 259.	5.8	63
15556	Loss of disease tolerance during <i>Citrobacter rodentium</i> infection is associated with impaired epithelial differentiation and hyperactivation of T cell responses. <i>Scientific Reports</i> , 2018, 8, 847.	1.6	15
15557	Integration of GWAS, pathway and network analyses reveals novel mechanistic insights into the synthesis of milk proteins in dairy cows. <i>Scientific Reports</i> , 2018, 8, 566.	1.6	39
15558	Analyzing DNA Methylation Patterns During Tumor Evolution. <i>Methods in Molecular Biology</i> , 2018, 1711, 27-53.	0.4	4
15559	Comparative proteomic analysis of hepatic effects induced by nanosilver, silver ions and nanoparticle coating in rats. <i>Food and Chemical Toxicology</i> , 2018, 113, 255-266.	1.8	17
15560	Analysis of Homologs of Cry-toxin Receptor-Related Proteins in the Midgut of a Non-Bt Target, <i>Nilaparvata lugens</i> (Stål) (Hemiptera: Delphacidae). <i>Journal of Insect Science</i> , 2018, 18, .	0.6	9
15561	Region-Specific Methylation Profiling in Acute Myeloid Leukemia. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 33-42.	2.2	11
15562	Alpha-1-antitrypsin: a novel predictor for long-term recovery of chronic disorder of consciousness. <i>Expert Review of Molecular Diagnostics</i> , 2018, 18, 307-313.	1.5	4
15563	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
15564	ANP32A regulates histone H3 acetylation and promotes leukemogenesis. <i>Leukemia</i> , 2018, 32, 1587-1597.	3.3	25
15565	Comparative transcriptome analysis reveals molecular response to salinity stress of salt-tolerant and sensitive genotypes of indica rice at seedling stage. <i>Scientific Reports</i> , 2018, 8, 2085.	1.6	74
15566	Epigenome-wide association study of DNA methylation in narcolepsy: an integrated genetic and epigenetic approach. <i>Sleep</i> , 2018, 41, .	0.6	16
15567	Time-dependent transcriptional response of GOT1 human small intestine neuroendocrine tumor after ¹⁷⁷ Lu[Lu]-octreotate therapy. <i>Nuclear Medicine and Biology</i> , 2018, 60, 11-18.	0.3	7
15568	Differential gene expression induced by anti-cancer agent plumbagin is mediated by androgen receptor in prostate cancer cells. <i>Scientific Reports</i> , 2018, 8, 2694.	1.6	20
15569	Microarray analysis reveals Tmub1 as a cell cycle-associated protein in rat hepatocytes. <i>Molecular Medicine Reports</i> , 2018, 17, 4337-4344.	1.1	7
15570	Genomic tools for behavioural ecologists to understand repeatable individual differences in behaviour. <i>Nature Ecology and Evolution</i> , 2018, 2, 944-955.	3.4	97
15571	Leukemia-propagating cells demonstrate distinctive gene expression profiles compared with other cell fractions from patients with de novo Philadelphia chromosome-positive ALL. <i>Annals of Hematology</i> , 2018, 97, 799-811.	0.8	0
15572	Genome sequence and description of <i>Haloferax massiliense</i> sp. nov., a new halophilic archaeon isolated from the human gut. <i>Extremophiles</i> , 2018, 22, 485-498.	0.9	14

#	ARTICLE	IF	CITATIONS
15573	Using intracellular markers to identify a novel set of surface markers for live cell purification from a heterogeneous hiPSC culture. <i>Scientific Reports</i> , 2018, 8, 804.	1.6	14
15574	Complete genomic and transcriptional landscape analysis using third-generation sequencing: a case study of <i>Saccharomyces cerevisiae</i> CEN.PK113-7D. <i>Nucleic Acids Research</i> , 2018, 46, e38-e38.	6.5	116
15575	ER α -Mediated Nuclear Sequestration of RSK2 Is Required for ER+ Breast Cancer Tumorigenesis. <i>Cancer Research</i> , 2018, 78, 2014-2025.	0.4	17
15576	Bioinformatics Approaches to Predict Drug Responses from Genomic Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1711, 277-296.	0.4	12
15577	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. <i>Nature Communications</i> , 2018, 9, 288.	5.8	59
15578	Projection-Based Clustering through Self-Organization and Swarm Intelligence. , 2018, , .		33
15579	EBI Metagenomics in 2017: enriching the analysis of microbial communities, from sequence reads to assemblies. <i>Nucleic Acids Research</i> , 2018, 46, D726-D735.	6.5	175
15580	An exact test for comparing a fixed quantitative property between gene sets. <i>Bioinformatics</i> , 2018, 34, 971-977.	1.8	5
15581	Assessing the Role of Muscle Protein Breakdown in Response to Nutrition and Exercise in Humans. <i>Sports Medicine</i> , 2018, 48, 53-64.	3.1	100
15582	RGBM: regularized gradient boosting machines for identification of the transcriptional regulators of discrete glioma subtypes. <i>Nucleic Acids Research</i> , 2018, 46, e39-e39.	6.5	32
15583	A network-based meta-analysis for characterizing the genetic landscape of human aging. <i>Biogerontology</i> , 2018, 19, 81-94.	2.0	16
15584	The pomegranate (<i>Punica granatum</i> L.) genome provides insights into fruit quality and ovule developmental biology. <i>Plant Biotechnology Journal</i> , 2018, 16, 1363-1374.	4.1	115
15585	Physiological and transcriptomic analyses of a yellow-green mutant with high photosynthetic efficiency in wheat (<i>Triticum aestivum</i> L.). <i>Functional and Integrative Genomics</i> , 2018, 18, 175-194.	1.4	21
15586	Gene Phylogenies and Orthologous Groups. <i>Methods in Molecular Biology</i> , 2018, 1704, 1-28.	0.4	11
15587	Comparative Genomics for Prokaryotes. <i>Methods in Molecular Biology</i> , 2018, 1704, 55-78.	0.4	15
15588	Identification of candidate serum biomarkers of childhood-onset growth hormone deficiency using SWATH-MS and feature selection. <i>Journal of Proteomics</i> , 2018, 175, 105-113.	1.2	14
15589	PECAplus: statistical analysis of time-dependent regulatory changes in dynamic single-omics and dual-omics experiments. <i>Npj Systems Biology and Applications</i> , 2018, 4, 3.	1.4	10
15590	A high parasite density environment induces transcriptional changes and cell death in <i>Plasmodium falciparum</i> blood stages. <i>FEBS Journal</i> , 2018, 285, 848-870.	2.2	21

#	ARTICLE	IF	CITATIONS
15591	Kernel differential subgraph reveals dynamic changes in biomolecular networks. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1750027.	0.3	2
15592	Network-based technologies for early drug discovery. <i>Drug Discovery Today</i> , 2018, 23, 626-635.	3.2	72
15593	Systems Biology Modeling to Study Pathogen-Host Interactions. <i>Methods in Molecular Biology</i> , 2018, 1734, 97-112.	0.4	13
15594	Tools for protein science. <i>Protein Science</i> , 2018, 27, 6-9.	3.1	2
15595	Minichromosome maintenance complex component 6 (MCM6) expression correlates with histological grade and survival in endometrioid endometrial adenocarcinoma. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2018, 472, 623-633.	1.4	22
15596	A Case Study Application of the Aggregate Exposure Pathway (AEP) and Adverse Outcome Pathway (AOP) Frameworks to Facilitate the Integration of Human Health and Ecological End Points for Cumulative Risk Assessment (CRA). <i>Environmental Science & Technology</i> , 2018, 52, 839-849.	4.6	21
15597	Gene Network Analysis of Interstitial Macrophages After Treatment with Induced Pluripotent Stem Cells Secretome (iPSC-cm) in the Bleomycin Injured Rat Lung. <i>Stem Cell Reviews and Reports</i> , 2018, 14, 412-424.	5.6	14
15598	<i>Trichinella spiralis</i> muscle larvae excretory-secretory products induce changes in cytoskeletal and myogenic transcription factors in primary myoblast cultures. <i>International Journal for Parasitology</i> , 2018, 48, 275-285.	1.3	13
15599	Evolutionary transition from blood feeding to obligate nonbiting in a mosquito. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1009-1014.	3.3	23
15600	Identifying a combined biomarker for bisphosphonate-related osteonecrosis of the jaw. <i>Clinical Implant Dentistry and Related Research</i> , 2018, 20, 191-198.	1.6	4
15602	Integrated microRNA and mRNA signatures in peripheral blood lymphocytes of familial epithelial ovarian cancer. <i>Biochemical and Biophysical Research Communications</i> , 2018, 496, 191-198.	1.0	5
15603	Molecular dissection of distinct symptoms induced by tomato chlorosis virus and tomato yellow leaf curl virus based on comparative transcriptome analysis. <i>Virology</i> , 2018, 516, 1-20.	1.1	46
15604	An amebic protein disulfide isomerase (PDI) complements the yeast PDI1 mutation but is unable to support cell viability under ER or thermal stress. <i>FEBS Open Bio</i> , 2018, 8, 49-55.	1.0	11
15605	A five-gene signature may predict sunitinib sensitivity and serve as prognostic biomarkers for renal cell carcinoma. <i>Journal of Cellular Physiology</i> , 2018, 233, 6649-6660.	2.0	40
15606	Discovery of microRNA-target modules of African rice (<i>Oryza glaberrima</i>) under salinity stress. <i>Scientific Reports</i> , 2018, 8, 570.	1.6	44
15607	Genetic analysis of very obese children with autism spectrum disorder. <i>Molecular Genetics and Genomics</i> , 2018, 293, 725-736.	1.0	7
15608	Transcriptomic analysis reveals the molecular mechanisms of <i>Camellia sinensis</i> in response to salt stress. <i>Plant Growth Regulation</i> , 2018, 84, 481-492.	1.8	54
15609	Whole transcriptome analysis reveals potential novel mechanisms of low-level linezolid resistance in <i>Enterococcus faecalis</i> . <i>Gene</i> , 2018, 647, 143-149.	1.0	22

#	ARTICLE	IF	CITATIONS
15610	Identification of Potential MR-Derived Biomarkers for Tumor Tissue Response to 177Lu-Octreotate Therapy in an Animal Model of Small Intestine Neuroendocrine Tumor. <i>Translational Oncology</i> , 2018, 11, 193-204.	1.7	9
15611	Large-scale aggregation analysis of eukaryotic proteins reveals an involvement of intrinsically disordered regions in protein folding. <i>Scientific Reports</i> , 2018, 8, 678.	1.6	26
15612	The role of introns in the conservation of the metabolic genes of <i>Arabidopsis thaliana</i> . <i>Genomics</i> , 2018, 110, 310-317.	1.3	30
15613	Graph regularized nonnegative matrix factorization for temporal link prediction in dynamic networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2018, 496, 121-136.	1.2	80
15614	Extracting a biologically relevant latent space from cancer transcriptomes with variational autoencoders. , 2018, , .		101
15616	Golgi Phosphoprotein 2 Is a Novel Regulator of IL-12 Production and Macrophage Polarization. <i>Journal of Immunology</i> , 2018, 200, 1480-1488.	0.4	9
15617	Matrix factorization-based data fusion for the prediction of lncRNA-disease associations. <i>Bioinformatics</i> , 2018, 34, 1529-1537.	1.8	157
15618	Human Accelerated Regions and Other Human-Specific Sequence Variations in the Context of Evolution and Their Relevance for Brain Development. <i>Genome Biology and Evolution</i> , 2018, 10, 166-188.	1.1	61
15619	Sequential feature selection and inference using multi-variate random forests. <i>Bioinformatics</i> , 2018, 34, 1336-1344.	1.8	7
15620	Human pain genetics database: a resource dedicated to human pain genetics research. <i>Pain</i> , 2018, 159, 749-763.	2.0	80
15622	An epigenome-wide methylation study of healthy individuals with or without depressive symptoms. <i>Journal of Human Genetics</i> , 2018, 63, 319-326.	1.1	9
15623	Exploring intrinsically disordered proteins in <i>Chlamydomonas reinhardtii</i> . <i>Scientific Reports</i> , 2018, 8, 6805.	1.6	25
15624	Transcriptome profiling to identify key mediators of granulosa cell proliferation upon FSH stimulation in the goose (<i>Anser cygnoides</i>). <i>British Poultry Science</i> , 2018, 59, 416-421.	0.8	15
15625	Studying microbial functionality within the gut ecosystem by systems biology. <i>Genes and Nutrition</i> , 2018, 13, 5.	1.2	31
15626	Identification of a cold-tolerant locus in rice (<i>Oryza sativa</i> L.) using bulked segregant analysis with a next-generation sequencing strategy. <i>Rice</i> , 2018, 11, 24.	1.7	58
15627	A hidden Markov tree model for testing multiple hypotheses corresponding to Gene Ontology gene sets. <i>BMC Bioinformatics</i> , 2018, 19, 107.	1.2	2
15628	Transcriptome profiling provides insights into dormancy release during cold storage of <i>Lilium pumilum</i> . <i>BMC Genomics</i> , 2018, 19, 196.	1.2	33
15629	Transcriptome profiling of genes related to light-induced anthocyanin biosynthesis in eggplant (<i>Solanum melongena</i> L.) before purple color becomes evident. <i>BMC Genomics</i> , 2018, 19, 201.	1.2	44

#	ARTICLE	IF	CITATIONS
15630	Comparisons of gene coexpression network modules in breast cancer and ovarian cancer. <i>BMC Systems Biology</i> , 2018, 12, 8.	3.0	11
15631	A homologous mapping method for three-dimensional reconstruction of protein networks reveals disease-associated mutations. <i>BMC Systems Biology</i> , 2018, 12, 13.	3.0	1
15632	QSurface: fast identification of surface expression markers in cancers. <i>BMC Systems Biology</i> , 2018, 12, 17.	3.0	6
15633	The mRNA and miRNA transcriptomic landscape of <i>Panax ginseng</i> under the high ambient temperature. <i>BMC Systems Biology</i> , 2018, 12, 27.	3.0	10
15634	Multi-target drug repositioning by bipartite block-wise sparse multi-task learning. <i>BMC Systems Biology</i> , 2018, 12, 55.	3.0	8
15635	miR-148b-3p functions as a tumor suppressor in GISTs by directly targeting KIT. <i>Cell Communication and Signaling</i> , 2018, 16, 16.	2.7	29
15636	Epigenetic impacts of stress priming of the neuroinflammatory response to sarin surrogate in mice: a model of Gulf War illness. <i>Journal of Neuroinflammation</i> , 2018, 15, 86.	3.1	47
15637	Pairwise gene GO-based measures for biclustering of high-dimensional expression data. <i>BioData Mining</i> , 2018, 11, 4.	2.2	8
15638	Gene-level differential analysis at transcript-level resolution. <i>Genome Biology</i> , 2018, 19, 53.	3.8	108
15639	Supporting shared hypothesis testing in the biomedical domain. <i>Journal of Biomedical Semantics</i> , 2018, 9, 9.	0.9	5
15640	Microbiome and ecotypic adaption of <i>Holcus lanatus</i> (L.) to extremes of its soil pH range, investigated through transcriptome sequencing. <i>Microbiome</i> , 2018, 6, 48.	4.9	29
15641	High quality draft genome sequences of <i>Mycoplasma agassizii</i> strains PS6T and 723 isolated from <i>Gopherus</i> tortoises with upper respiratory tract disease. <i>Standards in Genomic Sciences</i> , 2018, 13, 12.	1.5	4
15642	Development of a computational promoter with highly efficient expression in tumors. <i>BMC Cancer</i> , 2018, 18, 480.	1.1	2
15643	Constraints on signaling network logic reveal functional subgraphs on Multiple Myeloma OMIC data. <i>BMC Systems Biology</i> , 2018, 12, 32.	3.0	3
15644	Identification of novel drug targets for diamond-blackfan anemia based on RPS19 gene mutation using protein-protein interaction network. <i>BMC Systems Biology</i> , 2018, 12, 39.	3.0	15
15645	Network modules uncover mechanisms of skeletal muscle dysfunction in COPD patients. <i>Journal of Translational Medicine</i> , 2018, 16, 34.	1.8	22
15646	Differences in MWCNT- and SWCNT-induced DNA methylation alterations in association with the nuclear deposition. <i>Particle and Fibre Toxicology</i> , 2018, 15, 11.	2.8	57
15647	Proteomic analysis of protein interactions between <i>Eimeria maxima</i> sporozoites and chicken jejunal epithelial cells by shotgun LC-MS/MS. <i>Parasites and Vectors</i> , 2018, 11, 226.	1.0	16

#	ARTICLE	IF	CITATIONS
15648	Draft genome sequence of <i>Fermentimonas caenicola</i> strain SIT8, isolated from the human gut. <i>Standards in Genomic Sciences</i> , 2018, 13, 8.	1.5	7
15649	Strategies for high-altitude adaptation revealed from high-quality draft genome of non-violacein producing <i>Janthinobacterium lividum</i> ERGS5:01. <i>Standards in Genomic Sciences</i> , 2018, 13, 11.	1.5	32
15650	The thematic modelling of subtext. <i>Multimedia Tools and Applications</i> , 2018, 77, 28281-28308.	2.6	1
15651	Identifying influential genes in protein-protein interaction networks. <i>Information Sciences</i> , 2018, 454-455, 229-241.	4.0	25
15652	Remote Memory and Cortical Synaptic Plasticity Require Neuronal CCCTC-Binding Factor (CTCF). <i>Journal of Neuroscience</i> , 2018, 38, 5042-5052.	1.7	39
15654	Proteomics for Biomarker Identification and Clinical Application in Kidney Disease. <i>Advances in Clinical Chemistry</i> , 2018, 85, 91-113.	1.8	41
15655	Deciphering the genome and secondary metabolome of the plant pathogen <i>Fusarium culmorum</i> . <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	10
15656	Complete Genome Sequence of the Heavy-Metal-Tolerant Endophytic Type Strain of <i>Salinicola tamaricis</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	5
15657	Transcriptional regulatory networks underlying gene expression changes in Huntington's disease. <i>Molecular Systems Biology</i> , 2018, 14, e7435.	3.2	55
15658	Inflammatory genes are novel prognostic biomarkers for colorectal cancer. <i>International Journal of Molecular Medicine</i> , 2018, 42, 368-380.	1.8	24
15659	Accessing Expert-Curated Pharmacological Data in the IUPHAR/BPS Guide to PHARMACOLOGY. <i>Current Protocols in Bioinformatics</i> , 2018, 61, 1.34.1-1.34.46.	25.8	13
15660	The Knowledge Object Reference Ontology (<sc>KORO</sc>): A formalism to support management and sharing of computable biomedical knowledge for learning health systems. <i>Learning Health Systems</i> , 2018, 2, e10054.	1.1	31
15661	Big Semantic Data Processing in the Life Sciences Domain. , 2018, , 1-8.		1
15662	The multiple myeloma risk allele at 5q15 lowers ELL2 expression and increases ribosomal gene expression. <i>Nature Communications</i> , 2018, 9, 1649.	5.8	22
15663	Genetics in multiple sclerosis: Updates in the era of big data. <i>Clinical and Experimental Neuroimmunology</i> , 2018, 9, 19-24.	0.5	3
15664	Deep Sequencing of Small RNAs in Blood of Patients with Brain Arteriovenous Malformations. <i>World Neurosurgery</i> , 2018, 115, e570-e579.	0.7	16
15665	Complex network theory for the identification and assessment of candidate protein targets. <i>Computers in Biology and Medicine</i> , 2018, 97, 113-123.	3.9	5
15666	Identification of diverse target RNAs that are functionally regulated by human Pumilio proteins. <i>Nucleic Acids Research</i> , 2018, 46, 362-386.	6.5	80

#	ARTICLE	IF	CITATIONS
15667	A New Database for Drug Discovery Through Application of Data-Integration and Semantics. , 2018, , .		1
15668	Signatures of local adaptation along environmental gradients in a range-expanding damselfly (<i>Ischnura elegans</i>). <i>Molecular Ecology</i> , 2018, 27, 2576-2593.	2.0	82
15669	A Strategy for Discovery of Endocrine Interactions with Application to Whole-Body Metabolism. <i>Cell Metabolism</i> , 2018, 27, 1138-1155.e6.	7.2	58
15670	Environmental fluctuations accelerate molecular evolution of thermal tolerance in a marine diatom. <i>Nature Communications</i> , 2018, 9, 1719.	5.8	98
15671	Functional and structural characterization of osteocytic MLO-Y4 cell proteins encoded by genes differentially expressed in response to mechanical signals in vitro. <i>Scientific Reports</i> , 2018, 8, 6716.	1.6	11
15672	RNA Sequencing, <i>de novo</i> assembly, functional annotation and SSR analysis of the endangered diving beetle <i>Cybister chinensis</i> (= <i>Cybister japonicus</i>) using the Illumina platform. <i>Entomological Research</i> , 2018, 48, 60-72.	0.6	3
15673	Identifying genes as potential prognostic indicators in patients with serous ovarian cancer resistant to carboplatin using integrated bioinformatics analysis. <i>Oncology Reports</i> , 2018, 39, 2653-2663.	1.2	18
15674	Parallel evolution of gene expression between trophic specialists despite divergent genotypes and morphologies. <i>Evolution Letters</i> , 2018, 2, 62-75.	1.6	32
15675	MiRGOFS: a GO-based functional similarity measurement for miRNAs, with applications to the prediction of miRNA subcellular localization and miRNA-disease association. <i>Bioinformatics</i> , 2018, 34, 3547-3556.	1.8	50
15676	Tumor-Independent Host Secretomes Induced By Angiogenesis and Immune-Checkpoint Inhibitors. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 1602-1612.	1.9	6
15677	Automated brightfield morphometry of 3D organoid populations by OrganoSeg. <i>Scientific Reports</i> , 2018, 8, 5319.	1.6	92
15678	Identification of key genes and miRNAs associated with carotid atherosclerosis based on mRNA-seq data. <i>Medicine (United States)</i> , 2018, 97, e9832.	0.4	21
15679	Tolerance response and metabolism of acetic acid by biodegradation fungus <i>Amorphotheca resinae</i> ZN1. <i>Journal of Biotechnology</i> , 2018, 275, 31-39.	1.9	6
15680	Functional Precision Medicine Identifies Novel Druggable Targets and Therapeutic Options in Head and Neck Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 2828-2843.	3.2	20
15681	New Frontiers in Mining Complex Patterns. <i>Lecture Notes in Computer Science</i> , 2018, , .	1.0	0
15682	MicroRNA Expression Levels Are Altered in the Cerebrospinal Fluid of Patients with Young-Onset Alzheimer's Disease. <i>Molecular Neurobiology</i> , 2018, 55, 8826-8841.	1.9	111
15683	Identification of potential key protein interaction networks of BK virus nephropathy in patients receiving kidney transplantation. <i>Scientific Reports</i> , 2018, 8, 5017.	1.6	12
15684	microRNA expression profiles of scar and normal tissue from patients with posterior urethral stricture caused by pelvic fracture urethral distraction defects. <i>International Journal of Molecular Medicine</i> , 2018, 41, 2733-2743.	1.8	14

#	ARTICLE	IF	CITATIONS
15685	MicroRNA expression data analysis to identify key miRNAs associated with Alzheimer's disease. <i>Journal of Gene Medicine</i> , 2018, 20, e3014.	1.4	63
15686	Comparative Transcriptome Analysis of Seedling Stage of Two Sorghum Cultivars Under Salt Stress. <i>Journal of Plant Growth Regulation</i> , 2018, 37, 986-998.	2.8	24
15687	CD40 ligand deficiency causes functional defects of peripheral neutrophils that are improved by exogenous IFN- β . <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 1571-1588.e9.	1.5	21
15688	A single-cell RNA-seq survey of the developmental landscape of the human prefrontal cortex. <i>Nature</i> , 2018, 555, 524-528.	13.7	551
15689	LMTK3 confers chemo-resistance in breast cancer. <i>Oncogene</i> , 2018, 37, 3113-3130.	2.6	31
15690	Investigation of mechanisms of mesenchymal stem cells for treatment of diabetic nephropathy via construction of a miRNA-TF-mRNA network. <i>Renal Failure</i> , 2018, 40, 136-145.	0.8	14
15692	Transcriptomic characterization of MRI contrast with focus on the T1-w/T2-w ratio in the cerebral cortex. <i>NeuroImage</i> , 2018, 174, 504-517.	2.1	51
15693	U-Index, a dataset and an impact metric for informatics tools and databases. <i>Scientific Data</i> , 2018, 5, 180043.	2.4	7
15694	Using a hydro-reference ontology to provide improved computer-interpretable semantics for the groundwater markup language (GWML2). <i>International Journal of Geographical Information Science</i> , 2018, 32, 1138-1171.	2.2	11
15695	Integrating genetic analysis and crop modeling: A major QTL can finely adjust photoperiod-sensitive sorghum flowering. <i>Field Crops Research</i> , 2018, 221, 7-18.	2.3	11
15696	A computational biology approach of a genome-wide screen connected miRNAs to obesity and type 2 diabetes. <i>Molecular Metabolism</i> , 2018, 11, 145-159.	3.0	48
15697	Transcriptome Network Analysis Reveals Aging-Related Mitochondrial and Proteasomal Dysfunction and Immune Activation in Human Thyroid. <i>Thyroid</i> , 2018, 28, 656-666.	2.4	23
15698	PRECISION MEDICINE: FROM DILOTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES. , 2018, , .		3
15699	Screening for key lncRNAs in the progression of gallbladder cancer using bioinformatics analyses. <i>Molecular Medicine Reports</i> , 2018, 17, 6449-6455.	1.1	8
15700	Identification of potential genes and miRNAs associated with sepsis based on microarray analysis. <i>Molecular Medicine Reports</i> , 2018, 17, 6227-6234.	1.1	9
15701	Integrated SWATH-based and targeted-based proteomics provide insights into the retinal emmetropization process in guinea pig. <i>Journal of Proteomics</i> , 2018, 181, 1-15.	1.2	18
15702	A Deep Learning Framework for Robust and Accurate Prediction of ncRNA-Protein Interactions Using Evolutionary Information. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 11, 337-344.	2.3	116
15703	Vascular restenosis in coronary artery bypass grafting might be associated with VEGF-C/VEGFR-3 signaling pathway. <i>Heart and Vessels</i> , 2018, 33, 1106-1120.	0.5	8

#	ARTICLE	IF	CITATIONS
15704	Dynamics of chromatin marks and the role of JMJD3 during pancreatic endocrine cell fate commitment. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	26
15705	Whole-Exome Sequencing Identifies Two Discrete Druggable Signaling Pathways in Follicular Thyroid Cancer. <i>Journal of the American College of Surgeons</i> , 2018, 226, 950-959e5.	0.2	24
15706	RNA cytosine methylation and methyltransferases mediate chromatin organization and 5-azacytidine response and resistance in leukaemia. <i>Nature Communications</i> , 2018, 9, 1163.	5.8	132
15707	Role for Wnt Signaling in Retinal Neuropil Development: Analysis via RNA-Seq and In Vivo Somatic CRISPR Mutagenesis. <i>Neuron</i> , 2018, 98, 109-126.e8.	3.8	64
15708	PANDA: Protein function prediction using domain architecture and affinity propagation. <i>Scientific Reports</i> , 2018, 8, 3484.	1.6	14
15709	Evolutionary Interplay between Symbiotic Relationships and Patterns of Signal Peptide Gain and Loss. <i>Genome Biology and Evolution</i> , 2018, 10, 928-938.	1.1	9
15710	Comparative transcriptome profiling of the human and mouse dorsal root ganglia: an RNA-seq-based resource for pain and sensory neuroscience research. <i>Pain</i> , 2018, 159, 1325-1345.	2.0	306
15712	Inter-replicon Gene Flow Contributes to Transcriptional Integration in the <i>Sinorhizobium meliloti</i> Multipartite Genome. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1711-1720.	0.8	14
15713	Identification of the key genes associated with neuropathic pain. <i>Molecular Medicine Reports</i> , 2018, 17, 6371-6378.	1.1	16
15714	How nitrogen sources influence <i>Mortierella alpina</i> aging: From the lipid droplet proteome to the whole-cell proteome and metabolome. <i>Journal of Proteomics</i> , 2018, 179, 140-149.	1.2	18
15715	Regulation of the Hsp90 system. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2018, 1865, 889-897.	1.9	48
15717	Integrity, standards, and QC-related issues with big data in pre-clinical drug discovery. <i>Biochemical Pharmacology</i> , 2018, 152, 84-93.	2.0	3
15718	Priming integrin alpha 5 promotes the osteogenic differentiation of human periodontal ligament stem cells due to cytoskeleton and cell cycle changes. <i>Journal of Proteomics</i> , 2018, 179, 122-130.	1.2	27
15719	<i>m</i> -AAA and <i>i</i> -AAA complexes work coordinately regulating OMA1, the stress-activated supervisor of mitochondrial dynamics. <i>Journal of Cell Science</i> , 2018, 131, .	1.2	40
15720	Comprehensive analysis of differential expression profiles reveals potential biomarkers associated with the cell cycle and regulated by p53 in human small cell lung cancer. <i>Experimental and Therapeutic Medicine</i> , 2018, 15, 3273-3282.	0.8	13
15721	LINC00152 is a potential biomarker involved in the modulation of biological characteristics of residual colorectal cancer cells following chemoradiotherapy. <i>Oncology Letters</i> , 2018, 15, 4177-4184.	0.8	13
15722	De novo assembly, gene annotation, and marker development using Illumina paired-end transcriptome sequencing in the <i>Crassadoma gigantea</i> . <i>Gene</i> , 2018, 658, 54-62.	1.0	9
15723	Functional Validation of Candidate Genes Detected by Genomic Feature Models. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1659-1668.	0.8	14

#	ARTICLE	IF	CITATIONS
15724	Exploring the oncoproteomic response of human prostate cancer to therapeutic radiation using data-independent acquisition (DIA) mass spectrometry. <i>Prostate</i> , 2018, 78, 563-575.	1.2	23
15725	Root Development. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	3
15726	Chromatin Immunoprecipitation Sequencing (ChIP-Seq) for Transcription Factors and Chromatin Factors in <i>Arabidopsis thaliana</i> Roots: From Material Collection to Data Analysis. <i>Methods in Molecular Biology</i> , 2018, 1761, 231-248.	0.4	11
15727	New automatic fuzzy relational clustering algorithms using multi-objective NSGA-II. <i>Information Sciences</i> , 2018, 448-449, 112-133.	4.0	35
15728	OBO to UML: Support for the development of conceptual models in the biomedical domain. <i>Journal of Biomedical Informatics</i> , 2018, 80, 14-25.	2.5	3
15729	Draft genome analysis provides insights into the fiber yield, crude protein biosynthesis, and vegetative growth of domesticated ramie (<i>Boehmeria nivea</i> L. Gaud). <i>DNA Research</i> , 2018, 25, 173-181.	1.5	32
15730	Bioinformatics Analysis of Microarray Data to Reveal Novel Genes Related to Cold-Resistance of Maize. <i>Russian Journal of Plant Physiology</i> , 2018, 65, 278-285.	0.5	4
15731	Classification of State Trajectories in Gene Regulatory Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 68-82.	1.9	11
15732	Application of Genetic Programming (GP) Formalism for Building Disease Predictive Models from Protein-Protein Interactions (PPI) Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 27-37.	1.9	11
15733	Extracting Stage-Specific and Dynamic Modules Through Analyzing Multiple Networks Associated with Cancer Progression. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 647-658.	1.9	24
15734	Genome, transcriptome and proteome: the rise of omics data and their integration in biomedical sciences. <i>Briefings in Bioinformatics</i> , 2018, 19, 286-302.	3.2	498
15735	Detecting Essential Proteins Based on Network Topology, Gene Expression Data, and Gene Ontology Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 109-116.	1.9	44
15736	Introducing a Stable Bootstrap Validation Framework for Reliable Genomic Signature Extraction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 181-190.	1.9	17
15737	Evolutionary Graph Clustering for Protein Complex Identification. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 892-904.	1.9	23
15738	Index-Based Network Aligner of Protein-Protein Interaction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 330-336.	1.9	14
15739	A Novel Method on Information Recommendation via Hybrid Similarity. <i>IEEE Transactions on Systems, Man, and Cybernetics: Systems</i> , 2018, 48, 448-459.	5.9	33
15740	Sparse Pathway-Induced Dynamic Network Biomarker Discovery for Early Warning Signal Detection in Complex Diseases. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1028-1034.	1.9	6
15741	Elucidation of the dynamic nature of interactome networks: A practical tutorial. <i>Journal of Proteomics</i> , 2018, 171, 116-126.	1.2	1

#	ARTICLE	IF	CITATIONS
15742	MISAGA: An Algorithm for Mining Interesting Subgraphs in Attributed Graphs. <i>IEEE Transactions on Cybernetics</i> , 2018, 48, 1369-1382.	6.2	32
15743	Investigating the neuroimmunogenic architecture of schizophrenia. <i>Molecular Psychiatry</i> , 2018, 23, 1251-1260.	4.1	59
15744	HINMINE: heterogeneous information network mining with information retrieval heuristics. <i>Journal of Intelligent Information Systems</i> , 2018, 50, 29-61.	2.8	16
15745	An empirical evaluation of hierarchical feature selection methods for classification in bioinformatics datasets with gene ontology-based features. <i>Artificial Intelligence Review</i> , 2018, 50, 201-240.	9.7	24
15746	Genome-Wide DNA Methylation Patterns Analysis of Noncoding RNAs in Temporal Lobe Epilepsy Patients. <i>Molecular Neurobiology</i> , 2018, 55, 793-803.	1.9	36
15747	Transcriptome Analysis Identifies Multifaceted Regulatory Mechanisms Dictating a Genetic Switch from Neuronal Network Establishment to Maintenance During Postnatal Prefrontal Cortex Development. <i>Cerebral Cortex</i> , 2018, 28, 833-851.	1.6	15
15748	Functional, structural, and phylogenetic analysis of mitochondrial cytochrome b (cytb) in insects. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 236-249.	0.7	7
15749	Transcriptional analysis of the interaction between the oomycete biocontrol agent, <i>Pythium oligandrum</i> , and the roots of <i>Vitis vinifera</i> L.. <i>Biological Control</i> , 2018, 120, 26-35.	1.4	18
15750	Comprehensive functional analysis of large lists of genes and proteins. <i>Journal of Proteomics</i> , 2018, 171, 2-10.	1.2	80
15751	The benefits (and misfortunes) of SDS in top-down proteomics. <i>Journal of Proteomics</i> , 2018, 175, 75-86.	1.2	25
15752	Assessment of Semantic Similarity between Proteins Using Information Content and Topological Properties of the Gene Ontology Graph. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 839-849.	1.9	15
15753	The anatomy of phenotype ontologies: principles, properties and applications. <i>Briefings in Bioinformatics</i> , 2018, 19, 1008-1021.	3.2	66
15754	Gene expression analysis identify a metabolic and cell function alterations as a hallmark of obesity without metabolic syndrome in peripheral blood, a pilot study. <i>Clinical Nutrition</i> , 2018, 37, 1348-1353.	2.3	12
15755	Transcriptomic Profiling in Human Decidua of Severe Preeclampsia Detected by RNA Sequencing. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 607-615.	1.2	59
15756	DUSP1 and KCNJ2 mRNA upregulation can serve as a biomarker of mechanical asphyxia-induced death in cardiac tissue. <i>International Journal of Legal Medicine</i> , 2018, 132, 655-665.	1.2	10
15757	Adding biological meaning to human protein-protein interactions identified by yeast two-hybrid screenings: A guide through bioinformatics tools. <i>Journal of Proteomics</i> , 2018, 171, 127-140.	1.2	9
15758	Bioimage-based protein subcellular location prediction: a comprehensive review. <i>Frontiers of Computer Science</i> , 2018, 12, 26-39.	1.6	27
15759	Testing for differentially expressed genetic pathways with single-subject N-of-1 data in the presence of inter-gene correlation. <i>Statistical Methods in Medical Research</i> , 2018, 27, 3797-3813.	0.7	13

#	ARTICLE	IF	CITATIONS
15760	High-throughput metaproteomics data analysis with Unipept: A tutorial. <i>Journal of Proteomics</i> , 2018, 171, 11-22.	1.2	65
15761	NewGOA: Predicting New GO Annotations of Proteins by Bi-Random Walks on a Hybrid Graph. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1390-1402.	1.9	30
15762	Replicable and Coupled Changes in Innate and Adaptive Immune Gene Expression in Two Case-Control Studies of Blood Microarrays in Major Depressive Disorder. <i>Biological Psychiatry</i> , 2018, 83, 70-80.	0.7	158
15763	High-throughput Transcriptome Sequencing Reveals the Role of Anthocyanin Metabolism in <i>Begonia semperflorens</i> Under High Light Stress. <i>Photochemistry and Photobiology</i> , 2018, 94, 105-114.	1.3	19
15764	Integrated analysis of <i>SNP</i> , <i>CNV</i> and gene expression data in genetic association studies. <i>Clinical Genetics</i> , 2018, 93, 557-566.	1.0	20
15765	Thioredoxin-Mediated ROS Homeostasis Explains Natural Variation in Plant Regeneration. <i>Plant Physiology</i> , 2018, 176, 2231-2250.	2.3	46
15766	Species translatable blood gene signature as a marker of exposure to smoking: Computational approaches of the top ranked teams in the sbv IMPROVER Systems Toxicology Challenge. <i>Computational Toxicology</i> , 2018, 5, 25-30.	1.8	1
15767	DeepGO: predicting protein functions from sequence and interactions using a deep ontology-aware classifier. <i>Bioinformatics</i> , 2018, 34, 660-668.	1.8	318
15768	Thyroid State Regulates Gene Expression in Human Whole Blood. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 169-178.	1.8	14
15769	Comparative genomics and transcriptomics analysis-guided metabolic engineering of <i>Propionibacterium acidipropionici</i> for improved propionic acid production. <i>Biotechnology and Bioengineering</i> , 2018, 115, 483-494.	1.7	29
15770	Identification of differentially expressed genes regulated by molecular signature in breast cancer-associated fibroblasts by bioinformatics analysis. <i>Archives of Gynecology and Obstetrics</i> , 2018, 297, 161-183.	0.8	8
15771	Identification of the genomic region under epigenetic regulation during non-alcoholic fatty liver disease progression. <i>Hepatology Research</i> , 2018, 48, E320-E334.	1.8	30
15772	RCSB Protein Data Bank: Sustaining a living digital data resource that enables breakthroughs in scientific research and biomedical education. <i>Protein Science</i> , 2018, 27, 316-330.	3.1	219
15773	The DifferentialNet database of differential protein-protein interactions in human tissues. <i>Nucleic Acids Research</i> , 2018, 46, D522-D526.	6.5	71
15774	Expanded and updated data and a query pipeline for iBeetle-Base. <i>Nucleic Acids Research</i> , 2018, 46, D831-D835.	6.5	35
15775	Identification of breast cancer hub genes and analysis of prognostic values using integrated bioinformatics analysis. <i>Cancer Biomarkers</i> , 2018, 21, 373-381.	0.8	37
15776	Fast analytical methods for finding significant labeled graph motifs. <i>Data Mining and Knowledge Discovery</i> , 2018, 32, 504-531.	2.4	18
15777	Transcriptional determinants of individualized inflammatory responses at anatomically separate sites. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 805-808.	1.5	4

#	ARTICLE	IF	CITATIONS
15778	Cellular and molecular characterizations of a slow-growth variant provide insights into the fast growth of bamboo. <i>Tree Physiology</i> , 2018, 38, 641-654.	1.4	42
15779	Tip-Based Fractionation of Batch-Enriched Phosphopeptides Facilitates Easy and Robust Phosphoproteome Analysis. <i>Journal of Proteome Research</i> , 2018, 17, 46-54.	1.8	17
15780	The Transcriptional Landscape of Radiation-Treated Human Prostate Cancer: Analysis of a Prospective Tissue Cohort. <i>International Journal of Radiation Oncology Biology Physics</i> , 2018, 100, 188-198.	0.4	24
15781	Two's company: studying interspecies relationships with dual RNA-seq. <i>Current Opinion in Microbiology</i> , 2018, 42, 7-12.	2.3	54
15782	Transcriptome analysis of <i>Paecilomyces hepiali</i> at different growth stages and culture additives to reveal putative genes in cordycepin biosynthesis. <i>Genomics</i> , 2018, 110, 162-170.	1.3	20
15783	Argonaute Proteins. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	2
15784	Co-expression modules construction by WGCNA and identify potential prognostic markers of uveal melanoma. <i>Experimental Eye Research</i> , 2018, 166, 13-20.	1.2	180
15785	Profiling Open Chromatin Structure in the Ovarian Somatic Cells Using ATAC-seq. <i>Methods in Molecular Biology</i> , 2018, 1680, 165-177.	0.4	4
15786	De novo assembly and transcriptome characterization of the freshwater prawn <i>Palaemonetes argentinus</i> : Implications for a detoxification response. <i>Marine Genomics</i> , 2018, 37, 74-81.	0.4	6
15787	<i>MADS1</i> and <i>MaOFP1</i> regulate fruit quality in a tomato <i>ovate</i> mutant. <i>Plant Biotechnology Journal</i> , 2018, 16, 989-1001.	4.1	33
15788	<i>Biodiversity Informatics</i> . , 2018, , 375-399.		2
15789	Functional Interpretation of Gene Sets: Semantic-Based Clustering of Gene Ontology Terms on the BioTest Platform. <i>Advances in Intelligent Systems and Computing</i> , 2018, , 125-136.	0.5	3
15790	Dimensions of Semantic Similarity. <i>Studies in Computational Intelligence</i> , 2018, , 87-125.	0.7	2
15791	cDNA microarray analysis of human keratinocytes cells of patients submitted to chemoradiotherapy and oral photobiomodulation therapy: pilot study. <i>Lasers in Medical Science</i> , 2018, 33, 11-18.	1.0	12
15792	MicroRNA-induced silencing in epilepsy: Opportunities and challenges for clinical application. <i>Developmental Dynamics</i> , 2018, 247, 94-110.	0.8	53
15793	Co-expression analysis reveals key gene modules and pathway of human coronary heart disease. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 2102-2109.	1.2	29
15794	Genomic Analysis and Resistance Mechanisms in <i>Shigella flexneri</i> 2a Strain 301. <i>Microbial Drug Resistance</i> , 2018, 24, 323-336.	0.9	4
15795	Visualizing omics and clinical data: Which challenges for dealing with their variety?. <i>Methods</i> , 2018, 132, 3-18.	1.9	7

#	ARTICLE	IF	CITATIONS
15796	Integrating Imaging Genomic Data in the Quest for Biomarkers of Schizophrenia Disease. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1480-1491.	1.9	13
15797	CHEMGENIE: integration of chemogenomics data for applications in chemical biology. <i>Drug Discovery Today</i> , 2018, 23, 151-160.	3.2	13
15798	Proteomic composition of Nipah virus-like particles. <i>Journal of Proteomics</i> , 2018, 172, 190-200.	1.2	16
15799	Incorporating gene ontology into fuzzy relational clustering of microarray gene expression data. <i>BioSystems</i> , 2018, 163, 1-10.	0.9	19
15800	S-FLN: A sequence-based hierarchical approach for functional linkage network construction. <i>Journal of Theoretical Biology</i> , 2018, 437, 149-162.	0.8	0
15801	Identification of key gene modules and pathways of human breast cancer by co-expression analysis. <i>Breast Cancer</i> , 2018, 25, 213-223.	1.3	16
15802	Shared genetic etiology of hypertension and stroke: evidence from bioinformatics analysis of genome-wide association studies. <i>Journal of Human Hypertension</i> , 2018, 32, 34-39.	1.0	5
15803	Annotating gene sets by mining large literature collections with protein networks. , 2018, , .		6
15804	Proteomic Characterization of <i>Caenorhabditis elegans</i> Larval Development. <i>Proteomics</i> , 2018, 18, 1700238.	1.3	3
15805	Sex determination and differentiation genes in a functional hermaphrodite scallop, <i>Nodipecten subnodosus</i> . <i>Marine Genomics</i> , 2018, 37, 161-175.	0.4	16
15806	Proteomic analysis of six- and twelve-month hippocampus and cerebellum in a murine Down syndrome model. <i>Neurobiology of Aging</i> , 2018, 63, 96-109.	1.5	14
15807	Fantastic Beasts and How To Sequence Them: Ecological Genomics for Obscure Model Organisms. <i>Trends in Genetics</i> , 2018, 34, 121-132.	2.9	64
15808	Soldier-biased gene expression in a subterranean termite implies functional specialization of the defensive caste. <i>Evolution & Development</i> , 2018, 20, 3-16.	1.1	14
15809	Up-regulation of YPEL1 and YPEL5 and down-regulation of ITGA2 in erlotinib-treated EGFR-mutant non-small cell lung cancer: A bioinformatic analysis. <i>Gene</i> , 2018, 643, 74-82.	1.0	11
15810	The impact of protein interaction networks' characteristics on computational complex detection methods. <i>Journal of Theoretical Biology</i> , 2018, 439, 141-151.	0.8	14
15811	A Guide to Illumina BeadChip Data Analysis. <i>Methods in Molecular Biology</i> , 2018, 1708, 303-330.	0.4	23
15812	The complete genome sequence of <i>Colwellia</i> sp. NB097-1 reveals evidence for the potential genetic basis for its adaptation to cold environment. <i>Marine Genomics</i> , 2018, 37, 54-57.	0.4	8
15813	AgroPortal: A vocabulary and ontology repository for agronomy. <i>Computers and Electronics in Agriculture</i> , 2018, 144, 126-143.	3.7	87

#	ARTICLE	IF	CITATIONS
15814	Dynamic Modeling. , 2018, , 103-111.		0
15815	Evidence for a hierarchical transcriptional circuit in <i>Drosophila</i> male germline involving testis-specific TAF and two gene-specific transcription factors, Mod and Acj6. FEBS Letters, 2018, 592, 46-59.	1.3	4
15816	Database of transcription factors in lung cancer (DBTFLC): A novel resource for exploring transcription factors associated with lung cancer. Journal of Cellular Biochemistry, 2018, 119, 5253-5261.	1.2	9
15817	Integration of ENCODE RNAseq and eCLIP Data Sets. Methods in Molecular Biology, 2018, 1720, 111-129.	0.4	5
15818	Insights into the Proteome of Gastrointestinal Stromal Tumors-Derived Exosomes Reveals New Potential Diagnostic Biomarkers. Molecular and Cellular Proteomics, 2018, 17, 495-515.	2.5	47
15820	Proteomics analysis of human breast milk to assess breast cancer risk. Electrophoresis, 2018, 39, 653-665.	1.3	27
15821	Transcriptome analysis of the threatened snail <i>Ellobium chinense</i> reveals candidate genes for adaptation and identifies SSRs for conservation genetics. Genes and Genomics, 2018, 40, 333-347.	0.5	6
15822	Prediction of protein essentiality by the improved particle swarm optimization. Soft Computing, 2018, 22, 6657-6669.	2.1	8
15823	Aging and neurodegeneration are associated with increased mutations in single human neurons. Science, 2018, 359, 555-559.	6.0	496
15824	Cellular, ultrastructural and molecular analyses of epidermal cell development in the planarian <i>Schmidtea mediterranea</i> . Developmental Biology, 2018, 433, 357-373.	0.9	35
15825	Protein corona between nanoparticles and bacterial proteins in activated sludge: Characterization and effect on nanoparticle aggregation. Bioresource Technology, 2018, 250, 10-16.	4.8	22
15826	Systems Biology. Methods in Molecular Biology, 2018, , .	0.4	0
15827	Copy number variation regions in Nellore cattle: Evidences of environment adaptation. Livestock Science, 2018, 207, 51-58.	0.6	30
15828	Pectin methylesterase inhibitor (PMEI) family can be related to male sterility in Chinese cabbage (<i>Brassica rapa</i> ssp. <i>pekinensis</i>). Molecular Genetics and Genomics, 2018, 293, 343-357.	1.0	21
15829	Cln5 is secreted and functions as a glycoside hydrolase in <i>Dictyostelium</i> . Cellular Signalling, 2018, 42, 236-248.	1.7	45
15830	Capsaicin reduces genotoxicity, colonic cell proliferation and preneoplastic lesions induced by 1,2-dimethylhydrazine in rats. Toxicology and Applied Pharmacology, 2018, 338, 93-102.	1.3	31
15831	De novo transcriptome analysis of <i>Ammopiptanthus nanus</i> and its comparative analysis with <i>A. mongolicus</i> . Trees - Structure and Function, 2018, 32, 287-300.	0.9	15
15832	Signatures of selection in embryonic transcriptomes of lizards adapting in parallel to cool climate. Evolution; International Journal of Organic Evolution, 2018, 72, 67-81.	1.1	22

#	ARTICLE	IF	CITATIONS
15833	MicroRNA profiling in MDA-MB-231 human breast cancer cell exposed to the <i>Phaleria macrocarpa</i> (Boerl.) fruit ethyl acetate fraction (PMEAF) through Illumina Hi-Seq technologies and various in silico bioinformatics tools. <i>Journal of Ethnopharmacology</i> , 2018, 213, 118-131.	2.0	2
15834	Molecular Characterization of an Endozoicomonas-Like Organism Causing Infection in the King Scallop (<i>Pecten maximus</i> L.). <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	23
15835	Transcriptome analysis and discovery of genes involved in immune pathways from coelomocytes of <i>Onchidium struma</i> after bacterial challenge. <i>Fish and Shellfish Immunology</i> , 2018, 72, 528-543.	1.6	14
15836	<i>Pseudomonas silesiensis</i> sp. nov. strain A3T isolated from a biological pesticide sewage treatment plant and analysis of the complete genome sequence. <i>Systematic and Applied Microbiology</i> , 2018, 41, 13-22.	1.2	23
15837	Endothelial dysfunction is a superinducer of syndecan-4: fibrogenic role of its ectodomain. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2018, 314, H484-H496.	1.5	32
15838	Equipment selection knowledge base system for industrial styrene process. <i>Chinese Journal of Chemical Engineering</i> , 2018, 26, 1707-1712.	1.7	3
15839	Environmental variation partitioned into separate heritable components. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 136-152.	1.1	40
15840	A Method for Cross-Species Visualization and Analysis of RNA-Sequence Data. <i>Methods in Molecular Biology</i> , 2018, 1702, 291-305.	0.4	3
15841	Raising orphans from a metadata morass: A researcher's guide to re-use of public $\text{\textcircled{r}}$ omics data. <i>Plant Science</i> , 2018, 267, 32-47.	1.7	18
15842	Temporal variation in brain transcriptome is associated with the expression of female mimicry as a sequential male alternative reproductive tactic in fish. <i>Molecular Ecology</i> , 2018, 27, 789-803.	2.0	7
15843	Discerning molecular interactions: A comprehensive review on biomolecular interaction databases and network analysis tools. <i>Gene</i> , 2018, 642, 84-94.	1.0	117
15844	Protein Moonlighting Revealed by Noncatalytic Phenotypes of Yeast Enzymes. <i>Genetics</i> , 2018, 208, 419-431.	1.2	28
15845	Identification of a novel gene in ROD9 island of <i>Salmonella</i> Enteritidis involved in the alteration of virulence-associated genes expression. <i>Virulence</i> , 2018, 9, 348-362.	1.8	19
15846	Genome-wide association study for ketosis in US Jerseys using producer-recorded data. <i>Journal of Dairy Science</i> , 2018, 101, 413-424.	1.4	33
15847	Optimal Penalized Function-on-Function Regression Under a Reproducing Kernel Hilbert Space Framework. <i>Journal of the American Statistical Association</i> , 2018, 113, 1601-1611.	1.8	30
15848	Integrative miRNA analysis identifies hsa-miR-154, hsa-miR-7, and hsa-miR-600 as potential prognostic biomarker for cervical cancer. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 1558-1566.	1.2	48
15849	Beyond Representing Orthology Relations by Trees. <i>Algorithmica</i> , 2018, 80, 73-103.	1.0	7
15850	Complete genome sequence of human pathogen <i>Kosakonia cowanii</i> type strain 888-76 T. <i>Brazilian Journal of Microbiology</i> , 2018, 49, 16-17.	0.8	18

#	ARTICLE	IF	CITATIONS
15851	Human blood gene signature as a marker for smoking exposure: Computational approaches of the top ranked teams in the sbv IMPROVER Systems Toxicology challenge. <i>Computational Toxicology</i> , 2018, 5, 31-37.	1.8	3
15852	Evaluation of in vivo and in vitro models of toxicity by comparison of toxicogenomics data with the literature. <i>Methods</i> , 2018, 132, 57-65.	1.9	8
15853	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. <i>Molecular Psychiatry</i> , 2018, 23, 1169-1180.	4.1	32
15854	Gene co-expression network analysis identifies the hub genes associated with immune functions for nocturnal hemodialysis in patients with end-stage renal disease. <i>Medicine (United States)</i> , 2018, 97, e12018.	0.4	24
15855	PAX5A and PAX5B isoforms are both efficient to drive B cell differentiation. <i>Oncotarget</i> , 2018, 9, 32841-32854.	0.8	4
15856	Computerized Approach to Creating a Systematic Ontology of Hematology/Oncology Regimens. <i>JCO Clinical Cancer Informatics</i> , 2018, 2, 1-11.	1.0	18
15857	Constructing Datasets for Multi-hop Reading Comprehension Across Documents. <i>Transactions of the Association for Computational Linguistics</i> , 2018, 6, 287-302.	3.2	245
15858	Molecular Response to Extreme Summer Temperatures Differs Between Two Genetically Differentiated Populations of a Coral Reef Fish. <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	29
15859	InDePTH: detection of hub genes for developing gene expression networks under anticancer drug treatment. <i>Oncotarget</i> , 2018, 9, 29097-29111.	0.8	8
15860	Transcriptomic Characterization of the South American Freshwater Stingray <i>Potamotrygon motoro</i> Venom Apparatus. <i>Toxins</i> , 2018, 10, 544.	1.5	13
15861	<i>De novo</i> male gonad transcriptome draft for the marine mussel <i>Perumytilus purpuratus</i> with a focus on its reproductive-related proteins. <i>Journal of Genomics</i> , 2018, 6, 127-132.	0.6	10
15862	Genome-wide differences in DNA methylation changes in caprine ovaries between oestrous and dioestrous phases. <i>Journal of Animal Science and Biotechnology</i> , 2018, 9, 85.	2.1	28
15863	INTEGRO: an algorithm for data-integration and disease-gene association. , 2018, , .		10
15864	iDEP: an integrated web application for differential expression and pathway analysis of RNA-Seq data. <i>BMC Bioinformatics</i> , 2018, 19, 534.	1.2	803
15865	Representativeness of variation benchmark datasets. <i>BMC Bioinformatics</i> , 2018, 19, 461.	1.2	18
15866	GOnet: a tool for interactive Gene Ontology analysis. <i>BMC Bioinformatics</i> , 2018, 19, 470.	1.2	189
15867	Exploring Disease Similarity by Integrating Multiple Data Sources. , 2018, , .		2
15868	GLUE: a flexible software system for virus sequence data. <i>BMC Bioinformatics</i> , 2018, 19, 532.	1.2	84

#	ARTICLE	IF	CITATIONS
15869	RADAR: Representation Learning across Disease Information Networks for Similar Disease Detection. , 2018, , .		4
15870	Gene ontology concept recognition using named concept: understanding the various presentations of the gene functions in biomedical literature. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	2
15871	Semantic Multi-Classifer Systems Identify Predictive Processes in Heart Failure Models across Species. Biomolecules, 2018, 8, 158.	1.8	1
15872	Fusing heterogeneous genomic data to discover cancer progression related dynamic modules. , 2018, , .		5
15873	Expression reflects population structure. PLoS Genetics, 2018, 14, e1007841.	1.5	27
15874	Accelerating annotation of articles via automated approaches: evaluation of the neXtA5 curation-support tool by neXtProt. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	6
15875	A Partial least squares-based regression approach for analysis of frontotemporal dementia gene markers in human brain gene microarray data. , 2018, , .		1
15876	Toward an Interoperability and Integration Framework to Enable Digital Thread. Systems, 2018, 6, 46.	1.2	39
15877	A Study of Biclustering Coherence Measures for Gene Expression Data. , 2018, , .		1
15878	Connecting nutrition composition measures to biomedical research. BMC Research Notes, 2018, 11, 883.	0.6	2
15879	A hierarchical multi-label classification method based on neural networks for gene function prediction. Biotechnology and Biotechnological Equipment, 2018, 32, 1613-1621.	0.5	14
15880	Evaluating the impact of topological protein features on the negative examples selection. BMC Bioinformatics, 2018, 19, 417.	1.2	2
15881	High-quality-draft genome sequence of the heavy metal resistant and exopolysaccharides producing bacterium Mucilaginibacter pedocola TBZ30T. Standards in Genomic Sciences, 2018, 13, 34.	1.5	11
15882	Integrative Gene Selection on Gene Expression Data: Providing Biological Context to Traditional Approaches. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	15
15883	Harnessing the Power of Unified Metadata in an Ontology Repository: The Case of AgroPortal. Journal on Data Semantics, 2018, 7, 191-221.	2.0	14
15885	Systematic characterization of autophagy-related genes during the adipocyte differentiation using public-access data. Oncotarget, 2018, 9, 15526-15541.	0.8	13
15886	Optimizing gene set annotations combining GO structure and gene expression data. BMC Systems Biology, 2018, 12, 133.	3.0	0
15887	Variation in Mitochondria-Derived Transcript Levels Associated With DDT Resistance in the91-RStrain ofDrosophila melanogaster(Diptera: Drosophilidae). Journal of Insect Science, 2018, 18, .	0.6	2

#	ARTICLE	IF	CITATIONS
15888	Examining the key genes and pathways in hepatocellular carcinoma development from hepatitis B virusâ€‘positive cirrhosis. <i>Molecular Medicine Reports</i> , 2018, 18, 4940-4950.	1.1	20
15889	Differential Gene Expression to Characterize Spontaneously Regressing Metastatic Neuroblastoma. , 2018, , .		0
15890	Coexpression modules constructed by weighted gene coâ€‘expression network analysis indicate ubiquitinâ€‘mediated proteolysis as a potential biomarker of uveal melanoma. <i>Experimental and Therapeutic Medicine</i> , 2019, 17, 237-243.	0.8	4
15891	Hybrid natural language processing for high-performance patent and literature mining in IBM Watson for Drug Discovery. <i>IBM Journal of Research and Development</i> , 2018, 62, 8:1-8:12.	3.2	5
15892	Effects of Icaria on Atherosclerosis and Predicted Function Regulatory Network in ApoE Deficient Mice. <i>BioMed Research International</i> , 2018, 2018, 1-12.	0.9	11
15893	Natural selection in bats with historical exposure to white-nose syndrome. <i>BMC Zoology</i> , 2018, 3, .	0.3	17
15894	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
15895	A longitudinal feature selection method identifies relevant genes to distinguish complicated injury and uncomplicated injury over time. <i>BMC Medical Informatics and Decision Making</i> , 2018, 18, 115.	1.5	5
15896	Comparative transcriptome study provides insights into acquisition of embryogenic ability in upland cotton during somatic embryogenesis. <i>Journal of Cotton Research</i> , 2018, 1, .	1.0	9
15897	NeVOmics: An Enrichment Tool for Gene Ontology and Functional Network Analysis and Visualization of Data from OMICs Technologies. <i>Genes</i> , 2018, 9, 569.	1.0	16
15898	Integrative analysis of gene expression profiles reveals distinct molecular characteristics in oral tongue squamous cell carcinoma. <i>Oncology Letters</i> , 2018, 17, 2377-2387.	0.8	12
15899	Transcriptome Analysis and Functional Identification of Xa13 and Piâ€‘ta Orthologs in <i>Oryza granulata</i> . <i>Plant Genome</i> , 2018, 11, 170097.	1.6	2
15900	Mushroom Body Specific Transcriptome Analysis Reveals Dynamic Regulation of Learning and Memory Genes After Acquisition of Long-Term Courtship Memory in <i>Drosophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3433-3446.	0.8	30
15901	Identification of hub genes and pathways in glioblastoma by bioinformatics analysis. <i>Oncology Letters</i> , 2019, 17, 1035-1041.	0.8	7
15902	Generation and characterization of expressed sequence tags (ESTs) from coralloid root cDNA library of <i>Cycas debaoensis</i> . <i>Plant Diversity</i> , 2018, 40, 245-252.	1.8	1
15903	<i>Bacillus velezensis</i> YC7010 Enhances Plant Defenses Against Brown Planthopper Through Transcriptomic and Metabolic Changes in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 1904.	1.7	41
15904	Identification and comparison of microRNAs in pituitary gland during prenatal and postnatal stages of sheep by deep sequencing. <i>Journal of Genetics</i> , 2018, 97, 965-975.	0.4	7
15905	A Survey of Methods for Genome Functional Analysis in Comparative Genomics. <i>International Journal of Engineering and Technology(UAE)</i> , 2018, 7, 681.	0.2	3

#	ARTICLE	IF	CITATIONS
15906	A review on biclustering of gene expression microarray data: algorithms, effective measures and validations. <i>International Journal of Data Mining and Bioinformatics</i> , 2018, 21, 230.	0.1	3
15907	Clinical significance and effect of MTDH/AEG-1 in bladder urothelial cancer: a study based on immunohistochemistry, RNA-seq, and in vitro verification. <i>Cancer Management and Research</i> , 2018, Volume 10, 6921-6936.	0.9	1
15909	Protein Regulating Networks underlying Multiple Actions against Cancer Delivered by Ginseng. , 2018, , .		1
15910	Bioinformatics analysis and verification of key genes associated with recurrent respiratory tract infections. <i>International Journal of Molecular Medicine</i> , 2018, 42, 514-524.	1.8	2
15911	Weighted gene co-expression network analysis of microarray mRNA expression profiling in response to electroacupuncture. , 2018, , .		1
15912	Cantharidin Triggers Apoptosis via ALB and PPP2R4 against Lung Cancer. , 2018, , .		0
15913	Genome-Wide miRNA Expression Alterations in Nucleus Accumbens Provide Insights into Chronic Stress and Treatment in Depression. , 2018, , .		0
15914	Exome sequencing study of 20 patients with high myopia. <i>PeerJ</i> , 2018, 6, e5552.	0.9	13
15915	System analysis of the regulation of the immune response by CD147 and FOXC1 in cancer cell lines. <i>Oncotarget</i> , 2018, 9, 12918-12931.	0.8	8
15916	Gene expression profiles for predicting antibody-mediated kidney allograft rejection: Analysis of GEO datasets. <i>International Journal of Molecular Medicine</i> , 2018, 42, 2303-2311.	1.8	5
15917	Genome-wide detection of selective signatures in a Duroc pig population. <i>Journal of Integrative Agriculture</i> , 2018, 17, 2528-2535.	1.7	14
15918	Functional Mapping of Plant Growth in <i>Arabidopsis thaliana</i> . , 2018, , .		0
15919	Genetic Algorithm for Community Detection in Biological Networks. <i>Procedia Computer Science</i> , 2018, 126, 195-204.	1.2	7
15920	Analysis of NFkB-mediated regulation of mechanisms underlying the development of Hodgkin's lymphoma. <i>Molecular Medicine Reports</i> , 2018, 17, 8129-8136.	1.1	5
15921	A Lexical Approach to Identifying Subtype Inconsistencies in Biomedical Terminologies. , 2018, , .		5
15922	Quality Assurance of Concept Roles in the National Cancer Institute thesaurus. , 2018, , .		2
15923	Protein Regulating Network towards Tonifying Primal Qi Delivered by Ginseng. , 2018, , .		0
15926	Proteomic changes in traumatic brain injury: experimental approaches. <i>Current Opinion in Neurology</i> , 2018, 31, 709-717.	1.8	14

#	ARTICLE	IF	CITATIONS
15927	Quantitative proteomic analysis of aqueous humor from patients with drusen and reticular pseudodrusen in age-related macular degeneration. <i>BMC Ophthalmology</i> , 2018, 18, 289.	0.6	32
15928	Transcriptome profile analysis of leg muscle tissues between slow- and fast-growing chickens. <i>PLoS ONE</i> , 2018, 13, e0206131.	1.1	18
15929	A Genetic Circuit Compiler: Generating Combinatorial Genetic Circuits with Web Semantics and Inference. <i>ACS Synthetic Biology</i> , 2018, 7, 2812-2823.	1.9	2
15930	The EcoCyc Database. <i>EcoSal Plus</i> , 2018, 8, .	2.1	75
15931	Identification of Core Biomarkers Associated with Outcome in Glioma: Evidence from Bioinformatics Analysis. <i>Disease Markers</i> , 2018, 2018, 1-16.	0.6	22
15932	SyNDI: synchronous network data integration framework. <i>BMC Bioinformatics</i> , 2018, 19, 403.	1.2	1
15933	Integrated whole genome microarray analysis and immunohistochemical assay identifies COL11A1, GJB2 and CTRL as predictive biomarkers for pancreatic cancer. <i>Cancer Cell International</i> , 2018, 18, 174.	1.8	28
15934	Draft genome sequences of <i>Candidatus Chloroploca asiatica</i> ™ and <i>Candidatus Viridilinea mediisalina</i> ™, candidate representatives of the Chloroflexales order: phylogenetic and taxonomic implications. <i>Standards in Genomic Sciences</i> , 2018, 13, 24.	1.5	56
15935	Identification of critically carcinogenesis-related genes in basal cell carcinoma. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 6957-6967.	1.0	7
15936	Two histologically colorectal carcinomas subsets from the serrated pathway show different methylome signatures and diagnostic biomarkers. <i>Clinical Epigenetics</i> , 2018, 10, 141.	1.8	12
15937	Genomic and transcriptomic signals of thermal tolerance in heat-tolerant corals (<i>Platygyra</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 34	2.0	63
15938	Comparative Analyses of the Transcriptome and Proteome of Comte de Paris and Smooth Cayenne to Improve the Understanding of Ethephon-Induced Floral Transition in Pineapple. <i>Cellular Physiology and Biochemistry</i> , 2018, 50, 2139-2156.	1.1	11
15939	Identification and Analysis of Rice Yield-Related Candidate Genes by Walking on the Functional Network. <i>Frontiers in Plant Science</i> , 2018, 9, 1685.	1.7	4
15940	Transcriptome and Resistance-Related Genes Analysis of <i>Botrytis cinerea</i> B05.10 Strain to Different Selective Pressures of Cyprodinil and Fenhexamid. <i>Frontiers in Microbiology</i> , 2018, 9, 2591.	1.5	8
15941	Identification of hub genes with diagnostic values in pancreatic cancer by bioinformatics analyses and supervised learning methods. <i>World Journal of Surgical Oncology</i> , 2018, 16, 223.	0.8	24
15942	Transcriptomic Characterization of the Human Habenula Highlights Drug Metabolism and the Neuroimmune System. <i>Frontiers in Neuroscience</i> , 2018, 12, 742.	1.4	23
15943	Effect of single nucleotide polymorphisms on intramuscular fat content in Hungarian Simmental cattle. <i>Asian-Australasian Journal of Animal Sciences</i> , 2018, 31, 1415-1419.	2.4	10
15944	Whole-genome sequences of Malawi cichlids reveal multiple radiations interconnected by gene flow. <i>Nature Ecology and Evolution</i> , 2018, 2, 1940-1955.	3.4	358

#	ARTICLE	IF	CITATIONS
15945	The genome of an underwater architect, the caddisfly <i>Stenopsyche tienmushanensis</i> (Insecta: Trichoptera). <i>GigaScience</i> , 2018, 7, .	3.3	41
15946	Characterization of drought stress-responsive root transcriptome of faba bean (<i>Vicia faba</i> L.) using RNA sequencing. <i>3 Biotech</i> , 2018, 8, 502.	1.1	15
15947	Adipocyte-secreted BMP8b mediates adrenergic-induced remodeling of the neuro-vascular network in adipose tissue. <i>Nature Communications</i> , 2018, 9, 4974.	5.8	104
15948	PVCbase: an integrated web resource for the PVC bacterial proteomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	13
15949	Surgical adhesions in mice are derived from mesothelial cells and can be targeted by antibodies against mesothelial markers. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	70
15950	A new method for evaluating the impacts of semantic similarity measures on the annotation of gene sets. <i>PLoS ONE</i> , 2018, 13, e0208037.	1.1	3
15951	Inflammatory Cytokine TNF α Promotes the Long-Term Expansion of Primary Hepatocytes in 3D Culture. <i>Cell</i> , 2018, 175, 1607-1619.e15.	13.5	211
15952	MicroRNA 399 as a potential integrator of photo-response, phosphate homeostasis, and sucrose signaling under long day condition. <i>BMC Plant Biology</i> , 2018, 18, 290.	1.6	15
15953	Mutations in DNA repair genes are associated with increased neo-antigen load and activated T cell infiltration in lung adenocarcinoma. <i>Oncotarget</i> , 2018, 9, 7949-7960.	0.8	49
15954	CCNA2 acts as a novel biomarker in regulating the growth and apoptosis of colorectal cancer. <i>Cancer Management and Research</i> , 2018, Volume 10, 5113-5124.	0.9	83
15955	Chromatin Immunoprecipitation of Murine Brown Adipose Tissue. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	1
15956	Novel and differentially abundant microRNAs in sperm cells, seminal plasma, and serum of boars due to porcine reproduction and respiratory syndrome virus infection. <i>Animal Reproduction Science</i> , 2018, 199, 60-71.	0.5	7
15957	The draft genome sequence of <i>Nitrospira lenta</i> strain BS10, a nitrite oxidizing bacterium isolated from activated sludge. <i>Standards in Genomic Sciences</i> , 2018, 13, 32.	1.5	28
15958	A general framework dedicated to computational morphogenesis Part II $\hat{=}$ Knowledge representation and architecture. <i>BioSystems</i> , 2018, 173, 314-334.	0.9	2
15959	Evidence for genetic contribution to the increased risk of type 2 diabetes in schizophrenia. <i>Translational Psychiatry</i> , 2018, 8, 252.	2.4	73
15960	BioJupies: Automated Generation of Interactive Notebooks for RNA-Seq Data Analysis in the Cloud. <i>Cell Systems</i> , 2018, 7, 556-561.e3.	2.9	217
15961	Spn limits intestinal stem cell self-renewal. <i>PLoS Genetics</i> , 2018, 14, e1007773.	1.5	10
15962	Structural Variation, Functional Differentiation, and Activity Correlation of the Cytochrome P450 Gene Superfamily Revealed in Ginseng. <i>Plant Genome</i> , 2018, 11, 170106.	1.6	14

#	ARTICLE	IF	CITATIONS
15963	Identification of Grade-associated MicroRNAs in Brainstem Gliomas Based on Microarray Data. <i>Journal of Cancer</i> , 2018, 9, 4463-4476.	1.2	6
15964	ALS mutations of FUS suppress protein translation and disrupt the regulation of nonsense-mediated decay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11904-E11913.	3.3	138
15965	Computational discovery of direct associations between GO terms and protein domains. <i>BMC Bioinformatics</i> , 2018, 19, 413.	1.2	3
15966	Bioinformatics-based study to detect chemical compounds that show potential as treatments for pulmonary thromboembolism. <i>International Journal of Molecular Medicine</i> , 2019, 43, 276-284.	1.8	5
15967	Intrinsic-overlapping co-expression module detection with application to Alzheimer's Disease. <i>Computational Biology and Chemistry</i> , 2018, 77, 373-389.	1.1	16
15968	<i>Arabidopsis molybdenum</i> cofactor sulfurase ABA3 contributes to anthocyanin accumulation and oxidative stress tolerance in ABA-dependent and independent ways. <i>Scientific Reports</i> , 2018, 8, 16592.	1.6	43
15969	Unified Transcriptomic Signature of Arbuscular Mycorrhiza Colonization in Roots of <i>Medicago truncatula</i> by Integration of Machine Learning, Promoter Analysis, and Direct Merging Meta-Analysis. <i>Frontiers in Plant Science</i> , 2018, 9, 1550.	1.7	20
15970	Genome-wide transcriptome profiling and spatial expression analyses identify signals and switches of development in tapeworms. <i>EvoDevo</i> , 2018, 9, 21.	1.3	30
15971	Draft genome sequence of <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> strain Fito_F321, an endophyte microorganism from <i>Vitis vinifera</i> with biocontrol potential. <i>Standards in Genomic Sciences</i> , 2018, 13, 30.	1.5	25
15972	High-quality-draft genome sequence of the multiple heavy metal resistant bacterium <i>Pseudaminobacter manganicus</i> JH-7T. <i>Standards in Genomic Sciences</i> , 2018, 13, 29.	1.5	8
15973	Complete genome sequence of <i>Planococcus</i> sp. PAMC21323 isolated from Antarctica and its metabolic potential to detoxify pollutants. <i>Standards in Genomic Sciences</i> , 2018, 13, 31.	1.5	10
15974	Uncovering the Changing Gene Expression Profile of Honeybee (<i>Apis mellifera</i>) Worker Larvae Transplanted to Queen Cells. <i>Frontiers in Genetics</i> , 2018, 9, 416.	1.1	12
15975	Chemical Profiling of the Endoplasmic Reticulum Proteome Using Designer Labeling Reagents. <i>Journal of the American Chemical Society</i> , 2018, 140, 17060-17070.	6.6	37
15976	Transcriptomics Study on <i>Staphylococcus aureus</i> Biofilm Under Low Concentration of Ampicillin. <i>Frontiers in Microbiology</i> , 2018, 9, 2413.	1.5	51
15977	Born to Cry: A Genetic Dissection of Infant Vocalization. <i>Frontiers in Behavioral Neuroscience</i> , 2018, 12, 250.	1.0	24
15978	CMV2b-Dependent Regulation of Host Defense Pathways in the Context of Viral Infection. <i>Viruses</i> , 2018, 10, 618.	1.5	14
15979	Optimized Protein-Protein Interaction Network Usage with Context Filtering. <i>Methods in Molecular Biology</i> , 2018, 1819, 33-50.	0.4	2
15980	gLabTrie: A Data Structure for Motif Discovery with Constraints. <i>Data-centric Systems and Applications</i> , 2018, , 71-95.	0.2	3

#	ARTICLE	IF	CITATIONS
15981	CEA: Combination-based gene set functional enrichment analysis. <i>Scientific Reports</i> , 2018, 8, 13085.	1.6	4
15982	A GPU-based algorithm for fast node label learning in large and unbalanced biomolecular networks. <i>BMC Bioinformatics</i> , 2018, 19, 353.	1.2	2
15983	Feature related multi-view nonnegative matrix factorization for identifying conserved functional modules in multiple biological networks. <i>BMC Bioinformatics</i> , 2018, 19, 394.	1.2	24
15984	Transcriptome analysis of <i>Xenopus</i> orofacial tissues deficient in retinoic acid receptor function. <i>BMC Genomics</i> , 2018, 19, 795.	1.2	8
15985	Robust Innate Immunity of Young Rabbits Mediates Resistance to Rabbit Hemorrhagic Disease Caused by Lagovirus Europaeus GI.1 But Not GI.2. <i>Viruses</i> , 2018, 10, 512.	1.5	29
15987	Identification of miRNA profiling in prediction of tumor recurrence and progress and bioinformatics analysis for patients with primary esophageal cancer: Study based on TCGA database. <i>Pathology Research and Practice</i> , 2018, 214, 2081-2086.	1.0	13
15988	Comparative Transcriptional Profiling and Physiological Responses of Two Contrasting Oat Genotypes under Salt Stress. <i>Scientific Reports</i> , 2018, 8, 16248.	1.6	25
15989	Proteomics based analysis of the nicotine catabolism in <i>Paenarthrobacter nicotinovorans</i> pAO1. <i>Scientific Reports</i> , 2018, 8, 16239.	1.6	19
15990	Rooting Phylogenies and the Tree of Life While Minimizing Ad Hoc and Auxiliary Assumptions. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431880510.	0.6	40
15991	Genome-wide association studies and meta-analysis uncovers new candidate genes for growth and carcass traits in pigs. <i>PLoS ONE</i> , 2018, 13, e0205576.	1.1	16
15992	An Ontology-Based Decision Support System for Insect Pest Control in Crops. <i>Communications in Computer and Information Science</i> , 2018, , 3-14.	0.4	8
15993	Maternal depression during pregnancy and cord blood DNA methylation: findings from the Avon Longitudinal Study of Parents and Children. <i>Translational Psychiatry</i> , 2018, 8, 244.	2.4	44
15994	Parasitic Nematodes Exert Antimicrobial Activity and Benefit From Microbiota-Driven Support for Host Immune Regulation. <i>Frontiers in Immunology</i> , 2018, 9, 2282.	2.2	57
15995	Integrated systems analysis reveals conserved gene networks underlying response to spinal cord injury. <i>ELife</i> , 2018, 7, .	2.8	29
15996	Identity Noise and Adipogenic Traits Characterize Dermal Fibroblast Aging. <i>Cell</i> , 2018, 175, 1575-1590.e22.	13.5	168
15997	Draft genomes of <i>Cronobacter sakazakii</i> strains isolated from dried spices bring unique insights into the diversity of plant-associated strains. <i>Standards in Genomic Sciences</i> , 2018, 13, 35.	1.5	29
15998	Comparative Transcriptome and iTRAQ Proteome Analyses Reveal the Mechanisms of Diapause in <i>Aphidius gifuensis</i> Ashmead (Hymenoptera: Aphidiidae). <i>Frontiers in Physiology</i> , 2018, 9, 1697.	1.3	32
15999	A multi-omics approach for identifying important pathways and genes in human cancer. <i>BMC Bioinformatics</i> , 2018, 19, 479.	1.2	15

#	ARTICLE	IF	CITATIONS
16000	Interaction of Gravity with Cell Metabolism. SpringerBriefs in Space Life Sciences, 2018, , 33-94.	0.1	0
16001	Copper-Catalyzed Synthesis, Bio-Evaluation, and in Silico Studies of 2-Aryl-N-alkylbenzimidazoles as Neuroprotective Agents. Catalysts, 2018, 8, 433.	1.6	3
16002	Complete genome sequence of the nitrogen-fixing bacterium Azospirillum humicireducens type strain SgZ-5T. Standards in Genomic Sciences, 2018, 13, 28.	1.5	6
16003	Comparative De Novo transcriptome analysis of the Australian black-lip and Sydney rock oysters reveals expansion of repetitive elements in Saccostrea genomes. PLoS ONE, 2018, 13, e0206417.	1.1	3
16004	Ischemia-reperfusion injury in a rat microvascular skin free flap model: A histological, genetic, and blood flow study. PLoS ONE, 2018, 13, e0209624.	1.1	28
16005	Arabidopsis thaliana responds to colonisation of Piriformospora indica by secretion of symbiosis-specific proteins. PLoS ONE, 2018, 13, e0209658.	1.1	17
16006	Robust analysis of novel mRNA–lncRNA cross talk based on ceRNA hypothesis uncovers carcinogenic mechanism and promotes diagnostic accuracy in esophageal cancer. Cancer Management and Research, 2019, Volume 11, 347-358.	0.9	16
16007	Cytokines in adipose-derived mesenchymal stem cells promote the healing of liver disease. World Journal of Stem Cells, 2018, 10, 146-159.	1.3	19
16008	Transcriptome dataset of trunk neural crest cells migrating along the ventral pathway of chick embryos. Data in Brief, 2018, 21, 2547-2553.	0.5	9
16009	Transcriptome analysis of the typical freshwater rhodophytes Sheathia arcuata grown under different light intensities. PLoS ONE, 2018, 13, e0197729.	1.1	12
16010	Identification of hub genes and outcome in colon cancer based on bioinformatics analysis. Cancer Management and Research, 2019, Volume 11, 323-338.	0.9	28
16011	From Matrices to Knowledge: Using Semantic Networks to Annotate the Connectome. Frontiers in Neuroanatomy, 2018, 12, 111.	0.9	4
16012	Biological Pathways Leading From ANGPTL8 to Diabetes Mellitus"A Co-expression Network Based Analysis. Frontiers in Physiology, 2018, 9, 1841.	1.3	8
16013	A Novel Inorganic Sulfur Compound Metabolizing Ferroplasma-Like Population Is Suggested to Mediate Extracellular Electron Transfer. Frontiers in Microbiology, 2018, 9, 2945.	1.5	18
16014	Who Models the World?. Proceedings of the ACM on Human-Computer Interaction, 2018, 2, 1-18.	2.5	20
16015	Type 1 Diabetes Mellitus-Associated Genetic Variants Contribute to Overlapping Immune Regulatory Networks. Frontiers in Genetics, 2018, 9, 535.	1.1	39
16016	Analysis of Dendrobium huoshanense transcriptome unveils putative genes associated with active ingredients synthesis. BMC Genomics, 2018, 19, 978.	1.2	44
16017	GPCR-specific autoantibody signatures are associated with physiological and pathological immune homeostasis. Nature Communications, 2018, 9, 5224.	5.8	116

#	ARTICLE	IF	CITATIONS
16018	Role of miRNAs in skeletal muscle aging. <i>Clinical Interventions in Aging</i> , 2018, Volume 13, 2407-2419.	1.3	42
16019	Elucidating the Role of Chromatin State and Transcription Factors on the Regulation of the Yeast Metabolic Cycle: A Multi-Omic Integrative Approach. <i>Frontiers in Genetics</i> , 2018, 9, 578.	1.1	10
16020	Up-Regulation of hsa-miR-210 Promotes Venous Metastasis and Predicts Poor Prognosis in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2018, 8, 569.	1.3	25
16021	Induced Resistance Mechanism of Novel Curcumin Analogs Bearing a Quinazoline Moiety to Plant Virus. <i>International Journal of Molecular Sciences</i> , 2018, 19, 4065.	1.8	10
16022	Candidate Variants for Additive and Interactive Effects on Bioenergy Traits in Switchgrass (<i>Panicum virgatum</i> L.) Identified by Genome-Wide Association Analyses. <i>Plant Genome</i> , 2018, 11, 180002.	1.6	8
16023	A graph based model for multiple biological data sources integration. , 2018, , .		3
16024	Ontology-Based Data Access and Integration. , 2018, , 2590-2596.		9
16025	Gravitational Biology II. <i>SpringerBriefs in Space Life Sciences</i> , 2018, , .	0.1	2
16026	Circadian Proteomic Analysis Uncovers Mechanisms of Post-Transcriptional Regulation in Metabolic Pathways. <i>Cell Systems</i> , 2018, 7, 613-626.e5.	2.9	93
16027	Integrated PTR-ToF-MS, GWAS and biological pathway analyses reveal the contribution of cow's genome to cheese volatilome. <i>Scientific Reports</i> , 2018, 8, 17002.	1.6	5
16028	Fine-Grained Age Group Classification in the wild. , 2018, , .		5
16029	Mitoproteomics: Tackling Mitochondrial Dysfunction in Human Disease. <i>Oxidative Medicine and Cellular Longevity</i> , 2018, 2018, 1-26.	1.9	19
16030	Analysis of dynamic molecular networks for pancreatic ductal adenocarcinoma progression. <i>Cancer Cell International</i> , 2018, 18, 214.	1.8	37
16031	Transcriptomic and proteomic host response to <i>Aspergillus fumigatus</i> conidia in an air-liquid interface model of human bronchial epithelium. <i>PLoS ONE</i> , 2018, 13, e0209652.	1.1	29
16032	High-resolution mapping of cancer cell networks using co-functional interactions. <i>Molecular Systems Biology</i> , 2018, 14, e8594.	3.2	61
16033	Whole exome sequencing identifies recessive germline mutations in FAM160A1 in familial NK/T cell lymphoma. <i>Blood Cancer Journal</i> , 2018, 8, 111.	2.8	5
16034	Identification of biomarkers of chromophobe renal cell carcinoma by weighted gene co-expression network analysis. <i>Cancer Cell International</i> , 2018, 18, 206.	1.8	22
16035	Expression and potential molecular mechanisms of miR-204-5p in breast cancer, based on bioinformatics and a meta-analysis of 2,306 1/2 cases. <i>Molecular Medicine Reports</i> , 2018, 19, 1168-1184.	1.1	4

#	ARTICLE	IF	CITATIONS
16036	Measures of co-expression for improved function prediction of long non-coding RNAs. <i>BMC Bioinformatics</i> , 2018, 19, 533.	1.2	11
16037	Complete genome of <i>Rhizobium leguminosarum</i> Norway, an ineffective <i>Lotus</i> micro-symbiont. <i>Standards in Genomic Sciences</i> , 2018, 13, 36.	1.5	17
16038	Mycoextraction: Rapid Cadmium Removal by Macrofungi-Based Technology from Alkaline Soil. <i>Minerals (Basel, Switzerland)</i> , 2018, 8, 589.	0.8	3
16039	Functional genomics of the digestive tract in broilers. <i>BMC Genomics</i> , 2018, 19, 928.	1.2	8
16040	RNA sequencing and anthocyanin synthesis-related genes expression analyses in white-fruited <i>Vaccinium uliginosum</i> . <i>BMC Genomics</i> , 2018, 19, 930.	1.2	8
16041	Identification of core genes and prediction of miRNAs associated with osteoporosis using a bioinformatics approach. <i>Oncology Letters</i> , 2018, 17, 468-481.	0.8	5
16042	The codon sequences predict protein lifetimes and other parameters of the protein life cycle in the mouse brain. <i>Scientific Reports</i> , 2018, 8, 16913.	1.6	17
16043	EMBLmyGFF3: a converter facilitating genome annotation submission to European Nucleotide Archive. <i>BMC Research Notes</i> , 2018, 11, 584.	0.6	19
16044	Integrated analysis of microRNA and mRNA expression profiles in splenomegaly induced by non-cirrhotic portal hypertension in rats. <i>Scientific Reports</i> , 2018, 8, 17983.	1.6	3
16045	Prognostic value of sorting nexin 10 weak expression in stomach adenocarcinoma revealed by weighted gene co-expression network analysis. <i>World Journal of Gastroenterology</i> , 2018, 24, 4906-4919.	1.4	17
16046	Neuroinflammatory signals drive spinal curve formation in zebrafish models of idiopathic scoliosis. <i>Science Advances</i> , 2018, 4, eaav1781.	4.7	57
16047	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018, 362, .	6.0	516
16048	Integrated analysis reveals key genes with prognostic value in lung adenocarcinoma. <i>Cancer Management and Research</i> , 2018, Volume 10, 6097-6108.	0.9	36
16049	A two-circRNA signature predicts tumour recurrence in clinical non-functioning pituitary adenoma. <i>Oncology Reports</i> , 2018, 41, 113-124.	1.2	9
16050	<i>Daphnia galeata</i> responds to the exposure to an ichthyosporean gut parasite by down-regulation of immunity and lipid metabolism. <i>BMC Genomics</i> , 2018, 19, 932.	1.2	9
16051	Differential responses of <i>Lasiopodomys mandarinus</i> and <i>Lasiopodomys brandtii</i> to chronic hypoxia: a cross-species brain transcriptome analysis. <i>BMC Genomics</i> , 2018, 19, 901.	1.2	14
16052	Transcriptome Sequencing and Biochemical Analysis of Perianths and Coronas Reveal Flower Color Formation in <i>Narcissus pseudonarcissus</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 4006.	1.8	15
16053	Identifying the key genes and microRNAs in colorectal cancer liver metastasis by bioinformatics analysis and <i>in vitro</i> experiments. <i>Oncology Reports</i> , 2019, 41, 279-291.	1.2	39

#	ARTICLE	IF	CITATIONS
16054	Preliminary insights into the genetics of bank vole tolerance to Puumala hantavirus in Sweden. <i>Ecology and Evolution</i> , 2018, 8, 11273-11292.	0.8	9
16055	Comparative transcriptomics between high and low rubber producing <i>Taraxacum kok-saghyz</i> R. plants. <i>BMC Genomics</i> , 2018, 19, 875.	1.2	13
16056	Analysis of the transcriptome data in <i>Litopenaeus vannamei</i> reveals the immune basis and predicts the hub regulation-genes in response to high-pH stress. <i>PLoS ONE</i> , 2018, 13, e0207771.	1.1	20
16057	G-quadruplexes formation in the 5'UTRs of mRNAs associated with colorectal cancer pathways. <i>PLoS ONE</i> , 2018, 13, e0208363.	1.1	8
16058	Derivation and Validation of the Potential Core Genes in Pancreatic Cancer for Tumor-Stroma Crosstalk. <i>BioMed Research International</i> , 2018, 2018, 1-11.	0.9	14
16059	Complete genome sequence of <i>Arcticibacterium luteifluviistationis</i> SM1504T, a cytophagaceae bacterium isolated from Arctic surface seawater. <i>Standards in Genomic Sciences</i> , 2018, 13, 33.	1.5	3
16060	Genome-wide identification of lncRNAs and mRNAs differentially expressed in non-functioning pituitary adenoma and construction of a lncRNA-mRNA co-expression network. <i>Biology Open</i> , 2019, 8, .	0.6	22
16061	Improving the Gene Ontology Resource to Facilitate More Informative Analysis and Interpretation of Alzheimer's Disease Data. <i>Genes</i> , 2018, 9, 593.	1.0	15
16062	Comprehensive Analysis of <i>BAP1</i> Somatic Mutation in Clear Cell Renal Cell Carcinoma to Explore Potential Mechanisms <i>in Silico</i> . <i>Journal of Cancer</i> , 2018, 9, 4108-4116.	1.2	17
16063	Overview of Technological Advances and Predictive Assays. , 2018, , 664-679.		0
16064	Identification and validation of <i>NOLC1</i> as a potential target for enhancing sensitivity in multidrug resistant non-small cell lung cancer cells. <i>Cellular and Molecular Biology Letters</i> , 2018, 23, 54.	2.7	16
16065	Comparative transcriptomics identifies genes differentially expressed in the intestine of a new fast-growing strain of common carp with higher unsaturated fatty acid content in muscle. <i>PLoS ONE</i> , 2018, 13, e0206615.	1.1	14
16066	Linking single-cell measurements of mass, growth rate, and gene expression. <i>Genome Biology</i> , 2018, 19, 207.	3.8	42
16067	A Comparison of Proteins Expressed between Human and Mouse Adipose-Derived Mesenchymal Stem Cells by a Proteome Analysis through Liquid Chromatography with Tandem Mass Spectrometry. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3497.	1.8	11
16068	Selective expansion of myeloid and NK cells in humanized mice yields human-like vaccine responses. <i>Nature Communications</i> , 2018, 9, 5031.	5.8	39
16069	Sex Effects on Gene Expression in Lacrimal Glands of Mouse Models of Sjögren Syndrome. , 2018, 59, 5599.		18
16070	SWIM tool application to expression data of glioblastoma stem-like cell lines, corresponding primary tumors and conventional glioma cell lines. <i>BMC Bioinformatics</i> , 2018, 19, 436.	1.2	26
16071	Screening and clinical significance of tumor markers in head and neck squamous cell carcinoma through bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2019, 19, 143-154.	1.1	20

#	ARTICLE	IF	CITATIONS
16072	200+ Protein Concentrations in Healthy Human Blood Plasma: Targeted Quantitative SRM SIS Screening of Chromosomes 18, 13, Y, and the Mitochondrial Chromosome Encoded Proteome. <i>Journal of Proteome Research</i> , 2019, 18, 120-129.	1.8	17
16073	RNA Sequencing for Gene Expression Profiles in a Rat Model of Middle Cerebral Artery Occlusion. <i>BioMed Research International</i> , 2018, 2018, 1-14.	0.9	8
16074	Agronomic Linked Data (AgroLD): A knowledge-based system to enable integrative biology in agronomy. <i>PLoS ONE</i> , 2018, 13, e0198270.	1.1	13
16075	Comparative Proteomic Analysis. , 2018, , .		2
16076	Generation and classification of transcriptomes in two <i>Crotonia</i> species and molecular evolution of <i>CYC/TB1</i> genes in <i>Stemonaceae</i> . <i>Plant Diversity</i> , 2018, 40, 253-264.	1.8	1
16077	The transcriptomic landscape of yaks reveals molecular pathways for high altitude adaptation. <i>Genome Biology and Evolution</i> , 2019, 11, 72-85.	1.1	41
16078	Evaluation of Prioritization Methods of Extrinsic Apoptotic Signaling Pathway Genes for Retrieval of the New Candidates Associated with Major Depressive Disorder. <i>Russian Journal of Genetics</i> , 2018, 54, 1366-1374.	0.2	6
16079	Interplay Between MicroRNAs and Targeted Genes in Cellular Homeostasis of Adult Zebrafish (<i>Danio</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.7	5
16080	Comparative Transcriptomic and Metagenomic Analyses of Influenza Virus-Infected Nasal Epithelial Cells From Multiple Individuals Reveal Specific Nasal-Initiated Signatures. <i>Frontiers in Microbiology</i> , 2018, 9, 2685.	1.5	13
16081	Transcriptome Analysis Provides Insights into Gingerol Biosynthesis in Ginger (<i>Zingiber</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.6	19
16082	MicroRNA-mRNA integrated analysis based on a case of well-differentiated thyroid cancer with both metastasis and metastatic recurrence. <i>Oncology Reports</i> , 2018, 40, 3803-3811.	1.2	8
16083	An Evolutionary Tabu Search Algorithm for Matching Biomedical Ontologies. , 2018, , .		0
16084	Automatic detection of genomic regions with informative epigenetic patterns. <i>BMC Genomics</i> , 2018, 19, 847.	1.2	1
16085	Extraction of Association Rules from Tobacco Smoke Effect on the Placenta Microarray Dataset using Gene Ontology Based Optimized Association Rule Mining. , 2018, , .		1
16086	Comparative Transcriptome Profiling of mRNA and lncRNA Related to Tail Adipose Tissues of Sheep. <i>Frontiers in Genetics</i> , 2018, 9, 365.	1.1	43
16087	Development of an AmpliSeq™ Panel for Next-Generation Sequencing of a Set of Genetic Predictors of Persisting Pain. <i>Frontiers in Pharmacology</i> , 2018, 9, 1008.	1.6	3
16088	A systems-approach reveals human nestin is an endothelial-enriched, angiogenesis-independent intermediate filament protein. <i>Scientific Reports</i> , 2018, 8, 14668.	1.6	19
16089	Mutation pattern analysis reveals polygenic mini-drivers associated with relapse after surgery in lung adenocarcinoma. <i>Scientific Reports</i> , 2018, 8, 14830.	1.6	5

#	ARTICLE	IF	CITATIONS
16090	Systems biology primer: the basic methods and approaches. <i>Essays in Biochemistry</i> , 2018, 62, 487-500.	2.1	128
16091	ChemDIS 2: an update of chemical-disease inference system. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	7
16092	Methods and results from the genome-wide association group at GAW20. <i>BMC Genetics</i> , 2018, 19, 79.	2.7	0
16093	MicroRNA-transcription factor network analysis reveals miRNAs cooperatively suppress RORA in oral squamous cell carcinoma. <i>Oncogenesis</i> , 2018, 7, 79.	2.1	29
16094	Prediction of gene regulatory enhancers across species reveals evolutionarily conserved sequence properties. <i>PLoS Computational Biology</i> , 2018, 14, e1006484.	1.5	71
16095	Chimeric Antigen Receptor-T Cells with 4-1BB Co-Stimulatory Domain Present a Superior Treatment Outcome than Those with CD28 Domain Based on Bioinformatics. <i>Acta Haematologica</i> , 2018, 140, 131-140.	0.7	8
16096	A mitochondrial proteome profile indicative of type 2 diabetes mellitus in skeletal muscles. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-14.	3.2	34
16097	Microenvironmental niche divergence shapes BRCA1-dysregulated ovarian cancer morphological plasticity. <i>Nature Communications</i> , 2018, 9, 3917.	5.8	33
16098	Evolutionary insights from comparative transcriptome and transcriptome-wide coalescence analyses in <i>Tetrastigma hemsleyanum</i> . <i>BMC Plant Biology</i> , 2018, 18, 208.	1.6	11
16099	Single-Run Mass Spectrometry Analysis Provides Deep Insight into <i>E. coli</i> Proteome. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 2394-2401.	1.2	3
16100	Hemocytes transcriptome profile of the Chinese mitten crab (<i>Eriocheir sinensis</i>). <i>Aquaculture and Fisheries</i> , 2018, 3, 191-195.	1.2	0
16101	Quantitative proteomic analyses reveal that RBBI3.3, a trypsin inhibitor protein, plays an important role in <i>Magnaporthe oryzae</i> infection in rice. <i>Plant Growth Regulation</i> , 2018, 86, 365-374.	1.8	3
16102	Bioinformatics analyses of significant genes, related pathways and candidate prognostic biomarkers in glioblastoma. <i>Molecular Medicine Reports</i> , 2018, 18, 4185-4196.	1.1	39
16103	Genomic study for maternal related traits in Santa Inã's sheep breed. <i>Livestock Science</i> , 2018, 217, 76-84.	0.6	7
16104	Habitual aerobic exercise and circulating proteomic patterns in healthy adults: relation to indicators of healthspan. <i>Journal of Applied Physiology</i> , 2018, 125, 1646-1659.	1.2	19
16105	Exome scale map of genetic alterations promoting metastasis in colorectal cancer. <i>BMC Genetics</i> , 2018, 19, 85.	2.7	22
16106	Genetic variants analysis of three dromedary camels using whole genome sequencing data. <i>PLoS ONE</i> , 2018, 13, e0204028.	1.1	39
16107	Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. <i>ELife</i> , 2018, 7, .	2.8	180

#	ARTICLE	IF	CITATIONS
16108	A new tool for studying waterfowl immune and metabolic responses: Molecular level analysis using kinome profiling. <i>Ecology and Evolution</i> , 2018, 8, 8537-8546.	0.8	1
16109	A functional transcriptomic analysis in the relict marsupial <i>Dromiciops gliroides</i> reveals adaptive regulation of protective functions during hibernation. <i>Molecular Ecology</i> , 2018, 27, 4489-4500.	2.0	24
16110	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
16111	Plasma membrane profiling during enterohemorrhagic <i>E. coli</i> infection reveals that the metalloprotease StcE cleaves CD55 from host epithelial surfaces. <i>Journal of Biological Chemistry</i> , 2018, 293, 17188-17199.	1.6	7
16112	Comparative genomic analysis of the human and nematode <i>Caenorhabditis elegans</i> uncovers potential reproductive genes and disease associations in humans. <i>Physiological Genomics</i> , 2018, 50, 1002-1014.	1.0	21
16113	Prioritizing candidate genes post-GWAS using multiple sources of data for mastitis resistance in dairy cattle. <i>BMC Genomics</i> , 2018, 19, 656.	1.2	69
16114	Complete genome sequence of the Robinia pseudoacacia L. symbiont Mesorhizobium amorphae CCNWGS0123. <i>Standards in Genomic Sciences</i> , 2018, 13, 18.	1.5	8
16115	A miRNA Combination as Promising Biomarker for Hepatocellular Carcinoma Diagnosis: A Study Based on Bioinformatics Analysis. <i>Journal of Cancer</i> , 2018, 9, 3435-3446.	1.2	28
16116	Investigation of post-translational modifications in type 2 diabetes. <i>Clinical Proteomics</i> , 2018, 15, 32.	1.1	24
16117	ECPred: a tool for the prediction of the enzymatic functions of protein sequences based on the EC nomenclature. <i>BMC Bioinformatics</i> , 2018, 19, 334.	1.2	99
16118	Systematic analysis of lncRNA-miRNA-mRNA competing endogenous RNA network identifies four-lncRNA signature as a prognostic biomarker for breast cancer. <i>Journal of Translational Medicine</i> , 2018, 16, 264.	1.8	218
16119	Differentially Expressed Genes Associated with the Cabbage Yellow-Green-Leaf Mutant in the ygl-1 Mapping Interval with Recombination Suppression. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2936.	1.8	9
16120	Phenotypic and molecular consequences of stepwise temperature increase across generations in a coral reef fish. <i>Molecular Ecology</i> , 2018, 27, 4516-4528.	2.0	37
16121	Novel ecological and climatic conditions drive rapid adaptation in invasive Florida Burmese pythons. <i>Molecular Ecology</i> , 2018, 27, 4744-4757.	2.0	30
16122	Analysis of differentially upregulated proteins in ptsHlcr ⁺ and rppH ⁺ mutants in Escherichia coli during an adaptive laboratory evolution experiment. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 10193-10208.	1.7	9
16123	Gene Ontology Enrichment Improves Performances of Functional Similarity of Genes. <i>Scientific Reports</i> , 2018, 8, 12100.	1.6	22
16124	Genome-Wide DNA Methylation Profile of Gene cis-Acting Element Methylations in All-trans Retinoic Acid-Induced Mouse Cleft Palate. <i>DNA and Cell Biology</i> , 2018, 37, 993-1002.	0.9	8
16125	Dengue Epidemics Prediction: A Survey of the State-of-the-Art Based on Data Science Processes. <i>IEEE Access</i> , 2018, 6, 53757-53795.	2.6	42

#	ARTICLE	IF	CITATIONS
16126	A Robust Methodology for Assessing Differential Homeolog Contributions to the Transcriptomes of Allopolyploids. <i>Genetics</i> , 2018, 210, 883-894.	1.2	21
16127	De novo assembly and quantification reveal differentially expressed genes between soft-seed and hard-seed pomegranate (<i>Punica granatum</i> L.). <i>Acta Horticulturae</i> , 2018, , 131-146.	0.1	0
16128	MiRNA expression profiles in healthy OSAHS and OSAHS with arterial hypertension: potential diagnostic and early warning markers. <i>Respiratory Research</i> , 2018, 19, 194.	1.4	35
16129	Neurogenetic profiles delineate large-scale connectivity dynamics of the human brain. <i>Nature Communications</i> , 2018, 9, 3876.	5.8	48
16130	Improving protein function prediction using protein sequence and GO-term similarities. <i>Bioinformatics</i> , 2019, 35, 1116-1124.	1.8	21
16131	Comprehensive Transcriptome Profiling and Identification of Potential Genes Responsible for Salt Tolerance in Tall Fescue Leaves under Salinity Stress. <i>Genes</i> , 2018, 9, 466.	1.0	5
16132	Viewing the Meso-Scale Structures in Protein-Protein Interaction Networks Using 2-Clubs. <i>IEEE Access</i> , 2018, 6, 36780-36797.	2.6	3
16133	Gene multifunctionality scoring using gene ontology. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840018.	0.3	6
16134	Genome-wide identification and characterization of CONSTANS-like gene family in radish (<i>Raphanus</i>) Tj ETQq0 0 0 rBT /Overlock 10 Tf	1.1	23
16135	De Novo Sequence and Copy Number Variants Are Strongly Associated with Tourette Disorder and Implicate Cell Polarity in Pathogenesis. <i>Cell Reports</i> , 2018, 24, 3441-3454.e12.	2.9	91
16136	Transcriptome profiling analysis characterized the gene expression patterns responded to combined drought and heat stresses in soybean. <i>Computational Biology and Chemistry</i> , 2018, 77, 413-429.	1.1	46
16137	An RNAi screen in human cell lines reveals conserved DNA damage repair pathways that mitigate formaldehyde sensitivity. <i>DNA Repair</i> , 2018, 72, 1-9.	1.3	11
16138	Graphic Encoding of Macromolecules for Efficient High-Throughput Analysis. , 2018, , .		4
16139	Environmental pH modulates transcriptomic responses in the fungus <i>Fusarium</i> sp. associated with KSHB <i>Euwallacea</i> sp. near <i>fornicatus</i> . <i>BMC Genomics</i> , 2018, 19, 721.	1.2	15
16140	Transcriptomic approach to address low germination rate in <i>Cyclobalnopsis gilva</i> seeds. <i>South African Journal of Botany</i> , 2018, 119, 286-294.	1.2	15
16141	CRISPR Activation Screens Systematically Identify Factors that Drive Neuronal Fate and Reprogramming. <i>Cell Stem Cell</i> , 2018, 23, 758-771.e8.	5.2	161
16142	Prediction of Synergistic Toxicity of Binary Mixtures to <i>Vibrio fischeri</i> Based on Biomolecular Interaction Networks. <i>Chemical Research in Toxicology</i> , 2018, 31, 1138-1150.	1.7	7
16143	Signatures of genetic adaptation to extremely varied Australian environments in introduced European house sparrows. <i>Molecular Ecology</i> , 2018, 27, 4542-4555.	2.0	16

#	ARTICLE	IF	CITATIONS
16144	Gene module analysis of juvenile myelomonocytic leukemia and screening of anticancer drugs. <i>Oncology Reports</i> , 2018, 40, 3155-3170.	1.2	1
16145	Gene expression differences between thyroid carcinoma, thyroid adenoma and normal thyroid tissue. <i>Oncology Reports</i> , 2018, 40, 3359-3369.	1.2	24
16146	Transcriptomic analyses identify albino-associated genes of a novel albino tea germplasm "Huabai"™. <i>Horticulture Research</i> , 2018, 5, 54.	2.9	42
16147	Surface markers of human embryonic stem cells: a meta analysis of membrane proteomics reports. <i>Expert Review of Proteomics</i> , 2018, 15, 911-922.	1.3	8
16148	Genomic heterogeneity differentiates clinical and environmental subgroups of <i>Legionella pneumophila</i> sequence type 1. <i>PLoS ONE</i> , 2018, 13, e0206110.	1.1	9
16149	Fine Mapping of Lobed Leaf Genes in Two Brassica napus Lines Using SLAF Sequencing. <i>Crop Science</i> , 2018, 58, 1684-1692.	0.8	1
16150	Gene Mapping and Gene-Set Analysis for Milk Fever Incidence in Holstein Dairy Cattle. <i>Frontiers in Genetics</i> , 2018, 9, 465.	1.1	15
16151	The Hierarchical Modular Structure of HER2+ Breast Cancer Network. <i>Frontiers in Physiology</i> , 2018, 9, 1423.	1.3	40
16152	De Novo Hepatic Transcriptome Assembly and Systems Level Analysis of Three Species of Dietary Fish, <i>Sardinops sagax</i> , <i>Scomber japonicus</i> , and <i>Pleuronichthys verticalis</i> . <i>Genes</i> , 2018, 9, 521.	1.0	1
16153	Determinants of promoter and enhancer transcription directionality in metazoans. <i>Nature Communications</i> , 2018, 9, 4472.	5.8	22
16154	LOLAweb: a containerized web server for interactive genomic locus overlap enrichment analysis. <i>Nucleic Acids Research</i> , 2018, 46, W194-W199.	6.5	30
16155	Candidate Biomarkers and Molecular Mechanism Investigation for Glioblastoma Multiforme Utilizing WGCNA. <i>BioMed Research International</i> , 2018, 2018, 1-10.	0.9	72
16156	Identification of candidate genes or microRNAs associated with the lymph node metastasis of SCLC. <i>Cancer Cell International</i> , 2018, 18, 161.	1.8	20
16157	Transcriptomics reveal potential vaccine antigens and a drastic increase of upregulated genes during <i>Theileria parva</i> development from arthropod to bovine infective stages. <i>PLoS ONE</i> , 2018, 13, e0204047.	1.1	21
16158	Whole Genome Transcriptome Analysis of the Association between Obesity and Triple-Negative Breast Cancer in Caucasian Women. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 2338.	1.2	19
16159	Molecular Atlas of Postnatal Mouse Heart Development. <i>Journal of the American Heart Association</i> , 2018, 7, e010378.	1.6	65
16160	Innexins: Expression, Regulation, and Functions. <i>Frontiers in Physiology</i> , 2018, 9, 1414.	1.3	43
16161	Proteomic analysis of human prostate cancer PC-3M-1E8 cells and PC-3M-2B4 cells of same origin but with different metastatic potential. <i>PLoS ONE</i> , 2018, 13, e0206139.	1.1	5

#	ARTICLE	IF	CITATIONS
16162	Genomic distribution of a novel <i>Pyrenophora tritici-repentis</i> ToxA insertion element. <i>PLoS ONE</i> , 2018, 13, e0206586.	1.1	16
16163	Metallocluster transactions: dynamic protein interactions guide the biosynthesis of Fe-S clusters in bacteria. <i>Biochemical Society Transactions</i> , 2018, 46, 1593-1603.	1.6	18
16164	Identification of glioblastoma gene prognosis modules based on weighted gene co-expression network analysis. <i>BMC Medical Genomics</i> , 2018, 11, 96.	0.7	57
16165	WEADE: A workflow for enrichment analysis and data exploration. <i>PLoS ONE</i> , 2018, 13, e0204016.	1.1	3
16166	Identification of highly connected and differentially expressed gene subnetworks in metastasizing endometrial cancer. <i>PLoS ONE</i> , 2018, 13, e0206665.	1.1	11
16167	Prioritising candidate genes causing QTL using hierarchical orthologous groups. <i>Bioinformatics</i> , 2018, 34, i612-i619.	1.8	5
16168	From Affective Science to Psychiatric Disorder: Ontology as a Semantic Bridge. <i>Frontiers in Psychiatry</i> , 2018, 9, 487.	1.3	48
16169	Advances in Bioinformatics and Computational Biology. <i>Lecture Notes in Computer Science</i> , 2018, , .	1.0	0
16170	Indirubin attenuates mouse psoriasis-like skin lesion in a CD274-dependent manner: an achievement of RNA sequencing. <i>Bioscience Reports</i> , 2018, 38, .	1.1	13
16171	First genome sequencing and comparative analyses of <i>Corynebacterium pseudotuberculosis</i> strains from Mexico. <i>Standards in Genomic Sciences</i> , 2018, 13, 21.	1.5	8
16172	Extracellular Vesicles Secreted by Hypoxic AC10 Cardiomyocytes Modulate Fibroblast Cell Motility. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 152.	1.1	14
16174	Host Proteins Identified in Extracellular Viral Particles as Targets for Broad-Spectrum Antiviral Inhibitors. <i>Journal of Proteome Research</i> , 2018, 18, 7-17.	1.8	7
16175	The human gut microbiome in early-onset type 1 diabetes from the TEDDY study. <i>Nature</i> , 2018, 562, 589-594.	13.7	623
16176	A survey of inter-individual variation in DNA methylation identifies environmentally responsive co-regulated networks of epigenetic variation in the human genome. <i>PLoS Genetics</i> , 2018, 14, e1007707.	1.5	65
16177	Global Transcriptome Analysis During Adipogenic Differentiation and Involvement of Transthyretin Gene in Adipogenesis in Cattle. <i>Frontiers in Genetics</i> , 2018, 9, 463.	1.1	25
16178	Unraveling Rice Tolerance Mechanisms Against <i>Schizotetranychus oryzae</i> Mite Infestation. <i>Frontiers in Plant Science</i> , 2018, 9, 1341.	1.7	9
16179	Tissue-Specific Profiling of Oxidative Stress-Associated Transcriptome in a Healthy Mouse Model. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3174.	1.8	31
16180	Clust: automatic extraction of optimal co-expressed gene clusters from gene expression data. <i>Genome Biology</i> , 2018, 19, 172.	3.8	141

#	ARTICLE	IF	CITATIONS
16181	Comparative gene expression profile and DNA methylation status in diabetic patients of Kazak and Han people. <i>Medicine (United States)</i> , 2018, 97, e11982.	0.4	7
16182	Draft genome sequences of <i>Cylindrospermopsis raciborskii</i> strains CS-508 and MVCC14, isolated from freshwater bloom events in Australia and Uruguay. <i>Standards in Genomic Sciences</i> , 2018, 13, 26.	1.5	4
16183	The proteome of perilymph in patients with vestibular schwannoma. A possibility to identify biomarkers for tumor associated hearing loss?. <i>PLoS ONE</i> , 2018, 13, e0198442.	1.1	29
16184	<scp>FAANG</scp>, establishing metadata standards, validation and best practices for the farmed and companion animal community. <i>Animal Genetics</i> , 2018, 49, 520-526.	0.6	78
16185	Data Analytics Applications for Streaming Data From Social Media: What to Predict?. <i>Frontiers in Big Data</i> , 2018, 1, 2.	1.8	10
16186	GOGO: An improved algorithm to measure the semantic similarity between gene ontology terms. <i>Scientific Reports</i> , 2018, 8, 15107.	1.6	77
16187	Food perception without ingestion leads to metabolic changes and irreversible developmental arrest in <i>C. elegans</i> . <i>BMC Biology</i> , 2018, 16, 112.	1.7	17
16188	The Diurnal Timing of Starvation Differently Impacts Murine Hepatic Gene Expression and Lipid Metabolism – A Systems Biology Analysis Using Self-Organizing Maps. <i>Frontiers in Physiology</i> , 2018, 9, 1180.	1.3	10
16189	Computational Toxicology. , 2018, , 327-350.		2
16190	Identifying the dynamic gene regulatory network during latent HIV-1 reactivation using high-dimensional ordinary differential equations. <i>International Journal of Computational Biology and Drug Design</i> , 2018, 11, 135.	0.3	1
16191	MicroRNA-664-5p promotes myoblast proliferation and inhibits myoblast differentiation by targeting serum response factor and Wnt1. <i>Journal of Biological Chemistry</i> , 2018, 293, 19177-19190.	1.6	26
16192	Metabolic Remodeling during Liver Regeneration. <i>Developmental Cell</i> , 2018, 47, 425-438.e5.	3.1	86
16193	A Comparative Assessment of Human and Chimpanzee iPSC-derived Cardiomyocytes with Primary Heart Tissues. <i>Scientific Reports</i> , 2018, 8, 15312.	1.6	57
16194	Small RNA and degradome profiling involved in seed development and oil synthesis of <i>Brassica napus</i> . <i>PLoS ONE</i> , 2018, 13, e0204998.	1.1	23
16195	Transcriptome sequencing, de novo assembly and annotation of the freeze tolerant earthworm, <i>Dendrobaena octaedra</i> . <i>Gene Reports</i> , 2018, 13, 180-191.	0.4	8
16196	From Plant Ontology to Gene Ontology and back. <i>Current Plant Biology</i> , 2018, 14, 66-69.	2.3	5
16197	Neurogenetic contributions to amyloid beta and tau spreading in the human cortex. <i>Nature Medicine</i> , 2018, 24, 1910-1918.	15.2	135
16198	Hierarchical HotNet: identifying hierarchies of altered subnetworks. <i>Bioinformatics</i> , 2018, 34, i972-i980.	1.8	102

#	ARTICLE	IF	CITATIONS
16199	Evidence of the Red-Queen Hypothesis from Accelerated Rates of Evolution of Genes Involved in Biotic Interactions in Pneumocystis. <i>Genome Biology and Evolution</i> , 2018, 10, 1596-1606.	1.1	9
16200	Identification of Essential Proteins Using Improved Node and Edge Clustering Coefficient. , 2018, , .		2
16201	Pathogenicity Induced by Invasive Infection of <i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> in a Mouse Model of Diabetes. <i>Frontiers in Microbiology</i> , 2018, 9, 2128.	1.5	8
16202	Granulocyte-Colony-Stimulating Factor Alters the Proteomic Landscape of the Ventral Tegmental Area. <i>Proteomes</i> , 2018, 6, 35.	1.7	10
16203	De novo transcriptome based on next-generation sequencing reveals candidate genes with sex-specific expression in <i>Arapaima gigas</i> (Schinz, 1822), an ancient Amazonian freshwater fish. <i>PLoS ONE</i> , 2018, 13, e0206379.	1.1	13
16204	Targeting glycometabolic reprogramming to restore the sensitivity of leukemia drug-resistant K562/ADM cells to adriamycin. <i>Life Sciences</i> , 2018, 215, 1-10.	2.0	18
16205	Analysis of the <i>Trichuris suis</i> excretory/secretory proteins as a function of life cycle stage and their immunomodulatory properties. <i>Scientific Reports</i> , 2018, 8, 15921.	1.6	37
16206	Deep sequencing and miRNA profiles in alcohol-induced neuroinflammation and the TLR4 response in mice cerebral cortex. <i>Scientific Reports</i> , 2018, 8, 15913.	1.6	37
16207	Genome sequence of the cauliflower mushroom <i>Sparassis crispa</i> (Hanabiratake) and its association with beneficial usage. <i>Scientific Reports</i> , 2018, 8, 16053.	1.6	32
16208	Functional Simple Sequence Repeat (SSR) Biomarkers for Specific Gene Groups of <i>Oreochromis niloticus</i> . , 2018, , .		0
16209	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
16210	Functional Genomics. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1102, 11-30.	0.8	3
16211	Ontology-based validation and identification of regulatory phenotypes. <i>Bioinformatics</i> , 2018, 34, i857-i865.	1.8	5
16212	Distinct co-expression networks using multi-omic data reveal novel interventional targets in HPV-positive and negative head-and-neck squamous cell cancer. <i>Scientific Reports</i> , 2018, 8, 15254.	1.6	28
16213	MetaHCR: a web-enabled metagenome data management system for hydrocarbon resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, 1-10.	1.4	1
16214	One complete and three draft genome sequences of four <i>Brochothrix thermosphacta</i> strains, CD 337, TAP 175, BSAS1 3 and EBP 3070. <i>Standards in Genomic Sciences</i> , 2018, 13, 22.	1.5	10
16215	Bioinformatics Analysis and Functional Prediction of Transmembrane Proteins in <i>Entamoeba histolytica</i> . <i>Genes</i> , 2018, 9, 499.	1.0	5
16216	Identification of COL1A1 as an invasion-related gene in malignant astrocytoma. <i>International Journal of Oncology</i> , 2018, 53, 2542-2554.	1.4	31

#	ARTICLE	IF	CITATIONS
16217	HSP90-incorporating chaperome networks as biosensor for disease-related pathways in patient-specific midbrain dopamine neurons. <i>Nature Communications</i> , 2018, 9, 4345.	5.8	40
16218	Cycles of gene expression and genome response during mammalian tissue regeneration. <i>Epigenetics and Chromatin</i> , 2018, 11, 52.	1.8	13
16219	Comparative Proteomic and Physiological Analyses of Two Divergent Maize Inbred Lines Provide More Insights into Drought-Stress Tolerance Mechanisms. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3225.	1.8	41
16220	A histone acetylome-wide association study of Alzheimer's disease identifies disease-associated H3K27ac differences in the entorhinal cortex. <i>Nature Neuroscience</i> , 2018, 21, 1618-1627.	7.1	138
16221	Species groups distributed across elevational gradients reveal convergent and continuous genetic adaptation to high elevations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10634-E10641.	3.3	57
16222	Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy and Tools. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	1.9	14
16223	Prediction of Target Genes and Pathways Associated With Cetuximab Insensitivity in Colorectal Cancer. <i>Technology in Cancer Research and Treatment</i> , 2018, 17, 153303381880690.	0.8	11
16224	Insights into the draft genome sequence of bioactives-producing <i>Bacillus thuringiensis</i> DNG9 isolated from Algerian soil-oil slough. <i>Standards in Genomic Sciences</i> , 2018, 13, 25.	1.5	12
16225	Single-Locus and Multi-Locus Genome-Wide Association Studies in the Genetic Dissection of Fiber Quality Traits in Upland Cotton (<i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1083.	1.7	74
16226	Identification of Genes and Pathways Involved in Ovarian Epithelial Cancer by Bioinformatics Analysis. <i>Journal of Cancer</i> , 2018, 9, 3016-3022.	1.2	13
16227	CeleryDB: a genomic database for celery. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	27
16228	Identification of Missing Carbon Fixation Enzymes as Potential Drug Targets in <i>Mycobacterium Tuberculosis</i> . <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	8
16229	Identification of an eight-gene prognostic signature for lung adenocarcinoma. <i>Cancer Management and Research</i> , 2018, Volume 10, 3383-3392.	0.9	63
16230	Normal and Abortive Buds Transcriptomic Profiling of Broccoli ogu Cytoplasmic Male Sterile Line and Its Maintainer. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2501.	1.8	9
16231	Identifying miRNA-mRNA regulation network of major depressive disorder in ovarian cancer patients. <i>Oncology Letters</i> , 2018, 16, 5375-5382.	0.8	25
16232	Transcriptome analysis of the critically endangered Dabry's sturgeon (<i>Acipenser dabryanus</i>) head kidney response to <i>Aeromonas hydrophila</i> . <i>Fish and Shellfish Immunology</i> , 2018, 83, 249-261.	1.6	31
16233	Nuclear Factor I Represses the Notch Effector HEY1 in Glioblastoma. <i>Neoplasia</i> , 2018, 20, 1023-1037.	2.3	24
16234	Towards global data products of Essential Biodiversity Variables on species traits. <i>Nature Ecology and Evolution</i> , 2018, 2, 1531-1540.	3.4	163

#	ARTICLE	IF	CITATIONS
16235	DNA methylation in adolescents with anxiety disorder: a longitudinal study. <i>Scientific Reports</i> , 2018, 8, 13800.	1.6	13
16236	Molecular mechanism of activated T cells in breast cancer. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 5015-5024.	1.0	11
16237	Identification of novel genes involved in gingival epithelial cells responding to <i>Aggregatibacter actinomycetemcomitans</i> and <i>Porphyromonas gingivalis</i> infections. <i>Archives of Oral Biology</i> , 2018, 96, 113-121.	0.8	4
16238	Comparative transcriptome analysis of <i>Paphia undulata</i> with different foot colors. <i>Marine Genomics</i> , 2018, 42, 25-31.	0.4	1
16239	Sequence and structural variation in the genome of the <i>Biomphalaria glabrata</i> embryonic (Bge) cell line. <i>Parasites and Vectors</i> , 2018, 11, 496.	1.0	9
16240	Phenotypic Characterization, Fine Mapping, and Altered Expression Profiling of <i>Roses1</i> Mutation That Affects Organ Size and Water Loss Through Regulating Stomatal Density in Rice. <i>Crop Science</i> , 2018, 58, 486-506.	0.8	4
16241	A Review of Software Tools for Pathway Crosstalk Inference. <i>Current Bioinformatics</i> , 2018, 13, 64-72.	0.7	3
16242	Transcriptomic Insights Into the Growth Phase- and Sugar-Associated Changes in the Exopolysaccharide Production of a High EPS-Producing <i>Streptococcus thermophilus</i> ASCC 1275. <i>Frontiers in Microbiology</i> , 2018, 9, 1919.	1.5	48
16243	Shared Biological Pathways Between Alzheimer's Disease and Ischemic Stroke. <i>Frontiers in Neuroscience</i> , 2018, 12, 605.	1.4	13
16244	Molecular Networks of <i>Postia placenta</i> Involved in Degradation of Lignocellulosic Biomass Revealed from Metadata Analysis of Open Access Gene Expression Data. <i>International Journal of Biological Sciences</i> , 2018, 14, 237-252.	2.6	11
16245	Systematic transcriptomic analysis provides insights into lotus (<i>Nelumbo nucifera</i>) seed development. <i>Plant Growth Regulation</i> , 2018, 86, 339-350.	1.8	21
16246	Palmitate-Induced Insulin Hypersecretion and Later Secretory Decline Associated with Changes in Protein Expression Patterns in Human Pancreatic Islets. <i>Journal of Proteome Research</i> , 2018, 17, 3824-3836.	1.8	8
16247	PMLPR: A novel method for predicting subcellular localization based on recommender systems. <i>Scientific Reports</i> , 2018, 8, 12006.	1.6	12
16248	Genome-wide analysis of the FleQ direct regulon in <i>Pseudomonas fluorescens</i> F113 and <i>Pseudomonas putida</i> KT2440. <i>Scientific Reports</i> , 2018, 8, 13145.	1.6	44
16249	Exosomal zinc transporter ZIP4 promotes cancer growth and is a novel diagnostic biomarker for pancreatic cancer. <i>Cancer Science</i> , 2018, 109, 2946-2956.	1.7	116
16250	Systematic pharmacological screens uncover novel pathways involved in cerebral cavernous malformations. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	34
16251	Use of Proteomic Imaging Coupled With Transcriptomic Analysis to Identify Biomolecules Responsive to Cochlear Injury. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 243.	1.4	2
16252	One Way to Achieve Germination: Common Molecular Mechanism Induced by Ethylene and After-Ripening in Sunflower Seeds. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2464.	1.8	15

#	ARTICLE	IF	CITATIONS
16253	Transcriptomic responses to extreme low salinity among locally adapted populations of Olympia oyster (<i>Ostrea lurida</i>). <i>Molecular Ecology</i> , 2018, 27, 4225-4240.	2.0	41
16254	In silico Study of Iron, Zinc and Copper Binding Proteins of <i>Pseudomonas syringae</i> pv. <i>lapsa</i> : Emphasis on Secreted Metalloproteins. <i>Frontiers in Microbiology</i> , 2018, 9, 1838.	1.5	28
16255	Data on genome annotation and analysis of earthworm <i>Eisenia fetida</i> . <i>Data in Brief</i> , 2018, 20, 525-534.	0.5	6
16256	Exploring the Uncharacterized Human Proteome Using neXtProt. <i>Journal of Proteome Research</i> , 2018, 17, 4211-4226.	1.8	32
16257	Context-dependent prediction of protein complexes by SiComPre. <i>Npj Systems Biology and Applications</i> , 2018, 4, 37.	1.4	2
16258	Profiles for long non-coding RNAs in ovarian granulosa cells from women with PCOS with or without hyperandrogenism. <i>Reproductive BioMedicine Online</i> , 2018, 37, 613-623.	1.1	17
16259	Analysis of Transcription Factor-Related Regulatory Networks Based on Bioinformatics Analysis and Validation in Hepatocellular Carcinoma. <i>BioMed Research International</i> , 2018, 2018, 1-16.	0.9	42
16260	Microarray-Based Gene Expression Analysis Identifies Potential Diagnostic and Prognostic Biomarkers for Waldenström Macroglobulinemia. <i>Acta Haematologica</i> , 2018, 140, 87-96.	0.7	2
16261	Functional signaling and gene regulatory networks between the oocyte and the surrounding cumulus cells. <i>BMC Genomics</i> , 2018, 19, 351.	1.2	49
16262	LncRNA-135528 inhibits tumor progression by up-regulating CXCL10 through the JAK/STAT pathway. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2018, 23, 651-666.	2.2	30
16263	Genomic analysis reveals genes affecting distinct phenotypes among different Chinese and western pig breeds. <i>Scientific Reports</i> , 2018, 8, 13352.	1.6	37
16264	Impact of Inter-Individual Variance in the Expression of a Radiation-Responsive Gene Panel Used for Triage. <i>Radiation Research</i> , 2018, 190, 226.	0.7	24
16265	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
16266	Health information technology: promise and progress. <i>Health Systems</i> , 2018, 7, 161-165.	0.9	2
16267	ResearchMaps.org for integrating and planning research. <i>PLoS ONE</i> , 2018, 13, e0195271.	1.1	4
16268	Copy Number Alterations in Tumor Genomes Deleting Antineoplastic Drug Targets Partially Compensated by Complementary Amplifications. <i>Cancer Genomics and Proteomics</i> , 2018, 15, 365-378.	1.0	1
16269	Transcriptomic Analysis of Pseudoscorpion Venom Reveals a Unique Cocktail Dominated by Enzymes and Protease Inhibitors. <i>Toxins</i> , 2018, 10, 207.	1.5	26
16270	OBSOLETE: Bioinformatics Principles for Deciphering Cardiovascular Diseases. , 2018, , .		1

#	ARTICLE	IF	CITATIONS
16271	Analysis of miRNA signature differentially expressed in exosomes from adriamycin-resistant and parental human breast cancer cells. <i>Bioscience Reports</i> , 2018, 38, .	1.1	21
16272	Proteomic Analysis of Rapeseed Root Response to Waterlogging Stress. <i>Plants</i> , 2018, 7, 71.	1.6	23
16273	Proteomic analysis of human T cell-derived exosomes reveals differential RAS/MAPK signaling. <i>European Journal of Immunology</i> , 2018, 48, 1915-1917.	1.6	21
16274	Computational Approaches to Understand the Genome and Protein Sequences of Fungi. , 2018, , 635-649.		0
16275	SMRT-Cappable-seq reveals complex operon variants in bacteria. <i>Nature Communications</i> , 2018, 9, 3676.	5.8	80
16276	Transcriptomic analyses of cacao cell suspensions in light and dark provide target genes for controlled flavonoid production. <i>Scientific Reports</i> , 2018, 8, 13575.	1.6	14
16277	Biclustering of transcriptome sequencing data reveals human tissue-specific circular RNAs. <i>BMC Genomics</i> , 2018, 19, 958.	1.2	9
16278	System analysis of teratozoospermia mRNA profile based on integrated bioinformatics tools. <i>Molecular Medicine Reports</i> , 2018, 18, 1297-1304.	1.1	10
16279	Research Article Preliminary analysis on the developmental transcriptomes of swallowtail butterfly <i>Papilio polytes</i> (Lepidoptera: Papilioidea). <i>Genetics and Molecular Research</i> , 2018, 17, .	0.3	0
16280	Enumerating consistent sub-graphs of directed acyclic graphs: an insight into biomedical ontologies. <i>Bioinformatics</i> , 2018, 34, i313-i322.	1.8	7
16281	TRIQ: a new method to evaluate triclusters. <i>BioData Mining</i> , 2018, 11, 15.	2.2	7
16282	Metabolome and molecular basis for carbohydrate increase and nitrate reduction in burley tobacco seedlings by glycerol through upregulating carbon and nitrogen metabolism. <i>Scientific Reports</i> , 2018, 8, 13300.	1.6	10
16283	Transcriptome analysis of differentially expressed unigenes involved in flavonoid biosynthesis during flower development of <i>Chrysanthemum morifolium</i> 'Chuju'. <i>Scientific Reports</i> , 2018, 8, 13414.	1.6	43
16284	Role of Cyclic Adenosine Monophosphate in Myopic Scleral Remodeling in Guinea Pigs: A Microarray Analysis. , 2018, 59, 4318.		13
16285	The developmental and genetic trajectory of coloration in the guppy (<i>Poecilia reticulata</i>). <i>Evolution & Development</i> , 2018, 20, 207-218.	1.1	8
16286	Genome-Wide Characterization of Selection Signatures and Runs of Homozygosity in Ugandan Goat Breeds. <i>Frontiers in Genetics</i> , 2018, 9, 318.	1.1	126
16287	Factors Associated with Heritable Pulmonary Arterial Hypertension Exert Convergent Actions on the miR-130/301-Vascular Matrix Feedback Loop. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2289.	1.8	24
16288	Dynamics of alternative polyadenylation in human preimplantation embryos. <i>Biochemical and Biophysical Research Communications</i> , 2018, 504, 727-733.	1.0	3

#	ARTICLE	IF	CITATIONS
16289	FGFR1/FOXM1 pathway: a key regulator of glioblastoma stem cells radioresistance and a prognosis biomarker. <i>Oncotarget</i> , 2018, 9, 31637-31649.	0.8	33
16290	Hepatitis C virus core impacts expression of miR122 and miR204 involved in carcinogenic progression via regulation of TGFBRAP1 and HOTTIP expression. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 1173-1182.	1.0	10
16291	Exploring the Mechanism of Flavonoids Through Systematic Bioinformatics Analysis. <i>Frontiers in Pharmacology</i> , 2018, 9, 918.	1.6	36
16292	Transcriptome sequencing identifies key pathways and genes involved in gastric adenocarcinoma. <i>Molecular Medicine Reports</i> , 2018, 18, 3673-3682.	1.1	13
16293	Identification of six key miRNAs associated with breast cancer through screening large-scale microarray data. <i>Oncology Letters</i> , 2018, 16, 4159-4168.	0.8	7
16294	Transcriptome profiling uncovers Î²-galactosidases of diverse domain classes influencing hypocotyl development in jute (<i>Corchorus capsularis</i> L.). <i>Phytochemistry</i> , 2018, 156, 20-32.	1.4	8
16295	Tomato DCL2b is required for the biosynthesis of 22-nt small RNAs, the resulting secondary siRNAs, and the host defense against ToMV. <i>Horticulture Research</i> , 2018, 5, 62.	2.9	55
16296	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
16297	Microgravity-Induced Alterations of Inflammation-Related Mechanotransduction in Endothelial Cells on Board SJ-10 Satellite. <i>Frontiers in Physiology</i> , 2018, 9, 1025.	1.3	38
16298	Microarray data analysis to identify differentially expressed genes and biological pathways associated with asthma. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 1613-1620.	0.8	2
16299	Genetic dissection of bull fertility in Jersey dairy cattle. <i>Animal Genetics</i> , 2018, 49, 393-402.	0.6	38
16300	A Disease-Associated MicroRNA Cluster Links Inflammatory Pathways and an Altered Composition of Leukocyte Subsets to Noninfectious Uveitis. , 2018, 59, 878.		28
16301	De novo assembly and annotation of <i>Hyalomma dromedarii</i> tick (Acari: Ixodidae) sialotranscriptome with regard to gender differences in gene expression. <i>Parasites and Vectors</i> , 2018, 11, 314.	1.0	21
16302	A comprehensive comparison of four species of Onchidiidae provides insights on the morphological and molecular adaptations of invertebrates from shallow seas to wetlands. <i>PLoS ONE</i> , 2018, 13, e0196252.	1.1	7
16303	BdorOR88a Modulates the Responsiveness to Methyl Eugenol in Mature Males of <i>Bactrocera dorsalis</i> (Hendel). <i>Frontiers in Physiology</i> , 2018, 9, 987.	1.3	29
16304	FungiDB: An Integrated Bioinformatic Resource for Fungi and Oomycetes. <i>Journal of Fungi (Basel)</i> , Tj ETQq1 1 0.784314 rgBT/Overlook 1.5 309		
16305	PirVP genes causing AHPND identified in a new <i>Vibrio</i> species (<i>Vibrio punensis</i>) within the commensal Orientalis clade. <i>Scientific Reports</i> , 2018, 8, 13080.	1.6	96
16306	Computational characterization and identification of human polycystic ovary syndrome genes. <i>Scientific Reports</i> , 2018, 8, 12949.	1.6	20

#	ARTICLE	IF	CITATIONS
16307	Predictions of novel <i>Schistosoma mansoni</i> - human protein interactions consistent with experimental data. <i>Scientific Reports</i> , 2018, 8, 13092.	1.6	9
16308	Integrating MicroRNA Expression Profiling Studies to Systematically Evaluate the Diagnostic Value of MicroRNAs in Pancreatic Cancer and Validate Their Prognostic Significance with the Cancer Genome Atlas Data. <i>Cellular Physiology and Biochemistry</i> , 2018, 49, 678-695.	1.1	28
16309	Multiple model species selection for transcriptomics analysis of non-model organisms. <i>BMC Bioinformatics</i> , 2018, 19, 284.	1.2	8
16310	Stratification of candidate genes for Parkinson's disease using weighted protein-protein interaction network analysis. <i>BMC Genomics</i> , 2018, 19, 452.	1.2	35
16311	Transcriptome analysis of <i>Valsa mali</i> reveals its response mechanism to the biocontrol actinomycete <i>Saccharothrix yanglingensis</i> Hhs.015. <i>BMC Microbiology</i> , 2018, 18, 90.	1.3	9
16312	Differentially expressed proteins in positive versus negative HNSCC lymph nodes. <i>BMC Medical Genomics</i> , 2018, 11, 73.	0.7	6
16313	Transcriptome analysis of alcohol-treated microglia reveals downregulation of beta amyloid phagocytosis. <i>Journal of Neuroinflammation</i> , 2018, 15, 141.	3.1	34
16314	A network pharmacology approach to explore the mechanisms of Erxian decoction in polycystic ovary syndrome. <i>Chinese Medicine</i> , 2018, 13, 46.	1.6	25
16315	Models of cell signaling uncover molecular mechanisms of high-risk neuroblastoma and predict disease outcome. <i>Biology Direct</i> , 2018, 13, 16.	1.9	26
16316	The effect of chronic and acute stressors, and their interaction, on testes function: an experimental test during testicular recrudescence. <i>Journal of Experimental Biology</i> , 2018, 221, .	0.8	11
16317	Regulatory RNAs in Virulence and Host-Microbe Interactions. , 2018, , 305-337.		4
16318	A Study on machine learning methods and applications in genetics and genomics. <i>International Journal of Engineering and Technology(UAE)</i> , 2018, 7, 201.	0.2	0
16319	B cells with aberrant activation of Notch1 signaling promote Treg and Th2 cell-dominant T-cell responses via IL-33. <i>Blood Advances</i> , 2018, 2, 2282-2295.	2.5	19
16320	Transcriptome sequencing for identification of diapause-associated genes in fall webworm, <i>Hyphantria cunea</i> Drury. <i>Gene</i> , 2018, 668, 229-236.	1.0	15
16321	An ERK-Dependent Feedback Mechanism Prevents Hematopoietic Stem Cell Exhaustion. <i>Cell Stem Cell</i> , 2018, 22, 879-892.e6.	5.2	84
16322	The contribution of human sperm proteins to the development and epigenome of the preimplantation embryo. <i>Human Reproduction Update</i> , 2018, 24, 535-555.	5.2	131
16323	The Encyclopedia of Proteome Dynamics: a big data ecosystem for (prote)omics. <i>Nucleic Acids Research</i> , 2018, 46, D1202-D1209.	6.5	19
16324	ActiveDriverDB: human disease mutations and genome variation in post-translational modification sites of proteins. <i>Nucleic Acids Research</i> , 2018, 46, D901-D910.	6.5	82

#	ARTICLE	IF	CITATIONS
16325	Combined analysis of genome-wide expression profiling of maize (<i>Zea mays</i> L.) leaves infected with <i>Ustilago maydis</i> . <i>Genome</i> , 2018, 61, 505-513.	0.9	2
16326	Computational functional genomics-based approaches in analgesic drug discovery and repurposing. <i>Pharmacogenomics</i> , 2018, 19, 783-797.	0.6	23
16327	GIANT 2.0: genome-scale integrated analysis of gene networks in tissues. <i>Nucleic Acids Research</i> , 2018, 46, W65-W70.	6.5	59
16328	Genes and gene clusters related to genotype and drought-induced variation in saccharification potential, lignin content and wood anatomical traits in <i>Populus nigra</i> . <i>Tree Physiology</i> , 2018, 38, 320-339.	1.4	35
16330	In Silico Prediction and Validation of Novel RNA Binding Proteins and Residues in the Human Proteome. <i>Proteomics</i> , 2018, 18, e1800064.	1.3	19
16331	Floral pigmentation pattern in Oriental hybrid lily (<i>Lilium</i> spp.) cultivar "Dizzy"™ is caused by transcriptional regulation of anthocyanin biosynthesis genes. <i>Journal of Plant Physiology</i> , 2018, 228, 85-91.	1.6	21
16332	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	5.8	484
16333	Updated regulation curation model at the <i>Saccharomyces</i> Genome Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	2
16334	Identification of differentially expressed genes in childhood asthma. <i>Medicine (United States)</i> , 2018, 97, e10861.	0.4	8
16335	Identification and Verification of Candidate Genes Regulating Neural Stem Cells Behavior Under Hypoxia. <i>Cellular Physiology and Biochemistry</i> , 2018, 47, 212-222.	1.1	9
16336	Gene microarray analysis of lncRNA and mRNA expression profiles in patients with high-grade ovarian serous cancer. <i>International Journal of Molecular Medicine</i> , 2018, 42, 91-104.	1.8	17
16337	Graph Clustering with Local Density-Cut. <i>Lecture Notes in Computer Science</i> , 2018, , 187-202.	1.0	4
16338	An integrated analysis of genome-wide DNA methylation and gene expression data in hepatocellular carcinoma. <i>FEBS Open Bio</i> , 2018, 8, 1093-1103.	1.0	49
16339	Network Analysis of Gene Expression. <i>Methods in Molecular Biology</i> , 2018, 1783, 325-341.	0.4	9
16340	Investigation of the mechanism of adult-stage resistance to barley yellow dwarf virus associated with a wheat-Thinopyrum intermedium translocation. <i>Crop Journal</i> , 2018, 6, 394-405.	2.3	2
16341	Using ZFIN: Data Types, Organization, and Retrieval. <i>Methods in Molecular Biology</i> , 2018, 1757, 307-347.	0.4	12
16342	Gene Expression Analysis. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	3
16343	Systems Biology-Based Investigation of Host-Plasmodium Interactions. <i>Trends in Parasitology</i> , 2018, 34, 617-632.	1.5	19

#	ARTICLE	IF	CITATIONS
16344	Progression of whole-blood transcriptional signatures from interferon-induced to neutrophil-associated patterns in severe influenza. <i>Nature Immunology</i> , 2018, 19, 625-635.	7.0	119
16345	Leveraging Experimental Details for an Improved Understanding of Host-Pathogen Interactome. <i>Current Protocols in Bioinformatics</i> , 2018, 61, 8.26.1-8.26.12.	25.8	2
16346	EuPathDB: The Eukaryotic Pathogen Genomics Database Resource. <i>Methods in Molecular Biology</i> , 2018, 1757, 69-113.	0.4	80
16347	Altered mitochondrial acetylation profiles in a kainic acid model of temporal lobe epilepsy. <i>Free Radical Biology and Medicine</i> , 2018, 123, 116-124.	1.3	37
16348	A genome-wide cross-trait analysis from UK Biobank highlights the shared genetic architecture of asthma and allergic diseases. <i>Nature Genetics</i> , 2018, 50, 857-864.	9.4	191
16349	Integration of multi-omics data and deep phenotyping enables prediction of cytokine responses. <i>Nature Immunology</i> , 2018, 19, 776-786.	7.0	103
16350	Computational identification of specific genes for glioblastoma stem-like cells identity. <i>Scientific Reports</i> , 2018, 8, 7769.	1.6	48
16351	Genetic screening and multipotency in rhesus monkey haploid neural progenitor cells. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	18
16352	Microarray-based bioinformatics analysis of the prospective target gene network of key miRNAs influenced by long non-coding RNA PVT1 in HCC. <i>Oncology Reports</i> , 2018, 40, 226-240.	1.2	11
16353	Protein protein interaction network analysis of differentially expressed genes to understand involved biological processes in coronary artery disease and its different severity. <i>Gene Reports</i> , 2018, 12, 50-60.	0.4	4
16354	Anti-tumoral effects of exercise on hepatocellular carcinoma growth. <i>Hepatology Communications</i> , 2018, 2, 607-620.	2.0	30
16355	Developmental plasticity in reptiles: Insights from temperature-dependent gene expression in wall lizard embryos. <i>Journal of Experimental Zoology Part A: Ecological and Integrative Physiology</i> , 2018, 329, 351-361.	0.9	13
16356	Molecular characterization of proton beam-induced mutations in soybean using genotyping-by-sequencing. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1169-1180.	1.0	22
16357	Dynamic Proteome Alteration and Functional Modulation of Human Saliva Induced by Dietary Chemosensory Stimuli. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 5621-5634.	2.4	22
16358	Towards a complete map of the human long non-coding RNA transcriptome. <i>Nature Reviews Genetics</i> , 2018, 19, 535-548.	7.7	451
16359	Quantitative Proteome and Phosphoproteome Analyses of <i>Streptomyces coelicolor</i> Reveal Proteins and Phosphoproteins Modulating Differentiation and Secondary Metabolism. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1591-1611.	2.5	35
16360	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
16361	Gender-specific Effects of Selection for Drinking in the Dark on the Network Roles of Coding and Noncoding <i>RNA</i> s. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 1454-1465.	1.4	13

#	ARTICLE	IF	CITATIONS
16362	Correlated Gene Expression and Anatomical Communication Support Synchronized Brain Activity in the Mouse Functional Connectome. <i>Journal of Neuroscience</i> , 2018, 38, 5774-5787.	1.7	23
16363	Urinary transcriptomics reveals patterns associated with subclinical injury of the renal allograft. <i>Biomarkers in Medicine</i> , 2018, 12, 427-438.	0.6	3
16364	An Introduction to the <i>Saccharomyces</i> Genome Database (SGD). <i>Methods in Molecular Biology</i> , 2018, 1757, 21-30.	0.4	16
16365	A Primer for the <i>Rat</i> Genome Database (RGD). <i>Methods in Molecular Biology</i> , 2018, 1757, 163-209.	0.4	11
16366	Long non-coding RNA Gm2199 rescues liver injury and promotes hepatocyte proliferation through the upregulation of ERK1/2. <i>Cell Death and Disease</i> , 2018, 9, 602.	2.7	28
16367	Underutilised and Neglected Crops: Next Generation Sequencing Approaches for Crop Improvement and Better Food Security. , 2018, , 287-380.		3
16368	Transcriptome analysis of the adult human Klinefelter testis and cellularity-matched controls reveals disturbed differentiation of Sertoli- and Leydig cells. <i>Cell Death and Disease</i> , 2018, 9, 586.	2.7	33
16369	Sorting Five Human Tumor Types Reveals Specific Biomarkers and Background Classification Genes. <i>Scientific Reports</i> , 2018, 8, 8180.	1.6	8
16370	Transcriptome and miRNA analyses of the response to <i>Corynespora cassiicola</i> in cucumber. <i>Scientific Reports</i> , 2018, 8, 7798.	1.6	43
16371	Yeast mitochondria: an overview of mitochondrial biology and the potential of mitochondrial systems biology. <i>FEMS Yeast Research</i> , 2018, 18, .	1.1	94
16372	Ecological Engineering Helps Maximize Function in Algal Oil Production. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	6
16373	Developmental vascular regression is regulated by a Wnt/ β 2-catenin, MYC, P21 (CDKN1A) pathway that controls cell proliferation and cell death. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	26
16374	PomBase: The Scientific Resource for Fission Yeast. <i>Methods in Molecular Biology</i> , 2018, 1757, 49-68.	0.4	32
16375	Bayesian Network to Infer Drug-Induced Apoptosis Circuits from Connectivity Map Data. <i>Methods in Molecular Biology</i> , 2018, 1783, 361-378.	0.4	2
16376	Statistical and artificial neural network-based analysis to understand complexity and heterogeneity in preeclampsia. <i>Computational Biology and Chemistry</i> , 2018, 75, 222-230.	1.1	23
16377	RNA-binding proteins with basic-acidic dipeptide (BAD) domains self-assemble and aggregate in Alzheimer's disease. <i>Journal of Biological Chemistry</i> , 2018, 293, 11047-11066.	1.6	66
16378	Improving amphibian genomic resources: a multitissue reference transcriptome of an iconic invader. <i>GigaScience</i> , 2018, 7, 1-7.	3.3	23
16379	Two-Hybrid Systems. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	1

#	ARTICLE	IF	CITATIONS
16380	Analysis of the microRNA expression profiles in DEF cells infected with duck Tembusu virus. <i>Infection, Genetics and Evolution</i> , 2018, 63, 126-134.	1.0	14
16381	Socio-reproductive Conflicts and the Father's Curse Dilemma. <i>American Naturalist</i> , 2018, 192, 250-262.	1.0	3
16382	Identification of key genes in rheumatoid arthritis and osteoarthritis based on bioinformatics analysis. <i>Medicine (United States)</i> , 2018, 97, e10997.	0.4	27
16383	Identification of key candidate genes and pathways in hepatocellular carcinoma by integrated bioinformatical analysis. <i>Experimental and Therapeutic Medicine</i> , 2018, 15, 4932-4942.	0.8	15
16384	Microarray analysis for the identification of specific proteins and functional modules involved in the process of hepatocellular carcinoma originating from cirrhotic liver. <i>Molecular Medicine Reports</i> , 2018, 17, 5619-5626.	1.1	8
16385	Analyses of Protein Interaction Networks Using Computational Tools. <i>Methods in Molecular Biology</i> , 2018, 1794, 97-117.	0.4	6
16386	Identification of gene-specific DNA methylation signature for Colorectal Cancer. <i>Cancer Genetics</i> , 2018, 228-229, 5-11.	0.2	7
16388	Multiple network alignment via multiMAGNA++. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1-1.	1.9	36
16389	Using the Candida Genome Database. <i>Methods in Molecular Biology</i> , 2018, 1757, 31-47.	0.4	12
16390	The floral transcriptome of <i>Machilus yunnanensis</i> , a tree in the magnoliid family Lauraceae. <i>Computational Biology and Chemistry</i> , 2018, 77, 456-465.	1.1	1
16391	Embryonic transcriptome and proteome analyses on hepatic lipid metabolism in chickens divergently selected for abdominal fat content. <i>BMC Genomics</i> , 2018, 19, 384.	1.2	35
16392	Transcriptomic response of breast cancer cells to anacardic acid. <i>Scientific Reports</i> , 2018, 8, 8063.	1.6	32
16393	An integrative framework for protein interaction network and methylation data to discover epigenetic modules. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 16, 1-1.	1.9	24
16394	Genetic modifiers of radon-induced lung cancer risk: a genome-wide interaction study in former uranium miners. <i>International Archives of Occupational and Environmental Health</i> , 2018, 91, 937-950.	1.1	27
16395	Bioinformatics Principles for Deciphering Cardiovascular Diseases. , 2018, , 273-292.		3
16396	Gold-containing compound BDG-I inhibits the growth of A549 lung cancer cells through the deregulation of miRNA expression. <i>Saudi Pharmaceutical Journal</i> , 2018, 26, 1035-1043.	1.2	6
16397	De novo transcriptome assembly, gene expressions and metabolites for flower color variation of two garden species in Brassicaceae. <i>Scientia Horticulturae</i> , 2018, 240, 592-602.	1.7	12
16398	Transcriptome analysis reveals candidate genes involved in splay leg syndrome in piglets. <i>Journal of Applied Genetics</i> , 2018, 59, 475-483.	1.0	7

#	ARTICLE	IF	CITATIONS
16399	Synergistic co-regulation and competition by a SOX9-GLI-FOXA phasic transcriptional network coordinate chondrocyte differentiation transitions. <i>PLoS Genetics</i> , 2018, 14, e1007346.	1.5	56
16400	Identification and functional analysis of differentially expressed genes associated with cerebral ischemia/reperfusion injury through bioinformatics methods. <i>Molecular Medicine Reports</i> , 2018, 18, 1513-1523.	1.1	13
16401	Weighted gene co-expression network analysis in identification of key genes and networks for ischemic reperfusion remodeling myocardium. <i>Molecular Medicine Reports</i> , 2018, 18, 1955-1962.	1.1	9
16402	Transcriptome profiling analysis reveals biomarkers in colon cancer samples of various differentiation. <i>Oncology Letters</i> , 2018, 16, 48-54.	0.8	7
16403	Functional genomics of lipid metabolism in the oleaginous yeast <i>Rhodospiridium toruloides</i> . <i>ELife</i> , 2018, 7, .	2.8	98
16404	Identification of natural product compounds as quorum sensing inhibitors in <i>Pseudomonas fluorescens</i> P07 through virtual screening. <i>Bioorganic and Medicinal Chemistry</i> , 2018, 26, 4088-4099.	1.4	28
16405	Microarray Analysis of the Molecular Mechanism Involved in Parkinson's Disease. <i>Parkinson's Disease</i> , 2018, 2018, 1-12.	0.6	22
16406	Inheritance and Molecular Mapping of Tight-placenta Gene and Seed Traits in Chinese Hami Melon "Queen". <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2018, 53, 788-794.	0.5	3
16407	De novo assembly and annotation of <i>Didymium iridis</i> transcriptome and identification of stage-specific genes. <i>Biologia (Poland)</i> , 2018, 73, 393-402.	0.8	4
16408	Analysis Methods for Shotgun Metagenomics. <i>Computational Biology</i> , 2018, , 71-112.	0.1	1
16409	Molecular Mechanisms of Gastrointestinal Signaling. , 2018, , 227-315.		0
16410	CS for Non-CS Science Students. , 2018, , .		0
16411	Transcriptome analysis of hepatic gene expression and DNA methylation in methionine- and betaine-supplemented geese (<i>Anser cygnoides domesticus</i>). <i>Poultry Science</i> , 2018, 97, 3463-3477.	1.5	14
16412	DeepText2GO: Improving large-scale protein function prediction with deep semantic text representation. <i>Methods</i> , 2018, 145, 82-90.	1.9	58
16413	A whole-genome transcriptome analysis of articular chondrocytes in secondary osteoarthritis of the hip. <i>PLoS ONE</i> , 2018, 13, e0199734.	1.1	22
16414	Genomewide phenotypic analysis of growth, cell morphogenesis, and cell cycle events in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2018, 14, e7573.	3.2	69
16415	LncmiRSRN: identification and analysis of long non-coding RNA related miRNA sponge regulatory network in human cancer. <i>Bioinformatics</i> , 2018, 34, 4232-4240.	1.8	73
16416	Transcriptional and Translational Landscape of Equine Torovirus. <i>Journal of Virology</i> , 2018, 92, .	1.5	24

#	ARTICLE	IF	CITATIONS
16417	Analogical Reasoning in Clinical Practice with Description Logic $\{ELH\}$. Lecture Notes in Computer Science, 2018, , 179-204.	1.0	0
16418	Idiopathic Scoliosis Families Highlight Actin-Based and Microtubule-Based Cellular Projections and Extracellular Matrix in Disease Etiology. G3: Genes, Genomes, Genetics, 2018, 8, 2663-2672.	0.8	19
16419	Exploring the molecular pathogenesis associated with Tâ€cell polymphocytic leukemia based on a comprehensive bioinformatics analysis. Oncology Letters, 2018, 16, 301-307.	0.8	6
16420	Clinical Research Data. , 2018, , 547-557.		1
16421	Genome-Wide Analysis of Multidrug and Toxic Compound Extrusion (<i>MATE</i>) Family in <i>Gossypium raimondii</i> and <i>Gossypium arboreum</i> and Its Expression Analysis Under Salt, Cadmium, and Drought Stress. G3: Genes, Genomes, Genetics, 2018, 8, 2483-2500.	0.8	56
16423	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	9.4	893
16424	Deep Transcriptomic Analysis of Black Rockfish (<i>Sebastes schlegelii</i>) Provides New Insights on Responses to Acute Temperature Stress. Scientific Reports, 2018, 8, 9113.	1.6	53
16425	Identification of a complex population of chromatin-associated proteins in the European sea bass (<i>Dicentrarchus labrax</i>) sperm. Systems Biology in Reproductive Medicine, 2018, 64, 502-517.	1.0	12
16426	Time- and polarity-dependent proteomic changes associated with homeostatic scaling at central synapses. ELife, 2018, 7, .	2.8	49
16427	Discovering hidden knowledge through auditing clinical diagnostic knowledge bases. Journal of Biomedical Informatics, 2018, 84, 75-81.	2.5	5
16428	A meta-learning framework using representation learning to predict drug-drug interaction. Journal of Biomedical Informatics, 2018, 84, 136-147.	2.5	32
16429	Switching roles for DNA and histone methylation depend on evolutionary ages of human endogenous retroviruses. Genome Research, 2018, 28, 1147-1157.	2.4	82
16430	Melittin Constrains the Expression of Identified Key Genes Associated with Bladder Cancer. Journal of Immunology Research, 2018, 2018, 1-16.	0.9	10
16431	Gene family innovation, conservation and loss on the animal stem lineage. ELife, 2018, 7, .	2.8	149
16432	Data Mining Mycobacterium tuberculosis Pathogenic Gene Transcription Factors and Their Regulatory Network Nodes. International Journal of Genomics, 2018, 2018, 1-9.	0.8	6
16433	Transcriptome analysis demonstrates that long noncoding RNA is involved in the hypoxic response in <i>Larimichthys crocea</i> . Fish Physiology and Biochemistry, 2018, 44, 1333-1347.	0.9	15
16434	Histology and Transcriptome Profiles of the Mammary Gland across Critical Windows of Development in Sprague Dawley Rats. Journal of Mammary Gland Biology and Neoplasia, 2018, 23, 149-163.	1.0	6
16435	Gene expressionâ€based drug repurposing to target aging. Aging Cell, 2018, 17, e12819.	3.0	56

#	ARTICLE	IF	CITATIONS
16436	Non-classical monocytes as mediators of tissue destruction in arthritis. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 1490-1497.	0.5	65
16437	Prioritizing network communities. <i>Nature Communications</i> , 2018, 9, 2544.	5.8	37
16438	Multi-factored gene-gene proximity measures exploiting biological knowledge extracted from Gene Ontology : application in gene clustering. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	1.9	5
16439	De Novo Sequencing of a <i>Sparassis latifolia</i> Genome and Its Associated Comparative Analyses. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2018, 2018, 1-12.	0.7	9
16440	A machine-learned analysis of human gene polymorphisms modulating persisting pain points to major roles of neuroimmune processes. <i>European Journal of Pain</i> , 2018, 22, 1735-1756.	1.4	11
16442	An evolutionary transcriptomics approach links CD36 to membrane remodeling in replicative senescence. <i>Molecular Omics</i> , 2018, 14, 237-246.	1.4	12
16443	High-quality assembly of the reference genome for scarlet sage, <i>Salvia splendens</i> , an economically important ornamental plant. <i>GigaScience</i> , 2018, 7, .	3.3	49
16444	EviNet: a web platform for network enrichment analysis with flexible definition of gene sets. <i>Nucleic Acids Research</i> , 2018, 46, W163-W170.	6.5	22
16445	De novo sequencing, assembly and characterisation of <i>Aloe vera</i> transcriptome and analysis of expression profiles of genes related to saponin and anthraquinone metabolism. <i>BMC Genomics</i> , 2018, 19, 427.	1.2	36
16446	RNA-Seq transcriptome analysis of <i>Amaranthus palmeri</i> with differential tolerance to glufosinate herbicide. <i>PLoS ONE</i> , 2018, 13, e0195488.	1.1	35
16447	Regulators of Long-Term Memory Revealed by Mushroom Body-Specific Gene Expression Profiling in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2018, 209, 1167-1181.	1.2	27
16448	Co-expression analysis reveals key gene modules and pathways of oral squamous cell carcinoma. <i>Cancer Biomarkers</i> , 2018, 22, 763-771.	0.8	2
16449	De novo assembly and comparative transcriptome analysis: novel insights into sesquiterpenoid biosynthesis in <i>Matricaria chamomilla</i> L. <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	1
16450	Network Pharmacology-Based Approach to Investigate the Mechanisms of <i>Hedyotis diffusa</i> Willd. in the Treatment of Gastric Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-17.	0.5	39
16451	Transcriptomic Analysis of Hepatic Cells in Multicellular Organotypic Liver Models. <i>Scientific Reports</i> , 2018, 8, 11306.	1.6	8
16452	CD5L is upregulated in hepatocellular carcinoma and promotes liver cancer cell proliferation and antiapoptotic responses by binding to HSPA5 (GRP78). <i>FASEB Journal</i> , 2018, 32, 3878-3891.	0.2	43
16453	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
16454	A Meta-Analysis Characterizing Stem-Like Gene Expression in the Suprachiasmatic Nucleus and Its Circadian Clock. <i>BioMed Research International</i> , 2018, 2018, 1-11.	0.9	9

#	ARTICLE	IF	CITATIONS
16455	Transcriptomic response to GABA-producing <i>Lactobacillus plantarum</i> CGMCC 1.2437T induced by L-MSG. <i>PLoS ONE</i> , 2018, 13, e0199021.	1.1	36
16458	Truth selection for truth discovery models exploiting ordering relationship among values. <i>Knowledge-Based Systems</i> , 2018, 159, 298-308.	4.0	7
16459	Multi-omic elucidation of aromatic catabolism in adaptively evolved <i>Rhodococcus opacus</i> . <i>Metabolic Engineering</i> , 2018, 49, 69-83.	3.6	50
16460	CUP-SHAPED COTYLEDON1 (CUC1) and CUC2 regulate cytokinin homeostasis to determine ovule number in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2018, 69, 5169-5176.	2.4	52
16461	Sigmoid colon mucosal gene expression supports alterations of neuronal signaling in irritable bowel syndrome with constipation. <i>American Journal of Physiology - Renal Physiology</i> , 2018, 315, G140-G157.	1.6	18
16462	Differential aging of growth plate cartilage underlies differences in bone length and thus helps determine skeletal proportions. <i>PLoS Biology</i> , 2018, 16, e2005263.	2.6	48
16463	Single-cell transcriptomic analyses reveal distinct dorsal/ventral pancreatic programs. <i>EMBO Reports</i> , 2018, 19, .	2.0	26
16464	Computational Approaches in Reproductomics. , 2018, , 347-383.		0
16465	Prioritization of Candidate Genes for Congenital Diaphragmatic Hernia in a Critical Region on Chromosome 4p16 using a Machine-Learning Algorithm. <i>Journal of Pediatric Genetics</i> , 2018, 07, 164-173.	0.3	15
16466	Deciphering cellular biological processes to clinical application: a new perspective for T1±1 treatment targeting multiple diseases. <i>Expert Opinion on Biological Therapy</i> , 2018, 18, 23-31.	1.4	11
16467	Strong correlation of downregulated genes related to synaptic transmission and mitochondria in post-mortem autism cerebral cortex. <i>Journal of Neurodevelopmental Disorders</i> , 2018, 10, 18.	1.5	51
16468	The developmental transcriptomes of two sea biscuit species with differing larval types. <i>BMC Genomics</i> , 2018, 19, 368.	1.2	4
16469	Identifying differentially expressed genes from cross-site integrated data based on relative expression orderings. <i>International Journal of Biological Sciences</i> , 2018, 14, 892-900.	2.6	37
16470	Expression and network analysis of YBX1 interactors for identification of new drug targets in lung adenocarcinoma. <i>Journal of Genomics</i> , 2018, 6, 103-112.	0.6	10
16471	Active N6-Methyladenine Demethylation by DMAD Regulates Gene Expression by Coordinating with Polycomb Protein in Neurons. <i>Molecular Cell</i> , 2018, 71, 848-857.e6.	4.5	71
16472	GFAP Mutations in Astrocytes Impair Oligodendrocyte Progenitor Proliferation and Myelination in an hiPSC Model of Alexander Disease. <i>Cell Stem Cell</i> , 2018, 23, 239-251.e6.	5.2	91
16473	Monoassociation with <i>Lactobacillus plantarum</i> Disrupts Intestinal Homeostasis in Adult <i>Drosophila melanogaster</i> . <i>MBio</i> , 2018, 9, .	1.8	36
16474	Differences between fast and slow muscles in scallops revealed through proteomics and transcriptomics. <i>BMC Genomics</i> , 2018, 19, 377.	1.2	22

#	ARTICLE	IF	CITATIONS
16475	PathCORE-T: identifying and visualizing globally co-occurring pathways in large transcriptomic compendia. <i>BioData Mining</i> , 2018, 11, 14.	2.2	14
16476	Alternatively spliced variants in Atlantic cod (<i>Gadus morhua</i>) support response to variable salinity environment. <i>Scientific Reports</i> , 2018, 8, 11607.	1.6	11
16477	Transcriptome analysis highlights key differentially expressed genes involved in cellulose and lignin biosynthesis of sugarcane genotypes varying in fiber content. <i>Scientific Reports</i> , 2018, 8, 11612.	1.6	91
16478	Transferring knowledge of bacterial protein interaction networks to predict pathogen targeted human genes and immune signaling pathways: a case study on <i>M. tuberculosis</i> . <i>BMC Genomics</i> , 2018, 19, 505.	1.2	11
16479	Conducting metagenomic studies in microbiology and clinical research. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8629-8646.	1.7	26
16481	Transcriptomic analysis of porcine PBMCs in response to <i>Actinobacillus pleuropneumoniae</i> reveals the dynamic changes of differentially expressed genes related to immuno-inflammatory responses. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 2371-2384.	0.7	3
16482	Transcriptome analysis of sweet Sorghum inbred lines differing in salt tolerance provides novel insights into salt exclusion by roots. <i>Plant and Soil</i> , 2018, 430, 423-439.	1.8	52
16483	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a "Plug and Play" Domain. <i>Methods in Enzymology</i> , 2018, 606, 1-71.	0.4	99
16484	Activation of JAK/STAT3 restores NK cell function and improves immune defense after brain ischemia. <i>FASEB Journal</i> , 2018, 32, 2757-2767.	0.2	20
16485	PanACEA: a bioinformatics tool for the exploration and visualization of bacterial pan-chromosomes. <i>BMC Bioinformatics</i> , 2018, 19, 246.	1.2	9
16486	Gene expression analysis indicates reduced memory and cognitive functions in the hippocampus and increase in synaptic reorganization in the frontal cortex 3 weeks after MDMA administration in Dark Agouti rats. <i>BMC Genomics</i> , 2018, 19, 580.	1.2	12
16487	A semantics-oriented computational approach to investigate microRNA regulation on glucocorticoid resistance in pediatric acute lymphoblastic leukemia. <i>BMC Medical Informatics and Decision Making</i> , 2018, 18, 57.	1.5	12
16488	Family specific genetic predisposition to breast cancer: results from Tunisian whole exome sequenced breast cancer cases. <i>Journal of Translational Medicine</i> , 2018, 16, 158.	1.8	32
16489	Matrine Is Identified as a Novel Macropinocytosis Inducer by a Network Target Approach. <i>Frontiers in Pharmacology</i> , 2018, 9, 10.	1.6	39
16490	Dynamic Changes in Chemosensory Gene Expression during the <i>Dendrolimus punctatus</i> Mating Process. <i>Frontiers in Physiology</i> , 2017, 8, 1127.	1.3	25
16491	Dietary Safety Assessment of Flk1-Transgenic Fish. <i>Frontiers in Physiology</i> , 2018, 9, 8.	1.3	1
16492	Different Modes of Gene Duplication Show Divergent Evolutionary Patterns and Contribute Differently to the Expansion of Gene Families Involved in Important Fruit Traits in Pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 1076 50 97 T	1.7	36
16493	Genome-Wide Identification and Characterization of Long Non-Coding RNA in Wheat Roots in Response to Ca ²⁺ Channel Blocker. <i>Frontiers in Plant Science</i> , 2018, 9, 244.	1.7	36

#	ARTICLE	IF	CITATIONS
16494	MorphDB: Prioritizing Genes for Specialized Metabolism Pathways and Gene Ontology Categories in Plants. <i>Frontiers in Plant Science</i> , 2018, 9, 352.	1.7	7
16495	Identification of Putative Precursor Genes for the Biosynthesis of Cannabinoid-Like Compound in <i>Radula marginata</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 537.	1.7	28
16496	Sex-Dependent Variation of Pumpkin (<i>Cucurbita maxima</i> cv. Big Max) Nectar and Nectaries as Determined by Proteomics and Metabolomics. <i>Frontiers in Plant Science</i> , 2018, 9, 860.	1.7	17
16497	Circulating MicroRNA Expression Levels Associated With Internet Gaming Disorder. <i>Frontiers in Psychiatry</i> , 2018, 9, 81.	1.3	13
16498	Application of Public Knowledge Discovery Tool (PKDE4J) to Represent Biomedical Scientific Knowledge. <i>Frontiers in Research Metrics and Analytics</i> , 2018, 3, .	0.9	7
16499	Murine cytomegalovirus M72 promotes acute virus replication in vivo and is a substrate of the TRIC/CCT complex. <i>Virology</i> , 2018, 522, 92-105.	1.1	9
16500	MinOmics, an Integrative and Immersive Tool for Multi-Omics Analysis. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	25
16501	Understanding Forest Health with Remote Sensing, Part III: Requirements for a Scalable Multi-Source Forest Health Monitoring Network Based on Data Science Approaches. <i>Remote Sensing</i> , 2018, 10, 1120.	1.8	63
16502	Dissecting the expression landscape of mitochondrial genes in lung squamous cell carcinoma and lung adenocarcinoma. <i>Oncology Letters</i> , 2018, 16, 3992-4000.	0.8	6
16503	Cigarette Smoke-Induced Emphysema Exhausts Early Cytotoxic CD8+ T Cell Responses against Nascent Lung Cancer Cells. <i>Journal of Immunology</i> , 2018, 201, 1558-1569.	0.4	19
16504	MaxMIF: A New Method for Identifying Cancer Driver Genes through Effective Data Integration. <i>Advanced Science</i> , 2018, 5, 1800640.	5.6	37
16505	KampoDB, database of predicted targets and functional annotations of natural medicines. <i>Scientific Reports</i> , 2018, 8, 11216.	1.6	11
16506	High-throughput profiling of the circulating proteome suggests sexually dimorphic corticosteroid signaling following ischemic stroke. <i>Physiological Genomics</i> , 2018, 50, 876-883.	1.0	8
16507	Mitofusin2 Induces Cell Autophagy of Pancreatic Cancer through Inhibiting the PI3K/Akt/mTOR Signaling Pathway. <i>Oxidative Medicine and Cellular Longevity</i> , 2018, 2018, 1-8.	1.9	41
16508	Construction of a specific SVM classifier and identification of molecular markers for lung adenocarcinoma based on lncRNA-miRNA-mRNA network. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 3129-3140.	1.0	41
16509	Early Transcriptomic Response to Phosphate Deprivation in Soybean Leaves as Revealed by RNA-Sequencing. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2145.	1.8	19
16510	Identifying Cancer Specific Driver Modules Using a Network-Based Method. <i>Molecules</i> , 2018, 23, 1114.	1.7	5
16511	A head transcriptome provides insights into odorant binding proteins of the bamboo grasshopper. <i>Genes and Genomics</i> , 2018, 40, 991-1000.	0.5	14

#	ARTICLE	IF	CITATIONS
16512	An unsupervised machine learning method for discovering patient clusters based on genetic signatures. <i>Journal of Biomedical Informatics</i> , 2018, 85, 30-39.	2.5	71
16513	AMPK/GSK3 β - β -catenin cascade-triggered overexpression of CEMIP promotes migration and invasion in anoikis-resistant prostate cancer cells by enhancing metabolic reprogramming. <i>FASEB Journal</i> , 2018, 32, 3924-3935.	0.2	59
16514	Transcriptome response of human skeletal muscle to divergent exercise stimuli. <i>Journal of Applied Physiology</i> , 2018, 124, 1529-1540.	1.2	61
16515	Systems Pharmacological Approach to Investigate the Mechanism of <i>Acori Tatarinowii Rhizoma</i> for Alzheimer's Disease. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-20.	0.5	20
16516	Genetic variation associated with healthy traits and environmental conditions in <i>Vaccinium vitis-idaea</i> . <i>BMC Genomics</i> , 2018, 19, 4.	1.2	16
16517	Transcriptomics investigation of thyroid hormone disruption in the olfactory system of the <i>Rana [Lithobates] catesbeiana</i> tadpole. <i>Aquatic Toxicology</i> , 2018, 202, 46-56.	1.9	17
16518	Inhibition of EP300 and DDR1 synergistically alleviates pulmonary fibrosis in vitro and in vivo. <i>Biomedicine and Pharmacotherapy</i> , 2018, 106, 1727-1733.	2.5	30
16519	Identification of differentially expressed proteins in rats with spinal cord injury during the transitional phase using an iTRAQ-based quantitative analysis. <i>Gene</i> , 2018, 677, 66-76.	1.0	7
16520	High-quality whole-genome sequence of an abundant Holarctic odontocete, the harbour porpoise (<i>Phocoena phocoena</i>). <i>Molecular Ecology Resources</i> , 2018, 18, 1469-1481.	2.2	11
16521	Application of Transcriptomics to Compare the Carbohydrate Active Enzymes That Are Expressed by Diverse Genera of Anaerobic Fungi to Degrade Plant Cell Wall Carbohydrates. <i>Frontiers in Microbiology</i> , 2018, 9, 1581.	1.5	58
16522	RBPMetaDB: a comprehensive annotation of mouse RNA-Seq datasets with perturbations of RNA-binding proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	4
16523	Exploiting Functional Context in Biology: Reconsidering Classification of Bacterial Life. , 2018, , .		2
16524	Analysis and expression of the carotenoid biosynthesis genes from <i>Deinococcus wulumuqiensis</i> R12 in engineered <i>Escherichia coli</i> . <i>AMB Express</i> , 2018, 8, 94.	1.4	19
16525	Effect of single-nucleotide polymorphisms on the breeding value of fertility and breeding value of beef in Hungarian Simmental cattle. <i>Acta Veterinaria Hungarica</i> , 2018, 66, 215-225.	0.2	8
16526	The Psychiatric Cell Map Initiative: A Convergent Systems Biological Approach to Illuminating Key Molecular Pathways in Neuropsychiatric Disorders. <i>Cell</i> , 2018, 174, 505-520.	13.5	108
16527	Methods for Physical Characterization of Phase-Separated Bodies and Membrane-less Organelles. <i>Journal of Molecular Biology</i> , 2018, 430, 4773-4805.	2.0	124
16528	Lossless Compression of Binary Trees With Correlated Vertex Names. <i>IEEE Transactions on Information Theory</i> , 2018, 64, 6070-6080.	1.5	10
16529	Whole-genome resequencing of Ujumqin sheep to investigate the determinants of the multi-vertebral trait. <i>Genome</i> , 2018, 61, 653-661.	0.9	8

#	ARTICLE	IF	CITATIONS
16530	Integration of multiple networks and pathways identifies cancer driver genes in pan-cancer analysis. <i>BMC Genomics</i> , 2018, 19, 25.	1.2	46
16531	Full-length transcriptome sequences and the identification of putative genes for flavonoid biosynthesis in safflower. <i>BMC Genomics</i> , 2018, 19, 548.	1.2	85
16532	Gene set analysis methods: a systematic comparison. <i>BioData Mining</i> , 2018, 11, 8.	2.2	68
16533	Genome-Wide Characterization and Expression Analyses of <i>Pleurotus ostreatus</i> MYB Transcription Factors during Developmental Stages and under Heat Stress Based on de novo Sequenced Genome. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2052.	1.8	36
16534	Bioinformatics analysis of gene expression profiles to diagnose crucial and novel genes in glioblastoma multiform. <i>Pathology Research and Practice</i> , 2018, 214, 1395-1461.	1.0	7
16535	De novo transcriptome assembly based on RNA-seq and dynamic expression of key enzyme genes in loganin biosynthetic pathway of <i>Cornus officinalis</i> . <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	6
16536	Redesigning the Materials and Catalysts Database Construction Process Using Ontologies. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 1742-1754.	2.5	22
16537	Gene expression profiles in neurological tissues during West Nile virus infection: a critical meta-analysis. <i>BMC Genomics</i> , 2018, 19, 530.	1.2	10
16538	An overview of <i>Phoneutria nigriventer</i> spider venom using combined transcriptomic and proteomic approaches. <i>PLoS ONE</i> , 2018, 13, e0200628.	1.1	46
16539	<sc>Rhamnose $\hat{1}^2$ -hederin reverses chemoresistance of breast cancer cells by regulating exosome-mediated resistance transmission. <i>Bioscience Reports</i> , 2018, 38, .	1.1	16
16540	Transcription factor GATA4 associates with mesenchymal-like gene expression in human hepatoblastoma cells. <i>Tumor Biology</i> , 2018, 40, 101042831878549.	0.8	12
16541	MGOGP: a gene module-based heuristic algorithm for cancer-related gene prioritization. <i>BMC Bioinformatics</i> , 2018, 19, 215.	1.2	6
16542	Development and validation of an updated computational model of <i>Streptomyces coelicolor</i> primary and secondary metabolism. <i>BMC Genomics</i> , 2018, 19, 519.	1.2	20
16543	Bioinformatics Analysis Identifies p53 as a Candidate Prognostic Biomarker for Neuropathic Pain. <i>Frontiers in Genetics</i> , 2018, 9, 320.	1.1	40
16544	Metazoan Parasite Vaccines: Present Status and Future Prospects. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 67.	1.8	59
16545	Pleiotropic and Epistatic Network-Based Discovery: Integrated Networks for Target Gene Discovery. <i>Frontiers in Energy Research</i> , 2018, 6, .	1.2	32
16546	FSP: A Tool for Genome-Wide Prediction of smORF-Encoded Peptides and Their Functions. <i>Frontiers in Genetics</i> , 2018, 9, 96.	1.1	17
16547	<i>Litopenaeus vannamei</i> Transcriptome Profile of Populations Evaluated for Growth Performance and Exposed to White Spot Syndrome Virus (WSSV). <i>Frontiers in Genetics</i> , 2018, 9, 120.	1.1	19

#	ARTICLE	IF	CITATIONS
16548	Effects of Experimental Terrestrialization on the Skin Mucus Proteome of African Lungfish (<i>Protopterus dolloi</i>). <i>Frontiers in Immunology</i> , 2018, 9, 1259.	2.2	15
16549	Environmental Stress Responses and Experimental Handling Artifacts of a Model Organism, the Copepod <i>Acartia tonsa</i> (Dana). <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	13
16550	Surfaceome and Proteosurfaceome in Parietal Monoderm Bacteria: Focus on Protein Cell-Surface Display. <i>Frontiers in Microbiology</i> , 2018, 9, 100.	1.5	30
16551	Indigenous <i>Pseudomonas</i> spp. Strains from the Olive (<i>Olea europaea</i> L.) Rhizosphere as Effective Biocontrol Agents against <i>Verticillium dahliae</i> : From the Host Roots to the Bacterial Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 277.	1.5	79
16552	The LuxR Regulators PcoR and RfiA Co-regulate Antimicrobial Peptide and Alginate Production in <i>Pseudomonas corrugata</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 521.	1.5	16
16553	The Algicidal Fungus <i>Trametes versicolor</i> F21a Eliminating Blue Algae via Genes Encoding Degradation Enzymes and Metabolic Pathways Revealed by Transcriptomic Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 826.	1.5	16
16554	Comparative Metatranscriptomics of Wheat Rhizosphere Microbiomes in Disease Suppressive and Non-suppressive Soils for <i>Rhizoctonia solani</i> AG8. <i>Frontiers in Microbiology</i> , 2018, 9, 859.	1.5	66
16555	Metagenomic Approaches to Investigate the Contribution of the Vineyard Environment to the Quality of Wine Fermentation: Potentials and Difficulties. <i>Frontiers in Microbiology</i> , 2018, 9, 991.	1.5	90
16556	Differentially Expressed Genes in Osteomyelitis Induced by <i>Staphylococcus aureus</i> Infection. <i>Frontiers in Microbiology</i> , 2018, 9, 1093.	1.5	10
16557	Reduction of Proliferating Olfactory Cells and Low Expression of Extracellular Matrix Genes Are Hallmarks of the Aged Olfactory Mucosa. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 86.	1.7	33
16558	FindSim: A Framework for Integrating Neuronal Data and Signaling Models. <i>Frontiers in Neuroinformatics</i> , 2018, 12, 38.	1.3	8
16559	Sphingolipid Metabolism Is Dysregulated at Transcriptomic and Metabolic Levels in the Spinal Cord of an Animal Model of Amyotrophic Lateral Sclerosis. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 433.	1.4	52
16560	Regulation of Adult CNS Axonal Regeneration by the Post-transcriptional Regulator Cpeb1. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 445.	1.4	7
16561	Key Genes and Pathways Associated With Inner Ear Malformation in SOX10 ^{Δp.R109W} Mutation Pigs. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 181.	1.4	20
16562	Transcriptional Alterations in the Trigeminal Ganglia, Nucleus and Peripheral Blood Mononuclear Cells in a Rat Orofacial Pain Model. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 219.	1.4	24
16563	Nonredundant, Highly Connected MicroRNAs Control Functionality in Breast Cancer Networks. <i>International Journal of Genomics</i> , 2018, 2018, 1-10.	0.8	22
16564	Decoding the chromatin proteome of a single genomic locus by DNA sequencing. <i>PLoS Biology</i> , 2018, 16, e2005542.	2.6	14
16565	Geospatial Semantics. , 2018, , 80-94.		25

#	ARTICLE	IF	CITATIONS
16566	Socio-demographic, Clinical, and Genetic Determinants of Quality of Life in Lung Cancer Patients. <i>Scientific Reports</i> , 2018, 8, 10640.	1.6	16
16567	Application of ensemble learning to the differential gene expression in left-right breast tumors. , 2018, , .		1
16568	Data driven point packing for fast clustering. , 2018, , .		3
16569	Genome-wide association meta-analysis of age at first cannabis use. <i>Addiction</i> , 2018, 113, 2073-2086.	1.7	24
16570	Bacillales Members from the Olive Rhizosphere Are Effective Biological Control Agents against the Defoliating Pathotype of <i>Verticillium dahliae</i> . <i>Agriculture (Switzerland)</i> , 2018, 8, 90.	1.4	39
16571	Integrated Systems Approach Reveals Sphingolipid Metabolism Pathway Dysregulation in Association with Late-Onset Alzheimer's Disease. <i>Biology</i> , 2018, 7, 16.	1.3	6
16572	De Novo Sequencing and Assembly Analysis of Transcriptome in <i>Pinus bungeana</i> Zucc. ex Endl.. <i>Forests</i> , 2018, 9, 156.	0.9	7
16573	Genome-Wide Analysis of the <i>PYL</i> Gene Family and Identification of <i>PYL</i> Genes That Respond to Abiotic Stress in <i>Brassica napus</i> . <i>Genes</i> , 2018, 9, 156.	1.0	55
16574	Combining Targeted Metabolites Analysis and Transcriptomics to Reveal Chemical Composition Difference and Underlying Transcriptional Regulation in Maca (<i>Lepidium Meyenii</i> Walp.) Ecotypes. <i>Genes</i> , 2018, 9, 335.	1.0	6
16575	BIGO: A web application to analyse gene enrichment analysis results. <i>Computational Biology and Chemistry</i> , 2018, 76, 169-178.	1.1	1
16576	A comprehensive analysis of the Korean fir (<i>Abies koreana</i>) genes expressed under heat stress using transcriptome analysis. <i>Scientific Reports</i> , 2018, 8, 10233.	1.6	21
16577	A transcriptome study on <i>Macrobrachium nipponense</i> hepatopancreas experimentally challenged with white spot syndrome virus (WSSV). <i>PLoS ONE</i> , 2018, 13, e0200222.	1.1	24
16578	Integrated analysis of long noncoding RNA expression profiles in lymph node metastasis of hepatocellular carcinoma. <i>Gene</i> , 2018, 676, 47-55.	1.0	7
16579	LCK as a Potential Therapeutic Target for Acute Rejection after Kidney Transplantation: A Bioinformatics Clue. <i>Journal of Immunology Research</i> , 2018, 2018, 1-9.	0.9	8
16580	Traditional and systems biology based drug discovery for the rare tumor syndrome neurofibromatosis type 2. <i>PLoS ONE</i> , 2018, 13, e0197350.	1.1	17
16581	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
16582	Proteomics analysis of Xiangcaoliusuobingmi-treated <i>Capsicum annuum</i> L. infected with Cucumber mosaic virus. <i>Pesticide Biochemistry and Physiology</i> , 2018, 149, 113-122.	1.6	38
16583	ChemDIS-Mixture: an online tool for analyzing potential interaction effects of chemical mixtures. <i>Scientific Reports</i> , 2018, 8, 10047.	1.6	15

#	ARTICLE	IF	CITATIONS
16584	Onto2Vec: joint vector-based representation of biological entities and their ontology-based annotations. <i>Bioinformatics</i> , 2018, 34, i52-i60.	1.8	81
16585	Therapeutic Targeting of the Premetastatic Stage in Human Lung-to-Brain Metastasis. <i>Cancer Research</i> , 2018, 78, 5124-5134.	0.4	35
16586	Elevated Nrf-2 responses are insufficient to mitigate protein carbonylation in hepatospecific PTEN deletion mice. <i>PLoS ONE</i> , 2018, 13, e0198139.	1.1	12
16587	Antibacterial Evaluation and Virtual Screening of New Thiazolyl-Triazole Schiff Bases as Potential DNA-Gyrase Inhibitors. <i>International Journal of Molecular Sciences</i> , 2018, 19, 222.	1.8	38
16588	Comparative Transcriptome Analyses Uncover Key Candidate Genes Mediating Flight Capacity in <i>Bactrocera dorsalis</i> (Hendel) and <i>Bactrocera correcta</i> (Bezzi) (Diptera: Tephritidae). <i>International Journal of Molecular Sciences</i> , 2018, 19, 396.	1.8	14
16589	Dissection of the Mechanism for Compatible and Incompatible Graft Combinations of <i>Citrus grandis</i> (L.) Osbeck (â€™Hongmian Miyouâ€™™). <i>International Journal of Molecular Sciences</i> , 2018, 19, 505.	1.8	30
16590	Global Transcriptome Analysis of Brown Adipose Tissue of Diet-Induced Obese Mice. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1095.	1.8	17
16591	Genome-Wide Identification and Characterization of Warming-Related Genes in <i>Brassica rapa</i> ssp. <i>pekinensis</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 1727.	1.8	10
16592	Co-Expression Network Analysis of AMPK and Autophagy Gene Products during Adipocyte Differentiation. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1808.	1.8	10
16593	The Holo-Transcriptome of the Zoantharian <i>Protospalythoa variabilis</i> (Cnidaria: Anthozoa): A Plentiful Source of Enzymes for Potential Application in Green Chemistry, Industrial and Pharmaceutical Biotechnology. <i>Marine Drugs</i> , 2018, 16, 207.	2.2	10
16594	Screening of Genes Related to Early and Late Flowering in Tree Peony Based on Bulked Segregant RNA Sequencing and Verification by Quantitative Real-Time PCR. <i>Molecules</i> , 2018, 23, 689.	1.7	29
16595	Regularized Multi-View Subspace Clustering for Common Modules Across Cancer Stages. <i>Molecules</i> , 2018, 23, 1016.	1.7	12
16596	Comparative Proteomic Analysis of <i>Rana chensinensis</i> Oviduct. <i>Molecules</i> , 2018, 23, 1384.	1.7	6
16597	Feature Selection via Swarm Intelligence for Determining Protein Essentiality. <i>Molecules</i> , 2018, 23, 1569.	1.7	6
16598	MetaGOmics: A Web-Based Tool for Peptide-Centric Functional and Taxonomic Analysis of Metaproteomics Data. <i>Proteomes</i> , 2018, 6, 2.	1.7	43
16599	Transcriptome Analysis of Epithelioma Papulosum Cyprini Cells Infected by Reovirus Isolated from Allotrogeneic Silver Crucian Carp. <i>Viruses</i> , 2018, 10, 135.	1.5	3
16600	HFSP: high speed homology-driven function annotation of proteins. <i>Bioinformatics</i> , 2018, 34, i304-i312.	1.8	22
16601	dropEst: pipeline for accurate estimation of molecular counts in droplet-based single-cell RNA-seq experiments. <i>Genome Biology</i> , 2018, 19, 78.	3.8	159

#	ARTICLE	IF	CITATIONS
16602	Differentially expressed genes in hemocytes of <i>Litopenaeus vannamei</i> challenged with <i>Vibrio parahaemolyticus</i> AHPND (VPAHPND) and VPAHPND toxin. <i>Fish and Shellfish Immunology</i> , 2018, 81, 284-296.	1.6	36
16603	Regulatory RNAs in Virulence and Host-Microbe Interactions. <i>Microbiology Spectrum</i> , 2018, 6, .	1.2	34
16604	Identification of differential gene expression profile from peripheral blood cells of military pilots with hypertension by RNA sequencing analysis. <i>BMC Medical Genomics</i> , 2018, 11, 59.	0.7	14
16605	Adar3 Is Involved in Learning and Memory in Mice. <i>Frontiers in Neuroscience</i> , 2018, 12, 243.	1.4	54
16606	Increased Alternative Splicing as a Host Response to <i>Edwardsiella ictaluri</i> Infection in Catfish. <i>Marine Biotechnology</i> , 2018, 20, 729-738.	1.1	55
16607	Triflic Acid Treatment Enables LC-MS/MS Analysis of Insoluble Bacterial Biomass. <i>Journal of Proteome Research</i> , 2018, 17, 2978-2986.	1.8	5
16608	Pan-cancer adaptive immune resistance as defined by the Tumor Inflammation Signature (TIS): results from The Cancer Genome Atlas (TCGA). , 2018, 6, 63.		344
16609	Identification of potential target genes in pancreatic ductal adenocarcinoma by bioinformatics analysis. <i>Oncology Letters</i> , 2018, 16, 2453-2461.	0.8	26
16610	A promoter interaction map for cardiovascular disease genetics. <i>ELife</i> , 2018, 7, .	2.8	120
16611	Correlated Selection on Amino Acid Deletion and Replacement in Mammalian Protein Sequences. <i>Journal of Molecular Evolution</i> , 2018, 86, 365-378.	0.8	1
16612	RESKO: Repositioning drugs by using side effects and knowledge from ontologies. <i>Knowledge-Based Systems</i> , 2018, 160, 34-48.	4.0	8
16613	Molecular genetic overlap between migraine and major depressive disorder. <i>European Journal of Human Genetics</i> , 2018, 26, 1202-1216.	1.4	56
16614	Effects of Sepantronium Bromide (YM-155) on the Whole Transcriptome of MDA-MB-231 Cells: Highlight on Impaired ATR/ATM Fanconi Anemia DNA Damage Response. <i>Cancer Genomics and Proteomics</i> , 2018, 15, 249-264.	1.0	8
16615	Unlocking Human Brain Metabolism by Genome-Scale and Multiomics Metabolic Models: Relevance for Neurology Research, Health, and Disease. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 455-467.	1.0	14
16616	A Systems Biology Approach to Understanding the Pathophysiology of High-Grade Serous Ovarian Cancer: Focus on Iron and Fatty Acid Metabolism. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 502-513.	1.0	13
16617	Systems analysis of phosphate-limitation-induced lipid accumulation by the oleaginous yeast <i>Rhodospiridium toruloides</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 148.	6.2	78
16618	ProfPPIdb: Pairs of physical protein-protein interactions predicted for entire proteomes. <i>PLoS ONE</i> , 2018, 13, e0199988.	1.1	12
16619	A plant diterpene counteracts juvenile hormone-mediated gene regulation during <i>Drosophila melanogaster</i> larval development. <i>PLoS ONE</i> , 2018, 13, e0200706.	1.1	5

#	ARTICLE	IF	CITATIONS
16620	Computational identification and characterization of microRNAs and their targets in <i>Penaeus monodon</i> . <i>Journal of Oceanology and Limnology</i> , 2018, 36, 853-869.	0.6	1
16621	GOATOOLS: A Python library for Gene Ontology analyses. <i>Scientific Reports</i> , 2018, 8, 10872.	1.6	717
16622	Landscape of copy number variations in <i>Bos taurus</i> : individual and inter-breed variability. <i>BMC Genomics</i> , 2018, 19, 410.	1.2	25
16623	Genomic variations and association study of agronomic traits in flax. <i>BMC Genomics</i> , 2018, 19, 512.	1.2	46
16624	Analysis of codon usage patterns in <i>Hirudinaria manillensis</i> reveals a preference for GC-ending codons caused by dominant selection constraints. <i>BMC Genomics</i> , 2018, 19, 542.	1.2	41
16625	Overexpression of the Rybp Gene Inhibits Differentiation of Bovine Myoblasts into Myotubes. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2082.	1.8	5
16627	Identification of novel miRNAs and their target genes in <i>Eucalyptus grandis</i> . <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	10
16628	Transcriptome analysis of alternative splicing in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Plant Biology</i> , 2018, 18, 139.	1.6	21
16629	A comprehensive review of web-based resources of non-coding RNAs for plant science research. <i>International Journal of Biological Sciences</i> , 2018, 14, 819-832.	2.6	23
16630	Computing and Visualizing Gene Function Similarity and Coherence with NaviGO. <i>Methods in Molecular Biology</i> , 2018, 1807, 113-130.	0.4	2
16631	Combinatorial Targeting by MicroRNAs Co-ordinates Post-transcriptional Control of EMT. <i>Cell Systems</i> , 2018, 7, 77-91.e7.	2.9	92
16632	Hemolymph transcriptome analysis of Chinese mitten crab (<i>Eriocheir sinensis</i>) with intact, left cheliped autotomy and bilateral eyestalk ablation. <i>Fish and Shellfish Immunology</i> , 2018, 81, 266-275.	1.6	15
16633	MCENet: A database for maize conditional co-expression network and network characterization collaborated with multi-dimensional omics levels. <i>Journal of Genetics and Genomics</i> , 2018, 45, 351-360.	1.7	39
16634	Identification and characterization of known and novel microRNAs in strawberry fruits induced by <i>Botrytis cinerea</i> . <i>Scientific Reports</i> , 2018, 8, 10921.	1.6	14
16635	Construction and Applications of TeKnowbase. , 2018, , .		4
16636	Molecular mechanism of estrogen-mediated neuroprotection in the relief of brain ischemic injury. <i>BMC Genetics</i> , 2018, 19, 46.	2.7	8
16637	InfAcrOnt: calculating cross-ontology term similarities using information flow by a random walk. <i>BMC Genomics</i> , 2018, 19, 919.	1.2	98
16638	RNA-seq assistant: machine learning based methods to identify more transcriptional regulated genes. <i>BMC Genomics</i> , 2018, 19, 546.	1.2	40

#	ARTICLE	IF	CITATIONS
16639	Direct Reprogramming of Spiral Ganglion Non-neuronal Cells into Neurons: Toward Ameliorating Sensorineural Hearing Loss by Gene Therapy. <i>Frontiers in Cell and Developmental Biology</i> , 2018, 6, 16.	1.8	36
16640	An improved approach to infer protein-protein interaction based on a hierarchical vector space model. <i>BMC Bioinformatics</i> , 2018, 19, 161.	1.2	21
16641	Transcriptome analysis of response to <i>Plasmodiophora brassicae</i> infection in the Arabidopsis shoot and root. <i>BMC Genomics</i> , 2018, 19, 23.	1.2	96
16642	Novel candidate genes important for asthma and hypertension comorbidity revealed from associative gene networks. <i>BMC Medical Genomics</i> , 2018, 11, 15.	0.7	57
16643	Comprehensive subcellular topologies of polypeptides in <i>Streptomyces</i> . <i>Microbial Cell Factories</i> , 2018, 17, 43.	1.9	19
16644	Modeling and rescue of defective blood-brain barrier function of induced brain microvascular endothelial cells from childhood cerebral adrenoleukodystrophy patients. <i>Fluids and Barriers of the CNS</i> , 2018, 15, 9.	2.4	36
16645	Investigation of hypoxia networks in ovarian cancer via bioinformatics analysis. <i>Journal of Ovarian Research</i> , 2018, 11, 16.	1.3	28
16646	The bromodomain-containing protein Ibd1 links multiple chromatin-related protein complexes to highly expressed genes in <i>Tetrahymena thermophila</i> . <i>Epigenetics and Chromatin</i> , 2018, 11, 10.	1.8	16
16647	High quality draft genome sequence of <i>Mycoplasma testudineum</i> strain BH29T, isolated from the respiratory tract of a desert tortoise. <i>Standards in Genomic Sciences</i> , 2018, 13, 9.	1.5	3
16648	Activation of disease resistance against <i>Botryosphaeria dothidea</i> by downregulating the expression of MdSYP121 in apple. <i>Horticulture Research</i> , 2018, 5, 24.	2.9	39
16649	Regulation of osteogenesis by long noncoding RNAs: An epigenetic mechanism contributing to bone formation. <i>Connective Tissue Research</i> , 2018, 59, 35-41.	1.1	21
16650	A Novel Genetic Algorithm for Feature Selection in Hierarchical Feature Spaces. , 2018, , 738-746.		11
16651	The aquatic animals' transcriptome resource for comparative functional analysis. <i>BMC Genomics</i> , 2018, 19, 103.	1.2	5
16652	GraphTeams: a method for discovering spatial gene clusters in Hi-C sequencing data. <i>BMC Genomics</i> , 2018, 19, 308.	1.2	6
16653	Transcriptome sequencing and analysis during seed growth and development in <i>Euryale ferox</i> Salisb. <i>BMC Genomics</i> , 2018, 19, 343.	1.2	22
16654	Next generation sequencing for miRNA profile of spleen CD4 ⁺ T cells in the murine model of acute asthma. <i>Epigenomics</i> , 2018, 10, 1071-1083.	1.0	8
16655	Metagenomic insights into lignocellulose-degrading genes through Illumina-based & de novo sequencing of the microbiome in Vietnamese native goats' rumen. <i>Journal of General and Applied Microbiology</i> , 2018, 64, 108-116.	0.4	14
16656	Widespread epigenomic, transcriptomic and proteomic differences between hip osteophytic and articular chondrocytes in osteoarthritis. <i>Rheumatology</i> , 2018, 57, 1481-1489.	0.9	19

#	ARTICLE	IF	CITATIONS
16657	Urine proteomics of primary membranous nephropathy using nanoscale liquid chromatography tandem mass spectrometry analysis. <i>Clinical Proteomics</i> , 2018, 15, 5.	1.1	27
16658	Biomarker enhanced risk prediction for development of AKI after cardiac surgery. <i>BMC Nephrology</i> , 2018, 19, 102.	0.8	14
16659	Systematic target function annotation of human transcription factors. <i>BMC Biology</i> , 2018, 16, 4.	1.7	12
16660	Identification of key gene modules for human osteosarcoma by co-expression analysis. <i>World Journal of Surgical Oncology</i> , 2018, 16, 89.	0.8	21
16661	PhenoDis: a comprehensive database for phenotypic characterization of rare cardiac diseases. <i>Orphanet Journal of Rare Diseases</i> , 2018, 13, 22.	1.2	15
16662	Use of DAVID algorithms for clustering custom annotated gene lists in a non-model organism, rainbow trout. <i>BMC Research Notes</i> , 2018, 11, 63.	0.6	2
16663	The eXtensible ontology development (XOD) principles and tool implementation to support ontology interoperability. <i>Journal of Biomedical Semantics</i> , 2018, 9, 3.	0.9	57
16664	Improving the interoperability of biomedical ontologies with compound alignments. <i>Journal of Biomedical Semantics</i> , 2018, 9, 1.	0.9	40
16665	MIRO: guidelines for minimum information for the reporting of an ontology. <i>Journal of Biomedical Semantics</i> , 2018, 9, 6.	0.9	55
16666	CUILESS2016: a clinical corpus applying compositional normalization of text mentions. <i>Journal of Biomedical Semantics</i> , 2018, 9, 2.	0.9	7
16667	Effects of predation stress and food ration on perch gut microbiota. <i>Microbiome</i> , 2018, 6, 28.	4.9	67
16668	Commensal microbiota modulate gene expression in the skin. <i>Microbiome</i> , 2018, 6, 20.	4.9	147
16669	Integrated multi-omic analysis of host-microbiota interactions in acute oak decline. <i>Microbiome</i> , 2018, 6, 21.	4.9	49
16670	Transcriptomic analysis between self- and cross-pollinated pistils of tea plants (<i>Camellia sinensis</i>). <i>BMC Genomics</i> , 2018, 19, 289.	1.2	29
16671	Petri net-based prediction of therapeutic targets that recover abnormally phosphorylated proteins in muscle atrophy. <i>BMC Systems Biology</i> , 2018, 12, 26.	3.0	3
16672	High-quality draft genome of the methanotroph <i>Methylovulum psychrotolerans</i> Str. HV10-M2 isolated from plant material at a high-altitude environment. <i>Standards in Genomic Sciences</i> , 2018, 13, 10.	1.5	5
16673	Comprehensive analysis of differential expression profiles of mRNAs and lncRNAs and identification of a 14-lncRNA prognostic signature for patients with colon adenocarcinoma. <i>Oncology Reports</i> , 2018, 39, 2365-2375.	1.2	51
16674	Phenotypic Screening. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	0

#	ARTICLE	IF	CITATIONS
16675	Genome analysis of <i>Pseudomonas syringae</i> pv. <i>lachrymans</i> strain 814/98 indicates diversity within the pathovar. <i>European Journal of Plant Pathology</i> , 2018, 151, 663-676.	0.8	8
16676	De novo transcriptome analysis of an albino mutant <i>Pasphipedium pacificum</i> shamrock reveals reduced expression of genes related to chloroplast biosynthesis and division. <i>Horticulture Environment and Biotechnology</i> , 2018, 59, 411-421.	0.7	3
16677	Hypoxia-derived exosomes induce putative altered pathways in biosynthesis and ion regulatory channels in glioblastoma cells. <i>Biochemistry and Biophysics Reports</i> , 2018, 14, 104-113.	0.7	65
16678	Draft genome sequence of <i>Streptomyces hyaluromycini</i> MB-PO13T, a hyaluromycin producer. <i>Standards in Genomic Sciences</i> , 2018, 13, 2.	1.5	5
16679	Genomic insights into <i>Mycobacterium simiae</i> human colonization. <i>Standards in Genomic Sciences</i> , 2018, 13, 1.	1.5	18
16680	Transcriptome-based identification of genes related to resistance against <i>Botrytis elliptica</i> in <i>Lilium regale</i> . <i>Canadian Journal of Plant Science</i> , 2018, 98, 1058-1071.	0.3	17
16681	PANNZER2: a rapid functional annotation web server. <i>Nucleic Acids Research</i> , 2018, 46, W84-W88.	6.5	328
16682	Key signaling pathways, genes and transcription factors associated with hepatocellular carcinoma. <i>Molecular Medicine Reports</i> , 2018, 17, 8153-8160.	1.1	21
16683	Role of COL6A3 in colorectal cancer. <i>Oncology Reports</i> , 2018, 39, 2527-2536.	1.2	37
16684	Strategies for Taxonomic and Functional Annotation of Metagenomes. , 2018, , 55-79.		11
16685	Ancient horizontally transferred genes in the genome of California two-spot octopus, <i>Octopus bimaculoides</i> . <i>Gene</i> , 2018, 667, 34-44.	1.0	1
16686	Enhanced Quantitative LC-MS/MS Analysis of N-linked Glycans Derived from Glycoproteins Using Sodium Deoxycholate Detergent. <i>Journal of Proteome Research</i> , 2018, 17, 2668-2678.	1.8	19
16687	Effects of Zhizi Chuanxiong Capsule (æ€â€Šžèf¶âŠ) on the Abnormal Methylation in Rabbits with Atherosclerosis. <i>Chinese Journal of Integrative Medicine</i> , 2018, 24, 512-517.	0.7	5
16688	Interpretation of biological experiments changes with evolution of the Gene Ontology and its annotations. <i>Scientific Reports</i> , 2018, 8, 5115.	1.6	110
16689	Identification of target genes regulated by the <i>Drosophila</i> histone methyltransferase Eggless reveals a role of Decapentaplegic in apoptotic signaling. <i>Scientific Reports</i> , 2018, 8, 7123.	1.6	8
16690	Inferring ontology graph structures using OWL reasoning. <i>BMC Bioinformatics</i> , 2018, 19, 7.	1.2	21
16691	LocText: relation extraction of protein localizations to assist database curation. <i>BMC Bioinformatics</i> , 2018, 19, 15.	1.2	120
16692	Bio-SimVerb and Bio-SimLex: wide-coverage evaluation sets of word similarity in biomedicine. <i>BMC Bioinformatics</i> , 2018, 19, 33.	1.2	21

#	ARTICLE	IF	CITATIONS
16693	Complete genome sequence of <i>Thiodictyon syntrophicum</i> sp. nov. strain Cad16T, a photolithoautotrophic purple sulfur bacterium isolated from the alpine meromictic Lake Cadagno. <i>Standards in Genomic Sciences</i> , 2018, 13, 14.	1.5	12
16694	Role of plant respiratory burst oxidase homologs in stress responses. <i>Free Radical Research</i> , 2018, 52, 826-839.	1.5	76
16695	Co-expression of TIMP-1 and its cell surface binding partner CD63 in glioblastomas. <i>BMC Cancer</i> , 2018, 18, 270.	1.1	29
16696	Genome sequence of <i>Planktotalea frisia</i> type strain (SH6-1T), a representative of the <i>Roseobacter</i> group isolated from the North Sea during a phytoplankton bloom. <i>Standards in Genomic Sciences</i> , 2018, 13, 7.	1.5	5
16697	Effect of Larval Nutrition on Maternal mRNA Contribution to the <i>Drosophila</i> Egg. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1933-1941.	0.8	13
16698	Sex Determination in <i>Ceratopteris richardii</i> Is Accompanied by Transcriptome Changes That Drive Epigenetic Reprogramming of the Young Gametophyte. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2205-2214.	0.8	22
16699	Quantitative Prioritization of Tool Compounds for Phenotypic Screening. <i>Methods in Molecular Biology</i> , 2018, 1787, 195-206.	0.4	3
16700	p52 expression enhances lung cancer progression. <i>Scientific Reports</i> , 2018, 8, 6078.	1.6	15
16701	Draft Genome Sequence of the Crude Oil-Degrading and Biosurfactant-Producing Strain <i>Cobetia</i> sp. QF-1. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
16702	Taxon-Driven Functional Shifts Associated with Storm Flow in an Urban Stream Microbial Community. <i>MSphere</i> , 2018, 3, .	1.3	20
16703	Comprehensive gene expression profiling identifies distinct and overlapping transcriptional profiles in non-specific interstitial pneumonia and idiopathic pulmonary fibrosis. <i>Respiratory Research</i> , 2018, 19, 153.	1.4	66
16704	Identification of key genes and pathways involved in response to pain in goat and sheep by transcriptome sequencing. <i>Biological Research</i> , 2018, 51, 25.	1.5	15
16705	Reconstruction of the Protein-Protein Interaction Network for Protein Complexes Identification by Walking on the Protein Pair Fingerprints Similarity Network. <i>Frontiers in Genetics</i> , 2018, 9, 272.	1.1	13
16706	Comparative Transcriptomic Analysis of Two Actinorhizal Plants and the Legume <i>Medicago truncatula</i> Supports the Homology of Root Nodule Symbioses and Is Congruent With a Two-Step Process of Evolution in the Nitrogen-Fixing Clade of Angiosperms. <i>Frontiers in Plant Science</i> , 2018, 9, 1256.	1.7	38
16707	Assisted gene expression-based clustering with AWNCut. <i>Statistics in Medicine</i> , 2018, 37, 4386-4403.	0.8	8
16708	Comprehensive analysis of differentially expressed microRNAs and mRNAs in dorsal root ganglia from streptozotocin-induced diabetic rats. <i>PLoS ONE</i> , 2018, 13, e0202696.	1.1	14
16709	Alternate splicing of transcripts upon <i>Mycobacterium tuberculosis</i> infection impacts the expression of functional protein domains. <i>IUBMB Life</i> , 2018, 70, 845-854.	1.5	17
16710	Efficient proximity labeling in living cells and organisms with TurboID. <i>Nature Biotechnology</i> , 2018, 36, 880-887.	9.4	1,103

#	ARTICLE	IF	CITATIONS
16711	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. <i>Nature Genetics</i> , 2018, 50, 1240-1246.	9.4	199
16712	Robust prediction of response to immune checkpoint blockade therapy in metastatic melanoma. <i>Nature Medicine</i> , 2018, 24, 1545-1549.	15.2	473
16713	Discovery and control of culturable and viable but non-culturable cells of a distinctive <i>Lactobacillus harbinensis</i> strain from spoiled beer. <i>Scientific Reports</i> , 2018, 8, 11446.	1.6	41
16714	Proteomics: Clinical and research applications in respiratory diseases. <i>Respirology</i> , 2018, 23, 993-1003.	1.3	15
16715	New computational approaches to understanding molecular protein function. <i>PLoS Computational Biology</i> , 2018, 14, e1005756.	1.5	11
16716	From SNPs to pathways: Biological interpretation of type 2 diabetes (T2DM) genome wide association study (GWAS) results. <i>PLoS ONE</i> , 2018, 13, e0193515.	1.1	34
16717	Regional differences in thermal adaptation of a cold-water fish <i>Rhynchocypris oxycephalus</i> revealed by thermal tolerance and transcriptomic responses. <i>Scientific Reports</i> , 2018, 8, 11703.	1.6	14
16718	Constructing Node Embeddings for Human Phenotype Ontology to Assist Phenotypic Similarity Measurement. , 2018, , .		5
16719	Analysis of differentially expressed genes among human hair follicle-derived iPSCs, induced hepatocyte-like cells, and primary hepatocytes. <i>Stem Cell Research and Therapy</i> , 2018, 9, 211.	2.4	10
16720	Bioinformatics approach reveals the key role of C–X–C motif chemokine receptor 2 in endometriosis development. <i>Molecular Medicine Reports</i> , 2018, 18, 2841-2849.	1.1	6
16721	Excessive dietary lipid intake provokes an acquired form of lysosomal lipid storage disease in the kidney. <i>Journal of Pathology</i> , 2018, 246, 470-484.	2.1	32
16722	Evolutionary divergence of 3–UTRs in cichlid fishes. <i>BMC Genomics</i> , 2018, 19, 433.	1.2	20
16723	A proteomic analysis of chemoresistance development via sequential treatment with doxorubicin reveals novel players in MCF–7 breast cancer cells. <i>International Journal of Molecular Medicine</i> , 2018, 42, 1987-1997.	1.8	7
16724	Proteomic distinction of renal oncocytomas and chromophobe renal cell carcinomas. <i>Clinical Proteomics</i> , 2018, 15, 25.	1.1	8
16725	Rat BodyMap transcriptomes reveal unique circular RNA features across tissue types and developmental stages. <i>Rna</i> , 2018, 24, 1443-1456.	1.6	50
16726	Dysfunction of Sister Chromatids Separation Promotes Progression of Hepatocellular Carcinoma According to Analysis of Gene Expression Profiling. <i>Frontiers in Physiology</i> , 2018, 9, 1019.	1.3	14
16727	Databases and Tools for the Analysis of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018, , 377-394.	0.3	1
16729	Epigenetic regulation of the circadian gene <i>Per1</i> contributes to age-related changes in hippocampal memory. <i>Nature Communications</i> , 2018, 9, 3323.	5.8	118

#	ARTICLE	IF	CITATIONS
16730	From homogeneous to heterogeneous network alignment via colored graphlets. <i>Scientific Reports</i> , 2018, 8, 12524.	1.6	28
16731	Monitoring changes in the Gene Ontology and their impact on genomic data analysis. <i>GigaScience</i> , 2018, 7, .	3.3	4
16732	Deletion of the formin <i>Diaph1</i> protects from structural and functional abnormalities in the murine diabetic kidney. <i>American Journal of Physiology - Renal Physiology</i> , 2018, 315, F1601-F1612.	1.3	18
16733	Identification of biomarkers for Barcelona Clinic Liver Cancer staging and overall survival of patients with hepatocellular carcinoma. <i>PLoS ONE</i> , 2018, 13, e0202763.	1.1	40
16734	Divergent brain gene expression patterns associate with distinct cell-specific tau neuropathology traits in progressive supranuclear palsy. <i>Acta Neuropathologica</i> , 2018, 136, 709-727.	3.9	47
16735	A systemic approach to identify signaling pathways activated during short-term exposure to traffic-related urban air pollution from human blood. <i>Environmental Science and Pollution Research</i> , 2018, 25, 29572-29583.	2.7	1
16736	Unraveling the <i>Plasmodium vivax</i> sporozoite transcriptional journey from mosquito vector to human host. <i>Scientific Reports</i> , 2018, 8, 12183.	1.6	40
16737	Alterations of 63 hub genes during lingual carcinogenesis in C57BL/6J mice. <i>Scientific Reports</i> , 2018, 8, 12626.	1.6	7
16738	Systematic discovery of uncharacterized transcription factors in <i>Escherichia coli</i> K-12 MG1655. <i>Nucleic Acids Research</i> , 2018, 46, 10682-10696.	6.5	65
16739	Prediction of key genes and pathways involved in trastuzumab-resistant gastric cancer. <i>World Journal of Surgical Oncology</i> , 2018, 16, 174.	0.8	20
16740	Pan-cancer analysis of neoepitopes. <i>Scientific Reports</i> , 2018, 8, 12735.	1.6	17
16741	A compendium of conserved cleavage and polyadenylation events in mammalian genes. <i>Genome Research</i> , 2018, 28, 1427-1441.	2.4	81
16742	Construction and analysis of mRNA, miRNA, lncRNA, and TF regulatory networks reveal the key genes associated with prostate cancer. <i>PLoS ONE</i> , 2018, 13, e0198055.	1.1	58
16743	Deacetylase activity-independent transcriptional activation by HDAC2 during TPA-induced HL-60 cell differentiation. <i>PLoS ONE</i> , 2018, 13, e0202935.	1.1	4
16744	Monitoring sublethal changes in fish physiology following exposure to a light, unweathered crude oil. <i>Aquatic Toxicology</i> , 2018, 204, 27-45.	1.9	19
16745	Implications of Newly Identified Brain eQTL Genes and Their Interactors in Schizophrenia. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 12, 433-442.	2.3	63
16746	Transcriptomic Analysis of <i>Aedes aegypti</i> in Response to Mosquitocidal <i>Bacillus thuringiensis</i> LLP29 Toxin. <i>Scientific Reports</i> , 2018, 8, 12650.	1.6	10
16747	Comparative transcriptomic analyses and single-cell RNA sequencing of the freshwater planarian <i>Schmidtea mediterranea</i> identify major cell types and pathway conservation. <i>Genome Biology</i> , 2018, 19, 124.	3.8	44

#	ARTICLE	IF	CITATIONS
16748	Effects of 5-Aminolevulinic Acid on Gene Expression, Immunity, and ATP Levels in Pacific White Shrimp, <i>Litopenaeus vannamei</i> . <i>Marine Biotechnology</i> , 2018, 20, 829-843.	1.1	10
16749	Cx26 partial loss causes accelerated presbycusis by redox imbalance and dysregulation of Nfr2 pathway. <i>Redox Biology</i> , 2018, 19, 301-317.	3.9	50
16750	ESCC ATLAS: A population wide compendium of biomarkers for Esophageal Squamous Cell Carcinoma. <i>Scientific Reports</i> , 2018, 8, 12715.	1.6	22
16751	Physiological characterization of the emergence from diapause: A transcriptomics approach. <i>Scientific Reports</i> , 2018, 8, 12577.	1.6	40
16752	Identification of key genes and pathways using bioinformatics analysis in septic shock children. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 1163-1174.	1.1	20
16753	CLEC3B is downregulated and inhibits proliferation in clear cell renal cell carcinoma. <i>Oncology Reports</i> , 2018, 40, 2023-2035.	1.2	23
16754	Transcriptional effects of polyethylene microplastics ingestion in developing zebrafish (<i>Danio rerio</i>). <i>Environmental Pollution</i> , 2018, 243, 591-600.	3.7	122
16755	Instant Clue: A Software Suite for Interactive Data Visualization and Analysis. <i>Scientific Reports</i> , 2018, 8, 12648.	1.6	174
16756	OC-2-KB: integrating crowdsourcing into an obesity and cancer knowledge base curation system. <i>BMC Medical Informatics and Decision Making</i> , 2018, 18, 55.	1.5	22
16757	A clinical-pathogenetic approach on associated anomalies and chromosomal defects supports novel candidate critical regions and genes for gastroschisis. <i>Pediatric Surgery International</i> , 2018, 34, 931-943.	0.6	4
16758	Identification of Skt11-regulated genes in chondrocytes by integrated bioinformatics analysis. <i>Gene</i> , 2018, 677, 340-348.	1.0	9
16759	Comprehensive and in-depth analysis of microRNA and mRNA expression profile in salivary adenoid cystic carcinoma. <i>Gene</i> , 2018, 678, 349-360.	1.0	12
16760	Identification of prognostic risk factors for esophageal adenocarcinoma using bioinformatics analysis. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 4327-4337.	1.0	17
16761	Genome Variation in the Model Halophilic Bacterium <i>Salinibacter ruber</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1499.	1.5	12
16762	Unbiased shRNA screening, using a combination of FACS and high-throughput sequencing, enables identification of novel modifiers of Polycomb silencing. <i>Scientific Reports</i> , 2018, 8, 12128.	1.6	9
16763	Identification of cold-related miRNAs in sugarcane by small RNA sequencing and functional analysis of a cold inducible ScmiR393 to cold stress. <i>Environmental and Experimental Botany</i> , 2018, 155, 464-476.	2.0	21
16764	Efflux Pumps Represent Possible Evolutionary Convergence onto the \hat{I}^2 -Barrel Fold. <i>Structure</i> , 2018, 26, 1266-1274.e2.	1.6	19
16765	Comprehensive profiling of transcriptional networks specific for lactogenic differentiation of HC11 mammary epithelial stem-like cells. <i>Scientific Reports</i> , 2018, 8, 11777.	1.6	17

#	ARTICLE	IF	CITATIONS
16766	Studies on Aminoglycoside Susceptibility Identify a Novel Function of KsgA To Secure Translational Fidelity during Antibiotic Stress. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	23
16767	Genome sequencing and protein domain annotations of Korean Hanwoo cattle identify Hanwoo-specific immunity-related and other novel genes. <i>BMC Genetics</i> , 2018, 19, 37.	2.7	1
16768	Semantics for an Integrative and Immersive Pipeline Combining Visualization and Analysis of Molecular Data. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	20
16769	A Liquid Chromatography with Tandem Mass Spectrometry-Based Proteomic Analysis of Cells Cultured in DMEM 10% FBS and Chemically Defined Medium Using Human Adipose-Derived Mesenchymal Stem Cells. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2042.	1.8	8
16770	QTLTableMiner++: semantic mining of QTL tables in scientific articles. <i>BMC Bioinformatics</i> , 2018, 19, 183.	1.2	8
16771	Divergent genome evolution caused by regional variation in DNA gain and loss between human and mouse. <i>PLoS Computational Biology</i> , 2018, 14, e1006091.	1.5	2
16772	Identification of potential target genes of USP22 via CHIP-seq and RNA-seq analysis in HeLa cells. <i>Genetics and Molecular Biology</i> , 2018, 41, 488-495.	0.6	5
16773	Dehydration Stress Memory: Gene Networks Linked to Physiological Responses During Repeated Stresses of <i>Zea mays</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1058.	1.7	71
16774	Pan-Cancer Analysis Reveals Differential Susceptibility of Bidirectional Gene Promoters to DNA Methylation, Somatic Mutations, and Copy Number Alterations. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2296.	1.8	15
16775	A Methodological Assessment and Characterization of Genetically-Driven Variation in Three Human Phosphoproteomes. <i>Scientific Reports</i> , 2018, 8, 12106.	1.6	2
16776	SDREGION. , 2018, , .		8
16777	Bioinformatics analysis of microarray data to reveal the pathogenesis of diffuse intrinsic pontine glioma. <i>Biological Research</i> , 2018, 51, 26.	1.5	23
16778	Volatile Oil of <i>Amomum villosum</i> Inhibits Nonalcoholic Fatty Liver Disease via the Gut-Liver Axis. <i>BioMed Research International</i> , 2018, 2018, 1-16.	0.9	27
16779	Genes associated with inflammation and the cell cycle may serve as biomarkers for the diagnosis and prognosis of acute myocardial infarction in a Chinese population. <i>Molecular Medicine Reports</i> , 2018, 18, 1311-1322.	1.1	15
16780	Biases induced by using geography and environment to guide ex situ conservation. <i>Conservation Genetics</i> , 2018, 19, 1281-1293.	0.8	6
16781	The human iron-proteome. <i>Metallomics</i> , 2018, 10, 1223-1231.	1.0	106
16782	Specific expression pattern of IMP metabolism related-genes in chicken muscle between cage and free range conditions. <i>PLoS ONE</i> , 2018, 13, e0201736.	1.1	12
16783	Screening and identification of key biomarkers in bladder carcinoma: Evidence from bioinformatics analysis. <i>Oncology Letters</i> , 2018, 16, 3092-3100.	0.8	6

#	ARTICLE	IF	CITATIONS
16784	Identification of errors in the IEDB using ontologies. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	4
16785	The IUPHAR/BPS Guide to PHARMACOLOGY in 2018: updates and expansion to encompass the new guide to IMMUNOPHARMACOLOGY. Nucleic Acids Research, 2018, 46, D1091-D1106.	6.5	1,584
16786	RNA-seq analysis of aberrantly expressed long non-coding RNAs and mRNAs in a mouse model of ventilator-induced lung injury. Molecular Medicine Reports, 2018, 18, 882-892.	1.1	9
16787	Identification of miRNAs involved in SO ₂ preservation in <i>Vitis vinifera</i> L. by deep sequencing. Environmental and Experimental Botany, 2018, 153, 218-228.	2.0	17
16788	CommWalker: correctly evaluating modules in molecular networks in light of annotation bias. Bioinformatics, 2018, 34, 994-1000.	1.8	10
16789	Chemical-Induced Phenotypes at CTD Help Inform the Predisease State and Construct Adverse Outcome Pathways. Toxicological Sciences, 2018, 165, 145-156.	1.4	41
16790	Analysis of Gene Expression Changes in PHA-M Stimulated Lymphocytes – Unraveling PHA Activity as Prerequisite for Dicentric Chromosome Analysis. Radiation Research, 2018, 189, 579.	0.7	3
16791	A study of the key genes and inflammatory signaling pathways involved in HLA-B27-associated acute anterior uveitis families. International Journal of Molecular Medicine, 2018, 42, 259-269.	1.8	6
16792	Fungal Genomics. Methods in Molecular Biology, 2018, , .	0.4	3
16793	The Human Transcriptome. , 2018, , 135-164.		4
16794	Integration of Molecular and Cellular Pathogenesis. , 2018, , 243-249.		0
16795	Genomic atlas of the human plasma proteome. Nature, 2018, 558, 73-79.	13.7	1,180
16796	RNA Sequencing Reveals Novel Transcripts from Sympathetic Stellate Ganglia During Cardiac Sympathetic Hyperactivity. Scientific Reports, 2018, 8, 8633.	1.6	12
16797	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. Nucleic Acids Research, 2018, 46, D471-D476.	6.5	190
16798	A genome-wide association study of early maturation traits in upland cotton based on the CottonSNP80K array. Journal of Integrative Plant Biology, 2018, 60, 970-985.	4.1	28
16799	Expanding the horizons of microRNA bioinformatics. Rna, 2018, 24, 1005-1017.	1.6	27
16800	Potential candidate treatment agents for targeting of cholangiocarcinoma identified by gene expression profile analysis. Biomedical Reports, 2018, 9, 42-52.	0.9	6
16801	Bioinformatics analysis of microarray data to reveal the pathogenesis of brain ischemia. Molecular Medicine Reports, 2018, 18, 333-341.	1.1	6

#	ARTICLE	IF	CITATIONS
16802	Identification of proteins associated with paclitaxel resistance of epithelial ovarian cancer using iTRAQ-based proteomics. <i>Oncology Letters</i> , 2018, 15, 9793-9801.	0.8	6
16803	LearnSec: A Framework for Full Text Analysis. <i>Lecture Notes in Computer Science</i> , 2018, , 502-513.	1.0	3
16804	Comparative transcriptome analysis of dikaryotic mycelia and mature fruiting bodies in the edible mushroom <i>Lentinula edodes</i> . <i>Scientific Reports</i> , 2018, 8, 8983.	1.6	37
16805	A statistical method for measuring activation of gene regulatory networks. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2018, 17, .	0.2	1
16806	Gas41 links histone acetylation to H2A.Z deposition and maintenance of embryonic stem cell identity. <i>Cell Discovery</i> , 2018, 4, 28.	3.1	47
16807	Enhancer of zeste homolog 2 (Ezh2) controls bone formation and cell cycle progression during osteogenesis in mice. <i>Journal of Biological Chemistry</i> , 2018, 293, 12894-12907.	1.6	63
16808	Secretome Screening Reveals Fibroblast Growth Factors as Novel Inhibitors of Viral Replication. <i>Journal of Virology</i> , 2018, 92, .	1.5	32
16809	Systematic Identification, Characterization, and Conservation of Adjacent-Gene Coregulation in the Budding Yeast <i>Saccharomyces cerevisiae</i> . <i>MSphere</i> , 2018, 3, .	1.3	11
16810	The gonadal transcriptome of the unisexual Amazon molly <i>Poecilia formosa</i> in comparison to its sexual ancestors, <i>Poecilia mexicana</i> and <i>Poecilia latipinna</i> . <i>BMC Genomics</i> , 2018, 19, 12.	1.2	14
16811	Identification of specific metabolic pathways as druggable targets regulating the sensitivity to cyanide poisoning. <i>PLoS ONE</i> , 2018, 13, e0193889.	1.1	12
16812	A data mining paradigm for identifying key factors in biological processes using gene expression data. <i>Scientific Reports</i> , 2018, 8, 9083.	1.6	14
16813	LncRNA expression profiling of BMSCs in osteonecrosis of the femoral head associated with increased adipogenic and decreased osteogenic differentiation. <i>Scientific Reports</i> , 2018, 8, 9127.	1.6	45
16814	Biocuration: Distilling data into knowledge. <i>PLoS Biology</i> , 2018, 16, e2002846.	2.6	75
16815	Species-specific regulation of angiogenesis by glucocorticoids reveals contrasting effects on inflammatory and angiogenic pathways. <i>PLoS ONE</i> , 2018, 13, e0192746.	1.1	10
16816	Classifying the molecular functions of Rab GTPases in membrane trafficking using deep convolutional neural networks. <i>Analytical Biochemistry</i> , 2018, 555, 33-41.	1.1	65
16817	Detection of single alpha-helices in large protein sequence sets using hardware acceleration. <i>Journal of Structural Biology</i> , 2018, 204, 109-116.	1.3	6
16818	Massive expression of germ cell-specific genes is a hallmark of cancer and a potential target for novel treatment development. <i>Oncogene</i> , 2018, 37, 5694-5700.	2.6	45
16819	Prion-like Domains in Eukaryotic Viruses. <i>Scientific Reports</i> , 2018, 8, 8931.	1.6	43

#	ARTICLE	IF	CITATIONS
16820	Signature of Pareto optimization in the Escherichia coli proteome. <i>Scientific Reports</i> , 2018, 8, 9141.	1.6	8
16821	Prediction of novel target genes and pathways involved in bevacizumab-resistant colorectal cancer. <i>PLoS ONE</i> , 2018, 13, e0189582.	1.1	16
16822	Transcriptome profiling with focus on potential key genes for wing development and evolution in <i>Megalopterus caerulatus</i> , the damselfly species with the world's largest wings. <i>PLoS ONE</i> , 2018, 13, e0189898.	1.1	4
16823	Comparative analysis of miRNA and mRNA abundance in determinate cucumber by high-throughput sequencing. <i>PLoS ONE</i> , 2018, 13, e0190691.	1.1	9
16824	Implication of molecular vascular smooth muscle cell heterogeneity among arterial beds in arterial calcification. <i>PLoS ONE</i> , 2018, 13, e0191976.	1.1	25
16825	Genomic insights into the broad antifungal activity, plant-probiotic properties, and their regulation, in <i>Pseudomonas donghuensis</i> strain SVBP6. <i>PLoS ONE</i> , 2018, 13, e0194088.	1.1	42
16826	In silico identification of microRNAs predicted to regulate N-myristoyltransferase and Methionine Aminopeptidase 2 functions in cancer and infectious diseases. <i>PLoS ONE</i> , 2018, 13, e0194612.	1.1	5
16827	TnSeq of <i>Mycobacterium tuberculosis</i> clinical isolates reveals strain-specific antibiotic liabilities. <i>PLoS Pathogens</i> , 2018, 14, e1006939.	2.1	78
16828	Transcriptome analysis reveals the hawthorn response to the infection of apple chlorotic leaf spot virus. <i>Scientia Horticulturae</i> , 2018, 239, 171-180.	1.7	3
16829	Manual Gene Curation and Functional Annotation. <i>Methods in Molecular Biology</i> , 2018, 1775, 185-208.	0.4	10
16830	Genome-wide association study identifies genes associated with neuropathy in patients with head and neck cancer. <i>Scientific Reports</i> , 2018, 8, 8789.	1.6	18
16831	microRNA-199a/b-5p enhance imatinib efficacy via repressing WNT2 signaling-mediated protective autophagy in imatinib-resistant chronic myeloid leukemia cells. <i>Chemico-Biological Interactions</i> , 2018, 291, 144-151.	1.7	28
16832	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. <i>Nature Genetics</i> , 2018, 50, 928-936.	9.4	652
16833	Chemoproteomics reveals baicalin activates hepatic CPT1 to ameliorate diet-induced obesity and hepatic steatosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5896-E5905.	3.3	201
16834	Using Diagrams to Reason About Biological Mechanisms. <i>Lecture Notes in Computer Science</i> , 2018, , 264-279.	1.0	3
16835	Identifying changes in the wheat kernel proteome under heat stress using iTRAQ. <i>Crop Journal</i> , 2018, 6, 600-610.	2.3	23
16836	Quantitative phosphoproteomic analysis of the molecular substrates of sleep need. <i>Nature</i> , 2018, 558, 435-439.	13.7	195
16837	The Pathway Coexpression Network: Revealing pathway relationships. <i>PLoS Computational Biology</i> , 2018, 14, e1006042.	1.5	41

#	ARTICLE	IF	CITATIONS
16838	Biological Databases. <i>Translational Bioinformatics</i> , 2018, , 303-337.	0.0	0
16839	In vivo brain GPCR signaling elucidated by phosphoproteomics. <i>Science</i> , 2018, 360, .	6.0	105
16840	Clustering gene expression time series data using an infinite Gaussian process mixture model. <i>PLoS Computational Biology</i> , 2018, 14, e1005896.	1.5	123
16841	A comprehensive and quantitative comparison of text-mining in 15 million full-text articles versus their corresponding abstracts. <i>PLoS Computational Biology</i> , 2018, 14, e1005962.	1.5	112
16842	Hub connectivity, neuronal diversity, and gene expression in the <i>Caenorhabditis elegans</i> connectome. <i>PLoS Computational Biology</i> , 2018, 14, e1005989.	1.5	56
16843	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
16844	<i>Tbx20</i> Is Required in Mid-Gestation Cardiomyocytes and Plays a Central Role in Atrial Development. <i>Circulation Research</i> , 2018, 123, 428-442.	2.0	57
16845	A precision oncology approach to the pharmacological targeting of mechanistic dependencies in neuroendocrine tumors. <i>Nature Genetics</i> , 2018, 50, 979-989.	9.4	168
16846	Uncovering global metabolic response to cordycepin production in <i>Cordyceps militaris</i> through transcriptome and genome-scale network-driven analysis. <i>Scientific Reports</i> , 2018, 8, 9250.	1.6	30
16847	The Importance of Constraints and Control in Biological Mechanisms: Insights from Cancer Research. <i>Philosophy of Science</i> , 2018, 85, 573-593.	0.5	17
16848	Evidence of Rentian Scaling of Functional Modules in Diverse Biological Networks. <i>Neural Computation</i> , 2018, 30, 2210-2244.	1.3	3
16849	De novo and inherited private variants in MAP1B in periventricular nodular heterotopia. <i>PLoS Genetics</i> , 2018, 14, e1007281.	1.5	40
16850	Comparative Proteomics Analysis Reveals Trans Fatty Acid Isomers Activates Different Pathways in Human Umbilical Vein Endothelial Cell. <i>Lipids</i> , 2018, 53, 189-203.	0.7	1
16851	The extent of ribosome queuing in budding yeast. <i>PLoS Computational Biology</i> , 2018, 14, e1005951.	1.5	55
16852	<i>BioSankey</i> : Visualization of Microbial Communities Over Time. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	12
16853	MiR-139 in digestive system tumor diagnosis and detection: Bioinformatics and meta-analysis. <i>Clinica Chimica Acta</i> , 2018, 485, 33-41.	0.5	9
16854	Mapping biological process relationships and disease perturbations within a pathway network. <i>Npj Systems Biology and Applications</i> , 2018, 4, 22.	1.4	21
16855	ICBdocker: a Docker image for proteome annotation and visualization. <i>Bioinformatics</i> , 2018, 34, 3937-3938.	1.8	1

#	ARTICLE	IF	CITATIONS
16856	Protein Structure Databases. , 2019, , 460-471.		0
16857	A Bilinear Ranking SVM for Knowledge Based Relation Prediction and Classification. IEEE Transactions on Big Data, 2019, 5, 588-600.	4.4	2
16858	Evaluating the consistency of large-scale pharmacogenomic studies. Briefings in Bioinformatics, 2019, 20, 1734-1753.	3.2	8
16859	Alignment of Protein-Protein Interaction Networks. , 2019, , 997-1015.		0
16860	Identification of key gene modules and pathways of human glioma through coexpression network. Journal of Cellular Physiology, 2019, 234, 1862-1870.	2.0	3
16861	A computational system based on ontologies to automate the mapping process of medical reports into structured databases. Expert Systems With Applications, 2019, 115, 37-56.	4.4	9
16862	Evolutionary and structure-function analysis elucidates diversification of prokaryotic and eukaryotic trehalases. Journal of Biomolecular Structure and Dynamics, 2019, 37, 2926-2937.	2.0	5
16863	Effusion: prediction of protein function from sequence similarity networks. Bioinformatics, 2019, 35, 442-451.	1.8	12
16864	Complete Sequence of a Novel Multidrug-Resistant Pseudomonas putida Strain Carrying Two Copies of qnrVC6. Microbial Drug Resistance, 2019, 25, 1-7.	0.9	9
16865	Molecular footprints of inshore aquatic adaptation in Indo-Pacific humpback dolphin (Sousa Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF	1.3	10
16866	Investigating the effect of target of rapamycin kinase inhibition on the <i>Chlamydomonas reinhardtii</i> phosphoproteome: from known homologs to new targets. New Phytologist, 2019, 221, 247-260.	3.5	48
16867	Genome sequence and genetic transformation of a widely distributed and cultivated poplar. Plant Biotechnology Journal, 2019, 17, 451-460.	4.1	89
16868	MR4Cancer: a web server prioritizing master regulators for cancer. Bioinformatics, 2019, 35, 636-642.	1.8	6
16869	lrf3 from mandarin fish thymus initiates interferon transcription. Fish Physiology and Biochemistry, 2019, 45, 133-144.	0.9	8
16870	Genome sequence and description of Gracilibacillus timonensis sp. nov. strain Marseille P2481T, a moderate halophilic bacterium isolated from the human gut microflora. MicrobiologyOpen, 2019, 8, e00638.	1.2	8
16871	A Computational Workflow for the Automated Generation of Models of Genetic Designs. ACS Synthetic Biology, 2019, 8, 1548-1559.	1.9	27
16872	Integration of genetic and functional genomics data to uncover chemotherapeutic induced cytotoxicity. Pharmacogenomics Journal, 2019, 19, 178-190.	0.9	0
16873	Genomewide DNA Methylation Responses in Patients with β^2 -Thalassemia Treated with Yisui Shengxue Granules (益髓生血颗粒). Chinese Journal of Integrative Medicine, 2019, 25, 490-496.	0.7	3

#	ARTICLE	IF	CITATIONS
16874	Molecular Composition of Vestibular Hair Bundles. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a033209.	2.9	15
16875	Translational and Disease Bioinformatics. , 2019, , 1046-1057.		0
16876	Algorithms for Graph and Network Analysis: Graph Alignment. , 2019, , 102-109.		0
16877	Computing Languages for Bioinformatics: R. , 2019, , 199-205.		2
16878	Integrative Bioinformatics. , 2019, , 1092-1098.		0
16879	Biological Pathway Data Formats and Standards. , 2019, , 1063-1066.		0
16880	Biological Pathway Analysis. , 2019, , 1067-1070.		0
16881	Algorithms for Graph and Network Analysis: Clustering and Search of Motifs in Graphs. , 2019, , 95-101.		1
16882	Disease classification: from phenotypic similarity to integrative genomics and beyond. Briefings in Bioinformatics, 2019, 20, 1769-1780.	3.2	19
16883	Graphlets and Motifs in Biological Networks. , 2019, , 814-820.		4
16884	Information Retrieval in Life Sciences. , 2019, , 1104-1108.		1
16885	Ontology in Bioinformatics. , 2019, , 809-812.		0
16886	The Gene Ontology. , 2019, , 1-7.		3
16887	Metagenomic Analysis and its Applications. , 2019, , 184-193.		24
16888	Data Formats for Systems Biology and Quantitative Modeling. , 2019, , 884-893.		3
16889	Analyzing Transcriptome-Phenotype Correlations. , 2019, , 819-824.		1
16890	Biological and Medical Ontologies: Disease Ontology (DO). , 2019, , 838-847.		4
16891	Biological and Medical Ontologies: Human Phenotype Ontology (HPO). , 2019, , 848-857.		0

#	ARTICLE	IF	CITATIONS
16892	Tools for Semantic Analysis Based on Semantic Similarity. , 2019, , 889-895.		1
16893	Functional Enrichment Analysis Methods. , 2019, , 896-897.		1
16894	Gene Prioritization Using Semantic Similarity. , 2019, , 898-906.		0
16895	Visualization of Biomedical Networks. , 2019, , 1016-1035.		2
16896	Biomedical Text Mining. , 2019, , 1099-1109.		2
16897	SLIDE “ a web-based tool for interactive visualization of large-scale “ omics data. <i>Bioinformatics</i> , 2019, 35, 346-348.	1.8	6
16898	Data Integration and Transformation. , 2019, , 477-479.		0
16899	Design, synthesis, and insecticidal activity evaluation of novel 4- <i>N</i> , <i>Tj</i> ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 467 Td (N insecticides. <i>Pest Management Science</i> , 2019, 75, 427-437.	1.7	28
16900	Transcriptome Informatics. , 2019, , 324-340.		8
16901	Biological and Medical Ontologies: Introduction. , 2019, , 813-822.		0
16902	Biological and Medical Ontologies: GO and GOA. , 2019, , 823-831.		1
16903	A survey of computational methods in protein-protein interaction networks. <i>Annals of Operations Research</i> , 2019, 276, 35-87.	2.6	19
16904	Transcriptome Analysis. , 2019, , 792-805.		8
16905	Genome Informatics. , 2019, , 178-194.		0
16906	Genome Annotation. , 2019, , 195-209.		3
16907	Complete genome sequences of a H2O2-resistant psychrophilic bacterium <i>Colwellia</i> sp. Arc7-D isolated from Arctic Ocean sediment. <i>Marine Genomics</i> , 2019, 43, 65-67.	0.4	2
16908	Transcriptomic Analysis With the Progress of Symbiosis in “Crack-Entry” Legume <i>Arachis hypogaea</i> Highlights Its Contrast With “Infection Thread” Adapted Legumes. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 271-285.	1.4	59
16909	Discovering cellular protein-protein interactions: Technological strategies and opportunities. <i>Mass Spectrometry Reviews</i> , 2019, 38, 79-111.	2.8	70

#	ARTICLE	IF	CITATIONS
16910	Honey bee neurogenomic responses to affiliative and agonistic social interactions. <i>Genes, Brain and Behavior</i> , 2019, 18, e12509.	1.1	20
16911	The Exposome: Molecules to Populations. <i>Annual Review of Pharmacology and Toxicology</i> , 2019, 59, 107-127.	4.2	144
16912	Evolutionary biclustering algorithms: an experimental study on microarray data. <i>Soft Computing</i> , 2019, 23, 7671-7697.	2.1	10
16913	Learning for Personalized Medicine: A Comprehensive Review From a Deep Learning Perspective. <i>IEEE Reviews in Biomedical Engineering</i> , 2019, 12, 194-208.	13.1	63
16914	A comparison of mechanistic signaling pathway activity analysis methods. <i>Briefings in Bioinformatics</i> , 2019, 20, 1655-1668.	3.2	33
16915	Nuclear localized Raf1 isoform alters DNA-dependent protein kinase activity and the DNA damage response. <i>FASEB Journal</i> , 2019, 33, 1138-1150.	0.2	5
16916	PRSS8 suppresses colorectal carcinogenesis and metastasis. <i>Oncogene</i> , 2019, 38, 497-517.	2.6	24
16917	C5aR1 regulates migration of suppressive myeloid cells required for costimulatory blockade-induced murine allograft survival. <i>American Journal of Transplantation</i> , 2019, 19, 633-645.	2.6	25
16918	Bioinformatic analysis of the complete genome sequence of <i>Pectobacterium carotovorum</i> subsp. <i>brasiliense</i> BZA12 and candidate effector screening. <i>Journal of Plant Pathology</i> , 2019, 101, 39-49.	0.6	8
16919	Comparative transcriptome analyses of adzuki bean weevil (<i>Callosobruchus chinensis</i>) response to hypoxia and hypoxia/hypercapnia. <i>Bulletin of Entomological Research</i> , 2019, 109, 266-277.	0.5	4
16920	Combined Hypothesis Testing on Graphs With Applications to Gene Set Enrichment Analysis. <i>Journal of the American Statistical Association</i> , 2019, 114, 1320-1338.	1.8	1
16921	Random walk with restart on multiplex and heterogeneous biological networks. <i>Bioinformatics</i> , 2019, 35, 497-505.	1.8	183
16922	Characteristics of microbial communities and intestinal pathogenic bacteria for migrated <i>Larus ridibundus</i> in southwest China. <i>MicrobiologyOpen</i> , 2019, 8, e00693.	1.2	13
16923	Measuring Boundedness for Protein Complex Identification in PPI Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 967-979.	1.9	8
16924	Using Large Datasets to Understand Nanotechnology. <i>Advanced Materials</i> , 2019, 31, e1902798.	11.1	45
16925	Using Context-Sensitive Text Mining to Identify miRNAs in Different Stages of Atherosclerosis. <i>Thrombosis and Haemostasis</i> , 2019, 119, 1247-1264.	1.8	10
16926	Physics-based simulation ontology: an ontology to support modelling and reuse of data for physics-based simulation. <i>Journal of Engineering Design</i> , 2019, 30, 655-687.	1.1	16
16927	Nonsense-Mediated mRNA Decay Deficiency Affects the Auxin Response and Shoot Regeneration in <i>Arabidopsis</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 2000-2014.	1.5	9

#	ARTICLE	IF	CITATIONS
16928	Characterization of the prognostic values of the <i>NDRG</i> family in gastric cancer. <i>Therapeutic Advances in Gastroenterology</i> , 2019, 12, 175628481985850.	1.4	44
16929	Hybrid sequencing of the <i>Gynostemma pentaphyllum</i> transcriptome provides new insights into gypenoside biosynthesis. <i>BMC Genomics</i> , 2019, 20, 632.	1.2	16
16930	Comparative transcriptome analysis reveals the genetic basis underlying the biosynthesis of polysaccharides in <i>Hericium erinaceus</i> . , 2019, 60, 15.		14
16931	Pan-Cancer and Single-Cell Modeling of Genomic Alterations Through Gene Expression. <i>Frontiers in Genetics</i> , 2019, 10, 671.	1.1	22
16932	The Natural Compound Neobractatin Induces Cell Cycle Arrest by Regulating E2F1 and Gadd45 \pm . <i>Frontiers in Oncology</i> , 2019, 9, 654.	1.3	9
16933	Long Non-Coding RNAs Target Pathogenetically Relevant Genes and Pathways in Rheumatoid Arthritis. <i>Cells</i> , 2019, 8, 816.	1.8	17
16934	Effect of short-term oral prednisone therapy on blood gene expression: a randomised controlled clinical trial. <i>Respiratory Research</i> , 2019, 20, 176.	1.4	4
16935	Neural activities are unfavorable for the prognosis of ovarian cancer through mRNA expression analysis. <i>Biomarkers in Medicine</i> , 2019, 13, 663-673.	0.6	9
16936	Potential therapeutic drugs for ischemic stroke based on bioinformatics analysis. <i>International Journal of Neuroscience</i> , 2019, 129, 1098-1102.	0.8	3
16937	A dominant-negative effect drives selection of <i>TP53</i> missense mutations in myeloid malignancies. <i>Science</i> , 2019, 365, 599-604.	6.0	265
16938	Novel deep learning model for more accurate prediction of drug-drug interaction effects. <i>BMC Bioinformatics</i> , 2019, 20, 415.	1.2	86
16939	Identifying subpathway signatures for individualized anticancer drug response by integrating multi-omics data. <i>Journal of Translational Medicine</i> , 2019, 17, 255.	1.8	11
16940	An improved genome assembly of the fluke <i>Schistosoma japonicum</i> . <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007612.	1.3	50
16941	Discovery of stroke-related blood biomarkers from gene expression network models. <i>BMC Medical Genomics</i> , 2019, 12, 118.	0.7	14
16942	Long Non-Coding RNA Expression Levels Modulate Cell-Type-Specific Splicing Patterns by Altering Their Interaction Landscape with RNA-Binding Proteins. <i>Genes</i> , 2019, 10, 593.	1.0	16
16943	Evidence of association of the <i>DISC1</i> interactome gene set with schizophrenia from GWAS. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2019, 95, 109729.	2.5	16
16944	Multilayered Tuning of Dosage Compensation and Z-Chromosome Masculinization in the Wood White (<i>Leptidea sinapis</i>) Butterfly. <i>Genome Biology and Evolution</i> , 2019, 11, 2633-2652.	1.1	6
16945	ViSEAGO: a Bioconductor package for clustering biological functions using Gene Ontology and semantic similarity. <i>BioData Mining</i> , 2019, 12, 16.	2.2	99

#	ARTICLE	IF	CITATIONS
16946	Uncovering the Transcriptional Correlates of Hub Connectivity in Neural Networks. <i>Frontiers in Neural Circuits</i> , 2019, 13, 47.	1.4	20
16947	Identification of Wolbachia-Responsive miRNAs in the Small Brown Planthopper, <i>Laodelphax striatellus</i> . <i>Frontiers in Physiology</i> , 2019, 10, 928.	1.3	8
16948	EpiFIT: functional interpretation of transcription factors based on combination of sequence and epigenetic information. <i>Quantitative Biology</i> , 2019, 7, 233-243.	0.3	4
16949	Integrative Systems Biology Resources and Approaches in Disease Analytics. , 0, , .		1
16950	DeepGOPlus: improved protein function prediction from sequence. <i>Bioinformatics</i> , 2020, 36, 422-429.	1.8	242
16951	A Systematic View Exploring the Role of Chloroplasts in Plant Abiotic Stress Responses. <i>BioMed Research International</i> , 2019, 2019, 1-14.	0.9	14
16952	GWAS of Behavioral Traits. <i>Current Topics in Behavioral Neurosciences</i> , 2019, 42, 1-34.	0.8	0
16953	MCC: a Multiple Consensus Clustering Framework. <i>Journal of Classification</i> , 2019, 36, 414-434.	1.2	1
16954	Mammalian Annotation Database for improved annotation and functional classification of Omics datasets from less well-annotated organisms. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	13
16955	Syndromic immune disorder caused by a viable hypomorphic allele of spliceosome component Snrnp40. <i>Nature Immunology</i> , 2019, 20, 1322-1334.	7.0	7
16956	Investigation into the underlying regulatory mechanisms shaping inflorescence architecture in <i>Chenopodium quinoa</i> . <i>BMC Genomics</i> , 2019, 20, 658.	1.2	16
16957	MEK1/2 Inhibitors Unlock the Constrained Interferon Response in Macrophages Through IRF1 Signaling. <i>Frontiers in Immunology</i> , 2019, 10, 2020.	2.2	11
16958	Application of the High-Throughput TAB-Array for the Discovery of Novel 5-Hydroxymethylcytosine Biomarkers in Pancreatic Ductal Adenocarcinoma. <i>Epigenomes</i> , 2019, 3, 16.	0.8	15
16959	Experimental correlation analysis of bicluster coherence measures and gene ontology information. <i>Applied Soft Computing Journal</i> , 2019, 85, 105688.	4.1	1
16960	Draft Genome and Complete Hox-Cluster Characterization of the Sterlet (<i>Acipenser ruthenus</i>). <i>Frontiers in Genetics</i> , 2019, 10, 776.	1.1	34
16961	Discovery of core genes in colorectal cancer by weighted gene co-expression network analysis. <i>Oncology Letters</i> , 2019, 18, 3137-3149.	0.8	9
16962	Clinical value of microRNA-198-5p downregulation in lung adenocarcinoma and its potential pathways. <i>Oncology Letters</i> , 2019, 18, 2939-2954.	0.8	12
16963	Emerging concepts in pseudoenzyme classification, evolution, and signaling. <i>Science Signaling</i> , 2019, 12, .	1.6	80

#	ARTICLE	IF	CITATIONS
16964	Construction of subtype-specific prognostic gene signatures for early-stage non-small cell lung cancer using meta feature selection methods. <i>Oncology Letters</i> , 2019, 18, 2366-2375.	0.8	0
16965	Compression-induced expression of glycolysis genes in CAFs correlates with EMT and angiogenesis gene expression in breast cancer. <i>Communications Biology</i> , 2019, 2, 313.	2.0	38
16966	Comparative analysis of different methods revealing the involvement of proteins during ageing of rice seeds. <i>Plant Breeding</i> , 2019, 138, 830-839.	1.0	1
16967	Omics Driven Understanding of the Intestines of Parasitic Nematodes. <i>Frontiers in Genetics</i> , 2019, 10, 652.	1.1	13
16969	Comparison of dysregulated long noncoding RNAs in lung adenocarcinoma and spinal metastasis: A genome-wide analysis. <i>Neoplasia</i> , 2019, 66, 930-938.	0.7	0
16970	Possible epigenetic regulatory effect of dysregulated circular RNAs in Alzheimer's disease model. <i>Scientific Reports</i> , 2019, 9, 11956.	1.6	16
16971	Advances in gene ontology utilization improve statistical power of annotation enrichment. <i>PLoS ONE</i> , 2019, 14, e0220728.	1.1	10
16972	Decreased metabolism and increased tolerance to extreme environments in <i>Staphylococcus warneri</i> during long-term spaceflight. <i>MicrobiologyOpen</i> , 2019, 8, e917.	1.2	14
16973	RNA polymerase II (RNAP II)-associated factors are recruited to tRNA loci, revealing that RNAP II and RNAP III-mediated transcriptions overlap in yeast. <i>Journal of Biological Chemistry</i> , 2019, 294, 12349-12358.	1.6	2
16974	Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , 2019, 20, 147.	3.8	21
16975	pathfindR: An R Package for Comprehensive Identification of Enriched Pathways in Omics Data Through Active Subnetworks. <i>Frontiers in Genetics</i> , 2019, 10, 858.	1.1	247
16976	Nucleo-cytoplasmic Partitioning of ARF Proteins Controls Auxin Responses in <i>Arabidopsis thaliana</i> . <i>Molecular Cell</i> , 2019, 76, 177-190.e5.	4.5	165
16977	Establishment and characterisation of a new patient-derived model of myxoid liposarcoma with acquired resistance to trabectedin. <i>British Journal of Cancer</i> , 2019, 121, 464-473.	2.9	7
16978	Gene Fusions Derived by Transcriptional Readthrough are Driven by Segmental Duplication in Human. <i>Genome Biology and Evolution</i> , 2019, 11, 2678-2690.	1.1	7
16979	Replication timing networks reveal a link between transcription regulatory circuits and replication timing control. <i>Genome Research</i> , 2019, 29, 1415-1428.	2.4	12
16980	Identification of key genes and pathways between type I and type II endometrial cancer using bioinformatics analysis. <i>Oncology Letters</i> , 2019, 18, 2464-2476.	0.8	12
16981	Proteomics Links Ubiquitin Chain Topology Change to Transcription Factor Activation. <i>Molecular Cell</i> , 2019, 76, 126-137.e7.	4.5	24
16982	Inference of the gene regulatory network acting downstream of CROWN ROOTLESS1 in rice reveals a regulatory cascade linking genes involved in auxin signaling, crown root initiation, and root meristem specification and maintenance. <i>Plant Journal</i> , 2019, 100, 954-968.	2.8	13

#	ARTICLE	IF	CITATIONS
16983	Identification of key candidate targets and pathways for the targeted treatment of leukemia stem cells of chronic myelogenous leukemia using bioinformatics analysis. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e851.	0.6	10
16984	Analysis of methylation datasets identified significantly changed genes and functional pathways in osteoarthritis. <i>Clinical Rheumatology</i> , 2019, 38, 3529-3538.	1.0	5
16985	Retinal proteome associated with bradykinin-induced edema. <i>Experimental Eye Research</i> , 2019, 186, 107744.	1.2	8
16986	Identification of key pathways and genes in different types of chronic kidney disease based on WGCNA. <i>Molecular Medicine Reports</i> , 2019, 20, 2245-2257.	1.1	12
16987	Spatial Regulation of Mitochondrial Heterogeneity by Stromal Confinement in Micropatterned Tumor Models. <i>Scientific Reports</i> , 2019, 9, 11187.	1.6	15
16988	Cholestatic liver disease results increased production of reactive aldehydes and an atypical periportal hepatic antioxidant response. <i>Free Radical Biology and Medicine</i> , 2019, 143, 101-114.	1.3	13
16989	Extensive post-transcriptional buffering of gene expression in the response to severe oxidative stress in baker's yeast. <i>Scientific Reports</i> , 2019, 9, 11005.	1.6	50
16990	Exploration of Novel Biomarkers in Vasculitis by Integrated Bioinformatic Approaches. <i>Journal of Computational Biology</i> , 2019, 26, 1448-1457.	0.8	2
16991	Epitranscriptomic mechanisms of N6-methyladenosine methylation regulating mammalian hypertension development by determined spontaneously hypertensive rats pericytes. <i>Epigenomics</i> , 2019, 11, 1359-1370.	1.0	26
16992	Comparative Proteomics and Physiological Analyses Reveal Important Maize Filling-Kernel Drought-Responsive Genes and Metabolic Pathways. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3743.	1.8	36
16993	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. <i>Cell Host and Microbe</i> , 2019, 26, 252-264.e10.	5.1	274
16994	Effect of Reservoir Salinity between Bioacid and Carbonate Rock Based on Biometabolic Analysis. <i>Energy & Fuels</i> , 2019, 33, 8135-8144.	2.5	6
16995	Mapping anatomical related entities to human body parts based on wikipedia in discharge summaries. <i>BMC Bioinformatics</i> , 2019, 20, 430.	1.2	2
16996	Transcriptomic analysis of immune response to bacterial lipopolysaccharide in zebra finch (<i>Taeniopygia guttata</i>). <i>BMC Genomics</i> , 2019, 20, 647.	1.2	17
16997	ITRAQ-based proteomic analysis reveals possible target-related proteins in human adrenocortical adenomas. <i>BMC Genomics</i> , 2019, 20, 655.	1.2	7
16998	Intrinsically disordered proteins and structured proteins with intrinsically disordered regions have different functional roles in the cell. <i>PLoS ONE</i> , 2019, 14, e0217889.	1.1	84
16999	Integrated bioinformatics analysis to identify 15 hub genes in breast cancer. <i>Oncology Letters</i> , 2019, 18, 1023-1034.	0.8	16
17000	Exploration of fine-scale recombination rate variation in the domestic horse. <i>Genome Research</i> , 2019, 29, 1744-1752.	2.4	19

#	ARTICLE	IF	CITATIONS
17001	Distinct signatures of lung cancer types: aberrant mucin O-glycosylation and compromised immune response. <i>BMC Cancer</i> , 2019, 19, 824.	1.1	34
17002	Transcriptomic Analysis of Marine Gastropod <i>Hemifusus tuba</i> Provides Novel Insights into Conotoxin Genes. <i>Marine Drugs</i> , 2019, 17, 466.	2.2	6
17003	Dysregulation of DNA methylation patterns may identify patients with breast cancer resistant to endocrine therapy: A predictive classifier based on differentially methylated regions. <i>Oncology Letters</i> , 2019, 18, 1287-1303.	0.8	11
17004	Exome sequencing of 457 autism families recruited online provides evidence for autism risk genes. <i>Npj Genomic Medicine</i> , 2019, 4, 19.	1.7	163
17005	Chronic cadmium exposure decreases the dependency of MCF7 breast cancer cells on ER α . <i>Scientific Reports</i> , 2019, 9, 12135.	1.6	12
17006	Ligand Binding Site Structure Shapes Folding, Assembly and Degradation of Homomeric Protein Complexes. <i>Journal of Molecular Biology</i> , 2019, 431, 3871-3888.	2.0	5
17007	Long Noncoding RNA Expression Profile in BV2 Microglial Cells Exposed to Lipopolysaccharide. <i>BioMed Research International</i> , 2019, 2019, 1-9.	0.9	7
17008	Exploiting Differential Gene Expression to Discover Ionic and Osmotic-Associated Transcripts in the Halophyte Grass <i>Aeluropus litoralis</i> . <i>Biological Procedures Online</i> , 2019, 21, 14.	1.4	12
17009	Royal jelly-derived proteins enhance proliferation and migration of human epidermal keratinocytes in an in vitro scratch wound model. <i>BMC Complementary and Alternative Medicine</i> , 2019, 19, 175.	3.7	20
17010	Identification of key candidate genes involved in melanoma metastasis. <i>Molecular Medicine Reports</i> , 2019, 20, 903-914.	1.1	33
17011	RAC1 inhibition reverses cisplatin resistance in esophageal squamous cell carcinoma and induces downregulation of glycolytic enzymes. <i>Molecular Oncology</i> , 2019, 13, 2010-2030.	2.1	40
17012	Moonlighting Proteins and Cardiopathy in the Spatial Response of MCF7 Breast Cancer Cells to Tamoxifen. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1900029.	0.8	3
17013	Identification of important invasion and proliferation related genes in adrenocortical carcinoma. <i>Medical Oncology</i> , 2019, 36, 73.	1.2	19
17014	Predicting instances of pathway ontology classes for pathway integration. <i>Journal of Biomedical Semantics</i> , 2019, 10, 11.	0.9	1
17015	<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></p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 5037-5051.	1.0	13
17016	Multimodal Analytics for Next-Generation Big Data Technologies and Applications. , 2019, , .		1
17017	Transcriptome comparative analysis of immune tissues from asymptomatic and diseased <i>Epinephelus moara</i> naturally infected with nervous necrosis virus. <i>Fish and Shellfish Immunology</i> , 2019, 93, 99-107.	1.6	25
17018	Functionally significant metabolic differences between B and T lymphocyte lineages. <i>Immunology</i> , 2019, 158, 104-120.	2.0	21

#	ARTICLE	IF	CITATIONS
17019	Diagnostic and prognostic values of integrin α subfamily mRNA expression in colon adenocarcinoma. <i>Oncology Reports</i> , 2019, 42, 923-936.	1.2	13
17020	Predicting Sequence Features, Function, and Structure of Proteins Using MESSA. <i>Current Protocols in Bioinformatics</i> , 2019, 67, e84.	25.8	0
17021	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
17022	Shiny-Seq: advanced guided transcriptome analysis. <i>BMC Research Notes</i> , 2019, 12, 432.	0.6	28
17023	Quality assurance of complex ChEBI concepts based on number of relationship types. <i>Applied Ontology</i> , 2019, 14, 199-214.	1.0	2
17024	Identification and characterization of sexual dimorphism-linked gene expression profile in hepatocellular carcinoma. <i>Oncology Reports</i> , 2019, 42, 937-952.	1.2	10
17025	New SDC function prediction based on protein-protein interaction using bioinformatics tools. <i>Computational Biology and Chemistry</i> , 2019, 83, 107087.	1.1	10
17026	Strain-level metagenomic assignment and compositional estimation for long reads with MetaMaps. <i>Nature Communications</i> , 2019, 10, 3066.	5.8	98
17027	FunSet: an open-source software and web server for performing and displaying Gene Ontology enrichment analysis. <i>BMC Bioinformatics</i> , 2019, 20, 359.	1.2	22
17028	ET-GRU: using multi-layer gated recurrent units to identify electron transport proteins. <i>BMC Bioinformatics</i> , 2019, 20, 377.	1.2	54
17029	Revisiting the Phylogenetic History of Helminths Through Genomics, the Case of the New <i>Echinococcus oligarthrus</i> Genome. <i>Frontiers in Genetics</i> , 2019, 10, 708.	1.1	12
17030	AraPPINet: An Updated Interactome for the Analysis of Hormone Signaling Crosstalk in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 870.	1.7	12
17031	Cloudy with a Chance of Insights: Context Dependent Gene Regulation and Implications for Evolutionary Studies. <i>Genes</i> , 2019, 10, 492.	1.0	21
17032	Plasma proteomic changes during therapeutic hypothermia in resuscitated patients after cardiac arrest. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 1069-1080.	0.8	1
17033	Identification of potential diagnostic and therapeutic target genes for lung squamous cell carcinoma. <i>Oncology Letters</i> , 2019, 18, 169-180.	0.8	10
17034	Investigation of differentially expressed genes in nasopharyngeal carcinoma by integrated bioinformatics analysis. <i>Oncology Letters</i> , 2019, 18, 916-926.	0.8	4
17035	Integration of curated and high-throughput screening data to elucidate environmental influences on disease pathways. <i>Computational Toxicology</i> , 2019, 12, 100094.	1.8	13
17036	scOrange—a tool for hands-on training of concepts from single-cell data analytics. <i>Bioinformatics</i> , 2019, 35, i4-i12.	1.8	8

#	ARTICLE	IF	CITATIONS
17037	Genome wide characterization, evolution and expression analysis of FBA gene family under salt stress in <i>Gossypium</i> species. <i>Biologia (Poland)</i> , 2019, 74, 1539-1552.	0.8	3
17038	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
17039	Finding Functional Differences Between Species in a Microbial Community: Case Studies in Wine Fermentation and Kefir Culture. <i>Frontiers in Microbiology</i> , 2019, 10, 1347.	1.5	229
17040	Single-Cell Transcriptomics and Proteomics of Skeletal Muscle: Technology and Applications. , 2019, , 253-281.		0
17041	Systems-Level Understanding of Single-Cell Omics. , 2019, , 433-456.		0
17042	A gene expression network analysis of the pancreatic islets from lean and obese mice identifies complement 1q-like-3 secreted protein as a regulator of β -cell function. <i>Scientific Reports</i> , 2019, 9, 10119.	1.6	8
17043	Epimutations in Developmental Genes Underlie the Onset of Domestication in Farmed European Sea Bass. <i>Molecular Biology and Evolution</i> , 2019, 36, 2252-2264.	3.5	58
17044	Comprehensive in vivo identification of the c-Myc mRNA protein interactome using HyPR-MS. <i>Rna</i> , 2019, 25, 1337-1352.	1.6	15
17045	Regulation of tumor angiogenesis and mesenchymal endothelial transition by p38 through TGF- β 2 and JNK signaling. <i>Nature Communications</i> , 2019, 10, 3071.	5.8	96
17046	iOmicsPASS: network-based integration of multiomics data for predictive subnetwork discovery. <i>Npj Systems Biology and Applications</i> , 2019, 5, 22.	1.4	79
17047	Identification of expression signatures for non-small-cell lung carcinoma subtype classification. <i>Bioinformatics</i> , 2020, 36, 339-346.	1.8	26
17048	A new evolutionary rough fuzzy integrated machine learning technique for microRNA selection using next-generation sequencing data of breast cancer. , 2019, , .		1
17049	Co-expression analysis reveals dysregulated miRNAs and miRNA-mRNA interactions in the development of contrast-induced acute kidney injury. <i>PLoS ONE</i> , 2019, 14, e0218574.	1.1	9
17050	Gene Amplification-Driven Long Noncoding RNA SNHG17 Regulates Cell Proliferation and Migration in Human Non-Small-Cell Lung Cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 17, 405-413.	2.3	51
17051	Pigeon foot feathering reveals conserved limb identity networks. <i>Developmental Biology</i> , 2019, 454, 128-144.	0.9	19
17052	Unveiling the presence of biosynthetic pathways for bioactive compounds in the <i>Thalassiosira rotula</i> transcriptome. <i>Scientific Reports</i> , 2019, 9, 9893.	1.6	25
17053	<p></p>Bioinformatics analysis of dysregulated microRNAs in exosomes from docetaxel-resistant and parental human breast cancer cells</p>. <i>Cancer Management and Research</i> , 2019, Volume 11, 5425-5435.	0.9	15
17054	Identification of downstream target genes regulated by CX43 in hepatocellular carcinoma. <i>Neoplasma</i> , 2019, 66, 870-878.	0.7	1

#	ARTICLE	IF	CITATIONS
17055	RNA sequencing and transcriptome analysis of buffalo (<i>Bubalus bubalis</i>) blastocysts produced by somatic cell nuclear transfer and in vitro fertilization. <i>Molecular Reproduction and Development</i> , 2019, 86, 1149-1167.	1.0	9
17056	Novel significant stage-specific differentially expressed genes in hepatocellular carcinoma. <i>BMC Cancer</i> , 2019, 19, 663.	1.1	72
17057	Restoration of histone acetylation ameliorates disease and metabolic abnormalities in a FUS mouse model. <i>Acta Neuropathologica Communications</i> , 2019, 7, 107.	2.4	61
17058	Recent Advances in the Machine Learning-Based Drug-Target Interaction Prediction. <i>Current Drug Metabolism</i> , 2019, 20, 194-202.	0.7	48
17059	Combinatorial perturbation analysis reveals divergent regulations of mesenchymal genes during epithelial-to-mesenchymal transition. <i>Npj Systems Biology and Applications</i> , 2019, 5, 21.	1.4	65
17060	Evolutionary Proteomics Reveals Distinct Patterns of Complexity and Divergence between Lepidopteran Sperm Morphs. <i>Genome Biology and Evolution</i> , 2019, 11, 1838-1846.	1.1	12
17061	Disease gene prediction for molecularly uncharacterized diseases. <i>PLoS Computational Biology</i> , 2019, 15, e1007078.	1.5	26
17062	Transcriptomic correlates of electrophysiological and morphological diversity within and across excitatory and inhibitory neuron classes. <i>PLoS Computational Biology</i> , 2019, 15, e1007113.	1.5	28
17063	Transcriptome analysis of ovary in relatively greater and lesser egg producing Jinghai Yellow Chicken. <i>Animal Reproduction Science</i> , 2019, 208, 106114.	0.5	50
17064	Methylation analysis for postpartum depression: a case control study. <i>BMC Psychiatry</i> , 2019, 19, 190.	1.1	3
17065	The Farmed Atlantic Salmon (<i>Salmo salar</i>) Skin Mucus Proteome and Its Nutrient Potential for the Resident Bacterial Community. <i>Genes</i> , 2019, 10, 515.	1.0	26
17066	Inferring Regulatory Programs Governing Region Specificity of Neuroepithelial Stem Cells during Early Hindbrain and Spinal Cord Development. <i>Cell Systems</i> , 2019, 9, 167-186.e12.	2.9	13
17067	Three Biomarkers Predict Gastric Cancer Patients' Susceptibility To Fluorouracil-based Chemotherapy. <i>Journal of Cancer</i> , 2019, 10, 2953-2960.	1.2	9
17068	Quorum Quenching Enzyme APTM01, an Acylhomoserine-Lactone Acylase from Marine Bacterium of <i>Pseudoalteromonas tetradonis</i> Strain MQS005. <i>Current Microbiology</i> , 2019, 76, 1387-1397.	1.0	10
17069	Computational Drug Screening Identifies Compounds Targeting Renal Age-associated Molecular Profiles. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 843-853.	1.9	6
17070	Identification and characterization of a LuxI/R-type quorum sensing system in <i>Pseudoalteromonas</i> . <i>Research in Microbiology</i> , 2019, 170, 243-255.	1.0	19
17071	Estimating dispensable content in the human interactome. <i>Nature Communications</i> , 2019, 10, 3205.	5.8	9
17072	Identification of Key Genes and Candidated Pathways in Human Autosomal Dominant Polycystic Kidney Disease by Bioinformatics Analysis. <i>Kidney and Blood Pressure Research</i> , 2019, 44, 533-552.	0.9	14

#	ARTICLE	IF	CITATIONS
17073	Genome-wide identification of binding sites and gene targets of Alx1, a pivotal regulator of echinoderm skeletogenesis. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	23
17074	Differential regulation of mycelial growth and aflatoxin biosynthesis by <i>Aspergillus flavus</i> under different temperatures as revealed by strand-specific RNA-seq. <i>MicrobiologyOpen</i> , 2019, 8, e897.	1.2	11
17075	Describing Sequential Association Patterns from Longitudinal Microarray Data Sets in Humans. <i>Lecture Notes in Computer Science</i> , 2019, , 318-329.	1.0	1
17076	Identification of gene co-expression modules and hub genes associated with lymph node metastasis of papillary thyroid cancer. <i>Endocrine</i> , 2019, 66, 573-584.	1.1	35
17077	Accurate prediction of potential druggable proteins based on genetic algorithm and Bagging-SVM ensemble classifier. <i>Artificial Intelligence in Medicine</i> , 2019, 98, 35-47.	3.8	72
17078	FunFam protein families improve residue level molecular function prediction. <i>BMC Bioinformatics</i> , 2019, 20, 400.	1.2	20
17079	Why do eukaryotic proteins contain more intrinsically disordered regions?. <i>PLoS Computational Biology</i> , 2019, 15, e1007186.	1.5	70
17080	Multi-Omics Analysis of Fatty Alcohol Production in Engineered Yeasts <i>Saccharomyces cerevisiae</i> and <i>Yarrowia lipolytica</i> . <i>Frontiers in Genetics</i> , 2019, 10, 747.	1.1	32
17081	The ER Luminal Hsp70 Protein FpLhs1 Is Important for Conidiation and Plant Infection in <i>Fusarium pseudograminearum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1401.	1.5	24
17082	Proteomic Data Integration Highlights Central Actors Involved in Einkorn (<i>Triticum monococcum</i> ssp.) Tj ETQq1 1 0.784314 rgBT /Over Science, 2019, 10, 832.	1.7	2
17084	Using deep maxout neural networks to improve the accuracy of function prediction from protein interaction networks. <i>PLoS ONE</i> , 2019, 14, e0209958.	1.1	11
17085	<p></p>Gene expression profiling reveals candidate biomarkers and probable molecular mechanism in diabetic peripheral neuropathy</p><p></p>. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2019, Volume 12, 1213-1223.	1.1	13
17086	Label-Free Proteomic Analysis of Molecular Effects of 2-Methoxy-1,4-naphthoquinone on <i>Penicillium italicum</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 3459.	1.8	21
17087	Increased Immune Activation by Pathologic α -Synuclein in Parkinson's Disease. <i>Annals of Neurology</i> , 2019, 86, 593-606.	2.8	95
17088	Identification and Interaction Analysis of Significant Genes and MicroRNAs in Pterygium. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	10
17089	Analysis of gene expression in rheumatoid arthritis and related conditions offers insights into sex-bias, gene biotypes and co-expression patterns. <i>PLoS ONE</i> , 2019, 14, e0219698.	1.1	12
17090	Chromosome assembly of <i>Collichthys lucidus</i> , a fish of Sciaenidae with a multiple sex chromosome system. <i>Scientific Data</i> , 2019, 6, 132.	2.4	26
17091	Proteome Imaging: From Classic to Modern Mass Spectrometry-Based Molecular Histology. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1140, 55-98.	0.8	10

#	ARTICLE	IF	CITATIONS
17092	Viral abundance and diversity vary with depth in a southeastern United States agricultural ultisol. <i>Soil Biology and Biochemistry</i> , 2019, 137, 107546.	4.2	37
17093	A role for <i>PM19-Like 1</i> in seed dormancy in <i>Arabidopsis</i> . <i>Seed Science Research</i> , 2019, 29, 184-196.	0.8	9
17094	Complete Genome Sequence of <i>Brevibacillus laterosporus</i> Bl-zj, an Algicidal Bacterium Isolated from Soil. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
17095	Integrated identification of key genes and pathways in Alzheimer's disease via comprehensive bioinformatical analyses. <i>Hereditas</i> , 2019, 156, 25.	0.5	32
17096	ParaDB: A manually curated database containing genomic annotation for the human pathogenic fungi <i>Paracoccidioides</i> spp.. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007576.	1.3	3
17097	Hybrid gene misregulation in multiple developing tissues within a recent adaptive radiation of <i>Cyprinodon</i> pupfishes. <i>PLoS ONE</i> , 2019, 14, e0218899.	1.1	19
17098	The Gene Master Regulators (GMR) Approach Provides Legitimate Targets for Personalized, Time-Sensitive Cancer Gene Therapy. <i>Genes</i> , 2019, 10, 560.	1.0	16
17099	BioNorm: deep learning-based event normalization for the curation of reaction databases. <i>Bioinformatics</i> , 2020, 36, 611-620.	1.8	3
17100	Influence of metabolic status and genetic merit for fertility on proteomic composition of bovine oviduct fluid. <i>Biology of Reproduction</i> , 2019, 101, 893-905.	1.2	11
17101	Lack of long-term acclimation in Antarctic encrusting species suggests vulnerability to warming. <i>Nature Communications</i> , 2019, 10, 3383.	5.8	21
17102	Tripal v3: an ontology-based toolkit for construction of FAIR biological community databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	22
17103	mRNAs expression profiles of high glucose-induced memory in human umbilical vein endothelial cells. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2019, Volume 12, 1249-1261.	1.1	5
17104	MicroRNA Sequencing Reveals the Effect of Different Levels of Non-Fibrous Carbohydrate/Neutral Detergent Fiber on Rumen Development in Calves. <i>Animals</i> , 2019, 9, 496.	1.0	7
17105	Matching a Trope Ontology to the Basic Formal Ontology. <i>Philosophies</i> , 2019, 4, 40.	0.4	2
17106	Multigene Biomarkers of Pyrethroid Exposure: Exploratory Experiments. <i>Environmental Toxicology and Chemistry</i> , 2019, 38, 2436-2446.	2.2	3
17107	Transcriptome assembly and abiotic related gene expression analysis of date palm reveal candidate genes involved in response to cadmium stress. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2019, 225, 108569.	1.3	10
17108	Single-Cell RNA-Seq of the Developing Cardiac Outflow Tract Reveals Convergent Development of the Vascular Smooth Muscle Cells. <i>Cell Reports</i> , 2019, 28, 1346-1361.e4.	2.9	68
17109	The complete genome sequence of <i>Ethanoligenens harbinense</i> reveals the metabolic pathway of acetate-ethanol fermentation: A novel understanding of the principles of anaerobic biotechnology. <i>Environment International</i> , 2019, 131, 105053.	4.8	25

#	ARTICLE	IF	CITATIONS
17110	Development of a Chimeric Model to Study and Manipulate Human Microglia In Vivo. <i>Neuron</i> , 2019, 103, 1016-1033.e10.	3.8	218
17111	De novo transcriptome assembly of the fresh-cut white husk of <i>Juglans cathayensis</i> Dode: Insights for enzymatic browning mechanism of fresh-cut husk of walnut. <i>Scientia Horticulturae</i> , 2019, 257, 108654.	1.7	15
17112	Detailed modeling of positive selection improves detection of cancer driver genes. <i>Nature Communications</i> , 2019, 10, 3399.	5.8	49
17113	Genetically diverse <i>Pseudomonas aeruginosa</i> populations display similar transcriptomic profiles in a cystic fibrosis explanted lung. <i>Nature Communications</i> , 2019, 10, 3397.	5.8	68
17114	Transcriptome profiling of <i>Gerbera hybrida</i> reveals that stem bending is caused by water stress and regulation of abscisic acid. <i>BMC Genomics</i> , 2019, 20, 600.	1.2	14
17115	Whole genome sequence and de novo assembly revealed genomic architecture of Indian Mithun (<i>Bos</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.2	10
17116	Genomic Patterns of Local Adaptation under Gene Flow in <i>Arabidopsis lyrata</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 2557-2571.	3.5	61
17117	Genetic Diversity of Indigenous Pigs from South China Area Revealed by SNP Array. <i>Animals</i> , 2019, 9, 361.	1.0	19
17118	Complete Genome Sequences of <i>Colwellia</i> sp. Arc7-635, a Denitrifying Bacterium Isolated from Arctic Seawater. <i>Current Microbiology</i> , 2019, 76, 1061-1065.	1.0	5
17119	Integrated transcriptomic and phytochemical analyses provide insights into characteristic metabolites variation in leaves of 1-year-old grafted tea (<i>Camellia sinensis</i>). <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	6
17120	Mitochondrial respirasome works as a single unit and the cross-talk between complexes I, III2 and IV stimulates NADH dehydrogenase activity. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2019, 1860, 618-627.	0.5	12
17121	A genetics-led approach defines the drug target landscape of 30 immune-related traits. <i>Nature Genetics</i> , 2019, 51, 1082-1091.	9.4	157
17122	Identification of Key Genes and Circular RNAs in Human Gastric Cancer. <i>Medical Science Monitor</i> , 2019, 25, 2488-2504.	0.5	40
17123	Co-expression Network Analysis Elucidated a Core Module in Association With Prognosis of Non-functioning Non-invasive Human Pituitary Adenoma. <i>Frontiers in Endocrinology</i> , 2019, 10, 361.	1.5	23
17124	Physical confinement induces malignant transformation in mammary epithelial cells. <i>Biomaterials</i> , 2019, 217, 119307.	5.7	13
17125	A polysaccharide found in <i>Dendrobium nobile</i> Lindl stimulates calcium signaling pathway and enhances tobacco defense against TMV. <i>International Journal of Biological Macromolecules</i> , 2019, 137, 1286-1297.	3.6	19
17126	Identification and characterization of differentially expressed miRNAs in HepG2 cells under normoxic and hypoxic conditions. <i>RSC Advances</i> , 2019, 9, 16884-16891.	1.7	3
17127	The evolving concept of cell identity in the single cell era. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	115

#	ARTICLE	IF	CITATIONS
17128	Ontology mapping for semantically enabled applications. <i>Drug Discovery Today</i> , 2019, 24, 2068-2075.	3.2	25
17129	A systems biology pipeline identifies regulatory networks for stem cell engineering. <i>Nature Biotechnology</i> , 2019, 37, 810-818.	9.4	18
17130	Combining learning and constraints for genome-wide protein annotation. <i>BMC Bioinformatics</i> , 2019, 20, 338.	1.2	1
17131	pcaExplorer: an R/Bioconductor package for interacting with RNA-seq principal components. <i>BMC Bioinformatics</i> , 2019, 20, 331.	1.2	178
17132	Next generation community assessment of biomedical entity recognition web servers: metrics, performance, interoperability aspects of BeCalm. <i>Journal of Cheminformatics</i> , 2019, 11, 42.	2.8	4
17133	Identification of diagnostic long non-coding RNA biomarkers in patients with hepatocellular carcinoma. <i>Molecular Medicine Reports</i> , 2019, 20, 1121-1130.	1.1	29
17134	Screening key genes and signaling pathways in colorectal cancer by integrated bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2019, 20, 1259-1269.	1.1	28
17135	Analysis of the microRNA expression profiles in feline kidney cell line infected with feline panleukopenia virus. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103945.	1.0	8
17136	CTCF variants in 39 individuals with a variable neurodevelopmental disorder broaden the mutational and clinical spectrum. <i>Genetics in Medicine</i> , 2019, 21, 2723-2733.	1.1	48
17137	Transcriptomic profiling revealed genes involved in response to cold stress in maize. <i>Functional Plant Biology</i> , 2019, 46, 830.	1.1	63
17138	Comparative transcriptome analysis reveals genes related to the yolk ratio of duck eggs. <i>Animal Genetics</i> , 2019, 50, 484-492.	0.6	3
17139	GALL: An interactive webserver for inference and dynamic visualization of gene-gene associations based on gene ontology guided mining of biomedical literature. <i>PLoS ONE</i> , 2019, 14, e0219195.	1.1	5
17140	Significantly dysregulated genes in osteoarthritic labrum cells identified through gene expression profiling. <i>Molecular Medicine Reports</i> , 2019, 20, 1716-1724.	1.1	2
17141	Osteoclasts Modulate Bone Erosion in Cholesteatoma via RANKL Signaling. <i>JARO - Journal of the Association for Research in Otolaryngology</i> , 2019, 20, 449-459.	0.9	23
17142	Common and specific responses to iron and phosphorus deficiencies in roots of apple tree (<i>Malus ×</i>). <i>Trends in Plant Science</i> , 2019, 24, 101-115.	2.6	15
17143	HPO2Vec+: Leveraging heterogeneous knowledge resources to enrich node embeddings for the Human Phenotype Ontology. <i>Journal of Biomedical Informatics</i> , 2019, 96, 103246.	2.5	26
17144	Deep evolutionary origin of limb and fin regeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15106-15115.	3.3	46
17145	The Genome Sequence of the Anthelmintic-Susceptible New Zealand <i>Haemonchus contortus</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 1965-1970.	1.1	29

#	ARTICLE	IF	CITATIONS
17146	Expression and regulatory asymmetry of retained <i>Arabidopsis thaliana</i> transcription factor genes derived from whole genome duplication. <i>BMC Evolutionary Biology</i> , 2019, 19, 77.	3.2	20
17147	Analysis of potential functional significance of microRNA-3613-3p in human umbilical vein endothelial cells affected by heat stress. <i>Molecular Medicine Reports</i> , 2019, 20, 1846-1856.	1.1	1
17148	Isatin inhibits the invasion of human neuroblastoma SH-SY5Y cells, based on microarray analysis. <i>Molecular Medicine Reports</i> , 2019, 20, 1700-1706.	1.1	4
17149	Glial α -synuclein promotes neurodegeneration characterized by a distinct transcriptional program in vivo. <i>Glia</i> , 2019, 67, 1933-1957.	2.5	27
17150	Considering smoking status, coexpression network analysis of non-small cell lung cancer at different cancer stages, exhibits important genes and pathways. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 19172-19185.	1.2	5
17151	Integrated analysis identifying new lncRNA markers revealed in ceRNA network for tumor recurrence in papillary thyroid carcinoma and build of nomogram. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 19673-19683.	1.2	23
17152	Comprehensive Analysis of Core Genes and Potential Mechanisms in Rectal Cancer. <i>Journal of Computational Biology</i> , 2019, 26, 1262-1277.	0.8	15
17153	Long noncoding RNA NEAT1 mediates neuronal histone methylation and age-related memory impairment. <i>Science Signaling</i> , 2019, 12, .	1.6	81
17154	A periodic table of cell types. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	54
17155	Comparison of long non-coding RNA expression profiles in human dental follicle cells and human periodontal ligament cells. <i>Molecular Medicine Reports</i> , 2019, 20, 939-950.	1.1	5
17156	Identification of differentially expressed genes and functional annotations associated with metastases of the uveal melanoma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 19202-19214.	1.2	20
17157	Exploring the dark genome: implications for precision medicine. <i>Mammalian Genome</i> , 2019, 30, 192-200.	1.0	40
17158	Bioinformatics approach reveals the critical role of TGF- β 2 signaling pathway in pre-eclampsia development. <i>European Journal of Obstetrics, Gynecology and Reproductive Biology</i> , 2019, 240, 130-138.	0.5	13
17159	Draft genome sequence of cauliflower (<i>Brassica oleracea</i> L. var. botrytis) provides new insights into the C genome in Brassica species. <i>Horticulture Research</i> , 2019, 6, 82.	2.9	53
17160	Genome Sequence Resource for <i>Ilyonectria mors-panacis</i> , Causing Rusty Root Rot of <i>Panax notoginseng</i> . <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1468-1471.	1.4	13
17161	Cross-species functional modules link proteostasis to human normal aging. <i>PLoS Computational Biology</i> , 2019, 15, e1007162.	1.5	11
17162	FGF family members differentially regulate maturation and proliferation of stem cell-derived astrocytes. <i>Scientific Reports</i> , 2019, 9, 9610.	1.6	29
17163	Whole Transcriptome Sequencing Reveals How Acupuncture and Moxibustion Increase Pregnancy Rate in Patients Undergoing In Vitro Fertilization-Embryo Transplantation. <i>BioMed Research International</i> , 2019, 2019, 1-8.	0.9	10

#	ARTICLE	IF	CITATIONS
17164	Qianggan extract improved nonalcoholic steatohepatitis by modulating lncRNA/circRNA immune ceRNA networks. <i>BMC Complementary and Alternative Medicine</i> , 2019, 19, 156.	3.7	20
17165	<i>ProtDCalâ€Suite</i>: A web server for the numerical codification and functional analysis of proteins. <i>Protein Science</i> , 2019, 28, 1734-1743.	3.1	19
17166	Blinded Testing of Function Annotation for uPE1 Proteins by I-TASSER/COFACTOR Pipeline Using the 2018â€2019 Additions to neXtProt and the CAFA3 Challenge. <i>Journal of Proteome Research</i> , 2019, 18, 4154-4166.	1.8	20
17167	Chemical Probes Reveal Sirt2â€™s New Function as a Robust â€œEraserâ€of Lysine Lipoylation. <i>Journal of the American Chemical Society</i> , 2019, 141, 18428-18436.	6.6	37
17168	Dietary tryptophan links encephalogenicity of autoreactive T cells with gut microbial ecology. <i>Nature Communications</i> , 2019, 10, 4877.	5.8	69
17169	Differential expression and co-expression gene network analyses reveal molecular mechanisms and candidate biomarkers involved in breast muscle myopathies in chicken. <i>Scientific Reports</i> , 2019, 9, 14905.	1.6	43
17170	Multi-tissue network analysis for drug prioritization in knee osteoarthritis. <i>Scientific Reports</i> , 2019, 9, 15176.	1.6	13
17171	Proteomic analysis in cells treated with pristine carbon nano-onions and its subcellular localization. <i>Advances in Natural Sciences: Nanoscience and Nanotechnology</i> , 2019, 10, 035011.	0.7	4
17172	gep2pep: a bioconductor package for the creation and analysis of pathway-based expression profiles. <i>Bioinformatics</i> , 2019, , .	1.8	8
17173	Re-programing Chromatin with a Bifunctional LSD1/HDAC Inhibitor Induces Therapeutic Differentiation in DIPG. <i>Cancer Cell</i> , 2019, 36, 528-544.e10.	7.7	128
17174	Combined extracts of <i>Echinacea angustifolia</i> DC. and <i>Zingiber officinale</i> Roscoe in softgel capsules: Pharmacokinetics and immunomodulatory effects assessed by gene expression profiling. <i>Phytomedicine</i> , 2019, 65, 153090.	2.3	12
17175	GENAVi: a shiny web application for gene expression normalization, analysis and visualization. <i>BMC Genomics</i> , 2019, 20, 745.	1.2	40
17176	Search for Nutritional Fitness Traits in a Biological Pest Control Agent <i>Harmonia axyridis</i> Using Comparative Transcriptomics. <i>Frontiers in Physiology</i> , 2019, 10, 1148.	1.3	6
17177	Transcriptome Analysis Reveals Key Seed-Development Genes in Common Buckwheat (<i>Fagopyrum</i>) Tj ETQq1 1 0.784314 rgBI_Overlo	1.8	17
17178	Genomic Landscape and Immune Microenvironment Features of Preinvasive and Early Invasive Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2019, 14, 1912-1923.	0.5	105
17179	A high-quality <i>Actinidia chinensis</i> (kiwifruit) genome. <i>Horticulture Research</i> , 2019, 6, 117.	2.9	109
17180	Global agricultural concept space: lightweight semantics for pragmatic interoperability. <i>Npj Science of Food</i> , 2019, 3, 16.	2.5	6
17181	ModelBricksâ€™ modules for reproducible modeling improving model annotation and provenance. <i>Npj Systems Biology and Applications</i> , 2019, 5, 37.	1.4	13

#	ARTICLE	IF	CITATIONS
17182	Proteomic Analysis of Endothelial Cells Exposed to Ultrasmall Nanoparticles Reveals Disruption in Paracellular and Transcellular Transport. <i>Proteomics</i> , 2019, 19, e1800228.	1.3	4
17183	sRNA OsiA Stabilizes Catalase mRNA during Oxidative Stress Response of <i>Deinococcus radiodurans</i> R1. <i>Microorganisms</i> , 2019, 7, 422.	1.6	19
17184	Polymorphic Immune Mechanisms Regulate Commensal Repertoire. <i>Cell Reports</i> , 2019, 29, 541-550.e4.	2.9	55
17185	Identification of transcriptional isoforms associated with survival in cancer patient. <i>Journal of Genetics and Genomics</i> , 2019, 46, 413-421.	1.7	3
17186	Transcriptome of 17 β -hydroxysteroid dehydrogenase type 2 plays both hormone-dependent and hormone-independent roles in MCF-7 breast cancer cells. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2019, 195, 105471.	1.2	5
17187	DNAProDB: an expanded database and web-based tool for structural analysis of DNA-protein complexes. <i>Nucleic Acids Research</i> , 2019, 48, D277-D287.	6.5	41
17189	Transcriptomic profiling of gamma ray induced mutants from the CGL1 human hybrid cell system reveals novel insights into the mechanisms of radiation-induced carcinogenesis. <i>Free Radical Biology and Medicine</i> , 2019, 145, 300-311.	1.3	7
17190	Binding to medium and long chain fatty acyls is a common property of HEAT and ARM repeat modules. <i>Scientific Reports</i> , 2019, 9, 14226.	1.6	3
17191	Cancer classification of single-cell gene expression data by neural network. <i>Bioinformatics</i> , 2020, 36, 1360-1366.	1.8	39
17192	Concordance between gene expression in peripheral whole blood and colonic tissue in children with inflammatory bowel disease. <i>PLoS ONE</i> , 2019, 14, e0222952.	1.1	28
17193	Essentials of Bioinformatics, Volume II. , 2019, , .		1
17194	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
17195	Computational Methods for Identifying Similar Diseases. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 590-604.	2.3	102
17196	An Ontology-based Approach for Failure Classification in Predictive Maintenance Using Fuzzy C-means and SWRL Rules. <i>Procedia Computer Science</i> , 2019, 159, 630-639.	1.2	33
17197	Myo-REG: A Portal for Signaling Interactions in Muscle Regeneration. <i>Frontiers in Physiology</i> , 2019, 10, 1216.	1.3	8
17198	Rice Genome-Scale Network Integration Reveals Transcriptional Regulators of Grass Cell Wall Synthesis. <i>Frontiers in Plant Science</i> , 2019, 10, 1275.	1.7	14
17199	Zinc binding proteome of a phytopathogen <i>Xanthomonas translucens</i> pv. <i>undulosa</i> . <i>Royal Society Open Science</i> , 2019, 6, 190369.	1.1	10
17200	The Plant Ontology Facilitates Comparisons of Plant Development Stages Across Species. <i>Frontiers in Plant Science</i> , 2019, 10, 631.	1.7	36

#	ARTICLE	IF	CITATIONS
17201	A Bioinformatics Guide to Plant Microbiome Analysis. <i>Frontiers in Plant Science</i> , 2019, 10, 1313.	1.7	54
17203	ZC3H18 specifically binds and activates the BRCA1 promoter to facilitate homologous recombination in ovarian cancer. <i>Nature Communications</i> , 2019, 10, 4632.	5.8	21
17204	Aberrant dysregulated circular RNAs in the peripheral blood mononuclear cells of patients with rheumatoid arthritis revealed by RNA sequencing: novel diagnostic markers for RA. <i>Scandinavian Journal of Clinical and Laboratory Investigation</i> , 2019, 79, 551-559.	0.6	31
17205	S-Adenosylmethionine-Dependent Methyltransferase Helps <i>Pichia caribbica</i> Degrade Patulin. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 11758-11768.	2.4	32
17206	An Overview of Utilizing Knowledge Bases in Neural Networks for Question Answering. , 2019, , .		2
17207	Endocrine and local signaling interact to regulate spermatogenesis in zebrafish: Follicle-stimulating hormone, retinoic acid and androgens. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	13
17208	Investigating the Multi-Target Pharmacological Mechanism of <i>Hedyotis diffusa</i> Willd Acting on Prostate Cancer: A Network Pharmacology Approach. <i>Biomolecules</i> , 2019, 9, 591.	1.8	41
17209	The Long Noncoding RNA Paupar Modulates PAX6 Regulatory Activities to Promote Alpha Cell Development and Function. <i>Cell Metabolism</i> , 2019, 30, 1091-1106.e8.	7.2	45
17210	Loss of methionine sulfoxide reductases increases resistance to oxidative stress. <i>Free Radical Biology and Medicine</i> , 2019, 145, 374-384.	1.3	14
17211	Genetic interaction networks mediate individual statin drug response in <i>Saccharomyces cerevisiae</i> . <i>Npj Systems Biology and Applications</i> , 2019, 5, 35.	1.4	11
17212	Changes of Gene Expression in <i>Euglena gracilis</i> Obtained During the 29th DLR Parabolic Flight Campaign. <i>Scientific Reports</i> , 2019, 9, 14260.	1.6	10
17213	The MTH1 inhibitor TH588 is a microtubule-modulating agent that eliminates cancer cells by activating the mitotic surveillance pathway. <i>Scientific Reports</i> , 2019, 9, 14667.	1.6	19
17214	Transcriptomic analysis of early fruit development in Chinese white pear (<i>Pyrus bretschneideri</i> Rehd.) and functional identification of PbCCR1 in lignin biosynthesis. <i>BMC Plant Biology</i> , 2019, 19, 417.	1.6	33
17215	<i>Drosophila</i> Heterochromatin Stabilization Requires the Zinc-Finger Protein Small Ovary. <i>Genetics</i> , 2019, 213, 877-895.	1.2	15
17216	A Computational Pipeline for the Extraction of Actionable Biological Information From NGS-Phage Display Experiments. <i>Frontiers in Physiology</i> , 2019, 10, 1160.	1.3	6
17217	Differential Expression of Circular RNAs in Polytocous and Monotocous Uterus during the Reproductive Cycle of Sheep. <i>Animals</i> , 2019, 9, 797.	1.0	14
17218	Improved Biclustering Algorithm Based on Cuckoo Search and Firefly Algorithm. <i>Journal of Physics: Conference Series</i> , 2019, 1284, 012040.	0.3	0
17219	NKG2D Controls Natural Reactivity of $\hat{V}^{\beta}9\hat{V}^{\delta}2$ T Lymphocytes against Mesenchymal Glioblastoma Cells. <i>Clinical Cancer Research</i> , 2019, 25, 7218-7228.	3.2	28

#	ARTICLE	IF	CITATIONS
17220	Transcriptional Regulator TonEBP Mediates Oxidative Damages in Ischemic Kidney Injury. <i>Cells</i> , 2019, 8, 1284.	1.8	2
17221	Adult sox10+ Cardiomyocytes Contribute to Myocardial Regeneration in the Zebrafish. <i>Cell Reports</i> , 2019, 29, 1041-1054.e5.	2.9	29
17222	Transcriptome sequencing of hybrid bester sturgeon: Responses to poly (I:C) in the context of comparative immunogenomics. <i>Fish and Shellfish Immunology</i> , 2019, 93, 888-894.	1.6	12
17223	Identification of Key Hydroxymethylated Genes and Transcription Factors Associated with Alpha-Fetoprotein-Negative Hepatocellular Carcinoma. <i>DNA and Cell Biology</i> , 2019, 38, 1346-1356.	0.9	9
17224	Characterization of MRSA in Canada from 2007 to 2016. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, iv55-iv63.	1.3	19
17225	Characterization of the transient fluorescence wave phenomenon that occurs during H ₂ production in <i>Chlamydomonas reinhardtii</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 6321-6336.	2.4	15
17226	WormBase: a modern Model Organism Information Resource. <i>Nucleic Acids Research</i> , 2020, 48, D762-D767.	6.5	213
17227	Bovine Genome Database: new annotation tools for a new reference genome. <i>Nucleic Acids Research</i> , 2019, 48, D676-D681.	6.5	18
17228	Dynamic Modeling and Experimental Validation of Door-Opening Process by a Mobile Manipulator. <i>IEEE Access</i> , 2019, 7, 80916-80927.	2.6	4
17229	The heterotrimeric G protein $\hat{1}^2$ subunit RGB1 is required for seedling formation in rice. <i>Rice</i> , 2019, 12, 53.	1.7	18
17230	A seed-extended algorithm for detecting protein complexes based on density and modularity with topological structure and GO annotations. <i>BMC Genomics</i> , 2019, 20, 637.	1.2	11
17231	Genomic insights into a robust gamma-aminobutyric acid-producer <i>Lactobacillus brevis</i> CD0817. <i>AMB Express</i> , 2019, 9, 72.	1.4	29
17232	De novo Mutations From Whole Exome Sequencing in Neurodevelopmental and Psychiatric Disorders: From Discovery to Application. <i>Frontiers in Genetics</i> , 2019, 10, 258.	1.1	49
17234	Draft genome sequence data of <i>Cercospora kikuchii</i> , a causal agent of <i>Cercospora</i> leaf blight and purple seed stain of soybeans. <i>Data in Brief</i> , 2019, 27, 104693.	0.5	11
17235	Ionizing radiation induces endothelial transdifferentiation of glioblastoma stem-like cells through the Tie2 signaling pathway. <i>Cell Death and Disease</i> , 2019, 10, 816.	2.7	34
17236	Complete Genome of the Chitin-Degrading Bacterium, <i>Paenibacillus xylanilyticus</i> W4. <i>Genome Biology and Evolution</i> , 2019, 11, 3252-3255.	1.1	10
17237	Weighted single-step GWAS identified candidate genes associated with semen traits in a Duroc boar population. <i>BMC Genomics</i> , 2019, 20, 797.	1.2	27
17238	Rewiring of Cancer Cell Metabolism by Mitochondrial VDAC1 Depletion Results in Time-Dependent Tumor Reprogramming: Glioblastoma as a Proof of Concept. <i>Cells</i> , 2019, 8, 1330.	1.8	18

#	ARTICLE	IF	CITATIONS
17239	Bioinformatics for Marine Products: An Overview of Resources, Bottlenecks, and Perspectives. <i>Marine Drugs</i> , 2019, 17, 576.	2.2	26
17240	Antioxidant system of soiny mullet (<i>Liza haematocheila</i>) is responsive to dietary poly- $\hat{1}^2$ -hydroxybutyrate (PHB) supplementation based on immune-related enzyme activity and de novo transcriptome analysis. <i>Fish and Shellfish Immunology</i> , 2019, 95, 314-327.	1.6	15
17241	MiR-146a is over-expressed and controls IL-6 production in cystic fibrosis macrophages. <i>Scientific Reports</i> , 2019, 9, 16259.	1.6	33
17242	Genomic interrogation of familial short stature contributes to the discovery of the pathophysiological mechanisms and pharmaceutical drug repositioning. <i>Journal of Biomedical Science</i> , 2019, 26, 91.	2.6	2
17243	Mutation of the PTCH1 gene predicts recurrence of breast cancer. <i>Scientific Reports</i> , 2019, 9, 16359.	1.6	34
17244	The <i>Rhododendron</i> Genome and Chromosomal Organization Provide Insight into Shared Whole-Genome Duplications across the Heath Family (Ericaceae). <i>Genome Biology and Evolution</i> , 2019, 11, 3353-3371.	1.1	47
17245	Network Pharmacology and Reverse Molecular Docking-Based Prediction of the Molecular Targets and Pathways for Avicularin Against Cancer. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2019, 22, 4-12.	0.6	8
17246	Distinct gene expression characteristics in epithelial cell- <i><i>Porphyromonas gingivalis</i></i> interactions by integrating transcriptome analyses. <i>International Journal of Medical Sciences</i> , 2019, 16, 1320-1327.	1.1	6
17247	A Systems-Based Map of Human Brain Cell-Type Enriched Genes and Malignancy-Associated Endothelial Changes. <i>Cell Reports</i> , 2019, 29, 1690-1706.e4.	2.9	22
17248	DiNGO: standalone application for Gene Ontology and Human Phenotype Ontology term enrichment analysis. <i>Bioinformatics</i> , 2020, 36, 1981-1982.	1.8	2
17249	MGnify: the microbiome analysis resource in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D570-D578.	6.5	296
17250	Cisplatin-resistant triple-negative breast cancer subtypes: multiple mechanisms of resistance. <i>BMC Cancer</i> , 2019, 19, 1039.	1.1	77
17251	Alzheimer's Disease Progression in the 5 \hat{A} -FAD Mouse Captured with a Multiplex Gene Expression Array. <i>Journal of Alzheimer's Disease</i> , 2019, 72, 1177-1191.	1.2	7
17252	Phenotype Prediction and Genome-Wide Association Study Using Deep Convolutional Neural Network of Soybean. <i>Frontiers in Genetics</i> , 2019, 10, 1091.	1.1	78
17253	Deconvolution of the Genomic and Epigenomic Interaction Landscape of Triple-Negative Breast Cancer. <i>Cancers</i> , 2019, 11, 1692.	1.7	8
17254	Excluding Oct4 from Yamanaka Cocktail Unleashes the Developmental Potential of iPSCs. <i>Cell Stem Cell</i> , 2019, 25, 737-753.e4.	5.2	92
17255	SIGNOR 2.0, the SIGnaling Network Open Resource 2.0: 2019 update. <i>Nucleic Acids Research</i> , 2020, 48, D504-D510.	6.5	160
17256	Phenome-wide association study of TTR and RBP4 genes in 361,194 individuals reveals novel insights in the genetics of hereditary and wildtype transthyretin amyloidoses. <i>Human Genetics</i> , 2019, 138, 1331-1340.	1.8	14

#	ARTICLE	IF	CITATIONS
17257	Complete Genome Sequence of <i>Azoarcus</i> sp. Strain DD4, a Gram-Negative Propanotroph That Degrades 1,4-Dioxane and 1,1-Dichloroethylene. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7
17258	Systematic Discovery of Endogenous Human Ribonucleoprotein Complexes. <i>Cell Reports</i> , 2019, 29, 1351-1368.e5.	2.9	53
17259	Downregulation of GRK5 hampers the migration of breast cancer cells. <i>Scientific Reports</i> , 2019, 9, 15548.	1.6	13
17260	GenCLiP 3: mining human genes' functions and regulatory networks from PubMed based on co-occurrences and natural language processing. <i>Bioinformatics</i> , 2020, 36, 1973-1975.	1.8	60
17261	RACS: rapid analysis of ChIP-Seq data for contig based genomes. <i>BMC Bioinformatics</i> , 2019, 20, 533.	1.2	4
17262	Microevolution within ST11 group <i>Clostridioides difficile</i> isolates through mobile genetic elements based on complete genome sequencing. <i>BMC Genomics</i> , 2019, 20, 796.	1.2	5
17263	Multi-breed genome-wide association studies across countries for electronically recorded behavior traits in local dual-purpose cows. <i>PLoS ONE</i> , 2019, 14, e0221973.	1.1	6
17264	Omics Approaches to Understanding Muscle Biology. , 2019, , .		3
17265	Hepatic gene expression variations in response to high-fat diet-induced impaired glucose tolerance using RNAseq analysis in collaborative cross mouse population. <i>Mammalian Genome</i> , 2019, 30, 260-275.	1.0	13
17266	The Empusa code generator and its application to GBOL, an extendable ontology for genome annotation. <i>Scientific Data</i> , 2019, 6, 254.	2.4	13
17267	A specific fungal transcription factor controls effector gene expression and orchestrates the establishment of the necrotrophic pathogen lifestyle on wheat. <i>Scientific Reports</i> , 2019, 9, 15884.	1.6	34
17268	Oncogenes, tumor suppressor and differentiation genes represent the oldest human gene classes and evolve concurrently. <i>Scientific Reports</i> , 2019, 9, 16410.	1.6	17
17269	Trophectoderm regeneration to support full-term development in the inner cell mass isolated from bovine blastocyst. <i>Journal of Biological Chemistry</i> , 2019, 294, 19209-19223.	1.6	20
17270	SCNBase: a genomics portal for the soybean cyst nematode (<i>Heterodera glycines</i>). <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	9
17271	The IUPHAR/BPS Guide to PHARMACOLOGY in 2020: extending immunopharmacology content and introducing the IUPHAR/MMV Guide to MALARIA PHARMACOLOGY. <i>Nucleic Acids Research</i> , 2020, 48, D1006-D1021.	6.5	131
17272	Integrated transcriptomic analysis reveals hub genes involved in diagnosis and prognosis of pancreatic cancer. <i>Molecular Medicine</i> , 2019, 25, 47.	1.9	34
17273	In-silico prediction of microRNA targets and finding genes suggesting significant involvement in the development of <i>Glycine max</i> seed. <i>Vegetos</i> , 2019, 32, 450-463.	0.8	0
17274	Transcriptome sequencing of <i>Salvia miltiorrhiza</i> after infection by its endophytic fungi and identification of genes related to tanshinone biosynthesis. <i>Pharmaceutical Biology</i> , 2019, 57, 760-769.	1.3	25

#	ARTICLE	IF	CITATIONS
17275	The Year of the Rat: The Rat Genome Database at 20: a multi-species knowledgebase and analysis platform. <i>Nucleic Acids Research</i> , 2020, 48, D731-D742.	6.5	92
17276	Genetic and metabolic signatures of <i>Salmonella enterica</i> subsp. <i>enterica</i> associated with animal sources at the pangenomic scale. <i>BMC Genomics</i> , 2019, 20, 814.	1.2	29
17277	Lignin degradation potential and draft genome sequence of <i>Trametes trogii</i> S0301. <i>Biotechnology for Biofuels</i> , 2019, 12, 256.	6.2	16
17278	NLRP2 Regulates Proinflammatory and Antiapoptotic Responses in Proximal Tubular Epithelial Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 252.	1.8	31
17279	Bi-allelic Mutations in TTC29 Cause Male Subfertility with Asthenoteratospermia in Humans and Mice. <i>American Journal of Human Genetics</i> , 2019, 105, 1168-1181.	2.6	62
17280	Transcriptomic and metabolomic profiling provide novel insights into fruit development and flesh coloration in <i>Prunus mira</i> Koehne, a special wild peach species. <i>BMC Plant Biology</i> , 2019, 19, 463.	1.6	45
17281	Novel comparison of evaluation metrics for gene ontology classifiers reveals drastic performance differences. <i>PLoS Computational Biology</i> , 2019, 15, e1007419.	1.5	12
17282	Expression of Protein-Coding Gene Orthologs in Zebrafish and Mouse Inner Ear Non-sensory Supporting Cells. <i>Frontiers in Neuroscience</i> , 2019, 13, 1117.	1.4	12
17283	Transcriptome analysis of MAPK signaling pathway and associated genes to angiogenesis in chicken erythrocytes on response to thiram-induced tibial lesions. <i>Research in Veterinary Science</i> , 2019, 127, 65-75.	0.9	14
17284	Physiological and transcriptome analyses of photosynthesis and chlorophyll metabolism in variegated Citrus (<i>Shiranihi</i> and <i>Huangguogan</i>) seedlings. <i>Scientific Reports</i> , 2019, 9, 15670.	1.6	13
17285	Analysis of <i>Arabidopsis thaliana</i> Redox Gene Network Indicates Evolutionary Expansion of Class III Peroxidase in Plants. <i>Scientific Reports</i> , 2019, 9, 15741.	1.6	17
17286	Tissue-specific expression profiles and positive selection analysis in the tree swallow (<i>Tachycineta thalassina</i>) Tj ETQq1 1 0.784314 rgBT/Overload	1.6	39
17287	Mabellini: a genome-wide database for understanding the structural proteome and evaluating prospective antimicrobial targets of the emerging pathogen <i>Mycobacterium abscessus</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	12
17288	Differential regulatory network-based quantification and prioritization of key genes underlying cancer drug resistance based on time-course RNA-seq data. <i>PLoS Computational Biology</i> , 2019, 15, e1007435.	1.5	19
17289	A Combined Mass Spectrometry and Data Integration Approach to Predict the Mitochondrial Poly(A) RNA Interacting Proteome. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 283.	1.8	2
17290	Transcriptomic Analysis of mRNA-lncRNA-miRNA Interactions in Hepatocellular Carcinoma. <i>Scientific Reports</i> , 2019, 9, 16096.	1.6	58
17291	Identification of Hepatocellular Carcinoma-Related Potential Genes and Pathways Through Bioinformatic-Based Analyses. <i>Genetic Testing and Molecular Biomarkers</i> , 2019, 23, 766-777.	0.3	19
17292	Predicting Drug-Target Interactions With Multi-Label Classification and Label Partitioning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1596-1607.	1.9	34

#	ARTICLE	IF	CITATIONS
17293	Synthesis, Antiviral Activity, and Induction of Plant Resistance of Indole Analogues Bearing Dithioacetal Moiety. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 13882-13891.	2.4	53
17294	Visualizing Scientists's™ Cognitive Representation of Materials Data through the Application of Ontology. <i>Journal of Physical Chemistry Letters</i> , 2019, 10, 7482-7491.	2.1	16
17295	Exploring the Molecular Mechanism underlying the Stable Purple-Red Leaf Phenotype in <i>Lagerstroemia indica</i> cv. Ebony Embers. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5636.	1.8	23
17296	The neXtProt knowledgebase in 2020: data, tools and usability improvements. <i>Nucleic Acids Research</i> , 2020, 48, D328-D334.	6.5	121
17297	Elevated serum alpha-1 antitrypsin is a major component of GlycA-associated risk for future morbidity and mortality. <i>PLoS ONE</i> , 2019, 14, e0223692.	1.1	14
17298	Induction of human hemogenesis in adult fibroblasts by defined factors and hematopoietic coculture. <i>FEBS Letters</i> , 2019, 593, 3266-3287.	1.3	8
17299	Computational identification of vesicular transport proteins from sequences using deep gated recurrent units architecture. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1245-1254.	1.9	49
17300	Potential therapeutic drugs for ischemic stroke and stress disorder: A bioinformatics analysis. <i>Informatics in Medicine Unlocked</i> , 2019, 17, 100259.	1.9	4
17301	Proteomic profiling of cotton fiber developmental transition from cell elongation to secondary wall deposition. <i>Acta Biochimica Et Biophysica Sinica</i> , 2019, 51, 1168-1177.	0.9	10
17302	Intraocular VEGF deprivation induces degeneration and fibrogenic response in retina. <i>FASEB Journal</i> , 2019, 33, 13920-13934.	0.2	5
17303	Identification of key genes and pathways associated with different immune statuses of hepatitis B virus infection. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 7474-7489.	1.6	7
17304	Isolation of Cardiomyocytes Undergoing Mitosis With Complete Cytokinesis. <i>Circulation Research</i> , 2019, 125, 1070-1086.	2.0	14
17305	Comprehensive anatomic ontologies for lung development: A comparison of alveolar formation and maturation within mouse and human lung. <i>Journal of Biomedical Semantics</i> , 2019, 10, 18.	0.9	45
17306	Promising Prognosis Marker Candidates on the Status of Epithelial's Mesenchymal Transition and Glioma Stem Cells in Glioblastoma. <i>Cells</i> , 2019, 8, 1312.	1.8	23
17307	A deep learning ensemble for function prediction of hypothetical proteins from pathogenic bacterial species. <i>Computational Biology and Chemistry</i> , 2019, 83, 107147.	1.1	15
17308	Genetic Contributions to Health Literacy. <i>Twin Research and Human Genetics</i> , 2019, 22, 131-139.	0.3	0
17309	The whole-genome sequence analysis of <i>Morchella sextelata</i> . <i>Scientific Reports</i> , 2019, 9, 15376.	1.6	18
17310	The English People at War in the Age of Henry VIII, by Steven Gunn. <i>English Historical Review</i> , 2019, , .	0.0	0

#	ARTICLE	IF	CITATIONS
17311	Voluntary exercise normalizes the proteomic landscape in muscle and brain and improves the phenotype of progeroid mice. <i>Aging Cell</i> , 2019, 18, e13029.	3.0	25
17312	Genomic Analyses Provide Insights Into the Evolutionary History and Genetic Diversity of <i>Auricularia</i> Species. <i>Frontiers in Microbiology</i> , 2019, 10, 2255.	1.5	12
17313	Massive computational identification of somatic variants in exonic splicing enhancers using The Cancer Genome Atlas. <i>Cancer Medicine</i> , 2019, 8, 7372-7384.	1.3	1
17314	Screening and Identification of Potential Prognostic Biomarkers in Adrenocortical Carcinoma. <i>Frontiers in Genetics</i> , 2019, 10, 821.	1.1	28
17315	Genome-Wide Mining and Identification of Protein Kinase Gene Family Impacts Salinity Stress Tolerance in Highly Dense Genetic Map Developed from Interspecific Cross between <i>G. hirsutum</i> L. and <i>G. darwinii</i> G. Watt. <i>Agronomy</i> , 2019, 9, 560.	1.3	21
17316	Breaking the paradigm: Dr Insight empowers signature-free, enhanced drug repurposing. <i>Bioinformatics</i> , 2019, 35, 2818-2826.	1.8	36
17317	Biological process activity transformation of single cell gene expression for cross-species alignment. <i>Nature Communications</i> , 2019, 10, 4899.	5.8	29
17318	The U1 spliceosomal RNA is recurrently mutated in multiple cancers. <i>Nature</i> , 2019, 574, 712-716.	13.7	128
17319	Induction of metabolic quiescence defines the transitional to follicular B cell switch. <i>Science Signaling</i> , 2019, 12, .	1.6	35
17320	Clinical and Genetic Analysis of Children with Kartagener Syndrome. <i>Cells</i> , 2019, 8, 900.	1.8	26
17321	DeepCOP: deep learning-based approach to predict gene regulating effects of small molecules. <i>Bioinformatics</i> , 2020, 36, 813-818.	1.8	21
17322	Towards a Knowledge Base of Financial Relations: Overview and Project Description. , 2019, , .		0
17323	Multi-study reanalysis of 2,213 acute myeloid leukemia patients reveals age- and sex-dependent gene expression signatures. <i>Scientific Reports</i> , 2019, 9, 12413.	1.6	11
17324	Genome-Wide SNPs and InDels Characteristics of Three Chinese Cattle Breeds. <i>Animals</i> , 2019, 9, 596.	1.0	11
17325	Differential Proteomics Based on TMT and PRM Reveal the Resistance Response of <i>Bambusa pervariabilis</i> – <i>Dendrocalamopsis grandis</i> Induced by AP-Toxin. <i>Metabolites</i> , 2019, 9, 166.	1.3	8
17326	Transcriptome analysis of <i>Medicago lupulina</i> seedlings leaves treated by high calcium provides insights into calcium oxalate formation. <i>Plant and Soil</i> , 2019, 444, 299-314.	1.8	13
17327	Dynamics of Non-Canonical Amino Acid-Labeled Intra- and Extracellular Proteins in the Developing Mouse. <i>Cellular and Molecular Bioengineering</i> , 2019, 12, 495-509.	1.0	23
17328	<i>Bartonella massiliensis</i> sp. nov., a new bacterial species isolated from an <i>Ornithodoros sonrai</i> tick from Senegal. <i>New Microbes and New Infections</i> , 2019, 32, 100596.	0.8	10

#	ARTICLE	IF	CITATIONS
17329	Comparative transcription analysis of photosensitive and non-photosensitive eggplants to identify genes involved in dark regulated anthocyanin synthesis. <i>BMC Genomics</i> , 2019, 20, 678.	1.2	27
17330	Raptor genomes reveal evolutionary signatures of predatory and nocturnal lifestyles. <i>Genome Biology</i> , 2019, 20, 181.	3.8	11
17331	Current best practices in single-cell RNA-seq analysis: a tutorial. <i>Molecular Systems Biology</i> , 2019, 15, e8746.	3.2	1,322
17332	Structural Basis of the Subcellular Topology Landscape of <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1670.	1.5	25
17333	A high-quality genome assembly for the endangered golden snub-nosed monkey (<i>Rhinopithecus</i>) Tj ETQq0 0 0 rgBT/Overlock, 10 Tf 50 5	3.3	22
17334	RITAN: rapid integration of term annotation and network resources. <i>PeerJ</i> , 2019, 7, e6994.	0.9	17
17335	Customizing Functionalized Cofactor Mimics to Study the Human Pyridoxal 5â€²-Phosphate-Binding Proteome. <i>Cell Chemical Biology</i> , 2019, 26, 1461-1468.e7.	2.5	13
17336	Cross comparison and prognostic assessment of breast cancer multigene signatures in a large population-based contemporary clinical series. <i>Scientific Reports</i> , 2019, 9, 12184.	1.6	39
17337	The spatial distribution of extreme precipitation in Tibet based on Pareto. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 252, 042071.	0.2	0
17338	Analysis of Protein Synthesis in Cucumber Leaves after Inoculation with <i>Corynespora cassicola</i> : A Proteomic Approach. <i>Biochemistry (Moscow)</i> , 2019, 84, 963-977.	0.7	1
17339	Functional and transcriptional connectivity of communities in breast cancer co-expression networks. <i>Applied Network Science</i> , 2019, 4, .	0.8	29
17340	Regulation of Co-transcriptional Pre-mRNA Splicing by m6A through the Low-Complexity Protein hnRNPG. <i>Molecular Cell</i> , 2019, 76, 70-81.e9.	4.5	248
17341	In silico evidence of de novo interactions between ribosomal and Epstein - Barr virus proteins. <i>BMC Molecular and Cell Biology</i> , 2019, 20, 34.	1.0	3
17342	Identifying and exploiting gene-pathway interactions from RNA-seq data for binary phenotype. <i>BMC Genetics</i> , 2019, 20, 36.	2.7	2
17343	Transcriptional effects of ¹⁷⁷ Lu-octreotate therapy using a priming treatment schedule on GOT1 tumor in nude mice. <i>EJNMMI Research</i> , 2019, 9, 28.	1.1	3
17344	ComplexBrowser: A Tool for Identification and Quantification of Protein Complexes in Large-scale Proteomics Datasets. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2324-2334.	2.5	14
17345	Utilization of Bio-Ontologies for Enhancing Patent Information Retrieval. , 2019, , .		1
17346	Gene co-expression network analysis reveals pathways associated with graft healing by asymmetric profiling in tomato. <i>BMC Plant Biology</i> , 2019, 19, 373.	1.6	43

#	ARTICLE	IF	CITATIONS
17347	Pituitary cell translation and secretory capacities are enhanced cell autonomously by the transcription factor Creb3l2. <i>Nature Communications</i> , 2019, 10, 3960.	5.8	30
17348	Comparative analysis demonstrates cell type-specific conservation of SOX9 targets between mouse and chicken. <i>Scientific Reports</i> , 2019, 9, 12560.	1.6	22
17349	Comparative Analysis of MicroRNA and mRNA Profiles of Sperm with Different Freeze Tolerance Capacities in Boar (<i>Sus scrofa</i>) and Giant Panda (<i>Ailuropoda melanoleuca</i>). <i>Biomolecules</i> , 2019, 9, 432.	1.8	18
17350	The Role of Extracellular Matrix Expression, ERK1/2 Signaling and Cell Cohesiveness for Cartilage Yield from iPSCs. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4295.	1.8	19
17351	Amyloid-like Assembly Activates a Phosphatase in the Developing <i>Drosophila</i> Embryo. <i>Cell</i> , 2019, 178, 1403-1420.e21.	13.5	9
17352	Dual RNA-seq uncovers the immune response of <i>Larimichthys crocea</i> to the <i>secY</i> gene of <i>Pseudomonas plecoglossicida</i> from the perspective of host-pathogen interactions. <i>Fish and Shellfish Immunology</i> , 2019, 93, 949-957.	1.6	19
17353	Gene set enrichment analysis to create polygenic scores: a developmental examination of aggression. <i>Translational Psychiatry</i> , 2019, 9, 212.	2.4	16
17354	Signaling pathways and gene co-expression modules associated with cytoskeleton and axon morphology in breast cancer survivors with chronic paclitaxel-induced peripheral neuropathy. <i>Molecular Pain</i> , 2019, 15, 174480691987808.	1.0	10
17355	Network-guided analysis of hippocampal proteome identifies novel proteins that colocalize with A β 2 in a mice model of early-stage Alzheimer's disease. <i>Neurobiology of Disease</i> , 2019, 132, 104603.	2.1	13
17356	Region-specific gene expression in the epididymis of Yak. <i>Theriogenology</i> , 2019, 139, 132-146.	0.9	23
17357	SamPler " a novel method for selecting parameters for gene functional annotation routines. <i>BMC Bioinformatics</i> , 2019, 20, 454.	1.2	5
17358	Systems Pharmacological Approach to Investigate the Mechanism of <i>Hericium erinaceus</i> for Alzheimer's Disease. <i>Digital Chinese Medicine</i> , 2019, 2, 7-18.	0.5	3
17359	RNA-seq analysis of local tissue of <i>Carassius auratus gibelio</i> with pharyngeal myxobolosis: Insights into the pharyngeal mucosal immune response in a fish-parasite dialogue. <i>Fish and Shellfish Immunology</i> , 2019, 94, 99-112.	1.6	22
17360	Auxin-sensitive Aux/IAA proteins mediate drought tolerance in <i>Arabidopsis</i> by regulating glucosinolate levels. <i>Nature Communications</i> , 2019, 10, 4021.	5.8	155
17361	Characterization of an Environmental Multidrug-Resistant <i>Acinetobacter seifertii</i> and Comparative Genomic Analysis Reveals Co-occurrence of Antimicrobial Resistance and Metal Tolerance Determinants. <i>Frontiers in Microbiology</i> , 2019, 10, 2151.	1.5	16
17362	A pooled single-cell genetic screen identifies regulatory checkpoints in the continuum of the epithelial-to-mesenchymal transition. <i>Nature Genetics</i> , 2019, 51, 1389-1398.	9.4	150
17363	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
17364	DeepFunNet: Deep Learning for Gene Functional Similarity Network Construction. , 2019, , ,		0

#	ARTICLE	IF	CITATIONS
17365	Draft Genome Sequence of a <i>Chryseobacterium indologenes</i> Strain Isolated from a Blood Culture of a Hospitalized Child in Antananarivo, Madagascar. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
17366	<i>P4HB</i> , a Novel Hypoxia Target Gene Related to Gastric Cancer Invasion and Metastasis. <i>BioMed Research International</i> , 2019, 2019, 1-13.	0.9	35
17367	Integration analysis for novel lncRNA markers predicting tumor recurrence in human colon adenocarcinoma. <i>Journal of Translational Medicine</i> , 2019, 17, 299.	1.8	18
17368	Identification of modules and functional analysis in CRC subtypes by integrated bioinformatics analysis. <i>PLoS ONE</i> , 2019, 14, e0221772.	1.1	6
17369	Chemosensory Characteristics of Two <i>Semanotus bifasciatus</i> Populations. <i>Forests</i> , 2019, 10, 655.	0.9	4
17370	The Reason for Growth Inhibition of <i>Ulmus pumila</i> "Jinye": Lower Resistance and Abnormal Development of Chloroplasts Slow Down the Accumulation of Energy. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4227.	1.8	12
17371	The regulatory role of microRNA-mRNA co-expression in hepatitis B virus-associated acute liver failure. <i>Annals of Hepatology</i> , 2019, 18, 883-892.	0.6	6
17372	A Structure-Informed Atlas of Human-Virus Interactions. <i>Cell</i> , 2019, 178, 1526-1541.e16.	13.5	108
17373	Genetic variants in Forkhead box O1 associated with predisposition to sepsis in a Chinese Han population. <i>BMC Infectious Diseases</i> , 2019, 19, 781.	1.3	2
17374	H3K4me3, H3K9ac, H3K27ac, H3K27me3 and H3K9me3 Histone Tags Suggest Distinct Regulatory Evolution of Open and Condensed Chromatin Landmarks. <i>Cells</i> , 2019, 8, 1034.	1.8	64
17375	Identification and Classification of Differentially Expressed Genes and Network Meta-Analysis Reveals Potential Molecular Signatures Associated With Tuberculosis. <i>Frontiers in Genetics</i> , 2019, 10, 932.	1.1	26
17376	Protein Complex Identification and quantitative complexome by CN-PAGE. <i>Scientific Reports</i> , 2019, 9, 11523.	1.6	24
17377	Link clustering explains non-central and contextually essential genes in protein interaction networks. <i>Scientific Reports</i> , 2019, 9, 11672.	1.6	2
17378	The Functional 3D Organization of Unicellular Genomes. <i>Scientific Reports</i> , 2019, 9, 12734.	1.6	0
17379	Novel computational model of gastrula morphogenesis to identify spatial discriminator genes by self-organizing map (SOM) clustering. <i>Scientific Reports</i> , 2019, 9, 12597.	1.6	10
17380	Metamorphic Testing for Quality Assurance of Protein Function Prediction Tools. , 2019, , .		4
17381	Towards a Pancreatic Lesions Disease Classification System based on Ontologies. , 2019, , .		1
17382	Differential Regulation of Anthocyanins in Green and Purple Turnips Revealed by Combined De Novo Transcriptome and Metabolome Analysis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4387.	1.8	66

#	ARTICLE	IF	CITATIONS
17383	Migratory Neural Crest Cells Phagocytose Dead Cells in the Developing Nervous System. <i>Cell</i> , 2019, 179, 74-89.e10.	13.5	31
17384	Microbial Metabolism Modulates Antibiotic Susceptibility within the Murine Gut Microbiome. <i>Cell Metabolism</i> , 2019, 30, 800-823.e7.	7.2	70
17385	Mass spectrometry-based proteome profile may be useful to differentiate adenoid cystic carcinoma from polymorphous adenocarcinoma of salivary glands. <i>Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology</i> , 2019, 128, 639-650.	0.2	3
17386	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
17387	A human endogenous retrovirus encoded protease potentially cleaves numerous cellular proteins. <i>Mobile DNA</i> , 2019, 10, 36.	1.3	9
17388	Additive and heterozygous (dis)advantage GWAS models reveal candidate genes involved in the genotypic variation of maize hybrids to <i>Azospirillum brasilense</i> . <i>PLoS ONE</i> , 2019, 14, e0222788.	1.1	19
17389	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. <i>Nature Communications</i> , 2019, 10, 4267.	5.8	139
17390	cellHarmony: cell-level matching and holistic comparison of single-cell transcriptomes. <i>Nucleic Acids Research</i> , 2019, 47, e138-e138.	6.5	57
17391	Photoreceptor Activity Contributes to Contrasting Responses to Shade in Cardamine and Arabidopsis Seedlings. <i>Plant Cell</i> , 2019, 31, tpc.00275.2019.	3.1	23
17392	Synergistic Cytotoxicity of Renieramycin M and Doxorubicin in MCF-7 Breast Cancer Cells. <i>Marine Drugs</i> , 2019, 17, 536.	2.2	29
17393	High-coverage genomes to elucidate the evolution of penguins. <i>GigaScience</i> , 2019, 8, .	3.3	18
17394	Identifying Protein Complexes from Dynamic Temporal Interval Protein-Protein Interaction Networks. <i>BioMed Research International</i> , 2019, 2019, 1-17.	0.9	3
17395	Chlamydia pan-genomic analysis reveals balance between host adaptation and selective pressure to genome reduction. <i>BMC Genomics</i> , 2019, 20, 710.	1.2	20
17396	Discovery of leaf region and time point related modules and genes in maize (<i>Zea mays</i> L.) leaves by Weighted Gene Co-expression Network analysis (WGCNA) of gene expression profiles of carbon metabolism. <i>Journal of Integrative Agriculture</i> , 2019, 18, 350-360.	1.7	10
17397	<i>Chlorella vulgaris</i> supplementation effects on performances, oxidative stress and antioxidant genes expression in liver and ovaries of New Zealand White rabbits. <i>Heliyon</i> , 2019, 5, e02470.	1.4	27
17398	Exact hypothesis testing for shrinkage-based Gaussian graphical models. <i>Bioinformatics</i> , 2019, 35, 5011-5017.	1.8	8
17399	Mechanical Forces Regulate Cardiomyocyte Myofilament Maturation via the VCL-SSH1-CFL Axis. <i>Developmental Cell</i> , 2019, 51, 62-77.e5.	3.1	35
17400	Chronic Inflammation Directs an Olfactory Stem Cell Functional Switch from Neuroregeneration to Immune Defense. <i>Cell Stem Cell</i> , 2019, 25, 501-513.e5.	5.2	114

#	ARTICLE	IF	CITATIONS
17401	Effect of hyperoside on cervical cancer cells and transcriptome analysis of differentially expressed genes. <i>Cancer Cell International</i> , 2019, 19, 235.	1.8	24
17402	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
17403	Proteomics-Based Monitoring of Pathway Activity Reveals that Blocking Diacylglycerol Biosynthesis Rescues from Alpha-Synuclein Toxicity. <i>Cell Systems</i> , 2019, 9, 309-320.e8.	2.9	12
17404	Transcriptome analysis and the effects of polyunsaturated fatty acids on the immune responses of the critically endangered angtze sturgeon (<i>Acipenser dabryanus</i>). <i>Fish and Shellfish Immunology</i> , 2019, 94, 199-210.	1.6	13
17405	BINDER: computationally inferring a gene regulatory network for <i>Mycobacterium abscessus</i> . <i>BMC Bioinformatics</i> , 2019, 20, 466.	1.2	10
17406	Dissecting the genetic architecture of seed-cotton and lint yields in Upland cotton using genome-wide association mapping. <i>Breeding Science</i> , 2019, 69, 611-620.	0.9	2
17407	Proteogenomic Network Analysis of Context-Specific KRAS Signaling in Mouse-to-Human Cross-Species Translation. <i>Cell Systems</i> , 2019, 9, 258-270.e6.	2.9	44
17408	Identifying protein complexes based on an edge weight algorithm and core-attachment structure. <i>BMC Bioinformatics</i> , 2019, 20, 471.	1.2	21
17409	Integrative genomics analysis of hub genes and their relationship with prognosis and signaling pathways in esophageal squamous cell carcinoma. <i>Molecular Medicine Reports</i> , 2019, 20, 3649-3660.	1.1	21
17410	Worming into the Uncharacterized Human Proteome. <i>Journal of Proteome Research</i> , 2019, 18, 4143-4153.	1.8	7
17411	Pathway Analysis Integrating Genome-Wide and Functional Data Identifies <i>PLCG2</i> as a Candidate Gene for Age-Related Macular Degeneration. , 2019, 60, 4041.		10
17412	Metric learning on expression data for gene function prediction. <i>Bioinformatics</i> , 2020, 36, 1182-1190.	1.8	17
17413	Cross-Species Protein Function Prediction with Asynchronous-Random Walk. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1439-1450.	1.9	8
17414	Genomic Evidence for Local Adaptation of Hunter-Gatherers to the African Rainforest. <i>Current Biology</i> , 2019, 29, 2926-2935.e4.	1.8	40
17415	Identification of responsive miRNAs involved in combination stresses of phosphate starvation and salt stress in soybean root. <i>Environmental and Experimental Botany</i> , 2019, 167, 103823.	2.0	42
17416	Dynamic changes in epithelial cell morphology control thymic organ size during atrophy and regeneration. <i>Nature Communications</i> , 2019, 10, 4402.	5.8	46
17417	The in vivo transcriptome of <i>Schistosoma mansoni</i> in the prominent vector species <i>Biomphalaria pfeifferi</i> with supporting observations from <i>Biomphalaria glabrata</i> . <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007013.	1.3	12
17418	Predicting Phenotypic Diversity from Molecular and Genetic Data. <i>Genetics</i> , 2019, 213, 297-311.	1.2	3

#	ARTICLE	IF	CITATIONS
17419	IFN-Lambda 3 Mediates Antiviral Protection Against Porcine Epidemic Diarrhea Virus by Inducing a Distinct Antiviral Transcript Profile in Porcine Intestinal Epithelia. <i>Frontiers in Immunology</i> , 2019, 10, 2394.	2.2	37
17420	CircRNA Expression Pattern and ceRNA and miRNA-mRNA Networks Involved in Anther Development in the CMS Line of <i>Brassica campestris</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 4808.	1.8	34
17421	Screening and identification of biomarkers for systemic sclerosis via microarray technology. <i>International Journal of Molecular Medicine</i> , 2019, 44, 1753-1770.	1.8	11
17422	Draft genome sequence of <i>Solanum aethiopicum</i> provides insights into disease resistance, drought tolerance, and the evolution of the genome. <i>GigaScience</i> , 2019, 8, .	3.3	38
17423	Molecular Characterization of the Transcription Factors in Susceptible Poplar Infected with Virulent <i>Melampsora larici-populina</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 4806.	1.8	5
17424	Integrated bioinformatics analysis reveals role of the LINC01093/miR-96-5p/ZFAND5/NF- κ B signaling axis in hepatocellular carcinoma. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 3853-3860.	0.8	10
17425	Pro-angiogenesis effect and transcriptome profile of Shuxinyin formula in zebrafish. <i>Phytomedicine</i> , 2019, 65, 153083.	2.3	8
17426	Characterization of the Long Terminal Repeat of the Endogenous Retrovirus-derived microRNAs in the Olive Flounder. <i>Scientific Reports</i> , 2019, 9, 14007.	1.6	11
17427	Integrated Analysis of Multiple Microarray Studies to Identify Novel Gene Signatures in Non-alcoholic Fatty Liver Disease. <i>Frontiers in Endocrinology</i> , 2019, 10, 599.	1.5	46
17428	Genome-wide analysis of methylation in giant pandas with cataract by methylation-dependent restriction-site associated DNA sequencing (MethylRAD). <i>PLoS ONE</i> , 2019, 14, e0222292.	1.1	9
17429	Proteomic analysis of soluble proteins retrieved from <i>Duttaphrynus melanostictus</i> skin secretion by IEX-batch sample preparation. <i>Journal of Proteomics</i> , 2019, 209, 103525.	1.2	5
17430	Protective Role of Leaf Variegation in <i>Pittosporum tobira</i> under Low Temperature: Insights into the Physio-Biochemical and Molecular Mechanisms. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4857.	1.8	4
17431	Identification of potential key genes in esophageal adenocarcinoma using bioinformatics. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 3291-3298.	0.8	10
17432	S-allyl-cysteine sulfoxide (alliin) alleviates myocardial infarction by modulating cardiomyocyte necroptosis and autophagy. <i>International Journal of Molecular Medicine</i> , 2019, 44, 1943-1951.	1.8	15
17433	Comparative transcript profiling and cytological observation of the newly bred recessive genic male sterility non-heading Chinese cabbage (<i>Brassica rapa</i> ssp. <i>chinensis</i>) line WS24-3A. <i>Genes and Genomics</i> , 2019, 41, 1475-1492.	0.5	3
17434	A Survey of Gene Prioritization Tools for Mendelian and Complex Human Diseases. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	25
17435	Immunity-associated long non-coding RNA and expression in response to bacterial infection in large yellow croaker (<i>Larimichthys crocea</i>). <i>Fish and Shellfish Immunology</i> , 2019, 94, 634-642.	1.6	41
17436	The application of omics-based human liver platforms for investigating the mechanism of drug-induced hepatotoxicity in vitro. <i>Archives of Toxicology</i> , 2019, 93, 3067-3098.	1.9	21

#	ARTICLE	IF	CITATIONS
17437	Rhizophagus intraradices promotes alfalfa (<i>Medicago sativa</i>) defense against pea aphids (<i>Acyrtosiphon pisum</i>) revealed by RNA-Seq analysis. <i>Mycorrhiza</i> , 2019, 29, 623-635.	1.3	16
17438	Diesel exhaust particles dysregulate multiple immunological pathways in murine macrophages: Lessons from microarray and scRNA-seq technologies. <i>Archives of Biochemistry and Biophysics</i> , 2019, 678, 108116.	1.4	10
17439	Identification and characterization of jasmonic acid- and linolenic acid-mediated transcriptional regulation of secondary laticifer differentiation in <i>Hevea brasiliensis</i> . <i>Scientific Reports</i> , 2019, 9, 14296.	1.6	11
17440	Decreased ω -6: ω -3 PUFA ratio attenuates ethanol-induced alterations in intestinal homeostasis, microbiota, and liver injury. <i>Journal of Lipid Research</i> , 2019, 60, 2034-2049.	2.0	39
17441	Whole Genome Mapping Reveals Novel Genes and Pathways Involved in Milk Production Under Heat Stress in US Holstein Cows. <i>Frontiers in Genetics</i> , 2019, 10, 928.	1.1	52
17442	Expression of microRNA in human retinal pigment epithelial cells following infection with Zaire ebolavirus. <i>BMC Research Notes</i> , 2019, 12, 639.	0.6	10
17443	Association study reveals Th17, Treg, and Th2 loci related to resistance to <i>Haemonchus contortus</i> in Florida Native sheep1. <i>Journal of Animal Science</i> , 2019, 97, 4428-4444.	0.2	14
17444	Gene Ontology Causal Activity Modeling (GO-CAM) moves beyond GO annotations to structured descriptions of biological functions and systems. <i>Nature Genetics</i> , 2019, 51, 1429-1433.	9.4	76
17445	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
17446	Analysis of Small RNAs from <i>Solanum torvum</i> Swartz by Deep Sequencing. <i>Tropical Plant Biology</i> , 2019, 12, 44-54.	1.0	1
17447	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
17448	Impact of human milk on the transcriptomic response of fetal intestinal epithelial cells reveals expression changes of immune-related genes. <i>Food and Function</i> , 2019, 10, 140-150.	2.1	8
17449	Addiction Theories and Constructs: a new series. <i>Addiction</i> , 2019, 114, 955-956.	1.7	7
17450	Impact of Homologous Recombination on the Evolution of Prokaryotic Core Genomes. <i>MBio</i> , 2019, 10, .	1.8	60
17451	Transcriptome analysis identifies strong candidate genes for ginsenoside biosynthesis and reveals its underlying molecular mechanism in <i>Panax ginseng</i> C.A. Meyer. <i>Scientific Reports</i> , 2019, 9, 615.	1.6	24
17452	Widespread inter-individual gene expression variability in <i>Arabidopsis thaliana</i> . <i>Molecular Systems Biology</i> , 2019, 15, e8591.	3.2	55
17453	Imidazopyridines as Potent KDM5 Demethylase Inhibitors Promoting Reprogramming Efficiency of Human iPSCs. <i>IScience</i> , 2019, 12, 168-181.	1.9	24
17454	Exosomes Cause Preterm Birth in Mice: Evidence for Paracrine Signaling in Pregnancy. <i>Scientific Reports</i> , 2019, 9, 608.	1.6	84

#	ARTICLE	IF	CITATIONS
17455	Functional identity of hypothalamic melanocortin neurons depends on Tbx3. <i>Nature Metabolism</i> , 2019, 1, 222-235.	5.1	27
17456	GRIMM: GRaph IMputation and matching for HLA genotypes. <i>Bioinformatics</i> , 2019, 35, 3520-3523.	1.8	12
17457	p.E95K mutation in Indian hedgehog causing brachydactyly type A1 impairs IHH/Gli1 downstream transcriptional regulation. <i>BMC Genetics</i> , 2019, 20, 10.	2.7	5
17458	Thiol isomerase ERp57 targets and modulates the lectin pathway of complement activation. <i>Journal of Biological Chemistry</i> , 2019, 294, 4878-4888.	1.6	12
17459	CALD1, CNN1, and TAGLN identified as potential prognostic molecular markers of bladder cancer by bioinformatics analysis. <i>Medicine (United States)</i> , 2019, 98, e13847.	0.4	33
17460	Transcriptional Basis of Copper-Induced Olfactory Impairment in the Sea Lamprey, a Primitive Invasive Fish. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 933-941.	0.8	9
17461	High Throughput mRNA Sequencing Reveals Potential Therapeutic Targets of Tao-Hong-Si-Wu Decoction in Experimental Middle Cerebral Artery Occlusion. <i>Frontiers in Pharmacology</i> , 2018, 9, 1570.	1.6	17
17462	The putative mature peptide of piscidin-1 modulates global transcriptional profile and proliferation of splenic lymphocytes in orange-spotted grouper (<i>Epinephelus coioides</i>). <i>Fish and Shellfish Immunology</i> , 2019, 86, 1035-1043.	1.6	10
17463	Assessment of somatic single-nucleotide variation in brain tissue of cases with schizophrenia. <i>Translational Psychiatry</i> , 2019, 9, 21.	2.4	16
17464	Fibroblast activation and abnormal extracellular matrix remodelling as common hallmarks in three cancer-prone genodermatoses. <i>British Journal of Dermatology</i> , 2019, 181, 512-522.	1.4	46
17465	sAnr: a visual analytics framework for contextual analyses of private and public RNA-seq data. <i>BMC Genomics</i> , 2019, 20, 85.	1.2	0
17466	Smp38 MAP Kinase Regulation in <i>Schistosoma mansoni</i> : Roles in Survival, Oviposition, and Protection Against Oxidative Stress. <i>Frontiers in Immunology</i> , 2019, 10, 21.	2.2	29
17467	Complete Genome Sequence of <i>Streptomyces olivoreticuli</i> ATCC 31159 Which can Produce Anticancer Bestatin and Show Diverse Secondary Metabolic Potentials. <i>Current Microbiology</i> , 2019, 76, 370-375.	1.0	1
17468	Identification of coenzyme-binding proteins with machine learning algorithms. <i>Computational Biology and Chemistry</i> , 2019, 79, 185-192.	1.1	1
17469	WNT signaling modulates PD-L1 expression in the stem cell compartment of triple-negative breast cancer. <i>Oncogene</i> , 2019, 38, 4047-4060.	2.6	137
17470	Fungal Endophytes of <i>Populus trichocarpa</i> Alter Host Phenotype, Gene Expression, and Rhizobiome Composition. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 853-864.	1.4	52
17471	The Genetics of Mating Song Evolution Underlying Rapid Speciation: Linking Quantitative Variation to Candidate Genes for Behavioral Isolation. <i>Genetics</i> , 2019, 211, 1089-1104.	1.2	26
17472	Circular RNA Expression Alteration and Bioinformatics Analysis in Rats After Traumatic Spinal Cord Injury. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 497.	1.4	47

#	ARTICLE	IF	CITATIONS
17473	Inducing Hierarchical Multi-label Classification rules with Genetic Algorithms. <i>Applied Soft Computing Journal</i> , 2019, 77, 584-604.	4.1	18
17474	Molecular pathways of varicocele and its repair – A paired labelled shotgun proteomics approach. <i>Journal of Proteomics</i> , 2019, 196, 22-32.	1.2	20
17475	A sequential algorithm for false discovery rate control on directed acyclic graphs. <i>Biometrika</i> , 2019, 106, 69-86.	1.3	14
17476	Fuzzy Rough Set Based Feature Selection for Large-Scale Hierarchical Classification. <i>IEEE Transactions on Fuzzy Systems</i> , 2019, 27, 1891-1903.	6.5	63
17477	GOTrapper: a tool to navigate through branches of gene ontology hierarchy. <i>BMC Bioinformatics</i> , 2019, 20, 20.	1.2	11
17478	SMRT sequencing of the full-length transcriptome of the Sunda pangolin (<i>Manis javanica</i>). <i>Gene</i> , 2019, 692, 208-216.	1.0	19
17479	The Short Chain Fatty Acid Butyrate Imprints an Antimicrobial Program in Macrophages. <i>Immunity</i> , 2019, 50, 432-445.e7.	6.6	612
17480	Mechanotransduction of vocal fold fibroblasts and mesenchymal stromal cells in the context of the vocal fold mechanome. <i>Journal of Biomechanics</i> , 2019, 83, 227-234.	0.9	6
17481	Varanto: variant enrichment analysis and annotation. <i>Bioinformatics</i> , 2019, 35, 3154-3156.	1.8	1
17482	The Genome of <i>Armadillidium vulgare</i> (Crustacea, Isopoda) Provides Insights into Sex Chromosome Evolution in the Context of Cytoplasmic Sex Determination. <i>Molecular Biology and Evolution</i> , 2019, 36, 727-741.	3.5	43
17483	Predicting eukaryotic protein secretion without signals. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 140174.	1.1	19
17484	EDEn – Electroceutical Design Environment: Ion Channel Tissue Expression Database with Small Molecule Modulators. <i>IScience</i> , 2019, 11, 42-56.	1.9	24
17485	BNO – An ontology for understanding the transmittability of complex biomolecular networks. <i>Web Semantics</i> , 2019, 57, 100495.	2.2	1
17486	FOXO3 is involved in the tumor necrosis factor-driven inflammatory response in fibroblast-like synoviocytes. <i>Laboratory Investigation</i> , 2019, 99, 648-658.	1.7	20
17487	Inflammation-induced glycolytic switch controls suppressivity of mesenchymal stem cells via STAT1 glycosylation. <i>Leukemia</i> , 2019, 33, 1783-1796.	3.3	54
17488	Choice of Alternative Polyadenylation Sites, Mediated by the RNA-Binding Protein Elavl3, Plays a Role in Differentiation of Inhibitory Neuronal Progenitors. <i>Frontiers in Cellular Neuroscience</i> , 2018, 12, 518.	1.8	33
17489	Identification of key genes and pathways involved in microsatellite instability in colorectal cancer. <i>Molecular Medicine Reports</i> , 2019, 19, 2065-2076.	1.1	25
17490	Robust predictions of specialized metabolism genes through machine learning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2344-2353.	3.3	79

#	ARTICLE	IF	CITATIONS
17491	Canine CD4+ Tâ€cell lymphoma identified by flow cytometry exhibits a consistent histomorphology and gene expression profile. <i>Veterinary and Comparative Oncology</i> , 2019, 17, 253-264.	0.8	15
17492	Genomic changes associated with adaptation to arid environments in cactophilic <i>Drosophila</i> species. <i>BMC Genomics</i> , 2019, 20, 52.	1.2	22
17493	Analysis of synonymous codon usage pattern of genes in unique nonâ€bloodâ€sucking leech <i>Whitmania pigra</i> . <i>Journal of Cellular Biochemistry</i> , 2019, 120, 9850-9858.	1.2	1
17494	Complete genome sequence of <i>Bacillus megaterium</i> JX285 isolated from <i>Camellia oleifera</i> rhizosphere. <i>Computational Biology and Chemistry</i> , 2019, 79, 1-5.	1.1	18
17495	A first glimpse at genes important to the <i>Azolla</i> â€Nostoc symbiosis. <i>Symbiosis</i> , 2019, 78, 149-162.	1.2	26
17496	DNA Sequencing and the Evolution of the â€Omicsâ€, 2019, , 223-262.		0
17497	mRNA and microRNA transcriptomics analyses in intermuscular bones of two carp species, rice flower carp (<i>Cyprinus carpio</i> var. <i>Quanzhounensis</i>) and Jian carp (<i>Cyprinus carpio</i> var. <i>Jian</i>). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 30, 71-80.	0.4	7
17498	Lignocellulolytic characterization and comparative secretome analysis of a <i>Trichoderma erinaceum</i> strain isolated from decaying sugarcane straw. <i>Fungal Biology</i> , 2019, 123, 330-340.	1.1	7
17499	A polysaccharide found in <i>Paulownia fortunei</i> flowers can enhance cellular and humoral immunity in chickens. <i>International Journal of Biological Macromolecules</i> , 2019, 130, 213-219.	3.6	28
17500	Network Analysis Reveals TNF as a Major Hub of Reactive Inflammation Following Spinal Cord Injury. <i>Scientific Reports</i> , 2019, 9, 928.	1.6	12
17501	Comprehensive bioinformatics analysis of methylated and differentially expressed genes in esophageal squamous cell carcinoma. <i>Molecular Omics</i> , 2019, 15, 88-100.	1.4	9
17502	Transcriptome Analysis of Mesenchymal Stem Cells from Multiple Myeloma Patients Reveals Downregulation of Genes Involved in Cell Cycle Progression, Immune Response, and Bone Metabolism. <i>Scientific Reports</i> , 2019, 9, 1056.	1.6	28
17503	Interaction of roses with a biotrophic and a hemibiotrophic leaf pathogen leads to differences in defense transcriptome activation. <i>Plant Molecular Biology</i> , 2019, 99, 299-316.	2.0	29
17504	RT States: systematic annotation of the human genome using cell type-specific replication timing programs. <i>Bioinformatics</i> , 2019, 35, 2167-2176.	1.8	9
17505	CMSENN: Computational Modification Sites with Ensemble Neural Network. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2019, 185, 65-72.	1.8	20
17506	PomBase 2018: user-driven reimplementaion of the fission yeast database provides rapid and intuitive access to diverse, interconnected information. <i>Nucleic Acids Research</i> , 2019, 47, D821-D827.	6.5	157
17507	<p>Identification of key genes and pathways in seminoma by bioinformatics analysis</p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 3683-3693.	1.0	10
17508	Uncovering complex molecular networks in hostâ€pathogen interactions using systems biology. <i>Emerging Topics in Life Sciences</i> , 2019, 3, 371-378.	1.1	2

#	ARTICLE	IF	CITATIONS
17509	Identification of Genes Differentially Expressed in Simvastatin-Induced Alveolar Bone Formation. <i>JBMR Plus</i> , 2019, 3, e10122.	1.3	9
17510	Exploratory Gene Ontology Analysis with Interactive Visualization. <i>Scientific Reports</i> , 2019, 9, 7793.	1.6	10
17511	Genetic analyses of human fetal retinal pigment epithelium gene expression suggest ocular disease mechanisms. <i>Communications Biology</i> , 2019, 2, 186.	2.0	20
17512	Overlapping and unique roles played by ROCK1 and 2 in the modulation of coding and long noncoding RNA expression. <i>BMC Genomics</i> , 2019, 20, 409.	1.2	3
17513	A deficiency in SUMOylation activity disrupts multiple pathways leading to neural tube and heart defects in <i>Xenopus</i> embryos. <i>BMC Genomics</i> , 2019, 20, 386.	1.2	11
17514	Genomic characterization of <i>Escherichia coli</i> LCT-EC001, an extremely multidrug-resistant strain with an amazing number of resistance genes. <i>Gut Pathogens</i> , 2019, 11, 25.	1.6	8
17515	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , 2019, 38, 200-216.	0.7	154
17516	Differential gene expression analysis in blood of first episode psychosis patients. <i>Schizophrenia Research</i> , 2019, 209, 88-97.	1.1	27
17517	Homogeneity tests of covariance matrices with high-dimensional longitudinal data. <i>Biometrika</i> , 2019, 106, 619-634.	1.3	14
17518	Reporting and connecting cell type names and gating definitions through ontologies. <i>BMC Bioinformatics</i> , 2019, 20, 182.	1.2	9
17519	Ten quick tips for biocuration. <i>PLoS Computational Biology</i> , 2019, 15, e1006906.	1.5	21
17520	Screening of differentially expressed genes and identification of NUF2 as a prognostic marker in breast cancer. <i>International Journal of Molecular Medicine</i> , 2019, 44, 390-404.	1.8	19
17521	Rational creation and systematic analysis of cervical cancer kinase-inhibitor binding profile. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 689-698.	1.3	6
17522	An expanded proteome of cardiac t-tubules. <i>Cardiovascular Pathology</i> , 2019, 42, 15-20.	0.7	4
17523	Validating genome-wide CRISPR-Cas9 function improves screening in the oleaginous yeast <i>Yarrowia lipolytica</i> . <i>Metabolic Engineering</i> , 2019, 55, 102-110.	3.6	70
17524	Limits to a classic paradigm: most transcription factors in <i>E. coli</i> regulate genes involved in multiple biological processes. <i>Nucleic Acids Research</i> , 2019, 47, 6656-6667.	6.5	9
17525	Species interactions and distinct microbial communities in high Arctic permafrost affected cryosols are associated with the CH ₄ and CO ₂ gas fluxes. <i>Environmental Microbiology</i> , 2019, 21, 3711-3727.	1.8	23
17526	Quantitative proteomics analysis reveals proteins and pathways associated with anthocyanin accumulation in barley. <i>Food Chemistry</i> , 2019, 298, 124973.	4.2	21

#	ARTICLE	IF	CITATIONS
17527	Bioinformatic identification of key genes and molecular pathways in the spermatogenic process of cryptorchidism. <i>Genes and Diseases</i> , 2019, 6, 431-440.	1.5	5
17528	<i>Shigella</i> promotes major alteration of gut epithelial physiology and tissue invasion by shutting off host intracellular transport. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13582-13591.	3.3	23
17529	Novel interconnections of HOG signaling revealed by combined use of two proteomic software packages. <i>Cell Communication and Signaling</i> , 2019, 17, 66.	2.7	9
17530	Protein interactions and consensus clustering analysis uncover insights into herpesvirus virion structure and function relationships. <i>PLoS Biology</i> , 2019, 17, e3000316.	2.6	18
17531	Endogenous NO-mediated transcripts involved in photosynthesis and carbohydrate metabolism in alfalfa (<i>Medicago sativa</i> L.) seedlings under drought stress. <i>Plant Physiology and Biochemistry</i> , 2019, 141, 456-465.	2.8	11
17532	Gene Information eXtension (GIX): effortless retrieval of gene product information on any website. <i>Nature Methods</i> , 2019, 16, 665-666.	9.0	3
17533	Proteomics Analysis of Extracellular Matrix Remodeling During Zebrafish Heart Regeneration. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1745-1755.	2.5	51
17534	The Thm1 Zn(II) ₂ Cys ₆ transcription factor contributes to heat, membrane integrity and virulence in the insect pathogenic fungus <i>Beauveria bassiana</i> . <i>Environmental Microbiology</i> , 2019, 21, 3153-3171.	1.8	13
17535	Comprehensive epigenetic analyses reveal master regulators driving lung metastasis of breast cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 5415-5431.	1.6	17
17536	Machine learning with the TCGA-HNSC dataset: improving usability by addressing inconsistency, sparsity, and high-dimensionality. <i>BMC Bioinformatics</i> , 2019, 20, 339.	1.2	19
17537	Rational discovery of dual-indication multi-target PDE/Kinase inhibitor for precision anti-cancer therapy using structural systems pharmacology. <i>PLoS Computational Biology</i> , 2019, 15, e1006619.	1.5	37
17538	miR-142-3p suppresses uveal melanoma by targeting CDC25C, TGF β 1, GNAQ, WASL, and RAC1. <i>Cancer Management and Research</i> , 2019, Volume 11, 4729-4742.	0.9	19
17539	A First Study of the Virulence Potential of a <i>Bacillus subtilis</i> Isolate From Deep-Sea Hydrothermal Vent. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 183.	1.8	34
17540	Systems-level Analysis Reveals Multiple Modulators of Epithelial-mesenchymal Transition and Identifies DNAJB4 and CD81 as Novel Metastasis Inducers in Breast Cancer. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1756-1771.	2.5	29
17541	Circulating microvesicle protein is associated with renal transplant outcome. <i>Transplant Immunology</i> , 2019, 55, 101210.	0.6	9
17542	Transcriptional profiles of early stage red sea urchins (<i>Mesocentrotus franciscanus</i>) reveal differential regulation of gene expression across development. <i>Marine Genomics</i> , 2019, 48, 100692.	0.4	12
17543	Comparative transcriptome analysis reveals unique genetic adaptations conferring salt tolerance in a xerohalophyte. <i>Functional Plant Biology</i> , 2019, 46, 670.	1.1	10
17544	Randomised Trial of Lipiodol Uterine Bathing Effect (LUBE) in Women with Endometriosis-Related Infertility. <i>Fertility & Reproduction</i> , 2019, 01, 57-64.	0.0	4

#	ARTICLE	IF	CITATIONS
17545	Distilling a Materials Synthesis Ontology. <i>Matter</i> , 2019, 1, 8-12.	5.0	31
17546	MiRNA expression patterns are associated with tumor mutational burden in lung adenocarcinoma. <i>OncotImmunology</i> , 2019, 8, e1629260.	2.1	24
17547	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
17548	Metaproteomics: Sample Preparation and Methodological Considerations. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1073, 187-215.	0.8	26
17549	Transcriptional analysis of host responses related to immunity in chicken spleen tissues infected with reticuloendotheliosis virus strain SNV. <i>Infection, Genetics and Evolution</i> , 2019, 74, 103932.	1.0	20
17550	Chemoproteomic Method for Profiling Inhibitor-Bound Kinase Complexes. <i>Journal of the American Chemical Society</i> , 2019, 141, 11912-11922.	6.6	11
17551	Transcriptomic Insights into the Response of the Olfactory Bulb to Selenium Treatment in a Mouse Model of Alzheimer's Disease. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2998.	1.8	14
17552	Identification of differentially expressed genes in small and non-small cell lung cancer based on meta-analysis of mRNA. <i>Heliyon</i> , 2019, 5, e01707.	1.4	20
17553	Analysis of disease organ as a novel phenotype towards disease genetics understanding. <i>Journal of Biomedical Informatics</i> , 2019, 95, 103235.	2.5	1
17554	First-generation predictors of biological protein phase separation. <i>Current Opinion in Structural Biology</i> , 2019, 58, 88-96.	2.6	119
17555	Visualization and prediction of CRISPR incidence in microbial trait-space to identify drivers of antiviral immune strategy. <i>ISME Journal</i> , 2019, 13, 2589-2602.	4.4	34
17556	Survey of the <i>Bradysia odoriphaga</i> Transcriptome Using PacBio Single-Molecule Long-Read Sequencing. <i>Genes</i> , 2019, 10, 481.	1.0	8
17557	From parts to mechanisms: research heuristics for addressing heterogeneity in cancer genetics. <i>History and Philosophy of the Life Sciences</i> , 2019, 41, 27.	0.6	3
17558	MicroRNA profiling of patients with sporadic atrial septal defect. <i>Biotechnology and Biotechnological Equipment</i> , 2019, 33, 510-519.	0.5	4
17559	The Transcriptome Landscape of Walnut Interspecies Hybrid (<i>Juglans hindsii</i> × <i>Juglans regia</i>) and Regulation of Cambial Activity in Relation to Grafting. <i>Frontiers in Genetics</i> , 2019, 10, 577.	1.1	9
17560	DNA methylome and transcriptome alterations and cancer prevention by triterpenoid ursolic acid in UVB-induced skin tumor in mice. <i>Molecular Carcinogenesis</i> , 2019, 58, 1738-1753.	1.3	24
17561	Emerging Sample Treatments in Proteomics. <i>Advances in Experimental Medicine and Biology</i> , 2019, . .	0.8	6
17562	Analysis of the <i>Escherichia coli</i> extracellular vesicle proteome identifies markers of purity and culture conditions. <i>Journal of Extracellular Vesicles</i> , 2019, 8, 1632099.	5.5	79

#	ARTICLE	IF	CITATIONS
17563	Monozygotic twins and triplets discordant for amyotrophic lateral sclerosis display differential methylation and gene expression. <i>Scientific Reports</i> , 2019, 9, 8254.	1.6	36
17564	Trait ontology analysis based on association mapping studies bridges the gap between crop genomics and Phenomics. <i>BMC Genomics</i> , 2019, 20, 443.	1.2	8
17565	Transcriptomic analysis of two endophytes involved in enhancing salt stress ability of <i>Arabidopsis thaliana</i> . <i>Science of the Total Environment</i> , 2019, 686, 107-117.	3.9	52
17566	Aberrant NFATc1 signaling counteracts TGF β 2-mediated growth arrest and apoptosis induction in pancreatic cancer progression. <i>Cell Death and Disease</i> , 2019, 10, 446.	2.7	12
17567	Identification of core genes and clinical roles in pregnancy-associated breast cancer based on integrated analysis of different microarray profile datasets. <i>Bioscience Reports</i> , 2019, 39, .	1.1	16
17568	Transcriptome and excretory secretory proteome of infective-stage larvae of the nematode <i>Gnathostoma spinigerum</i> reveal potential immunodiagnostic targets for development. <i>Parasite</i> , 2019, 26, 34.	0.8	12
17569	Endometriosis Knowledgebase: a gene-based resource on endometriosis. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	16
17570	AtTRAPPC11/ROG2: A Role for TRAPPs in Maintenance of the Plant Trans-Golgi Network/Early Endosome Organization and Function. <i>Plant Cell</i> , 2019, 31, 1879-1898.	3.1	26
17571	A survey of transcriptome complexity using PacBio single-molecule real-time analysis combined with Illumina RNA sequencing for a better understanding of ricinoleic acid biosynthesis in <i>Ricinus communis</i> . <i>BMC Genomics</i> , 2019, 20, 456.	1.2	25
17572	Prediction of genes and protein-protein interaction networking for miR-221-5p using bioinformatics analysis. <i>Gene Reports</i> , 2019, 16, 100426.	0.4	2
17573	High expression of Annexin A2 is associated with DNA repair, metabolic alteration, and worse survival in pancreatic ductal adenocarcinoma. <i>Surgery</i> , 2019, 166, 150-156.	1.0	29
17574	Identification of key pathways and genes changes in pancreatic cancer cells (BXPc-3) after cross-talk with primary pancreatic stellate cells using bioinformatics analysis. <i>Neoplasma</i> , 2019, 66, 681-693.	0.7	7
17575	Cytological effects of honokiol treatment and its potential mechanism of action in non-small cell lung cancer. <i>Biomedicine and Pharmacotherapy</i> , 2019, 117, 109058.	2.5	15
17576	PTEN interacts with the transcription machinery on chromatin and regulates RNA polymerase II-mediated transcription. <i>Nucleic Acids Research</i> , 2019, 47, 5573-5586.	6.5	24
17577	Comparative transcriptomic and proteomic analysis of yellow shell and black shell pearl oysters, <i>Pinctada fucata martensii</i> . <i>BMC Genomics</i> , 2019, 20, 469.	1.2	25
17578	Contribution of Gene Regulatory Networks to Heritability of Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2019, 73, 2946-2957.	1.2	45
17579	Transcriptomics of host-specific interactions in natural populations of the parasitic plant purple witchweed (<i>Striga hermonthica</i>). <i>Weed Science</i> , 2019, 67, 397-411.	0.8	16
17580	The complexity of alternative splicing and landscape of tissue-specific expression in lotus (<i>Nelumbo</i>) Tj ETQq1 1 0.784314 rgBT /Overl 2019, 26, 301-311.	1.5	28

#	ARTICLE	IF	CITATIONS
17581	Culturing C2C12 myotubes on micromolded gelatin hydrogels accelerates myotube maturation. <i>Skeletal Muscle</i> , 2019, 9, 17.	1.9	80
17582	BRCA1/BRCA2-containing complex subunit 3 controls oligodendrocyte differentiation by dynamically regulating lysine 63-linked ubiquitination. <i>Glia</i> , 2019, 67, 1775-1792.	2.5	12
17583	After the Taxonomic Identification Phase: Addressing the Functions of Symbiotic Communities Within Marine Invertebrates. , 2019, , 105-144.		2
17584	eIF2B Mutations Cause Mitochondrial Malfunction in Oligodendrocytes. <i>NeuroMolecular Medicine</i> , 2019, 21, 303-313.	1.8	13
17585	Hippocampal sub-regional differences in the microRNA response to forebrain ischemia. <i>Molecular and Cellular Neurosciences</i> , 2019, 98, 164-178.	1.0	7
17586	Mitochondrial proteome profiling of <i>Leishmania tropica</i> . <i>Microbial Pathogenesis</i> , 2019, 133, 103542.	1.3	7
17587	Analysis of the role of DAMTC in lung adenocarcinoma cells based on the DNA microarrays. <i>Oncology Letters</i> , 2019, 17, 4787-4794.	0.8	1
17588	Distinct fibroblast subsets drive inflammation and damage in arthritis. <i>Nature</i> , 2019, 570, 246-251.	13.7	550
17589	Graph Algorithms for Condensing and Consolidating Gene Set Analysis Results. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S141-S152.	2.5	17
17590	Towards an Effective and Efficient Management of Genome Data: An Information Systems Engineering Perspective. <i>Lecture Notes in Business Information Processing</i> , 2019, , 99-110.	0.8	6
17591	Identification of Proteins Differentially Expressed by Adipose-derived Mesenchymal Stem Cells Isolated from Immunodeficient Mice. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2672.	1.8	7
17592	Transcriptomics Analysis Reveals New Insights into the Roles of Notch1 Signaling on Macrophage Polarization. <i>Scientific Reports</i> , 2019, 9, 7999.	1.6	23
17593	LION/web: a web-based ontology enrichment tool for lipidomic data analysis. <i>GigaScience</i> , 2019, 8, .	3.3	128
17594	Identify differential gene expressions in fatty infiltration process in rotator cuff. <i>Journal of Orthopaedic Surgery and Research</i> , 2019, 14, 158.	0.9	5
17595	Towards the automated economic assessment of newborn screening for rare diseases. <i>Journal of Biomedical Informatics</i> , 2019, 95, 103216.	2.5	2
17596	Map and model—moving from observation to prediction in toxicogenomics. <i>GigaScience</i> , 2019, 8, .	3.3	14
17597	Pergola-web: a web server for the visualization and analysis of longitudinal behavioral data using repurposed genomics tools and standards. <i>Nucleic Acids Research</i> , 2019, 47, W600-W604.	6.5	2
17598	The Oncogene ECT2 Contributes to a Hyperplastic, Proliferative Lung Epithelial Cell Phenotype in Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 61, 713-726.	1.4	15

#	ARTICLE	IF	CITATIONS
17599	Genome Analysis of <i>Hypomyces perniciosus</i> , the Causal Agent of Wet Bubble Disease of Button Mushroom (<i>Agaricus bisporus</i>). <i>Genes</i> , 2019, 10, 417.	1.0	17
17600	Phosphoproteomic and proteomic profiling of serine/threonine protein kinase PkaE of <i>Streptomyces coelicolor</i> A3(2) and its role in secondary metabolism and morphogenesis. <i>Bioscience, Biotechnology and Biochemistry</i> , 2019, 83, 1843-1850.	0.6	5
17601	LnCompare: gene set feature analysis for human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2019, 47, W523-W529.	6.5	20
17602	SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. <i>Neuron</i> , 2019, 103, 217-234.e4.	3.8	518
17603	Comparison of liver transcriptome from high- and low-intramuscular fat Chaohu ducks provided additional candidate genes for lipid selection. <i>3 Biotech</i> , 2019, 9, 251.	1.1	6
17604	The important role of phagocytosis and interleukins for Nile tilapia (<i>Oreochromis niloticus</i>) to defense infection of <i>Aeromonas hydrophila</i> based on transcriptome analysis. <i>Fish and Shellfish Immunology</i> , 2019, 92, 54-63.	1.6	33
17605	Regional Heterogeneity in Gene Expression, Regulation, and Coherence in the Frontal Cortex and Hippocampus across Development and Schizophrenia. <i>Neuron</i> , 2019, 103, 203-216.e8.	3.8	158
17606	Detecting evolving communities in dynamic networks using graph regularized evolutionary nonnegative matrix factorization. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2019, 530, 121279.	1.2	8
17607	IL-27 promotes the expansion of self-renewing CD8+ T cells in persistent viral infection. <i>Journal of Experimental Medicine</i> , 2019, 216, 1791-1808.	4.2	45
17608	Incorporating Pathway Information into Feature Selection towards Better Performed Gene Signatures. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	12
17609	Global serum proteomic changes in water buffaloes infected with <i>Fasciola gigantica</i> . <i>Parasites and Vectors</i> , 2019, 12, 281.	1.0	13
17610	Protein Structure and Modeling. , 2019, , .		3
17611	Genome-wide survey and expression analyses of the GRAS gene family in <i>Brassica napus</i> reveals their roles in root development and stress response. <i>Planta</i> , 2019, 250, 1051-1072.	1.6	30
17612	Endodermal Maternal Transcription Factors Establish Super-Enhancers during Zygotic Genome Activation. <i>Cell Reports</i> , 2019, 27, 2962-2977.e5.	2.9	31
17613	VCF/Plotein: visualization and prioritization of genomic variants from human exome sequencing projects. <i>Bioinformatics</i> , 2019, 35, 4803-4805.	1.8	6
17614	The prediction of early preeclampsia: Results from a longitudinal proteomics study. <i>PLoS ONE</i> , 2019, 14, e0217273.	1.1	81
17615	Comprehensive transcriptome analysis reveals genes potentially involved in isoflavone biosynthesis in <i>Pueraria thomsonii</i> Benth. <i>PLoS ONE</i> , 2019, 14, e0217593.	1.1	25
17616	PRC2-Mediated H3K27me3 Contributes to Transcriptional Regulation of FIT-Dependent Iron Deficiency Response. <i>Frontiers in Plant Science</i> , 2019, 10, 627.	1.7	22

#	ARTICLE	IF	CITATIONS
17617	NetR and AttR, Two New Bioinformatic Tools to Integrate Diverse Datasets into Cytoscape Network and Attribute Files. <i>Genes</i> , 2019, 10, 423.	1.0	1
17618	Transcriptomics analysis of sirolimus treatment in lupus nephritis. <i>Molecular Medicine Reports</i> , 2019, 20, 245-251.	1.1	3
17619	The Draft Genome of Eggplant. <i>Compendium of Plant Genomes</i> , 2019, , 55-63.	0.3	0
17620	Improving Energy Metabolism of Deproteinized Extract of Calf Blood Through Regulation of Hmgcs2, Cpt1a, Angptl4, Cyp8b1, and Ehhadh Genes in Mice. <i>Chemical Research in Chinese Universities</i> , 2019, 35, 427-433.	1.3	1
17621	Bioinformatics Analysis of Stromal Molecular Signatures Associated with Breast and Prostate Cancer. <i>Journal of Computational Biology</i> , 2019, 26, 1130-1139.	0.8	12
17622	ANASTASIA: An Automated Metagenomic Analysis Pipeline for Novel Enzyme Discovery Exploiting Next Generation Sequencing Data. <i>Frontiers in Genetics</i> , 2019, 10, 469.	1.1	21
17623	Bioinformatics analysis of the regulatory lncRNA-miRNA-mRNA network and drug prediction in patients with hypertrophic cardiomyopathy. <i>Molecular Medicine Reports</i> , 2019, 20, 549-558.	1.1	24
17624	Identify CRNDE and LINC00152 as the key lncRNAs in age-related degeneration of articular cartilage through comprehensive and integrative analysis. <i>PeerJ</i> , 2019, 7, e7024.	0.9	9
17625	Prediction of key regulators and downstream targets of E. coli induced mastitis. <i>Journal of Applied Genetics</i> , 2019, 60, 367-373.	1.0	28
17626	Deciphering the non-coding RNA-level response to arsenic stress in rice (<i>Oryza sativa</i>). <i>Plant Signaling and Behavior</i> , 2019, 14, 1629268.	1.2	22
17627	Development of a Zebrafish S1500+ Sentinel Gene Set for High-Throughput Transcriptomics. <i>Zebrafish</i> , 2019, 16, 331-347.	0.5	5
17628	Phenotypical profile and global transcriptomic profile of Hypervirulent <i>Klebsiella pneumoniae</i> due to carbapenemase-encoding plasmid acquisition. <i>BMC Genomics</i> , 2019, 20, 480.	1.2	17
17629	The initiation of puberty in Atlantic salmon brings about large changes in testicular gene expression that are modulated by the energy status. <i>BMC Genomics</i> , 2019, 20, 475.	1.2	15
17630	Identification of miRNAs and their target genes in <i>Larix olgensis</i> and verified of differential expression miRNAs. <i>BMC Plant Biology</i> , 2019, 19, 247.	1.6	8
17631	Cyberinfrastructure to Improve Forest Health and Productivity: The Role of Tree Databases in Connecting Genomes, Phenomes, and the Environment. <i>Frontiers in Plant Science</i> , 2019, 10, 813.	1.7	24
17632	Transcriptomic analysis of pollen-pistil interactions in almond (<i>Prunus dulcis</i>) identifies candidate genes for components of gametophytic self-incompatibility. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	13
17633	lncRNA Gm10451 regulates PTIP to facilitate iPSCs-derived β -like cell differentiation by targeting miR-338-3p as a ceRNA. <i>Biomaterials</i> , 2019, 216, 119266.	5.7	29
17634	Graphlet Laplacians for topology-function and topology-disease relationships. <i>Bioinformatics</i> , 2019, 35, 5226-5234.	1.8	8

#	ARTICLE	IF	CITATIONS
17635	Protein-protein interaction prediction using a hybrid feature representation and a stacked generalization scheme. <i>BMC Bioinformatics</i> , 2019, 20, 308.	1.2	44
17636	A novel mRNA-miRNA-lncRNA competing endogenous RNA triple sub-network associated with prognosis of pancreatic cancer. <i>Aging</i> , 2019, 11, 2610-2627.	1.4	170
17637	AXL knockdown gene signature reveals a drug repurposing opportunity for a class of antipsychotics to reduce growth and metastasis of triple-negative breast cancer. <i>Oncotarget</i> , 2019, 10, 2055-2067.	0.8	32
17638	On the presence of short-range periodicities in protein structures that are not related to established secondary structure elements. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 966-978.	1.5	0
17639	Specialized eRpL22 paralogue-specific ribosomes regulate specific mRNA translation in spermatogenesis in <i>Drosophila melanogaster</i> . <i>Molecular Biology of the Cell</i> , 2019, 30, 2240-2253.	0.9	28
17640	Navigating the disease landscape: knowledge representations for contextualizing molecular signatures. <i>Briefings in Bioinformatics</i> , 2019, 20, 609-623.	3.2	16
17641	A perfusion bioreactor-based 3D model of the subarachnoid space based on a meningeal tissue construct. <i>Fluids and Barriers of the CNS</i> , 2019, 16, 17.	2.4	8
17642	Comprehensive analysis of full genome sequence and Bd-miRNA/target mRNAs to discover the mechanism of hypovirulence in <i>Botryosphaeria dothidea</i> strains on pear infection with BdCV1 and BdPV1. <i>IMA Fungus</i> , 2019, 10, 3.	1.7	11
17643	De novo transcriptome assembly and co-expression network analysis of <i>Cynanchum thesioides</i> : Identification of genes involved in resistance to drought stress. <i>Gene</i> , 2019, 710, 375-386.	1.0	11
17644	ARtPM: Article Retrieval for Precision Medicine. <i>Journal of Biomedical Informatics</i> , 2019, 95, 103224.	2.5	7
17645	Decoding the human serum interactome of snake-derived antimicrobial peptide Ctn[15-34]: Toward an explanation for unusually long half-life. <i>Journal of Proteomics</i> , 2019, 204, 103372.	1.2	10
17646	Clinical expression and antigenic profiles of a <i>Plasmodium vivax</i> vaccine candidate: merozoite surface protein 7 (PvMSP-7). <i>Malaria Journal</i> , 2019, 18, 197.	0.8	7
17647	Genome-wide association study of multisite chronic pain in UK Biobank. <i>PLoS Genetics</i> , 2019, 15, e1008164.	1.5	144
17648	Transcriptomic profiles of 33 opium poppy samples in different tissues, growth phases, and cultivars. <i>Scientific Data</i> , 2019, 6, 66.	2.4	7
17649	NetGO: improving large-scale protein function prediction with massive network information. <i>Nucleic Acids Research</i> , 2019, 47, W379-W387.	6.5	86
17650	The human amniotic fluid mesenchymal stem cells therapy on SKOV3, ovarian cancer cell line. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e00726.	0.6	16
17651	Novel susceptibility genes were found in a targeted sequencing of stroke patients with or without depression in the Chinese Han population. <i>Journal of Affective Disorders</i> , 2019, 255, 1-9.	2.0	11
17652	Draft genome of the big-headed turtle <i>Platysternon megacephalum</i> . <i>Scientific Data</i> , 2019, 6, 60.	2.4	26

#	ARTICLE	IF	CITATIONS
17653	The genome resources for conservation of Indo-Pacific humpback dolphin, <i>Sousa chinensis</i> . <i>Scientific Data</i> , 2019, 6, 68.	2.4	3
17655	Transcriptomic Response to Feeding and Starvation in a Herbivorous Dinoflagellate. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	7
17656	Latent Model-Based Clustering for Biological Discovery. <i>IScience</i> , 2019, 14, 125-135.	1.9	5
17657	Sub-cytotoxic doses of pharmaceutical silica nanoparticles show significant impact on the proteome of HepG2 cells. <i>Journal of Controlled Release</i> , 2019, 306, 1-14.	4.8	3
17658	Iso-Seq analysis of the <i>Taxus cuspidata</i> transcriptome reveals the complexity of Taxol biosynthesis. <i>BMC Plant Biology</i> , 2019, 19, 210.	1.6	49
17659	Preclinical rationale for entinostat in embryonal rhabdomyosarcoma. <i>Skeletal Muscle</i> , 2019, 9, 12.	1.9	17
17660	Transcriptomic Analysis of <i>Trichoderma atroviride</i> Overgrowing Plant-Wilting <i>Verticillium dahliae</i> Reveals the Role of a New M14 Metalloprotease CPA1 in Biocontrol. <i>Frontiers in Microbiology</i> , 2019, 10, 1120.	1.5	50
17661	Identification of Temporal Characteristic Networks of Peripheral Blood Changes in Alzheimer's Disease Based on Weighted Gene Co-expression Network Analysis. <i>Frontiers in Aging Neuroscience</i> , 2019, 11, 83.	1.7	25
17662	Molecular Interaction Networks to Select Factors for Cell Conversion. <i>Methods in Molecular Biology</i> , 2019, 1975, 333-361.	0.4	2
17663	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
17664	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
17665	PiPred " a deep-learning method for prediction of β -helices in protein sequences. <i>Scientific Reports</i> , 2019, 9, 6888.	1.6	15
17666	PhyloToL: A Taxon/Gene-Rich Phylogenomic Pipeline to Explore Genome Evolution of Diverse Eukaryotes. <i>Molecular Biology and Evolution</i> , 2019, 36, 1831-1842.	3.5	23
17667	High-density genetic map construction and QTL mapping of first flower node in pepper (<i>Capsicum</i>) Tj ETQq1 1 0.784314 rgBTJ/Overl	1.6	34
17668	The Proteome of Pancreatic Cancer-Derived Exosomes Reveals Signatures Rich in Key Signaling Pathways. <i>Proteomics</i> , 2019, 19, e1800394.	1.3	19
17669	An ontology for representing hematologic malignancies: the cancer cell ontology. <i>BMC Bioinformatics</i> , 2019, 20, 181.	1.2	7
17670	Transcriptome analysis reveals pathways facilitating the growth of tobacco powdery mildew in <i>Arabidopsis</i> . <i>Phytopathology Research</i> , 2019, 1, .	0.9	9
17671	Cyclin C Regulated Oxidative Stress Responsive Transcriptome in <i>Mus musculus</i> Embryonic Fibroblasts. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1901-1908.	0.8	13

#	ARTICLE	IF	CITATIONS
17672	Filamentation Regulatory Pathways Control Adhesion-Dependent Surface Responses in Yeast. <i>Genetics</i> , 2019, 212, 667-690.	1.2	20
17673	Identifying Disease-Gene Associations With Graph-Regularized Manifold Learning. <i>Frontiers in Genetics</i> , 2019, 10, 270.	1.1	19
17674	Superantigen SpeA attenuates the biofilm forming capacity of <i>Streptococcus pyogenes</i> . <i>Journal of Microbiology</i> , 2019, 57, 626-636.	1.3	10
17675	Transcriptome analysis of activated sludge microbiomes reveals an unexpected role of minority nitrifiers in carbon metabolism. <i>Communications Biology</i> , 2019, 2, 179.	2.0	35
17676	modEnrichr: a suite of gene set enrichment analysis tools for model organisms. <i>Nucleic Acids Research</i> , 2019, 47, W183-W190.	6.5	62
17677	A comparative analysis of egg provisioning using mass spectrometry during rapid life history evolution in sea urchins. <i>Evolution & Development</i> , 2019, 21, 188-204.	1.1	20
17678	Involvement of Salicylic Acid in Anthracnose Infection in Tea Plants Revealed by Transcriptome Profiling. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2439.	1.8	29
17679	Microarray analysis reveals the changes of circular RNA expression and molecular mechanism in acute lung injury mouse model. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 16658-16667.	1.2	18
17680	TiO ₂ nanotubes promote osteogenic differentiation of mesenchymal stem cells via regulation of lncRNA CCL3-AS. <i>Colloids and Surfaces B: Biointerfaces</i> , 2019, 181, 416-425.	2.5	10
17681	Morpholinos Do Not Elicit an Innate Immune Response during Early <i>Xenopus</i> Embryogenesis. <i>Developmental Cell</i> , 2019, 49, 643-650.e3.	3.1	12
17682	A MICOSâ€“TIM22 Association Promotes Carrier Import into Human Mitochondria. <i>Journal of Molecular Biology</i> , 2019, 431, 2835-2851.	2.0	43
17683	Testosterone Influence on Gene Expression in Lacrimal Glands of Mouse Models of SjÃ¶rgren Syndrome. , 2019, 60, 2181.		15
17684	Microarray Bioinformatics. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	4
17685	Network Biology, Sequence, Pathway and Ontology Informatics. <i>Learning Materials in Biosciences</i> , 2019, , 175-187.	0.2	0
17686	Quantitative proteomic study of arsenic treated mouse liver sinusoidal endothelial cells using a reverse super-SILAC method. <i>Biochemical and Biophysical Research Communications</i> , 2019, 514, 475-481.	1.0	4
17687	Transcriptome analysis of differentially expressed genes during anther development stages on male sterility and fertility in <i>Cucumis melo</i> L. line. <i>Gene</i> , 2019, 707, 65-77.	1.0	11
17688	R-DeeP: Proteome-wide and Quantitative Identification of RNA-Dependent Proteins by Density Gradient Ultracentrifugation. <i>Molecular Cell</i> , 2019, 75, 184-199.e10.	4.5	77
17689	Immunophenotypic, cytotoxic, proteomic and genomic characterization of human cord blood vs. peripheral blood CD56 ^{Dim} NK cells. <i>Innate Immunity</i> , 2019, 25, 294-304.	1.1	8

#	ARTICLE	IF	CITATIONS
17690	Comparative transcriptome analysis of trout skin pigment cells. <i>BMC Genomics</i> , 2019, 20, 359.	1.2	25
17691	Transcriptional changes associated with advancing stages of heart failure underlie atrial and ventricular arrhythmogenesis. <i>PLoS ONE</i> , 2019, 14, e0216928.	1.1	2
17692	TRPV2 Calcium Channel Gene Expression and Outcomes in Gastric Cancer Patients: A Clinically Relevant Association. <i>Journal of Clinical Medicine</i> , 2019, 8, 662.	1.0	24
17693	Age-dependent alterations of Kir4.1 expression in neural crest-derived cells of the mouse and human cochlea. <i>Neurobiology of Aging</i> , 2019, 80, 210-222.	1.5	17
17694	Unbiased Boolean analysis of public gene expression data for cell cycle gene identification. <i>Molecular Biology of the Cell</i> , 2019, 30, 1770-1779.	0.9	28
17695	g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019) Tj ETQq1 1 0.784314 rgBT /Overlock 10 6.58 3,302	6.58	3,302
17696	OMDP: An ontology-based model for diagnosis and treatment of diabetes patients in remote healthcare systems. <i>International Journal of Distributed Sensor Networks</i> , 2019, 15, 155014771984711.	1.3	30
17697	Identification of novel biomarkers and candidate small molecule drugs in non-small-cell lung cancer by integrated microarray analysis. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 3545-3563.	1.0	32
17698	Interscapular and Perivascular Brown Adipose Tissue Respond Differently to a Short-Term High-Fat Diet. <i>Nutrients</i> , 2019, 11, 1065.	1.7	12
17699	A novel long noncoding RNA FAF inhibits apoptosis via upregulating FGF9 through PI3K/AKT signaling pathway in ischemia/hypoxia cardiomyocytes. <i>Journal of Cellular Physiology</i> , 2019, 234, 21973-21987.	2.0	25
17700	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
17701	mirTime: Identifying Condition-Specific Targets of MicroRNA in Time-series Transcript Data using Gaussian Process Model and Spherical Vector Clustering. <i>Bioinformatics</i> , 2019, , .	1.8	8
17702	Tracing the phylogenetic history of the Crl regulon through the Bacteria and Archaea genomes. <i>BMC Genomics</i> , 2019, 20, 299.	1.2	8
17703	What lies beneath? Molecular evolution during the radiation of caecilian amphibians. <i>BMC Genomics</i> , 2019, 20, 354.	1.2	7
17705	Identification of global mRNA expression profiles and comprehensive bioinformatic analyses of abnormally expressed genes in cholestatic liver disease. <i>Gene</i> , 2019, 707, 9-21.	1.0	11
17706	Alternative classification of identical concepts in different terminologies: Different ways to view the world. <i>Journal of Biomedical Informatics</i> , 2019, 94, 103193.	2.5	3
17707	Germline Structural Variations Are Preferential Sites of DNA Replication Timing Plasticity during Development. <i>Genome Biology and Evolution</i> , 2019, 11, 1663-1678.	1.1	1
17708	Leveraging implicit knowledge in neural networks for functional dissection and engineering of proteins. <i>Nature Machine Intelligence</i> , 2019, 1, 225-235.	8.3	18

#	ARTICLE	IF	CITATIONS
17709	Small Molecule Inhibitors of KDM5 Histone Demethylases Increase the Radiosensitivity of Breast Cancer Cells Overexpressing JARID1B. <i>Molecules</i> , 2019, 24, 1739.	1.7	25
17710	The Role of Long Non-coding RNA Prostate Cancer-Associated Transcript 1 in Prostate Cancer. <i>Journal of Computational Biology</i> , 2019, 26, 975-984.	0.8	2
17711	Identification of a regeneration-organizing cell in the <i>Xenopus</i> tail. <i>Science</i> , 2019, 364, 653-658.	6.0	108
17712	RNA-seq Transcriptome Analysis in Ovarian Tissue of Pelibuey Breed to Explore the Regulation of Prolificacy. <i>Genes</i> , 2019, 10, 358.	1.0	17
17713	Reconstructed Skin Models Revealed Unexpected Differences in Epidermal African and Caucasian Skin. <i>Scientific Reports</i> , 2019, 9, 7456.	1.6	24
17714	Tracking transcriptomic responses to endogenous and exogenous variation in cetaceans in the Southern California Bight. , 2019, 7, coz018.		8
17715	ODAE: Ontology-based systematic representation and analysis of drug adverse events and its usage in study of adverse events given different patient age and disease conditions. <i>BMC Bioinformatics</i> , 2019, 20, 199.	1.2	10
17716	Detailed prediction of protein sub-nuclear localization. <i>BMC Bioinformatics</i> , 2019, 20, 205.	1.2	2
17717	An annual cycle of gene regulation in the red-legged salamander mental gland: from hypertrophy to expression of rapidly evolving pheromones. <i>BMC Developmental Biology</i> , 2019, 19, 10.	2.1	7
17718	Muscle Gene Sets: a versatile methodological aid to functional genomics in the neuromuscular field. <i>Skeletal Muscle</i> , 2019, 9, 10.	1.9	8
17719	CiliaCarta: An integrated and validated compendium of ciliary genes. <i>PLoS ONE</i> , 2019, 14, e0216705.	1.1	104
17720	Genome-Wide Signatures of Selection Detection in Three South China Indigenous Pigs. <i>Genes</i> , 2019, 10, 346.	1.0	29
17721	Genome-wide association studies for 30 haematological and blood clinical-biochemical traits in Large White pigs reveal genomic regions affecting intermediate phenotypes. <i>Scientific Reports</i> , 2019, 9, 7003.	1.6	55
17722	Sex-specific Tau methylation patterns and synaptic transcriptional alterations are associated with neural vulnerability during chronic neuroinflammation. <i>Journal of Autoimmunity</i> , 2019, 101, 56-69.	3.0	11
17723	A small molecule promotes cartilage extracellular matrix generation and inhibits osteoarthritis development. <i>Nature Communications</i> , 2019, 10, 1914.	5.8	134
17724	In silico learning of tumor evolution through mutational time series. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9501-9510.	3.3	18
17725	Placental DNA methylation levels at CYP2E1 and IRS2 are associated with child outcome in a prospective autism study. <i>Human Molecular Genetics</i> , 2019, 28, 2659-2674.	1.4	57
17726	Feature Selection for Longitudinal Data by Using Sign Averages to Summarize Gene Expression Values over Time. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	3

#	ARTICLE	IF	CITATIONS
17727	Interactions between Germline and Somatic Mutated Genes in Aggressive Prostate Cancer. <i>Prostate Cancer</i> , 2019, 2019, 1-11.	0.4	9
17728	Abnormal methylation of spermatozoa induced by benzo(a)pyrene in rats. <i>Human and Experimental Toxicology</i> , 2019, 38, 846-856.	1.1	5
17729	A Pathway-Based Strategy to Identify Biomarkers for Lung Cancer Diagnosis and Prognosis. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431983849.	0.6	6
17730	Identification of significant genes with poor prognosis in ovarian cancer via bioinformatical analysis. <i>Journal of Ovarian Research</i> , 2019, 12, 35.	1.3	111
17731	Comparative analysis of mRNA expression profiles in Type 1 and Type 2 diabetes mellitus. <i>Epigenomics</i> , 2019, 11, 685-699.	1.0	5
17732	microRNA-messenger RNA regulatory network of esophageal squamous cell carcinoma and the identification of miR-1 as a biomarker of patient survival. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 12259-12272.	1.2	14
17733	The promising novel biomarkers and candidate small molecule drugs in lower-grade glioma: Evidence from bioinformatics analysis of high-throughput data. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 15106-15118.	1.2	22
17734	Construction and Analysis of miRNA Regulatory Networks. <i>Methods in Molecular Biology</i> , 2019, 1970, 121-167.	0.4	0
17735	A Perspective on Comparative and Functional Genomics. <i>Computational Biology</i> , 2019, , 361-372.	0.1	1
17736	Resistance mechanisms and cross-resistance for a pyridine-pyrimidine amide inhibitor of microtubule polymerization. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2019, 29, 1647-1653.	1.0	4
17737	Disordered APC/C-mediated cell cycle progression and IGF1/PI3K/AKT signalling are the potential basis of Sertoli cell-only syndrome. <i>Andrologia</i> , 2019, 51, e13288.	1.0	12
17738	Studying alcohol use disorder using <i>Drosophila melanogaster</i> in the era of "Big Data". <i>Behavioral and Brain Functions</i> , 2019, 15, 7.	1.4	20
17739	BRB-seq: ultra-affordable high-throughput transcriptomics enabled by bulk RNA barcoding and sequencing. <i>Genome Biology</i> , 2019, 20, 71.	3.8	125
17740	Predicting synthetic lethal interactions using conserved patterns in protein interaction networks. <i>PLoS Computational Biology</i> , 2019, 15, e1006888.	1.5	34
17741	Investigating architecture and structure-function relationships in cold shock DNA-binding domain family using structural genomics-based approach. <i>International Journal of Biological Macromolecules</i> , 2019, 133, 484-494.	3.6	17
17742	A robust data-driven genomic signature for idiopathic pulmonary fibrosis with applications for translational model selection. <i>PLoS ONE</i> , 2019, 14, e0215565.	1.1	6
17743	Metaproteomics of Freshwater Microbial Communities. <i>Methods in Molecular Biology</i> , 2019, 1977, 145-155.	0.4	1
17744	TAF5L and TAF6L Maintain Self-Renewal of Embryonic Stem Cells via the MYC Regulatory Network. <i>Molecular Cell</i> , 2019, 74, 1148-1163.e7.	4.5	36

#	ARTICLE	IF	CITATIONS
17745	CACNA2D3 Enhances the Chemosensitivity of Esophageal Squamous Cell Carcinoma to Cisplatin via Inducing Ca ²⁺ -Mediated Apoptosis and Suppressing PI3K/Akt Pathways. <i>Frontiers in Oncology</i> , 2019, 9, 185.	1.3	20
17746	In silico markers: an evolutionary and statistical approach to select informative genes of human breast cancer subtypes. <i>Genes and Genomics</i> , 2019, 41, 1371-1382.	0.5	3
17747	Deciphering the three-domain architecture in schlafens and the structures and roles of human schlafen12 and serpinB12 in transcriptional regulation. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 90, 59-76.	1.3	9
17748	FuncTree2: an interactive radial tree for functional hierarchies and omics data visualization. <i>Bioinformatics</i> , 2019, 35, 4519-4521.	1.8	15
17749	Integrating Imaging and Omics: Computational Methods and Challenges. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 175-197.	2.8	33
17750	Evolutionary conservation of MLO gene promoter signatures. <i>BMC Plant Biology</i> , 2019, 19, 150.	1.6	14
17751	Comparative analysis of microRNA expression profiles of adult <i>Schistosoma japonicum</i> isolated from water buffalo and yellow cattle. <i>Parasites and Vectors</i> , 2019, 12, 196.	1.0	6
17752	Defining inflammatory cell states in rheumatoid arthritis joint synovial tissues by integrating single-cell transcriptomics and mass cytometry. <i>Nature Immunology</i> , 2019, 20, 928-942.	7.0	760
17753	Genomic knockout of <i>alms1</i> in zebrafish recapitulates Alström syndrome and provides insight into metabolic phenotypes. <i>Human Molecular Genetics</i> , 2019, 28, 2212-2223.	1.4	16
17754	Plasma Fibronectin Levels Identified via Quantitative Proteomics Profiling Predicts Hepatitis B Surface Antigen Seroclearance in Chronic Hepatitis B. <i>Journal of Infectious Diseases</i> , 2019, 220, 940-950.	1.9	3
17755	Cistrome-GO: a web server for functional enrichment analysis of transcription factor ChIP-seq peaks. <i>Nucleic Acids Research</i> , 2019, 47, W206-W211.	6.5	76
17756	A Multigene Assay Determines Risk of Recurrence in Patients with Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2019, 79, 3466-3478.	0.4	32
17757	Classification tree algorithm for grouped variables. <i>Computational Statistics</i> , 2019, 34, 1613-1648.	0.8	6
17758	Promiscuous Targeting of Cellular Proteins by Vpr Drives Systems-Level Proteomic Remodeling in HIV-1 Infection. <i>Cell Reports</i> , 2019, 27, 1579-1596.e7.	2.9	75
17759	Footprint-based functional analysis of multiomic data. <i>Current Opinion in Systems Biology</i> , 2019, 15, 82-90.	1.3	39
17760	Differential methylation of enhancer at IGF2 is associated with abnormal dopamine synthesis in major psychosis. <i>Nature Communications</i> , 2019, 10, 2046.	5.8	55
17761	UVGD 1.0: a gene-centric database bridging ultraviolet radiation and molecular biology effects in organisms. <i>International Journal of Radiation Biology</i> , 2019, 95, 1172-1177.	1.0	0
17762	Identification and characterization of a novel stay-green QTL that increases yield in maize. <i>Plant Biotechnology Journal</i> , 2019, 17, 2272-2285.	4.1	45

#	ARTICLE	IF	CITATIONS
17763	Disrupted folate metabolism with anesthesia leads to myelination deficits mediated by epigenetic regulation of ERMN. <i>EBioMedicine</i> , 2019, 43, 473-486.	2.7	40
17764	The genomes of pecan and Chinese hickory provide insights into <i>Carya</i> evolution and nut nutrition. <i>GigaScience</i> , 2019, 8, .	3.3	88
17765	Impact of Combined Acidic and Hyperosmotic Shock Conditions on the Proteome of <i>Listeria monocytogenes</i> ATCC 19115 in a Time-Course Study. <i>Journal of Food Quality</i> , 2019, 2019, 1-12.	1.4	2
17766	m6Acomet: large-scale functional prediction of individual m6A RNA methylation sites from an RNA co-methylation network. <i>BMC Bioinformatics</i> , 2019, 20, 223.	1.2	32
17767	Analyses of circRNA profiling during the development from pre-receptive to receptive phases in the goat endometrium. <i>Journal of Animal Science and Biotechnology</i> , 2019, 10, 34.	2.1	29
17768	Developing a vocabulary and ontology for modeling insect natural history data: example data, use cases, and competency questions. <i>Biodiversity Data Journal</i> , 2019, 7, e33303.	0.4	3
17769	Proteomic analysis of the fast-twitch muscle of pacu (<i>Piaractus mesopotamicus</i>) after prolonged fasting and compensatory growth. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 30, 321-332.	0.4	11
17770	Multi-species transcriptome analyses for the regulation of crocins biosynthesis in <i>Crocus</i> . <i>BMC Genomics</i> , 2019, 20, 320.	1.2	16
17771	Genomic characterization of <i>Kerstersia gyiorum</i> SWMUKG01, an isolate from a patient with respiratory infection in China. <i>PLoS ONE</i> , 2019, 14, e0214686.	1.1	3
17772	Anticandidal Potential of Stem Bark Extract from <i>Schima superba</i> and the Identification of Its Major Anticandidal Compound. <i>Molecules</i> , 2019, 24, 1587.	1.7	3
17773	Loss of Msh2 and a single-radiation hit induce common, genome-wide, and persistent epigenetic changes in the intestine. <i>Clinical Epigenetics</i> , 2019, 11, 65.	1.8	11
17774	Direct 3D bioprinted full-thickness skin constructs recapitulate regulatory signaling pathways and physiology of human skin. <i>Bioprinting</i> , 2019, 15, e00051.	2.9	78
17775	Eggplant Domestication: Pervasive Gene Flow, Feralization, and Transcriptomic Divergence. <i>Molecular Biology and Evolution</i> , 2019, 36, 1359-1372.	3.5	47
17776	Impact of ROS-Induced Damage of TCA Cycle Enzymes on Metabolism and Virulence of <i>Salmonella enterica</i> serovar Typhimurium. <i>Frontiers in Microbiology</i> , 2019, 10, 762.	1.5	33
17777	The Transcriptomic Toolbox: Resources for Interpreting Large Gene Expression Data within a Precision Medicine Context for Metabolic Disease Atherosclerosis. <i>Journal of Personalized Medicine</i> , 2019, 9, 21.	1.1	6
17778	Distinct Requirements of CHD4 during B Cell Development and Antibody Response. <i>Cell Reports</i> , 2019, 27, 1472-1486.e5.	2.9	11
17779	Genomic data mining of an Antarctic deep-sea actinobacterium, <i>Janibacter limosus</i> P3-3-X1. <i>Marine Genomics</i> , 2019, 48, 100684.	0.4	7
17780	Dual inhibition of glutaminase and carnitine palmitoyltransferase decreases growth and migration of glutaminase inhibition-resistant triple-negative breast cancer cells. <i>Journal of Biological Chemistry</i> , 2019, 294, 9342-9357.	1.6	53

#	ARTICLE	IF	CITATIONS
17781	In Silico Integration Approach Reveals Key MicroRNAs and Their Target Genes in Follicular Thyroid Carcinoma. <i>BioMed Research International</i> , 2019, 2019, 1-9.	0.9	11
17782	Conserved Secondary Structures in Viral mRNAs. <i>Viruses</i> , 2019, 11, 401.	1.5	22
17783	Genes with High Network Connectivity Are Enriched for Disease Heritability. <i>American Journal of Human Genetics</i> , 2019, 104, 896-913.	2.6	46
17784	Benchmark: An Unbiased, Association-Data-Driven Strategy to Evaluate Gene Prioritization Algorithms. <i>American Journal of Human Genetics</i> , 2019, 104, 1025-1039.	2.6	16
17785	Association Analysis of Deep Genomic Features Extracted by Denoising Autoencoders in Breast Cancer. <i>Cancers</i> , 2019, 11, 494.	1.7	15
17786	Mutational spectrum and associations with clinical features in patients with acute myeloid leukaemia based on next-generation sequencing. <i>Molecular Medicine Reports</i> , 2019, 19, 4147-4158.	1.1	4
17787	I-TASSER gateway: A protein structure and function prediction server powered by XSEDE. <i>Future Generation Computer Systems</i> , 2019, 99, 73-85.	4.9	80
17788	Meta-path Based Prioritization of Functional Drug Actions with Multi-Level Biological Networks. <i>Scientific Reports</i> , 2019, 9, 5469.	1.6	1
17789	Deep Robust Framework for Protein Function Prediction using Variable-Length Protein Sequences. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	1.9	15
17790	Abnormalities in endothelial form of nitric oxide synthase is pathogenic in limited cutaneous systemic sclerosis. <i>Journal of Cosmetic Dermatology</i> , 2019, 18, 1938-1946.	0.8	0
17791	Highly efficient hypothesis testing methods for regression-type tests with correlated observations and heterogeneous variance structure. <i>BMC Bioinformatics</i> , 2019, 20, 185.	1.2	3
17792	In-depth transcriptome characterization uncovers distinct gene family expansions for <i>Cupressus gigantea</i> important to this long-lived species's adaptability to environmental cues. <i>BMC Genomics</i> , 2019, 20, 213.	1.2	12
17793	Simultaneous Interrogation of Cancer Omics to Identify Subtypes With Significant Clinical Differences. <i>Frontiers in Genetics</i> , 2019, 10, 236.	1.1	51
17794	Integration of Multiple Data Sources for Gene Network Inference Using Genetic Perturbation Data. <i>Journal of Computational Biology</i> , 2019, 26, 1113-1129.	0.8	7
17795	DNAmoD: the DNA modification database. <i>Journal of Cheminformatics</i> , 2019, 11, 30.	2.8	53
17796	Screening common signaling pathways associated with drug resistance in non-small cell lung cancer via gene expression profile analysis. <i>Cancer Medicine</i> , 2019, 8, 3059-3071.	1.3	9
17797	Microarray analyses of lncRNAs and mRNAs expression profiling associated with diabetic peripheral neuropathy in rats. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 15347-15359.	1.2	34
17798	An Open Science Approach to Artificial Intelligence in Healthcare. <i>Yearbook of Medical Informatics</i> , 2019, 28, 047-051.	0.8	29

#	ARTICLE	IF	CITATIONS
17799	Chemical suppression of specific C-C chemokine signaling pathways enhances cardiac reprogramming. <i>Journal of Biological Chemistry</i> , 2019, 294, 9134-9146.	1.6	20
17800	A penalized regression model for the joint estimation of eQTL associations and gene network structure. <i>Annals of Applied Statistics</i> , 2019, 13, .	0.5	2
17801	Improving the classification of neuropsychiatric conditions using gene ontology terms as features. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 508-518.	1.1	4
17802	Extended Multitarget Pharmacology of Anticancer Drugs. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 3006-3017.	2.5	17
17803	The Molecular Clock in the Evolution of Protein Structures. <i>Systematic Biology</i> , 2019, 68, 987-1002.	2.7	14
17804	Plasma Protein and MicroRNA Biomarkers of Insulin Resistance: A Network-Based Integrative -Omics Analysis. <i>Frontiers in Physiology</i> , 2019, 10, 379.	1.3	28
17805	<i>Aestuariusphingobium litorale</i> gen. nov., sp. nov., a novel proteobacterium isolated from a water sample of Pearl River estuary. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1357-1367.	0.7	8
17806	PseudoFuN: Deriving functional potentials of pseudogenes from integrative relationships with genes and microRNAs across 32 cancers. <i>GigaScience</i> , 2019, 8, .	3.3	18
17807	MGSEA – a multivariate Gene set enrichment analysis. <i>BMC Bioinformatics</i> , 2019, 20, 145.	1.2	11
17808	Long-read based assembly and synteny analysis of a reference <i>Drosophila subobscura</i> genome reveals signatures of structural evolution driven by inversions recombination-suppression effects. <i>BMC Genomics</i> , 2019, 20, 223.	1.2	15
17809	<i>Drosophila</i> mRNA Localization During Later Development: Past, Present, and Future. <i>Frontiers in Genetics</i> , 2019, 10, 135.	1.1	15
17810	Adapting Community Detection Algorithms for Disease Module Identification in Heterogeneous Biological Networks. <i>Frontiers in Genetics</i> , 2019, 10, 164.	1.1	38
17811	Elucidating Genotype-to-Phenotype Relationships via Analyses of Human Tissue Interactomes. , 2019, , 459-489.		0
17812	Dynamic host immune response in virus-associated cancers. <i>Communications Biology</i> , 2019, 2, 109.	2.0	34
17813	Primate piRNA Cluster Evolution Suggests Limited Relevance of Pseudogenes in piRNA-Mediated Gene Regulation. <i>Genome Biology and Evolution</i> , 2019, 11, 1088-1104.	1.1	10
17814	Assessing the Functional Relevance of Variants in the IKAROS Family Zinc Finger Protein 1 (IKZF1) in a Cohort of Patients With Primary Immunodeficiency. <i>Frontiers in Immunology</i> , 2019, 10, 568.	2.2	37
17815	Transcriptomic analysis of contrasting inbred lines and F2 segregant of Chinese cabbage provides valuable information on leaf morphology. <i>Genes and Genomics</i> , 2019, 41, 811-829.	0.5	1
17816	A transcriptional and functional analysis of heat hardening in two invasive fruit fly species, <i>Bactrocera dorsalis</i> and <i>Bactrocera correcta</i> . <i>Evolutionary Applications</i> , 2019, 12, 1147-1163.	1.5	26

#	ARTICLE	IF	CITATIONS
17817	Comparative Genome and Transcriptome Study of the Gene Expression Difference Between Pathogenic and Environmental Strains of <i>Prototheca zopfii</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 443.	1.5	16
17818	micro-RNAs dependent regulation of DNMT and HIF1 α gene expression in thrombotic disorders. <i>Scientific Reports</i> , 2019, 9, 4815.	1.6	6
17819	High levels of PIWI-interacting RNAs are present in the small RNA landscape of prostate epithelium from vitamin D clinical trial specimens. <i>Prostate</i> , 2019, 79, 840-855.	1.2	11
17820	Tandem-running and scouting behaviour are characterized by up-regulation of learning and memory formation genes within the ant brain. <i>Molecular Ecology</i> , 2019, 28, 2342-2359.	2.0	19
17821	Quantification and discovery of sequence determinants of protein-mRNA amount in human tissues. <i>Molecular Systems Biology</i> , 2019, 15, e8513.	3.2	63
17822	KIF15 promotes bladder cancer proliferation via the MEK-ERK signaling pathway. <i>Cancer Management and Research</i> , 2019, Volume 11, 1857-1868.	0.9	22
17823	Differential inflammatory landscape stimulus during titanium surfaces obtained osteogenic phenotype. <i>Journal of Biomedical Materials Research - Part A</i> , 2019, 107, 1597-1604.	2.1	11
17824	iTRAQ-based proteomic analysis reveals the accumulation of bioactive compounds in Chinese wild rice (<i>Zizania latifolia</i>) during germination. <i>Food Chemistry</i> , 2019, 289, 635-644.	4.2	35
17825	The Balancing Act of Intrinsically Disordered Proteins: Enabling Functional Diversity while Minimizing Promiscuity. <i>Journal of Molecular Biology</i> , 2019, 431, 1650-1670.	2.0	41
17826	Curating gene sets: challenges and opportunities for integrative analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	5
17827	Genome-wide genotyping uncovers genetic diversity, phylogeny, signatures of selection, and population structure of Chinese Jiangquhai pigs in a global perspective. <i>Journal of Animal Science</i> , 2019, 97, 1491-1500.	0.2	18
17828	White Matter is the Predilection Site of Late-Delayed Radiation-Induced Brain Injury in Non-Human Primates. <i>Radiation Research</i> , 2019, 191, 217.	0.7	18
17829	Transcriptional Reprogramming of <i>Arabidopsis thaliana</i> Defence Pathways by the Entomopathogen <i>Beauveria bassiana</i> Correlates With Resistance Against a Fungal Pathogen but Not Against Insects. <i>Frontiers in Microbiology</i> , 2019, 10, 615.	1.5	37
17830	A microRNA profile of pediatric glioblastoma: The role of NUCKS1 upregulation. <i>Molecular and Clinical Oncology</i> , 2019, 10, 331-338.	0.4	13
17831	Human iPSC-derived MSCs (iMSCs) from aged individuals acquire a rejuvenation signature. <i>Stem Cell Research and Therapy</i> , 2019, 10, 100.	2.4	90
17832	Fine mapping of <i>lcm1</i> , a gene conferring chlorophyll-deficient golden leaf in Chinese cabbage (<i>Brassica</i>) Tj ETQq1 1.0, 784314, ggBT / Ome	1.0	15
17833	High-Resolution Mapping of the <i>Escherichia coli</i> Chromosome Reveals Positions of High and Low Transcription. <i>Cell Systems</i> , 2019, 8, 212-225.e9.	2.9	79
17834	Drug Repurposing From Transcriptome Data: Methods and Applications. , 2019, , 303-327.		2

#	ARTICLE	IF	CITATIONS
17835	Caffeine Content and Related Gene Expression: Novel Insight into Caffeine Metabolism in <i>Camellia</i> Plants Containing Low, Normal, and High Caffeine Concentrations. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 3400-3411.	2.4	61
17836	A transcriptome-wide analysis deciphers distinct roles of G1 cyclins in temporal organization of the yeast cell cycle. <i>Scientific Reports</i> , 2019, 9, 3343.	1.6	9
17837	Integrated Analysis of Whole Exome Sequencing and Copy Number Evaluation in Parkinson's Disease. <i>Scientific Reports</i> , 2019, 9, 3344.	1.6	31
17838	Genome-wide analysis reveals the genomic features of the turkey vulture (<i>Cathartes aura</i>) as a scavenger. <i>Molecular Genetics and Genomics</i> , 2019, 294, 679-692.	1.0	10
17839	Hepatocytes direct the formation of a pro-metastatic niche in the liver. <i>Nature</i> , 2019, 567, 249-252.	13.7	263
17840	PAI-1 augments mucosal damage in colitis. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	44
17841	Repository of Enriched Structures of Proteins Involved in the Red Blood Cell Environment (RESPIRE). <i>PLoS ONE</i> , 2019, 14, e0211043.	1.1	5
17842	Integrative Analysis Reveals Key Circular RNA in Atrial Fibrillation. <i>Frontiers in Genetics</i> , 2019, 10, 108.	1.1	18
17843	Combined Genomic, Transcriptomic, Proteomic, and Physiological Characterization of the Growth of <i>Pecoramyces</i> sp. F1 in Monoculture and Co-culture With a Syntrophic Methanogen. <i>Frontiers in Microbiology</i> , 2019, 10, 435.	1.5	25
17844	A gene signature associated with prognosis and immune processes in head and neck squamous cell carcinoma. <i>Head and Neck</i> , 2019, 41, 2581-2590.	0.9	13
17845	Gonadal microRNA Expression Profiles and Their Potential Role in Sex Differentiation and Gonadal Maturation of Mud Crab <i>Scylla paramamosain</i> . <i>Marine Biotechnology</i> , 2019, 21, 320-334.	1.1	22
17846	The Genome of <i>Cucurbita argyrosperma</i> (Silver-Seed Gourd) Reveals Faster Rates of Protein-Coding Gene and Long Noncoding RNA Turnover and Neofunctionalization within <i>Cucurbita</i> . <i>Molecular Plant</i> , 2019, 12, 506-520.	3.9	48
17847	Succinyl-proteome profiling of <i>Pyricularia oryzae</i> , a devastating phytopathogenic fungus that causes rice blast disease. <i>Scientific Reports</i> , 2019, 9, 3490.	1.6	14
17848	Automated exploration of gene ontology term and pathway networks with ClueGO-REST. <i>Bioinformatics</i> , 2019, 35, 3864-3866.	1.8	48
17849	A new <i>MEIOB</i> mutation is a recurrent cause for azoospermia and testicular meiotic arrest. <i>Human Reproduction</i> , 2019, 34, 666-671.	0.4	50
17850	Functional protein representations from biological networks enable diverse cross-species inference. <i>Nucleic Acids Research</i> , 2019, 47, e51-e51.	6.5	23
17851	In Silico Databases and Tools for Drug Repurposing. , 2019, , 703-742.		7
17852	Identification and expression analysis of candidate chemosensory receptors based on the antennal transcriptome of <i>Lissorhoptrus oryzophilus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 30, 133-142.	0.4	9

#	ARTICLE	IF	CITATIONS
17853	Target discovery of chlorogenic acid derivatives from the flower buds of <i>Lonicera macranthoides</i> and their MAO B inhibitory mechanism. <i>FÄ-toterapÄ-Äç</i> , 2019, 134, 297-304.	1.1	19
17854	Gene expression profiling meta-analysis reveals novel gene signatures and pathways shared between tuberculosis and rheumatoid arthritis. <i>PLoS ONE</i> , 2019, 14, e0213470.	1.1	21
17855	LncRNAs GIHCG and SPINT1-AS1 Are Crucial Factors for Pan-Cancer Cells Sensitivity to Lapatinib. <i>Frontiers in Genetics</i> , 2019, 10, 25.	1.1	23
17856	Growth Factor Screening in Dystrophic Muscles Reveals PDGFB/PDGFRB-Mediated Migration of Interstitial Stem Cells. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1118.	1.8	12
17858	Connective Tissue Growth Factor Inhibition Enhances Cardiac Repair and Limits Fibrosis After Myocardial Infarction. <i>JACC Basic To Translational Science</i> , 2019, 4, 83-94.	1.9	48
17859	Enhancing the prediction of diseaseâ€“gene associations with multimodal deep learning. <i>Bioinformatics</i> , 2019, 35, 3735-3742.	1.8	52
17860	Comparative and Functional Algal Genomics. <i>Annual Review of Plant Biology</i> , 2019, 70, 605-638.	8.6	76
17861	A modular analysis of microglia gene expression, insights into the aged phenotype. <i>BMC Genomics</i> , 2019, 20, 164.	1.2	24
17862	Identification of novel candidate indicators for assessing zinc status during pregnancy in mice from microarray data. <i>BMC Pharmacology & Toxicology</i> , 2019, 20, 12.	1.0	1
17863	Integrative analysis of Paneth cell proteomic and transcriptomic data from intestinal organoids reveals functional processes dependent on autophagy. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	1.2	20
17864	Shared Gene Expression Between Multiple Sclerosis and Ischemic Stroke. <i>Frontiers in Genetics</i> , 2018, 9, 598.	1.1	9
17865	Identification of survivalâ€“associated key genes and long nonâ€“coding RNAs in glioblastoma multiforme by weighted gene coâ€“expression network analysis. <i>International Journal of Molecular Medicine</i> , 2019, 43, 1709-1722.	1.8	13
17866	Complete Genome Sequence of <i>Arthrobacter sp</i> . Strain MN05-02, a UV-Resistant Bacterium from a Manganese Deposit in the Sonoran Desert. <i>Journal of Genomics</i> , 2019, 7, 18-25.	0.6	2
17867	Emergent functions of proteins in non-stoichiometric supramolecular assemblies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 970-979.	1.1	49
17868	Comparative genomics sheds light on the predatory lifestyle of accipitrids and owls. <i>Scientific Reports</i> , 2019, 9, 2249.	1.6	14
17869	Chronic hypoxia changes gene expression profile of primary rat carotid body cells: consequences on the expression of NOS isoforms and ET-1 receptors. <i>Physiological Genomics</i> , 2019, 51, 109-124.	1.0	6
17870	Genomic Features of Exceptional Response in Vemurafenib Ä± Cobimetinibâ€“treated Patients with <i>BRAF</i> -mutated Metastatic Melanoma. <i>Clinical Cancer Research</i> , 2019, 25, 3239-3246.	3.2	32
17871	Systematic Review of the Prognostic Role of the Immune System After Surgery of Colorectal Liver Metastases. <i>Frontiers in Oncology</i> , 2019, 9, 148.	1.3	11

#	ARTICLE	IF	CITATIONS
17872	Identification of Potential Genes Responsible for Thermotolerance in Wheat under High Temperature Stress. <i>Genes</i> , 2019, 10, 174.	1.0	22
17873	Integrative analysis of cancer driver genes in prostate adenocarcinoma. <i>Molecular Medicine Reports</i> , 2019, 19, 2707-2715.	1.1	28
17874	Metabolism disruption analysis of zebrafish larvae in response to BPA and BPA analogs based on RNA-Seq technique. <i>Ecotoxicology and Environmental Safety</i> , 2019, 174, 181-188.	2.9	30
17875	A novel matched-pairs feature selection method considering with tumor purity for differential gene expression analyses. <i>Mathematical Biosciences</i> , 2019, 311, 39-48.	0.9	4
17876	Proteomic Identification of Protein Glutathionylation in Cardiomyocytes. <i>Journal of Proteome Research</i> , 2019, 18, 1806-1818.	1.8	19
17877	CausalTAB: the PSI-MITAB 2.8 updated format for signalling data representation and dissemination. <i>Bioinformatics</i> , 2019, 35, 3779-3785.	1.8	32
17878	Functional geometry of protein interactomes. <i>Bioinformatics</i> , 2019, 35, 3727-3734.	1.8	5
17879	High-throughput sequencing of small RNAs and analysis of differentially expressed microRNAs associated with high-fat diet-induced hepatic insulin resistance in mice. <i>Genes and Nutrition</i> , 2019, 14, 6.	1.2	16
17880	Integrated Analysis of miRNA and mRNA Expression Profiles in Spleen of Specific Pathogen-Free Chicken Infected with Avian Reticuloendotheliosis Virus Strain SNV. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1041.	1.8	13
17881	Prediction of platinum resistance patients of gastric cancer using bioinformatics. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 13478-13486.	1.2	6
17882	Origination and evolution of orphan genes and de novo genes in the genome of <i>Caenorhabditis elegans</i> . <i>Science China Life Sciences</i> , 2019, 62, 579-593.	2.3	21
17883	Epigenetic effects of paternal cocaine on reward stimulus behavior and accumbens gene expression in mice. <i>Behavioural Brain Research</i> , 2019, 367, 68-81.	1.2	14
17884	Interaction of Discoidin Domain Receptor 1 with a 14-3-3-Becn1-Akt1 Complex Modulates Glioblastoma Therapy Sensitivity. <i>Cell Reports</i> , 2019, 26, 3672-3683.e7.	2.9	48
17885	De novo transcriptome sequencing and gene expression profiling of sweet potato leaves during low temperature stress and recovery. <i>Gene</i> , 2019, 700, 23-30.	1.0	18
17886	Prediction of new vaccine targets in the core genome of <i>Corynebacterium pseudotuberculosis</i> through omics approaches and reverse vaccinology. <i>Gene</i> , 2019, 702, 36-45.	1.0	31
17887	De novo assembly and characterization of the transcriptome of the northern mauxia shrimp <i>Acetes chinensis</i> . <i>Marine Genomics</i> , 2019, 47, 100672.	0.4	4
17888	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. <i>Nature Genetics</i> , 2019, 51, 659-674.	9.4	154
17889	Safeguard function of PU.1 shapes the inflammatory epigenome of neutrophils. <i>Nature Immunology</i> , 2019, 20, 546-558.	7.0	40

#	ARTICLE	IF	CITATIONS
17890	Metatranscriptomic exploration of microbial functioning in clouds. <i>Scientific Reports</i> , 2019, 9, 4383.	1.6	68
17891	Ontologies to interpret remote sensing images: why do we need them?. <i>GIScience and Remote Sensing</i> , 2019, 56, 911-939.	2.4	38
17892	A gene for resistance to the <i>Varroa</i> mite (Acari) in honey bee (<i>Apis mellifera</i>) pupae. <i>Molecular Ecology</i> , 2019, 28, 2958-2966.	2.0	33
17893	Integrative Bioinformatics Analysis Reveals Potential Gene Biomarkers and Analysis of Function in Human Degenerative Disc Annulus Fibrosus Cells. <i>BioMed Research International</i> , 2019, 2019, 1-8.	0.9	8
17894	Genetic and genomic analyses of latent variables related to the milk fatty acid profile, milk composition, and udder health in dairy cattle. <i>Journal of Dairy Science</i> , 2019, 102, 5254-5265.	1.4	32
17895	Prediction of key gene function in spinal muscular atrophy using guilt by association method based on network and gene ontology. <i>Experimental and Therapeutic Medicine</i> , 2019, 17, 2561-2566.	0.8	4
17896	Genome-wide DNA methylation profile of thymomas and potential epigenetic regulation of thymoma subtypes. <i>Oncology Reports</i> , 2019, 41, 2762-2774.	1.2	10
17897	Too Many False Targets for MicroRNAs: Challenges and Pitfalls in Prediction of miRNA Targets and Their Gene Ontology in Model and Non-model Organisms. <i>BioEssays</i> , 2019, 41, e1800169.	1.2	56
17898	Essentials of Bioinformatics, Volume I. , 2019, , .		8
17899	Simultaneous clustering of multiview biomedical data using manifold optimization. <i>Bioinformatics</i> , 2019, 35, 4029-4037.	1.8	13
17900	Genome-Wide Identification, Characterization, and Expression Analysis of the Grapevine Superoxide Dismutase (SOD) Family. <i>International Journal of Genomics</i> , 2019, 2019, 1-13.	0.8	25
17901	Encircling the regions of the pharmacogenomic landscape that determine drug response. <i>Genome Medicine</i> , 2019, 11, 17.	3.6	14
17902	Selection of a Real-Time PCR Housekeeping Gene Panel in Human Endothelial Colony Forming Cells for Cellular Senescence Studies. <i>Frontiers in Medicine</i> , 2019, 6, 33.	1.2	17
17903	Integrating Germline and Somatic Mutation Information for the Discovery of Biomarkers in Triple-Negative Breast Cancer. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 1055.	1.2	14
17904	Polyadenylation sites and their characteristics in the genome of channel catfish (<i>Ictalurus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 Td <i>Genomics and Proteomics</i> , 2019, 30, 248-255.	0.4	0
17905	Death of female flower microsporocytes progresses independently of meiosis-like process and can be accelerated by specific transcripts in <i>Asparagus officinalis</i> . <i>Scientific Reports</i> , 2019, 9, 2703.	1.6	5
17906	Proteomic profiling and integrated analysis with transcriptomic data bring new insights in the stress responses of <i>Kluyveromyces marxianus</i> after an arrest during high-temperature ethanol fermentation. <i>Biotechnology for Biofuels</i> , 2019, 12, 49.	6.2	24
17907	Comparative genomics reveals the unique evolutionary status of <i>Plasmodiophora brassicae</i> and the essential role of GPCR signaling pathways. <i>Phytopathology Research</i> , 2019, 1, .	0.9	17

#	ARTICLE	IF	CITATIONS
17908	Transcriptional Analysis of Immunohistochemically Defined Subgroups of Non-Muscle-Invasive Papillary High-Grade Upper Tract Urothelial Carcinoma. <i>International Journal of Molecular Sciences</i> , 2019, 20, 570.	1.8	16
17909	Investigating the role of <i>Osiris</i> genes in <i>Drosophila sechellia</i> larval resistance to a host plant toxin. <i>Ecology and Evolution</i> , 2019, 9, 1922-1933.	0.8	21
17910	Transcriptional profiling of lactic acid treated reconstructed human epidermis reveals pathways underlying stinging and itch. <i>Toxicology in Vitro</i> , 2019, 57, 164-173.	1.1	12
17911	Salt-Enhanced Reproductive Development of <i>Suaeda salsa</i> L. Coincided With Ion Transporter Gene Upregulation in Flowers and Increased Pollen K ⁺ Content. <i>Frontiers in Plant Science</i> , 2019, 10, 333.	1.7	37
17912	From the Amazon: A comprehensive liver transcriptome dataset of the teleost fish tambaqui, <i>Colossoma macropomum</i> . <i>Data in Brief</i> , 2019, 23, 103751.	0.5	3
17913	Collective influencers in protein interaction networks. <i>Scientific Reports</i> , 2019, 9, 3948.	1.6	7
17914	Integrated analyses of lncRNAs microarray profiles and mRNA lncRNA coexpression in smooth muscle cells under hypoxic and normoxic conditions. <i>Bioscience Reports</i> , 2019, 39, .	1.1	12
17915	Identifying Genome-Wide Sequence Variations and Candidate Genes Implicated in Self-Incompatibility by Resequencing <i>Fragaria viridis</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 1039.	1.8	6
17916	Comprehensive Analysis of Driver Genes in Personal Genomes of Clear Cell Renal Cell Carcinoma. <i>Technology in Cancer Research and Treatment</i> , 2019, 18, 153303381983096.	0.8	3
17917	Characterization of the <i>Rosa roxburghii</i> Tratt transcriptome and analysis of MYB genes. <i>PLoS ONE</i> , 2019, 14, e0203014.	1.1	20
17918	Genome Sequencing Illustrates the Genetic Basis of the Pharmacological Properties of <i>Gloeostereum incarnatum</i> . <i>Genes</i> , 2019, 10, 188.	1.0	33
17919	Proteomic Analysis of Horseweed (<i>Conyza canadensis</i>) Subjected to Caprylic Acid Stress. <i>Proteomics</i> , 2019, 19, 1800294.	1.3	3
17920	Deep transcriptome analysis of the heat shock response in an Atlantic sturgeon (<i>Acipenser</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 T	1.6	13
17921	A new genomic blueprint of the human gut microbiota. <i>Nature</i> , 2019, 568, 499-504.	13.7	901
17922	MorCVD: A Unified Database for Host-Pathogen Protein-Protein Interactions of Cardiovascular Diseases Related to Microbes. <i>Scientific Reports</i> , 2019, 9, 4039.	1.6	10
17923	Genome-wide DNA methylation changes in transformed foci induced by nongenotoxic carcinogens. <i>Environmental and Molecular Mutagenesis</i> , 2019, 60, 576-587.	0.9	6
17925	Gene grouping strategy for network modeling from a small time-series dataset: An illustrative analysis of human organogenesis. <i>BioSystems</i> , 2019, 179, 24-29.	0.9	0
17926	Comparative transcriptome analysis of dioecious, unisexual floral development in <i>Ribes diacanthum</i> pall. <i>Gene</i> , 2019, 699, 43-53.	1.0	5

#	ARTICLE	IF	CITATIONS
17927	TACCO, a Database Connecting Transcriptome Alterations, Pathway Alterations and Clinical Outcomes in Cancers. <i>Scientific Reports</i> , 2019, 9, 3877.	1.6	19
17928	Integrative microRNA-mRNA Analysis of Muscle Tissues in Qianhua Mutton Merino and Small Tail Han Sheep Reveals Key Roles for oar-miR-655-3p and oar-miR-381-5p. <i>DNA and Cell Biology</i> , 2019, 38, 423-435.	0.9	17
17929	The Genome of <i>Drosophila innubila</i> Reveals Lineage-Specific Patterns of Selection in Immune Genes. <i>Molecular Biology and Evolution</i> , 2019, 36, 1405-1417.	3.5	37
17930	GenTree, an integrated resource for analyzing the evolution and function of primate-specific coding genes. <i>Genome Research</i> , 2019, 29, 682-696.	2.4	67
17931	Handling Big Data Scalability in Biological Domain Using Parallel and Distributed Processing: A Case of Three Biological Semantic Similarity Measures. <i>BioMed Research International</i> , 2019, 2019, 1-20.	0.9	3
17932	Expression Divergence as an Evolutionary Alternative Mechanism Adopted by Two Rice Subspecies Against Rice Blast Infection. <i>Rice</i> , 2019, 12, 12.	1.7	9
17933	Combined analysis and validation for DNA methylation and gene expression profiles associated with prostate cancer. <i>Cancer Cell International</i> , 2019, 19, 50.	1.8	28
17934	Plastid genome and composition analysis of two medical ferns: <i>Dryopteris crassirhizoma</i> Nakai and <i>Osmunda japonica</i> Thunb.. <i>Chinese Medicine</i> , 2019, 14, 9.	1.6	8
17935	Comparative analysis of the transcriptome of the Amazonian fish species <i>Colossoma macropomum</i> (tambaqui) and hybrid tambacu by next generation sequencing. <i>PLoS ONE</i> , 2019, 14, e0212755.	1.1	12
17936	Neuronal Apolipoprotein E4 Expression Results in Proteome-Wide Alterations and Compromises Bioenergetic Capacity by Disrupting Mitochondrial Function. <i>Journal of Alzheimer's Disease</i> , 2019, 68, 991-1011.	1.2	57
17937	The Protein-Protein Interaction Network of <i>Litopenaeus vannamei</i> Haemocytes. <i>Frontiers in Physiology</i> , 2019, 10, 156.	1.3	9
17938	myDIG: Personalized Illicit Domain-Specific Knowledge Discovery with No Programming. <i>Future Internet</i> , 2019, 11, 59.	2.4	8
17939	Construction of a cDNA library and preliminary analysis of the expressed sequence tags of the earthworm <i>Eisenia fetida</i> (Savigny, 1826). <i>Molecular Medicine Reports</i> , 2019, 19, 2537-2550.	1.1	0
17940	Public data sources to support systems toxicology applications. <i>Current Opinion in Toxicology</i> , 2019, 16, 17-24.	2.6	10
17941	Field transcriptome revealed a novel relationship between nitrate transport and flowering in Japanese beech. <i>Scientific Reports</i> , 2019, 9, 4325.	1.6	18
17942	Comprehensive analysis of the GATA transcription factor gene family in breast carcinoma using gene microarrays, online databases and integrated bioinformatics. <i>Scientific Reports</i> , 2019, 9, 4467.	1.6	16
17943	Differentially expressed genes ASPN, COL1A1, FN1, VCAN and MUC5AC are potential prognostic biomarkers for gastric cancer. <i>Oncology Letters</i> , 2019, 17, 3191-3202.	0.8	54
17944	Protein-Level Statistical Analysis of Quantitative Label-Free Proteomics Data with ProStaR. <i>Methods in Molecular Biology</i> , 2019, 1959, 225-246.	0.4	11

#	ARTICLE	IF	CITATIONS
17945	The International Cancer Genome Consortium Data Portal. <i>Nature Biotechnology</i> , 2019, 37, 367-369.	9.4	332
17946	Transcriptome analysis of the curry tree (<i>Berbera koenigii</i> L., Rutaceae) during leaf development. <i>Scientific Reports</i> , 2019, 9, 4230.	1.6	2
17947	Quantitative evaluation of ontology design patterns for combining pathology and anatomy ontologies. <i>Scientific Reports</i> , 2019, 9, 4025.	1.6	13
17948	Gene Expression Pattern and Regulatory Network of $\hat{\pm}$ -Toxin Treatment in <i>Bombyx mori</i> . <i>International Journal of Genomics</i> , 2019, 2019, 1-11.	0.8	1
17949	Integrating germline and somatic variation information using genomic data for the discovery of biomarkers in prostate cancer. <i>BMC Cancer</i> , 2019, 19, 229.	1.1	19
17950	Powerful gene set analysis in GWAS with the Generalized Berk-Jones statistic. <i>PLoS Genetics</i> , 2019, 15, e1007530.	1.5	35
17951	Comparative transcriptome analysis of salt-sensitive and salt-tolerant maize reveals potential mechanisms to enhance salt resistance. <i>Genes and Genomics</i> , 2019, 41, 781-801.	0.5	50
17952	Clinical and Genome-wide Analysis of Cisplatin-induced Tinnitus Implicates Novel Ototoxic Mechanisms. <i>Clinical Cancer Research</i> , 2019, 25, 4104-4116.	3.2	27
17953	Comparative transcriptome analyses revealed different heat stress responses in high- and low-GS <i>Brassica alboglabra</i> sprouts. <i>BMC Genomics</i> , 2019, 20, 269.	1.2	16
17954	MicroRNA Target Identification. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	2
17955	Xenbase: Facilitating the Use of <i>Xenopus</i> to Model Human Disease. <i>Frontiers in Physiology</i> , 2019, 10, 154.	1.3	61
17956	A Systematic Workflow for Design and Computational Analysis of Protein Microarrays. , 2019, , 213-222.		1
17957	Evaluation of synthetic gene encoding $\hat{\pm}$ -galactosidase through metagenomic sequencing of paddy soil. <i>Journal of Bioscience and Bioengineering</i> , 2019, 128, 274-282.	1.1	7
17958	<i>Prunus</i> genetics and applications after de novo genome sequencing: achievements and prospects. <i>Horticulture Research</i> , 2019, 6, 58.	2.9	121
17959	Context-specific interaction networks from vector representation of words. <i>Nature Machine Intelligence</i> , 2019, 1, 181-190.	8.3	9
17960	Salicylic acid treats acne vulgaris by suppressing $\langle scp \rangle$ AMPK $\langle /scp \rangle$ / $\langle scp \rangle$ SREBP $\langle /scp \rangle$ 1 pathway in sebocytes. <i>Experimental Dermatology</i> , 2019, 28, 786-794.	1.4	35
17961	Differential expression analysis of <i>Trichoderma virens</i> RNA reveals a dynamic transcriptome during colonization of <i>Zea mays</i> roots. <i>BMC Genomics</i> , 2019, 20, 280.	1.2	33
17962	Genomic signature of parity in the breast of premenopausal women. <i>Breast Cancer Research</i> , 2019, 21, 46.	2.2	29

#	ARTICLE	IF	CITATIONS
17963	The Promoter Regions of Intellectual Disability-Associated Genes Are Uniquely Enriched in LTR Sequences of the MER41 Primate-Specific Endogenous Retrovirus: An Evolutionary Connection Between Immunity and Cognition. <i>Frontiers in Genetics</i> , 2019, 10, 321.	1.1	10
17964	Actomyosin contraction during cellularization is regulated in part by Src64 control of Actin 5C protein levels. <i>Genesis</i> , 2019, 57, e23297.	0.8	4
17965	Mass Spectrometry of Proteins. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	0
17966	CBSSD: community-based semantic subgroup discovery. <i>Journal of Intelligent Information Systems</i> , 2019, 53, 265-304.	2.8	11
17967	Genetic effects of welding fumes on the development of respiratory system diseases. <i>Computers in Biology and Medicine</i> , 2019, 108, 142-149.	3.9	30
17968	Apple whole genome sequences: recent advances and new prospects. <i>Horticulture Research</i> , 2019, 6, 59.	2.9	77
17969	Elucidating the transcriptional program of feline injection-site sarcoma using a cross-species mRNA-sequencing approach. <i>BMC Cancer</i> , 2019, 19, 311.	1.1	7
17970	Identification of pharmacodynamic biomarker hypotheses through literature analysis with IBM Watson. <i>PLoS ONE</i> , 2019, 14, e0214619.	1.1	6
17971	Identification of hub genes in chronically hypoxic myocardium using bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2019, 19, 3871-3881.	1.1	1
17972	Network and Pathway-Based Analysis of Single-Nucleotide Polymorphism of miRNA in Temporal Lobe Epilepsy. <i>Molecular Neurobiology</i> , 2019, 56, 7022-7031.	1.9	8
17973	Independent Microevolution Mediated by Mobile Genetic Elements of Individual <i>Clostridium difficile</i> Isolates from Clade 4 Revealed by Whole-Genome Sequencing. <i>MSystems</i> , 2019, 4, .	1.7	16
17974	Causal Disturbance Analysis: A Novel Graph Centrality Based Method for Pathway Enrichment Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	1.9	1
17975	Fine-tuned adaptation of embryoâ€‘endometrium pairs at implantation revealed by transcriptome analyses in <i>Bos taurus</i> . <i>PLoS Biology</i> , 2019, 17, e3000046.	2.6	14
17976	Mining Featured Biomarkers Linked with Epithelial Ovarian Cancer Based on Bioinformatics. <i>Diagnostics</i> , 2019, 9, 39.	1.3	3
17977	Entity Resolution. <i>SpringerBriefs in Computer Science</i> , 2019, , 33-57.	0.2	1
17978	Ecosystems. <i>SpringerBriefs in Computer Science</i> , 2019, , 75-87.	0.2	0
17979	Protein interactome of the deamidase phosphoribosylformylglycinamide synthetase (PFAS) by LC-MS/MS. <i>Biochemical and Biophysical Research Communications</i> , 2019, 513, 746-752.	1.0	10
17980	Identification of the gene cluster for bistropolone-humulene meroterpenoid biosynthesis in <i>Phoma</i> sp.. <i>Fungal Genetics and Biology</i> , 2019, 129, 7-15.	0.9	26

#	ARTICLE	IF	CITATIONS
17981	Aligning the Aligners: Comparison of RNA Sequencing Data Alignment and Gene Expression Quantification Tools for Clinical Breast Cancer Research. <i>Journal of Personalized Medicine</i> , 2019, 9, 18.	1.1	17
17982	A photocleavable surfactant for top-down proteomics. <i>Nature Methods</i> , 2019, 16, 417-420.	9.0	82
17983	Identification of candidate cancer predisposing variants by performing whole-exome sequencing on index patients from BRCA1 and BRCA2-negative breast cancer families. <i>BMC Cancer</i> , 2019, 19, 313.	1.1	39
17984	Informatics and Computational Methods in Natural Product Drug Discovery: A Review and Perspectives. <i>Frontiers in Genetics</i> , 2019, 10, 368.	1.1	95
17985	Alkylaminophenol Induces G1/S Phase Cell Cycle Arrest in Glioblastoma Cells Through p53 and Cyclin-Dependent Kinase Signaling Pathway. <i>Frontiers in Pharmacology</i> , 2019, 10, 330.	1.6	42
17986	Computational Methods to Investigate the Impact of miRNAs on Pathways. <i>Methods in Molecular Biology</i> , 2019, 1970, 183-209.	0.4	5
17987	Genome-wide analysis of differentially expressed lncRNA in sporadic parathyroid tumors. <i>Osteoporosis International</i> , 2019, 30, 1511-1519.	1.3	8
17988	Transcriptomic analysis of the interaction of choriocarcinoma spheroids with receptive vs. non-receptive endometrial epithelium cell lines: an in vitro model for human implantation. <i>Journal of Assisted Reproduction and Genetics</i> , 2019, 36, 857-873.	1.2	13
17989	Yeast Ataxin-2 Forms an Intracellular Condensate Required for the Inhibition of TORC1 Signaling during Respiratory Growth. <i>Cell</i> , 2019, 177, 697-710.e17.	13.5	73
17990	Integrative transcriptomic analysis suggests new autoregulatory splicing events coupled with nonsense-mediated mRNA decay. <i>Nucleic Acids Research</i> , 2019, 47, 5293-5306.	6.5	49
17991	Genetic control of cellular morphogenesis in Müller glia. <i>Glia</i> , 2019, 67, 1401-1411.	2.5	20
17992	Four novel biomarkers for bladder cancer identified by weighted gene coexpression network analysis. <i>Journal of Cellular Physiology</i> , 2019, 234, 19073-19087.	2.0	22
17993	A new class of metrics for learning on real-valued and structured data. <i>Data Mining and Knowledge Discovery</i> , 2019, 33, 995-1016.	2.4	7
17994	Quantitative proteomics suggest a potential link between early embryonic death and trisomy 16. <i>Reproduction, Fertility and Development</i> , 2019, 31, 1116.	0.1	3
17995	GO functional similarity clustering depends on similarity measure, clustering method, and annotation completeness. <i>BMC Bioinformatics</i> , 2019, 20, 155.	1.2	19
17996	Discovery of Covalent CDK14 Inhibitors with Pan-TAIRE Family Specificity. <i>Cell Chemical Biology</i> , 2019, 26, 804-817.e12.	2.5	19
17997	A comprehensive review of feature based methods for drug target interaction prediction. <i>Journal of Biomedical Informatics</i> , 2019, 93, 103159.	2.5	104
17998	Î±1ACT Is Essential for Survival and Early Cerebellar Programming in a Critical Neonatal Window. <i>Neuron</i> , 2019, 102, 770-785.e7.	3.8	25

#	ARTICLE	IF	CITATIONS
17999	The identification of differentially expressed genes between extremes of placental efficiency in maternal line gilts on day 95 of gestation. <i>BMC Genomics</i> , 2019, 20, 254.	1.2	11
18000	Maternal diet deficient in riboflavin induces embryonic death associated with alterations in the hepatic proteome of duck embryos. <i>Nutrition and Metabolism</i> , 2019, 16, 19.	1.3	21
18001	Transcriptome sequencing of Himalayan Raspberry (<i>Rubus ellipticus</i>) and development of simple sequence repeat markers. <i>3 Biotech</i> , 2019, 9, 161.	1.1	11
18002	iMotor-CNN: Identifying molecular functions of cytoskeleton motor proteins using 2D convolutional neural network via Chou's 5-step rule. <i>Analytical Biochemistry</i> , 2019, 575, 17-26.	1.1	52
18003	Effects of adding a reverse edge across a stem in a directed acyclic graph. <i>Automatica</i> , 2019, 103, 254-260.	3.0	19
18004	A mouse model for SPG48 reveals a block of autophagic flux upon disruption of adaptor protein complex five. <i>Neurobiology of Disease</i> , 2019, 127, 419-431.	2.1	26
18005	A siphonous macroalgal genome suggests convergent functions of homeobox genes in algae and land plants. <i>DNA Research</i> , 2019, 26, 183-192.	1.5	35
18006	Combining microfluidics and RNA-sequencing to assess the inducible defensome of a mushroom against nematodes. <i>BMC Genomics</i> , 2019, 20, 243.	1.2	19
18007	Other Biological Databases. , 2019, , 75-96.		0
18008	Transcriptomic analysis of overexpressed SOX4 and SOX8 in TM4 Sertoli cells with emphasis on cell-to-cell interactions. <i>Biochemical and Biophysical Research Communications</i> , 2019, 512, 678-683.	1.0	8
18009	Biological Networks: Tools, Methods, and Analysis. , 2019, , 255-286.		1
18010	Identification of alternative oxidase encoding genes in <i>Caulerpa cylindracea</i> by de novo RNA-Seq assembly analysis. <i>Marine Genomics</i> , 2019, 46, 41-48.	0.4	5
18011	Metascape provides a biologist-oriented resource for the analysis of systems-level datasets. <i>Nature Communications</i> , 2019, 10, 1523.	5.8	7,886
18012	exRNA Atlas Analysis Reveals Distinct Extracellular RNA Cargo Types and Their Carriers Present across Human Biofluids. <i>Cell</i> , 2019, 177, 463-477.e15.	13.5	228
18013	Genome sequencing for rightward hemispheric language dominance. <i>Genes, Brain and Behavior</i> , 2019, 18, e12572.	1.1	14
18014	Prioritizing candidate genes for fertility in dairy cows using gene-based analysis, functional annotation and differential gene expression. <i>BMC Genomics</i> , 2019, 20, 255.	1.2	30
18015	Differential changes in bone strength of two inbred mouse strains following administration of a sclerostin-neutralizing antibody during growth. <i>PLoS ONE</i> , 2019, 14, e0214520.	1.1	1
18016	Triggering method in assisted reproduction alters the cumulus cell transcriptome. <i>Reproductive BioMedicine Online</i> , 2019, 39, 211-224.	1.1	7

#	ARTICLE	IF	CITATIONS
18017	Weighted gene coexpression network analysis identifies specific transcriptional modules and hub genes related to intramuscular fat traits in chicken breast muscle. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 13625-13639.	1.2	11
18018	Advanced Topic: Knowledge Graph Completion. <i>SpringerBriefs in Computer Science</i> , 2019, , 59-74.	0.2	1
18019	Utility of ankyrin 3 as a prognostic marker in androgen-receptor-positive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019, 176, 63-73.	1.1	7
18020	Gene expression profile of extraocular muscles following resection strabismus surgery. <i>Experimental Eye Research</i> , 2019, 182, 182-193.	1.2	2
18021	Middle-aged healthy women and Alzheimer's disease patients present an overlapping of brain cell transcriptional profile. <i>Neuroscience</i> , 2019, 406, 333-344.	1.1	25
18022	Transcriptional profiling of <i>Auricularia cornea</i> in selenium accumulation. <i>Scientific Reports</i> , 2019, 9, 5641.	1.6	17
18023	Prognostic risk model construction and molecular marker identification in glioblastoma multiforme based on mRNA/microRNA/long non-coding RNA analysis using random survival forest method. <i>Neoplasma</i> , 2019, 66, 459-469.	0.7	11
18024	Reducing waste in nutritional epidemiology: review and perspectives. <i>Proceedings of the Nutrition Society</i> , 2019, 78, 475-483.	0.4	2
18025	FunMappOne: a tool to hierarchically organize and visually navigate functional gene annotations in multiple experiments. <i>BMC Bioinformatics</i> , 2019, 20, 79.	1.2	30
18026	Identification of key pathways and gene changes in primary pancreatic stellate cells after cross-talk with pancreatic cancer cells (BXPC-3) using bioinformatics analysis. <i>Neoplasma</i> , 2019, 66, 446-458.	0.7	4
18027	Identification of 8â€miRNAs as biomarkers for nonalcoholic fatty liver disease. <i>Journal of Cellular Physiology</i> , 2019, 234, 17361-17369.	2.0	6
18028	Stressâ€induced mRNP granules: Form and function of processing bodies and stress granules. <i>Wiley Interdisciplinary Reviews RNA</i> , 2019, 10, e1524.	3.2	121
18029	Depletion of Î²3-adrenergic receptor induces left ventricular diastolic dysfunction via potential regulation of energy metabolism and cardiac contraction. <i>Gene</i> , 2019, 697, 1-10.	1.0	10
18030	A Model Information Management Plan for Molecular Pathology Sequence Data Using Standards. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 408-417.	1.2	5
18031	Predicted secreted protein analysis reveals synaptogenic function of <i>Clstn3</i> during WAT browning and BAT activation in mice. <i>Acta Pharmacologica Sinica</i> , 2019, 40, 999-1009.	2.8	9
18032	Identification of Potential Key Genes and Pathways in Early-Onset Colorectal Cancer Through Bioinformatics Analysis. <i>Cancer Control</i> , 2019, 26, 107327481983126.	0.7	46
18033	Characterization of Endothelial and Smooth Muscle Cells From Different Canine Vessels. <i>Frontiers in Physiology</i> , 2019, 10, 101.	1.3	20
18034	Comprehensive analysis of differentially expressed profiles of long non-coding RNAs and messenger RNAs in kaolin-induced hydrocephalus. <i>Gene</i> , 2019, 697, 184-193.	1.0	8

#	ARTICLE	IF	CITATIONS
18035	Functional genomic analysis of the human receptive endometrium transcriptome upon administration of mifepristone at the time of follicle rupture. <i>Molecular and Cellular Endocrinology</i> , 2019, 485, 88-96.	1.6	3
18036	Computational translation of genomic responses from experimental model systems to humans. <i>PLoS Computational Biology</i> , 2019, 15, e1006286.	1.5	37
18038	OGER++: hybrid multi-type entity recognition. <i>Journal of Cheminformatics</i> , 2019, 11, 7.	2.8	28
18039	RNA Sequencing Characterizes Transcriptomes Differences in Cold Response Between Northern and Southern <i>Alternanthera philoxeroides</i> and Highlight Adaptations Associated With Northward Expansion. <i>Frontiers in Plant Science</i> , 2019, 10, 24.	1.7	10
18041	Decreased mRNA and protein stability of W1282X limits response to modulator therapy. <i>Journal of Cystic Fibrosis</i> , 2019, 18, 606-613.	0.3	42
18042	Cellular Response of <i>Escherichia coli</i> to Photocatalysis: Flagellar Assembly Variation and Beyond. <i>ACS Nano</i> , 2019, 13, 2004-2014.	7.3	17
18043	Label-free Quantitative Analysis of Protein Expression Alterations in miR-26a-Knockout HeLa Cells using SWATH-MS Technology. <i>Scientific Reports</i> , 2019, 9, 1399.	1.6	5
18044	Complete Genome Sequence of <i>Pseudomonas</i> sp. Strain phDV1, an Isolate Capable of Efficient Degradation of Aromatic Hydrocarbons. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
18045	Ulcerative colitis: functional analysis of the in-depth proteome. <i>Clinical Proteomics</i> , 2019, 16, 4.	1.1	25
18046	Transcriptomics Identifies Modules of Differentially Expressed Genes and Novel Cyclotides in <i>Viola pubescens</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 156.	1.7	12
18047	Candidate Gene Selection for Cytoplasmic Male Sterility in Pepper (<i>Capsicum annum</i> L.) through Whole Mitochondrial Genome Sequencing. <i>International Journal of Molecular Sciences</i> , 2019, 20, 578.	1.8	24
18048	A Systems Pharmacology Approach for Identifying the Multiple Mechanisms of Action of the Wei Pi Xiao Decoction for the Treatment of Gastric Precancerous Lesions. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-15.	0.5	32
18049	Abrogation of Stem Loop Binding Protein (Slbp) function leads to a failure of cells to transition from proliferation to differentiation, retinal coloboma and midline axon guidance deficits. <i>PLoS ONE</i> , 2019, 14, e0211073.	1.1	9
18050	Comparative Analysis of Normalization Methods for Network Propagation. <i>Frontiers in Genetics</i> , 2019, 10, 4.	1.1	17
18051	Draft Genome Analysis Offers Insights Into the Mechanism by Which <i>Streptomyces chartreusis</i> WZS021 Increases Drought Tolerance in Sugarcane. <i>Frontiers in Microbiology</i> , 2018, 9, 3262.	1.5	39
18052	Biclustering Analysis of Co-regulation Patterns in Nuclear-Encoded Mitochondrial Genes and Metabolic Pathways. <i>Methods in Molecular Biology</i> , 2019, 1928, 469-478.	0.4	1
18053	Sex-Dependent Sensory Phenotypes and Related Transcriptomic Expression Profiles Are Differentially Affected by Angelman Syndrome. <i>Molecular Neurobiology</i> , 2019, 56, 5998-6016.	1.9	21
18054	First RNA-seq approach to study fruit set and parthenocarpy in zucchini (<i>Cucurbita pepo</i> L.). <i>BMC Plant Biology</i> , 2019, 19, 61.	1.6	19

#	ARTICLE	IF	CITATIONS
18055	O-GlcNAcylation alters the selection of mRNAs for translation and promotes 4E-BP1-dependent mitochondrial dysfunction in the retina. <i>Journal of Biological Chemistry</i> , 2019, 294, 5508-5520.	1.6	21
18056	The first chromosome-level genome for a marine mammal as a resource to study ecology and evolution. <i>Molecular Ecology Resources</i> , 2019, 19, 944-956.	2.2	27
18057	De Novo Transcriptome Assembly of Agave H11648 by Illumina Sequencing and Identification of Cellulose Synthase Genes in Agave Species. <i>Genes</i> , 2019, 10, 103.	1.0	22
18058	Genomewide analysis of 6-methyladenine DNA in peripheral blood mononuclear cells of systemic lupus erythematosus. <i>Lupus</i> , 2019, 28, 359-364.	0.8	4
18059	Genome-wide associations and detection of potential candidate genes for direct genetic and maternal genetic effects influencing dairy cattle body weight at different ages. <i>Genetics Selection Evolution</i> , 2019, 51, 4.	1.2	33
18060	Comparative transcriptome analysis reveals K ⁺ transporter gene contributing to salt tolerance in eggplant. <i>BMC Plant Biology</i> , 2019, 19, 67.	1.6	25
18061	Conserved Disease Modules Extracted From Multilayer Heterogeneous Disease and Gene Networks for Understanding Disease Mechanisms and Predicting Disease Treatments. <i>Frontiers in Genetics</i> , 2019, 9, 745.	1.1	52
18062	Identification of Candidate Genes for the Plateau Adaptation of a Tibetan Amphipod, <i>Gammarus lacustris</i> , Through Integration of Genome and Transcriptome Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 53.	1.1	14
18063	Unveiling the Link Between Inflammation and Adaptive Immunity in Breast Cancer. <i>Frontiers in Immunology</i> , 2019, 10, 56.	2.2	9
18064	Repurposing of Drugs as Novel Influenza Inhibitors From Clinical Gene Expression Infection Signatures. <i>Frontiers in Immunology</i> , 2019, 10, 60.	2.2	44
18065	Identification of critical genes associated with spinal cord injury based on the gene expression profile of spinal cord tissues from <i>trkB.T1</i> knockout mice. <i>Molecular Medicine Reports</i> , 2019, 19, 2013-2020.	1.1	3
18066	GWAS and Beyond: Using Omics Approaches to Interpret SNP Associations. <i>Current Genetic Medicine Reports</i> , 2019, 7, 30-40.	1.9	4
18067	Using mouse genetics to understand human skeletal disease. <i>Bone</i> , 2019, 126, 27-36.	1.4	5
18068	Development of Orthogonal Linear Separation Analysis (OLSA) to Decompose Drug Effects into Basic Components. <i>Scientific Reports</i> , 2019, 9, 1824.	1.6	10
18069	Genome-Wide mRNA-Seq Profiling Reveals that <i>LEF1</i> and <i>SMAD3</i> Regulate Epithelial-Mesenchymal Transition Through the Hippo Signaling Pathway During Palatal Fusion. <i>Genetic Testing and Molecular Biomarkers</i> , 2019, 23, 197-203.	0.3	4
18070	PPI-Detect: A support vector machine model for sequence-based prediction of protein-protein interactions. <i>Journal of Computational Chemistry</i> , 2019, 40, 1233-1242.	1.5	54
18071	H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. <i>Acta Neuropathologica</i> , 2019, 137, 637-655.	3.9	85
18072	In silico identification of copper-binding proteins of <i>Xanthomonas translucens</i> pv. <i>undulosa</i> for their probable role in plant-pathogen interactions. <i>Physiological and Molecular Plant Pathology</i> , 2019, 106, 187-195.	1.3	14

#	ARTICLE	IF	CITATIONS
18073	Brain transcriptome of honey bees (<i>Apis mellifera</i>) exhibiting impaired olfactory learning induced by a sublethal dose of imidacloprid. <i>Pesticide Biochemistry and Physiology</i> , 2019, 156, 36-43.	1.6	61
18074	Lymphocyte innateness defined by transcriptional states reflects a balance between proliferation and effector functions. <i>Nature Communications</i> , 2019, 10, 687.	5.8	136
18075	Targeted mutation detection in breast cancer using MammaSeq. <i>Breast Cancer Research</i> , 2019, 21, 22.	2.2	28
18076	Utilizing iVariantGuide for Variant Assessment of Next-Generation Sequencing. <i>Current Protocols in Bioinformatics</i> , 2019, 65, e73.	25.8	2
18077	Profiling of nuclear copper-binding proteins under hypoxic condition. <i>BioMetals</i> , 2019, 32, 329-341.	1.8	3
18078	Genomic Characterization of a Newly Isolated Rhizobacteria <i>Sphingomonas panacis</i> Reveals Plant Growth Promoting Effect to Rice. <i>Biotechnology and Bioprocess Engineering</i> , 2019, 24, 119-125.	1.4	10
18079	Reversible regulation of SATB1 ubiquitination by USP47 and SMURF2 mediates colon cancer cell proliferation and tumor progression. <i>Cancer Letters</i> , 2019, 448, 40-51.	3.2	61
18080	Computational prediction of the bioactivity potential of proteomes based on expert knowledge. <i>Journal of Biomedical Informatics</i> , 2019, 91, 103121.	2.5	2
18081	mTORC2-mediated PDHE1 nuclear translocation links EBV-LMP1 reprogrammed glucose metabolism to cancer metastasis in nasopharyngeal carcinoma. <i>Oncogene</i> , 2019, 38, 4669-4684.	2.6	40
18082	Obesity-associated inflammation triggers an autophagy-lysosomal response in adipocytes and causes degradation of perilipin 1. <i>Cell Death and Disease</i> , 2019, 10, 121.	2.7	52
18083	A genome-wide scan shows evidence for local adaptation in a widespread keystone Neotropical forest tree. <i>Heredity</i> , 2019, 123, 117-137.	1.2	24
18084	Retinal transcriptome and eQTL analyses identify genes associated with age-related macular degeneration. <i>Nature Genetics</i> , 2019, 51, 606-610.	9.4	201
18085	A network biology approach to unraveling inherited axonopathies. <i>Scientific Reports</i> , 2019, 9, 1692.	1.6	18
18086	Molecular signature of human bone marrow-derived mesenchymal stromal cell subsets. <i>Scientific Reports</i> , 2019, 9, 1774.	1.6	35
18087	Comparative analyses of phytochelatin synthase (<i>PCS</i>) genes in higher plants. <i>Biotechnology and Biotechnological Equipment</i> , 2019, 33, 178-194.	0.5	36
18088	Modular decomposition of protein structure using community detection. <i>Journal of Complex Networks</i> , 2019, 7, 101-113.	1.1	6
18089	Identification of potential blood biomarkers for Parkinson's disease by gene expression and DNA methylation data integration analysis. <i>Clinical Epigenetics</i> , 2019, 11, 24.	1.8	63
18090	Retroelement-Linked Transcription Factor Binding Patterns Point to Quickly Developing Molecular Pathways in Human Evolution. <i>Cells</i> , 2019, 8, 130.	1.8	11

#	ARTICLE	IF	CITATIONS
18091	Identification of common genetic risk variants for autism spectrum disorder. <i>Nature Genetics</i> , 2019, 51, 431-444.	9.4	1,538
18092	Circadian regulation in human white adipose tissue revealed by transcriptome and metabolic network analysis. <i>Scientific Reports</i> , 2019, 9, 2641.	1.6	55
18093	Metabolic gene NR4A1 as a potential therapeutic target for non-smoking female small cell lung cancer patients. <i>Thoracic Cancer</i> , 2019, 10, 715-727.	0.8	10
18094	Nitrate affects transcriptional regulation of UPBEAT1 and ROS localisation in roots of <i>Zea mays</i> L. <i>Physiologia Plantarum</i> , 2019, 166, 794-811.	2.6	16
18095	Functional homogeneity and specificity of topological modules in human proteome. <i>BMC Bioinformatics</i> , 2019, 19, 553.	1.2	2
18096	Predicting Gene Ontology Function of Human MicroRNAs by Integrating Multiple Networks. <i>Frontiers in Genetics</i> , 2019, 10, 3.	1.1	44
18097	The Ethylene Signaling Pathway Negatively Impacts CBF/DREB-Regulated Cold Response in Soybean (<i>Glycine max</i>). <i>Frontiers in Plant Science</i> , 2019, 10, 121.	1.7	43
18098	Genetic variants differentially associated with rheumatoid arthritis and systemic lupus erythematosus reveal the disease-specific biology. <i>Scientific Reports</i> , 2019, 9, 2739.	1.6	13
18099	Bioinformatics Analysis of Key Genes and Pathways in Colorectal Cancer. <i>Journal of Computational Biology</i> , 2019, 26, 364-375.	0.8	14
18100	Draft genome of the river water buffalo. <i>Ecology and Evolution</i> , 2019, 9, 3378-3388.	0.8	32
18101	FAM92A Underlies Nonsyndromic Postaxial Polydactyly in Humans and an Abnormal Limb and Digit Skeletal Phenotype in Mice. <i>Journal of Bone and Mineral Research</i> , 2019, 34, 375-386.	3.1	27
18102	<i>IDUA</i> , <i>NDST1</i> , <i>SAP30L</i> , <i>CRYBA4</i> , and <i>SLC11A1</i> as novel prognostic signatures clear cell renal cell carcinoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 16320-16327.	2.0	8
18103	Computational Intelligence Methods for Bioinformatics and Biostatistics. <i>Lecture Notes in Computer Science</i> , 2019, . .	1.0	0
18104	Disease-Genes Must Guide Data Source Integration in the Gene Prioritization Process. <i>Lecture Notes in Computer Science</i> , 2019, , 60-69.	1.0	0
18105	Transcriptomic information from the ovaries of red swamp crayfish (<i>Procambarus clarkii</i>) provides new insights into development of ovaries and embryos. <i>Aquaculture</i> , 2019, 505, 333-343.	1.7	12
18106	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
18107	Mesenchymal-Epithelial Interactome Analysis Reveals Essential Factors Required for Fibroblast-Free Alveolosphere Formation. <i>iScience</i> , 2019, 11, 318-333.	1.9	31
18108	Genetic and expression differences between putative ecotypes of <i>Sphagnum denticulatum</i> Brid. (Sphagnaceae: Bryophyta) subjected to drought stress and rehydration. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2019, 37, 39-52.	1.1	4

#	ARTICLE	IF	CITATIONS
18109	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
18110	Addressing systematic inconsistencies between in vitro and in vivo transcriptomic mode of action signatures. <i>Toxicology in Vitro</i> , 2019, 58, 1-12.	1.1	15
18111	Coacervation of Lipid Bilayer in Natural Cell Membranes for Extraction, Fractionation, and Enrichment of Proteins in Proteomics Studies. <i>Journal of Proteome Research</i> , 2019, 18, 1595-1606.	1.8	11
18112	Function Prediction for G Protein-Coupled Receptors through Text Mining and Induction Matrix Completion. <i>ACS Omega</i> , 2019, 4, 3045-3054.	1.6	2
18113	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates APOE, tau, immunity and lipid processing. <i>Nature Genetics</i> , 2019, 51, 414-430.	9.4	1,962
18114	Native aortic valve derived extracellular matrix hydrogel for three dimensional culture analyses with improved biomimetic properties. <i>Biomedical Materials (Bristol)</i> , 2019, 14, 035014.	1.7	11
18115	Genome Sequencing of <i>Cladobotryum protrusum</i> Provides Insights into the Evolution and Pathogenic Mechanisms of the Cobweb Disease Pathogen on Cultivated Mushroom. <i>Genes</i> , 2019, 10, 124.	1.0	25
18116	A MST1-FOXO1 cascade establishes endothelial tip cell polarity and facilitates sprouting angiogenesis. <i>Nature Communications</i> , 2019, 10, 838.	5.8	65
18117	Towards a data-integrated cell. <i>Nature Communications</i> , 2019, 10, 805.	5.8	37
18118	Genomic evidence for shared common ancestry of East African hunting-gathering populations and insights into local adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4166-4175.	3.3	40
18119	The complete chloroplast genome of a rare species <i>Capparis versicolor</i> Griff. (Rhoadales: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 Td 0.2 0	0.2	0
18120	CERENKOV2: improved detection of functional noncoding SNPs using data-space geometric features. <i>BMC Bioinformatics</i> , 2019, 20, 63.	1.2	5
18121	Targeting JUN, CEBPB, and HDAC3: A Novel Strategy to Overcome Drug Resistance in Hypoxic Glioblastoma. <i>Frontiers in Oncology</i> , 2019, 9, 33.	1.3	17
18122	Tree Response to Herbivory Is Affected by Endogenous Rhythmic Growth and Attenuated by Cotreatment With a Mycorrhizal Fungus. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 770-781.	1.4	5
18123	Comprehensive mass spectrometry-guided phenotyping of plant specialized metabolites reveals metabolic diversity in the cosmopolitan plant family Rhamnaceae. <i>Plant Journal</i> , 2019, 98, 1134-1144.	2.8	59
18124	BO-LSTM: classifying relations via long short-term memory networks along biomedical ontologies. <i>BMC Bioinformatics</i> , 2019, 20, 10.	1.2	44
18125	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
18126	Evaluation of cardiovascular system state by urine proteome after manned space flight. <i>Acta Astronautica</i> , 2019, 160, 594-600.	1.7	4

#	ARTICLE	IF	CITATIONS
18127	Human IFIT proteins inhibit lytic replication of KSHV: A new feed-forward loop in the innate immune system. <i>PLoS Pathogens</i> , 2019, 15, e1007609.	2.1	32
18128	Secretome profiling of heterotypic spheroids suggests a role of fibroblasts in HIF-1 pathway modulation and colorectal cancer photodynamic resistance. <i>Cellular Oncology (Dordrecht)</i> , 2019, 42, 173-196.	2.1	20
18129	Homozygous loss-of-function mutations in FSIP2 cause male infertility with asthenoteratospermia. <i>Journal of Genetics and Genomics</i> , 2019, 46, 53-56.	1.7	31
18130	Transcriptional regulation of the genes involved in protein metabolism and processing in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	1
18131	Genome-wide methylotyping resolves breast cancer epigenetic heterogeneity and suggests novel therapeutic perspectives. <i>Epigenomics</i> , 2019, 11, 605-617.	1.0	26
18132	Analysis of Predicted Host-Parasite Interactomes Reveals Commonalities and Specificities Related to Parasitic Lifestyle and Tissues Tropism. <i>Frontiers in Immunology</i> , 2019, 10, 212.	2.2	34
18133	Hypersensitive IFN Responses in Lupus Keratinocytes Reveal Key Mechanistic Determinants in Cutaneous Lupus. <i>Journal of Immunology</i> , 2019, 202, 2121-2130.	0.4	44
18134	Multiple microarray analysis for identification of hub genes involved in tubulointerstitial injury in diabetic nephropathy. <i>Journal of Cellular Physiology</i> , 2019, 234, 16447-16462.	2.0	43
18135	Genome sequence of a spore-laccase forming, BPA-degrading <i>Bacillus</i> sp. GZB isolated from an electronic-waste recycling site reveals insights into BPA degradation pathways. <i>Archives of Microbiology</i> , 2019, 201, 623-638.	1.0	15
18136	Genomic Characterization of the Zinc Transcriptional Regulatory Element Reveals Potential Functional Roles of ZNF658. <i>Biological Trace Element Research</i> , 2019, 192, 83-90.	1.9	3
18137	Genome-wide analysis of developmental stage-specific transcriptome in <i>Bradysia odoriphaga</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 30, 45-54.	0.4	4
18138	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. <i>Genome Research</i> , 2019, 29, 576-589.	2.4	39
18139	Gene expression atlas of embryo development in <i>Arabidopsis</i> . <i>Plant Reproduction</i> , 2019, 32, 93-104.	1.3	15
18140	Visualization and Analysis of Epiroteome Dynamics. <i>Journal of Molecular Biology</i> , 2019, 431, 1519-1539.	2.0	10
18141	Phosphoregulated FMRP phase separation models activity-dependent translation through bidirectional control of mRNA granule formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4218-4227.	3.3	249
18142	Harmonizing semantic annotations for computational models in biology. <i>Briefings in Bioinformatics</i> , 2019, 20, 540-550.	3.2	52
18143	A role for the <i>Saccharomyces cerevisiae</i> ABCF protein New1 in translation termination/recycling. <i>Nucleic Acids Research</i> , 2019, 47, 8807-8820.	6.5	26
18144	Molecular Profiling of the <i>Drosophila</i> Antenna Reveals Conserved Genes Underlying Olfaction in Insects. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3753-3771.	0.8	25

#	ARTICLE	IF	CITATIONS
18145	Computational Prediction of Human Body-Fluid Protein. , 2019, , .		2
18146	Maternal Experience Leads to Lasting Gene Expression Changes in Some Regions of the Mouse Brain. G3: Genes, Genomes, Genetics, 2019, 9, 2623-2628.	0.8	7
18147	PDBMine: A Reformulation of the Protein Data Bank to Facilitate Structural Data Mining. , 2019, , .		5
18148	Differential expression profile analysis of cisplatin-â€regulated miRNAs in a human gastric cancer cell line. Molecular Medicine Reports, 2019, 20, 1966-1976.	1.1	6
18149	Screening and authentication of molecular markers in malignant glioblastoma based on gene expression profiles. Oncology Letters, 2019, 18, 4593-4604.	0.8	11
18150	The Genome Sequence of the Eastern Woodchuck (<i>Marmota monax</i>) â€ A Preclinical Animal Model for Chronic Hepatitis B. G3: Genes, Genomes, Genetics, 2019, 9, 3943-3952.	0.8	13
18151	Network-Based Functional Prediction Augments Genetic Association To Predict Candidate Genes for Histamine Hypersensitivity in Mice. G3: Genes, Genomes, Genetics, 2019, 9, 4223-4233.	0.8	13
18152	Whole Genome Sequence of the Commercially Relevant Mushroom Strain <i>Agaricus bisporus</i> var. <i>bisporus</i> ARP23. G3: Genes, Genomes, Genetics, 2019, 9, 3057-3066.	0.8	13
18153	On Finding and Enumerating Maximal and Maximum k-Partite Cliques in k-Partite Graphs. Algorithms, 2019, 12, 23.	1.2	10
18154	The Eminence of Co-Expressed Ties in Schizophrenia Network Communities. Data, 2019, 4, 149.	1.2	0
18155	The 2nd U.S. Semantic Technologies Symposium (US2TS 2019). Semantic Web, 2019, 10, 631-635.	1.1	0
18156	Screening and identification of key biomarkers in adrenocortical carcinoma based on bioinformatics analysis. Oncology Letters, 2019, 18, 4667-4676.	0.8	11
18157	The Alliance of Genome Resources: Building a Modern Data Ecosystem for Model Organism Databases. Genetics, 2019, 213, 1189-1196.	1.2	41
18158	Mechanisms of <i>Atractylodis Macrocephalae</i> Rhizoma against Chronic Gastritis. , 2019, , .		0
18159	Anti-rheumatoid Arthritis Mechanisms of <i>Angelicae Pubescentis</i> Radix. , 2019, , .		0
18160	PAGWAS: a manually curated web-based knowledge database of GWAS pathway analysis. , 2019, , .		0
18161	The global transcriptomic signature in sinonasal tissues reveals roles for tissue type and chronic rhinosinusitis disease phenotype. Rhinology, 2020, 58, 273-283.	0.7	8
18162	Healing Functions of <i>Carthami Flos</i> against Contusion and Other Potential Damages. , 2019, , .		0

#	ARTICLE	IF	CITATIONS
18163	Healing Functions of Carthami Flos against Contusion and Other Potential Damages. , 2019, , .		0
18164	TEADs, Yap, Taz, Vgll4s transcription factors control the establishment of Left-Right asymmetry in zebrafish. <i>ELife</i> , 2019, 8, .	2.8	17
18165	Processing of association rules with ontology in distributed NoSQL systems. <i>Web Intelligence</i> , 2019, 17, 285-296.	0.1	1
18166	Therapeutic Mechanisms of Persicae Semen towards Healing Processes. , 2019, , .		0
18167	Cell Adhesion-Related Molecules Play a Key Role in Renal Cancer Progression by Multinetwork Analysis. <i>BioMed Research International</i> , 2019, 2019, 1-10.	0.9	17
18168	Minimum Information and Quality Standards for Conducting, Reporting, and Organizing In Vitro Research. <i>Handbook of Experimental Pharmacology</i> , 2019, 257, 177-196.	0.9	12
18169	Learning a Low-Rank Tensor of Pharmacogenomic Multi-relations from Biomedical Networks. , 2019, , .		7
18170	Identifying miRNA synergism using multiple-intervention causal inference. <i>BMC Bioinformatics</i> , 2019, 20, 613.	1.2	14
18171	The Paf1 Complex Broadly Impacts the Transcriptome of <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2019, 212, 711-728.	1.2	10
18172	Measuring consistency among gene set analysis methods: A systematic study. <i>Journal of Bioinformatics and Computational Biology</i> , 2019, 17, 1940010.	0.3	11
18173	Ontology-Based Interactive Visualization of Patient-Generated Research Questions. <i>Applied Clinical Informatics</i> , 2019, 10, 377-386.	0.8	3
18174	A gene regulatory network controls the balance between mesendoderm and ectoderm at pluripotency exit. <i>Molecular Systems Biology</i> , 2019, 15, e9043.	3.2	20
18175	Favorable Alleles of GRAIN-FILLING RATE1 Increase the Grain-Filling Rate and Yield of Rice. <i>Plant Physiology</i> , 2019, 181, 1207-1222.	2.3	30
18176	An Ontology-Independent Representation Learning for Similar Disease Detection Based on Multi-layer Similarity Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	1.9	6
18177	SeqScreen: a biocuration platform for robust taxonomic and biological process characterization of nucleic acid sequences of interest. , 2019, , .		7
18178	Multifaced regulator: RNA binding proteins and their roles in hematopoiesis. <i>Blood Science</i> , 2019, 1, 69-72.	0.4	0
18180	Genomics Analysis of L-DOPA Exposure in <i>Drosophila sechellia</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3973-3980.	0.8	8
18181	Persistence of skewed X-chromosome inactivation in pre-B acute lymphoblastic leukemia of a female ATRX mutation carrier. <i>Blood Advances</i> , 2019, 3, 2627-2631.	2.5	2

#	ARTICLE	IF	CITATIONS
18182	Topology Analysis of Protein-protein Interaction Network and Identification of Gene Ontology for Obstructive Sleep Apnea and Associated Diseases Using Bioinformatics Tools. , 2019, , .		0
18183	TPM2 as a potential predictive biomarker for atherosclerosis. <i>Aging</i> , 2019, 11, 6960-6982.	1.4	44
18184	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
18185	Biomedical ontologies and their development, management, and applications in and beyond China. <i>Journal of Bio-X Research</i> , 2019, 2, 178-184.	0.3	3
18186	5. Metagenomics of extreme environments: methods and applications. , 2019, , 93-126.		0
18187	Knowledge Extraction and Applications utilizing Context Data in Knowledge Graphs. , 0, , .		10
18188	Nonnegative Matrix Factorization for Dynamic Modules in Cancer Attribute Temporal Networks. , 2019, , .		1
18189	Visualizing multifunctional PPI network with Gene Ontology annotation. , 2019, , .		0
18190	Ontology-based transporter substrate annotation for benchmark datasets. , 2019, , .		5
18191	Refining modules to determine functionally significant clusters in molecular networks. <i>BMC Genomics</i> , 2019, 20, 901.	1.2	2
18192	Differences in the prognosis of gastric cancer patients of different sexes and races and the molecular mechanisms involved. <i>International Journal of Oncology</i> , 2019, 55, 1049-1068.	1.4	20
18193	Reconstruction and analysis of competitive endogenous RNA network reveals regulatory role of long non-coding RNAs in hepatic fibrosis. <i>Molecular Medicine Reports</i> , 2019, 20, 4091-4100.	1.1	5
18194	Functional Annotations of Novel Cancer-Associated lncRNAs Identified Using Machine Learning Algorithms. , 2019, , .		0
18195	Circular RNA expression alterations in colon tissues of Crohn's disease patients. <i>Molecular Medicine Reports</i> , 2019, 19, 4500-4506.	1.1	14
18196	Comparative Genomics Reveals a Well-Conserved Intrinsic Resistome in the Emerging Multidrug-Resistant Pathogen <i>Cupriavidus gilardii</i> . <i>MSphere</i> , 2019, 4, .	1.3	9
18197	Tumorigenic effects of TLX overexpression in HEK 293T cells. <i>Cancer Reports</i> , 2019, 2, e1204.	0.6	2
18198	Multiple freshwater invasions of the tapertail anchovy (<i>Clupeiformes: Engraulidae</i>) of the Yangtze River. <i>Ecology and Evolution</i> , 2019, 9, 12202-12215.	0.8	10
18199	Synthetic Activators of Cell Migration Designed by Constructive Machine Learning. <i>ChemistryOpen</i> , 2019, 8, 1303-1308.	0.9	9

#	ARTICLE	IF	CITATIONS
18200	DeepDRBP-2L: A New Genome Annotation Predictor for Identifying DNA-Binding Proteins and RNA-Binding Proteins Using Convolutional Neural Network and Long Short-Term Memory. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1451-1463.	1.9	30
18201	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	3.8	261
18202	Genome-Scale Metabolic Networks Shed Light on the Carotenoid Biosynthesis Pathway in the Brown Algae <i>Saccharina japonica</i> and <i>Cladosiphon okamuranus</i> . <i>Antioxidants</i> , 2019, 8, 564.	2.2	19
18203	ENCORE. , 2019, 2019, 5-14.		8
18204	Comparative analysis of cellular expression pattern of schizophrenia risk genes in human versus mouse cortex. <i>Cell and Bioscience</i> , 2019, 9, 89.	2.1	8
18205	Early Root Transcriptomic Changes in Wheat Seedlings Colonized by <i>Trichoderma harzianum</i> Under Different Inorganic Nitrogen Supplies. <i>Frontiers in Microbiology</i> , 2019, 10, 2444.	1.5	23
18206	Transcriptional Regulation of Autophagy Genes via Stage-Specific Activation of CEBPB and PPARC during Adipogenesis: A Systematic Study Using Public Gene Expression and Transcription Factor Binding Datasets. <i>Cells</i> , 2019, 8, 1321.	1.8	15
18207	The assessment of efficient representation of drug features using deep learning for drug repositioning. <i>BMC Bioinformatics</i> , 2019, 20, 577.	1.2	16
18208	Integrated transcriptome and miRNA analysis uncovers molecular regulators of aerial stem-to-rhizome transition in the medical herb <i>Gynostemma pentaphyllum</i> . <i>BMC Genomics</i> , 2019, 20, 865.	1.2	9
18209	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
18210	Mapping platforms into a new open science model for machine learning. <i>IT - Information Technology</i> , 2019, 61, 197-208.	0.6	4
18211	Synergistic Genetic Interactions between <i>Pkhd1</i> and <i>Pkd1</i> Result in an ARPKD-Like Phenotype in Murine Models. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 2113-2127.	3.0	39
18212	Broad regulation of gene isoform expression by Wnt signaling in cancer. <i>Rna</i> , 2019, 25, 1696-1713.	1.6	5
18213	Genetic Regulators and Physiological Significance of Glycogen Storage in <i>Candida albicans</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2019, 5, 102.	1.5	8
18214	An Acoustic Password Enhances Auditory Learning in Juvenile Brood Parasitic Cowbirds. <i>Current Biology</i> , 2019, 29, 4045-4051.e3.	1.8	17
18215	Network pharmacology-based study on the mechanism of <i>Œliu Wei Zhu Huang San</i> in respiratory tract infections treatment. <i>European Journal of Integrative Medicine</i> , 2019, 32, 101013.	0.8	1
18216	Toward Phylomics in Entomology: Current Systematic and Evolutionary Morphology. <i>Insect Systematics and Diversity</i> , 2019, 3, .	0.7	3
18217	MultiSourcDSim: an integrated approach for exploring disease similarity. <i>BMC Medical Informatics and Decision Making</i> , 2019, 19, 269.	1.5	12

#	ARTICLE	IF	CITATIONS
18218	Analysis of tumour ecological balance reveals resource-dependent adaptive strategies of ovarian cancer. <i>EBioMedicine</i> , 2019, 48, 224-235.	2.7	8
18219	In-silico definition of the <i>Drosophila melanogaster</i> matrisome. <i>Matrix Biology Plus</i> , 2019, 4, 100015.	1.9	32
18220	Association of functional variants and protein-to-protein physical interactions of human MutY homolog linked with familial adenomatous polyposis and colorectal cancer syndrome. <i>Non-coding RNA Research</i> , 2019, 4, 155-173.	2.4	1
18221	Patterns of diverse gene functions in genomic neighborhoods predict gene function and phenotype. <i>Scientific Reports</i> , 2019, 9, 19537.	1.6	19
18222	A network-based approach reveals novel invasion and Maurer's clefts-related proteins in <i>Plasmodium falciparum</i> . <i>Molecular Omics</i> , 2019, 15, 431-441.	1.4	4
18223	Profiling of the plasma proteome across different stages of human heart failure. <i>Nature Communications</i> , 2019, 10, 5830.	5.8	53
18224	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. <i>Nature Communications</i> , 2019, 10, 5817.	5.8	160
18225	The Use of Whole Exome Sequencing in a Cohort of Transgender Individuals to Identify Rare Genetic Variants. <i>Scientific Reports</i> , 2019, 9, 20099.	1.6	18
18226	Lipid and DHA-production in <i>Aurantiochytrium</i> sp. "Responses to nitrogen starvation and oxygen limitation revealed by analyses of production kinetics and global transcriptomes. <i>Scientific Reports</i> , 2019, 9, 19470.	1.6	48
18227	The transcriptome analysis of males musk gland in <i>Moschus berezovskii</i> (<i>Artiodactyla</i> :) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T		4
18228	The Heat Shock Response in Yeast Maintains Protein Homeostasis by Chaperoning and Replenishing Proteins. <i>Cell Reports</i> , 2019, 29, 4593-4607.e8.	2.9	67
18229	Transcriptome analysis reveals plasticity in gene regulation due to environmental cues in <i>Primula sikkimensis</i> , a high altitude plant species. <i>BMC Genomics</i> , 2019, 20, 989.	1.2	10
18230	Novel findings to the biosynthetic pathway of magnoflorine and taspine through transcriptomic and metabolomic analysis of <i>Croton draco</i> (<i>Euphorbiaceae</i>). <i>BMC Plant Biology</i> , 2019, 19, 560.	1.6	7
18231	Comparative transcriptome reveals the potential modulation mechanisms of estradiol affecting ovarian development of female <i>Portunus trituberculatus</i> . <i>PLoS ONE</i> , 2019, 14, e0226698.	1.1	15
18232	Conjoint Analysis of SMRT- and Illumina-Based RNA-Sequencing Data of <i>Fenneropenaeus chinensis</i> Provides Insight Into Sex-Biased Expression Genes Involved in Sexual Dimorphism. <i>Frontiers in Genetics</i> , 2019, 10, 1175.	1.1	5
18233	High-level integration of murine intestinal transcriptomics data highlights the importance of the complement system in mucosal homeostasis. <i>BMC Genomics</i> , 2019, 20, 1028.	1.2	14
18234	A 2018 workshop: vaccine and drug ontology studies (VDOS 2018). <i>BMC Bioinformatics</i> , 2019, 20, 705.	1.2	1
18235	OHMI: the ontology of host-microbiome interactions. <i>Journal of Biomedical Semantics</i> , 2019, 10, 25.	0.9	6

#	ARTICLE	IF	CITATIONS
18236	Bioinformatics analysis of key biomarkers and pathways in KSHV infected endothelial cells. <i>Medicine (United States)</i> , 2019, 98, e16277.	0.4	5
18237	Predicting associations among drugs, targets and diseases by tensor decomposition for drug repositioning. <i>BMC Bioinformatics</i> , 2019, 20, 628.	1.2	20
18238	Comprehensive analysis of chromosomal mobile genetic elements in the gut microbiome reveals phylum-level niche-adaptive gene pools. <i>PLoS ONE</i> , 2019, 14, e0223680.	1.1	59
18239	Extending the information content of the MALDI analysis of biological fluids via multi-million shot analysis. <i>PLoS ONE</i> , 2019, 14, e0226012.	1.1	15
18240	Transcriptome Analysis Identifies Immune Markers Related to Visceral Leishmaniasis Establishment in the Experimental Model of BALB/c Mice. <i>Frontiers in Immunology</i> , 2019, 10, 2749.	2.2	13
18241	A Phylogenomic Analysis of the Floral Transcriptomes of Sexually Deceptive and Rewarding European Orchids, <i>Ophrys</i> and <i>Gymnadenia</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1553.	1.7	26
18242	Battling Glioblastoma: A Novel Tyrosine Kinase Inhibitor with Multi-Dimensional Anti-Tumor Effect. <i>Cells</i> , 2019, 8, 1624.	1.8	5
18243	Genetic mapping in Diversity Outbred mice identifies a <i>Trpa1</i> variant influencing late-phase formalin response. <i>Pain</i> , 2019, 160, 1740-1753.	2.0	22
18244	Master Regulators of Signaling Pathways: An Application to the Analysis of Gene Regulation in Breast Cancer. <i>Frontiers in Genetics</i> , 2019, 10, 1180.	1.1	19
18245	Combined De Novo Transcriptome and Metabolome Analysis of Common Bean Response to <i>Fusarium oxysporum</i> f. sp. <i>phaseoli</i> Infection. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6278.	1.8	63
18246	Pan-genome diversification and recombination in <i>Cronobacter sakazakii</i> , an opportunistic pathogen in neonates, and insights to its xerotolerant lifestyle. <i>BMC Microbiology</i> , 2019, 19, 306.	1.3	12
18247	Expression alteration of microRNAs in Nucleus Accumbens is associated with chronic stress and antidepressant treatment in rats. <i>BMC Medical Informatics and Decision Making</i> , 2019, 19, 271.	1.5	12
18248	The essentiality landscape of cell cycle related genes in human pluripotent and cancer cells. <i>Cell Division</i> , 2019, 14, 15.	1.1	13
18249	Microarray-assisted size-effect study of amorphous silica nanoparticles on human bronchial epithelial cells. <i>Nanoscale</i> , 2019, 11, 22907-22923.	2.8	18
18250	The in vivo ISGylome links ISG15 to metabolic pathways and autophagy upon <i>Listeria monocytogenes</i> infection. <i>Nature Communications</i> , 2019, 10, 5383.	5.8	63
18251	Ontology-based prediction of cancer driver genes. <i>Scientific Reports</i> , 2019, 9, 17405.	1.6	16
18252	Repeated sex chromosome evolution in vertebrates supported by expanded avian sex chromosomes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20192051.	1.2	42
18253	Identifying gene function and module connections by the integration of multispecies expression compendia. <i>Genome Research</i> , 2019, 29, 2034-2045.	2.4	36

#	ARTICLE	IF	CITATIONS
18254	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
18255	Genomic Analysis of Spontaneous Abortion in Holstein Heifers and Primiparous Cows. <i>Genes</i> , 2019, 10, 954.	1.0	6
18256	Full-length transcriptome sequencing from multiple tissues of duck, <i>Anas platyrhynchos</i> . <i>Scientific Data</i> , 2019, 6, 275.	2.4	26
18257	Identified the Synergistic Mechanism of <i>Drynariae Rhizoma</i> for Treating Fracture Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-19.	0.5	12
18258	BNC1 regulates cell heterogeneity in human pluripotent stem cell derived-epicardium. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	24
18259	The Cellular Transcriptome in the Maternal Circulation During Normal Pregnancy: A Longitudinal Study. <i>Frontiers in Immunology</i> , 2019, 10, 2863.	2.2	43
18260	Comparative analysis of functional assay evidence use by ClinGen Variant Curation Expert Panels. <i>Genome Medicine</i> , 2019, 11, 77.	3.6	34
18261	The transcriptional regulator CBX2 and ovarian function: A whole genome and whole transcriptome approach. <i>Scientific Reports</i> , 2019, 9, 17033.	1.6	12
18262	Identification of DNAH6 mutations in infertile men with multiple morphological abnormalities of the sperm flagella. <i>Scientific Reports</i> , 2019, 9, 15864.	1.6	42
18263	Neogenin-1 distinguishes between myeloid-biased and balanced <i>Hoxb5</i> ⁺ mouse long-term hematopoietic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25115-25125.	3.3	26
18264	Comparative Analysis of Transcriptome Responses to Cold Stress in <i>Galeruca daurica</i> (Coleoptera: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	8.6	24
18265	Single-cell transcriptomics of the naked mole-rat reveals unexpected features of mammalian immunity. <i>PLoS Biology</i> , 2019, 17, e3000528.	2.6	80
18266	A Comparative Peptidomic Characterization of Cultured Skeletal Muscle Tissues Derived From db/db Mice. <i>Frontiers in Endocrinology</i> , 2019, 10, 741.	1.5	3
18267	Omega-3 Fatty Acids Activate Ciliary FFAR4 to Control Adipogenesis. <i>Cell</i> , 2019, 179, 1289-1305.e21.	13.5	159
18268	Predicting novel genomic regions linked to genetic disorders using GWAS and chromosome conformation data – a case study of schizophrenia. <i>Scientific Reports</i> , 2019, 9, 17940.	1.6	6
18269	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. <i>GigaScience</i> , 2019, 8, .	3.3	106
18270	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	5.8	197
18271	Full-Length Transcriptome Survey and Expression Analysis of Parasitoid Wasp <i>Chouioia cunea</i> upon Exposure to 1-Dodecene. <i>Scientific Reports</i> , 2019, 9, 18167.	1.6	4

#	ARTICLE	IF	CITATIONS
18272	Transcriptomics of Tasmanian Devil (<i>Sarcophilus harrisii</i>) Ear Tissue Reveals Homogeneous Gene Expression Patterns across a Heterogeneous Landscape. <i>Genes</i> , 2019, 10, 801.	1.0	6
18273	Identification of a Major QTL (qRRs-10.1) That Confers Resistance to <i>Ralstonia solanacearum</i> in Pepper (<i>Capsicum annuum</i>) Using SLAF-BSA and QTL Mapping. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5887.	1.8	35
18274	A Cross-Platform Comparison of Affymetrix, Agilent, and Illumina Microarray Reveals Functional Genomics in Colorectal Cancer Progression. , 2019, 2019, 252-255.		1
18275	The Cyclic AMP Receptor Protein Regulates Quorum Sensing and Global Gene Expression in <i>Yersinia pestis</i> during Planktonic Growth and Growth in Biofilms. <i>MBio</i> , 2019, 10, .	1.8	24
18276	GPCRs show widespread differential mRNA expression and frequent mutation and copy number variation in solid tumors. <i>PLoS Biology</i> , 2019, 17, e3000434.	2.6	55
18277	The impact of genetic adaptation on chimpanzee subspecies differentiation. <i>PLoS Genetics</i> , 2019, 15, e1008485.	1.5	15
18278	Comparative Proteomic Analysis Reveals Key Proteins Linked to the Accumulation of Soluble Sugars and Organic Acids in the Mature Fruits of the Wild <i>Malus</i> Species. <i>Plants</i> , 2019, 8, 488.	1.6	13
18279	Monocytes affect bone mineral density in pre- and postmenopausal women through ribonucleoprotein complex biogenesis by integrative bioinformatics analysis. <i>Scientific Reports</i> , 2019, 9, 17290.	1.6	11
18280	Network inference with ensembles of bi-clustering trees. <i>BMC Bioinformatics</i> , 2019, 20, 525.	1.2	12
18281	The genomes of two parasitic wasps that parasitize the diamondback moth. <i>BMC Genomics</i> , 2019, 20, 893.	1.2	17
18282	Identifying Acetylation Protein by Fusing Its PseAAC and Functional Domain Annotation. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 311.	2.0	10
18283	Profiling Transcriptional Regulation and Functional Roles of <i>Schistosoma mansoni</i> c-Jun N-Terminal Kinase. <i>Frontiers in Genetics</i> , 2019, 10, 1036.	1.1	11
18284	A Complete Transcriptional Landscape Analysis of <i>Pinus elliottii</i> Engelm. Using Third-Generation Sequencing and Comparative Analysis in the <i>Pinus</i> Phylogeny. <i>Forests</i> , 2019, 10, 942.	0.9	10
18285	ROBOKOP KG and KGB: Integrated Knowledge Graphs from Federated Sources. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 4968-4973.	2.5	36
18286	Representing glycophenotypes: semantic unification of glycobiology resources for disease discovery. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	5
18287	Systems Medicine as a Transforming Tool for Cardiovascular Genetics. <i>Cardiac and Vascular Biology</i> , 2019, , 359-379.	0.2	0
18288	Fast, sensitive and accurate integration of single-cell data with Harmony. <i>Nature Methods</i> , 2019, 16, 1289-1296.	9.0	3,494
18289	An exome-wide rare variant analysis of Korean men identifies three novel genes predisposing to prostate cancer. <i>Scientific Reports</i> , 2019, 9, 17173.	1.6	6

#	ARTICLE	IF	CITATIONS
18290	A Graphic Encoding Method for Quantitative Classification of Protein Structure and Representation of Conformational Changes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1336-1349.	1.9	4
18291	RNASeqR: An R Package for Automated Two-Group RNA-Seq Analysis Workflow. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2023-2031.	1.9	6
18292	A mechanistic evaluation of the angiogenic properties of a dehydrated amnion chorion membrane in vitro and in vivo. <i>Wound Repair and Regeneration</i> , 2019, 27, 609-621.	1.5	16
18293	Transcriptomic and microstructural analyses in <i>Liriodendron tulipifera</i> Linn. reveal candidate genes involved in nectary development and nectar secretion. <i>BMC Plant Biology</i> , 2019, 19, 531.	1.6	13
18294	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
18295	Current status and future perspective of computational toxicology in drug safety assessment under ontological intellection. <i>Journal of Toxicological Sciences</i> , 2019, 44, 721-735.	0.7	5
18296	Integrative In Silico and In Vitro Transcriptomics Analysis Revealed Gene Expression Changes and Oncogenic Features of Normal Cholangiocytes after Chronic Alcohol Exposure. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5987.	1.8	3
18297	Searching for the Genetic Determinants of Peripheral Arterial Disease. <i>Cardiology in Review</i> , 2019, 27, 145-152.	0.6	2
18298	Integrative Analysis of ceRNA Network Reveals Functional lncRNAs in Intrahepatic Cholangiocarcinoma. <i>BioMed Research International</i> , 2019, 2019, 1-9.	0.9	12
18299	Study on the Multitarget Mechanism and Key Active Ingredients of Herba Siegesbeckiae and Volatile Oil against Rheumatoid Arthritis Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-15.	0.5	28
18300	Expression Quantitative Trait Loci in Equine Skeletal Muscle Reveals Heritable Variation in Metabolism and the Training Responsive Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 1215.	1.1	11
18301	PHI-Nets: A Network Resource for Ascomycete Fungal Pathogens to Annotate and Identify Putative Virulence Interacting Proteins and siRNA Targets. <i>Frontiers in Microbiology</i> , 2019, 10, 2721.	1.5	8
18302	Novel Breast-Specific Long Non-coding RNA LINC00993 Acts as a Tumor Suppressor in Triple-Negative Breast Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 1325.	1.3	28
18303	Supervised and Unsupervised End-to-End Deep Learning for Gene Ontology Classification of Neural In Situ Hybridization Images. <i>Entropy</i> , 2019, 21, 221.	1.1	2
18304	Molecular Analysis of UV-C Induced Resveratrol Accumulation in <i>Polygonum cuspidatum</i> Leaves. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6185.	1.8	16
18305	A System-Level Investigation into the Mechanisms of Apigenin Against Inflammation. <i>Natural Product Communications</i> , 2019, 14, 1934578X1987860.	0.2	3
18306	PROMO: an interactive tool for analyzing clinically-labeled multi-omic cancer datasets. <i>BMC Bioinformatics</i> , 2019, 20, 732.	1.2	22
18307	Transcriptome analysis of the almond moth, <i>Cadra cautella</i> , female abdominal tissues and identification of reproduction control genes. <i>BMC Genomics</i> , 2019, 20, 883.	1.2	4

#	ARTICLE	IF	CITATIONS
18308	Classification of adaptor proteins using recurrent neural networks and PSSM profiles. BMC Genomics, 2019, 20, 966.	1.2	19
18309	Direct comparison of Arabidopsis gene expression reveals different responses to melatonin versus auxin. BMC Plant Biology, 2019, 19, 567.	1.6	37
18310	Integrated analyses of miRNAome and transcriptome reveal zinc deficiency responses in rice seedlings. BMC Plant Biology, 2019, 19, 585.	1.6	27
18311	Joint learning improves protein abundance prediction in cancers. BMC Biology, 2019, 17, 107.	1.7	16
18312	Evolutionarily novel genes are expressed in transgenic fish tumors and their orthologs are involved in development of progressive traits in humans. Infectious Agents and Cancer, 2019, 14, 46.	1.2	8
18313	Nuclear factor erythroid 2 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
18314	Drosophila Rps12 controls translation, growth, and cell competition through Xrp1. PLoS Genetics, 2019, 15, e1008513.	1.5	41
18315	Identification of Key Genes Involved in Embryo Development and Differential Oil Accumulation in Two Contrasting Maize Genotypes. Genes, 2019, 10, 993.	1.0	13
18316	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income. Nature Communications, 2019, 10, 5741.	5.8	110
18317	TRANSNAP: a web database providing comprehensive information on Japanese pear transcriptome. Scientific Reports, 2019, 9, 18922.	1.6	10
18318	ReVac: a reverse vaccinology computational pipeline for prioritization of prokaryotic protein vaccine candidates. BMC Genomics, 2019, 20, 981.	1.2	18
18319	Affected Sib-Pair Analyses Identify Signaling Networks Associated With Social Behavioral Deficits in Autism. Frontiers in Genetics, 2019, 10, 1186.	1.1	2
18320	Transcriptomic Characterization of the Human Insular Cortex and Claustrum. Frontiers in Neuroanatomy, 2019, 13, 94.	0.9	12
18321	Spermidine Increases the Sucrose Content in Inferior Grain of Wheat and Thereby Promotes Its Grain Filling. Frontiers in Plant Science, 2019, 10, 1309.	1.7	21
18322	An Integrated Pan-Cancer Analysis and Structure-Based Virtual Screening of GPR15. International Journal of Molecular Sciences, 2019, 20, 6226.	1.8	15
18324	Discrimination of Dormant and Active Hematopoietic Stem Cells by G0 Marker Reveals Dormancy Regulation by Cytoplasmic Calcium. Cell Reports, 2019, 29, 4144-4158.e7.	2.9	27
18325	Multi-omics analysis of multiple missions to space reveal a theme of lipid dysregulation in mouse liver. Scientific Reports, 2019, 9, 19195.	1.6	46
18326	Di (2-ethylhexyl) Phthalate Exposure Impairs the microRNAs Expression Profile During Primordial Follicle Assembly. Frontiers in Endocrinology, 2019, 10, 877.	1.5	10

#	ARTICLE	IF	CITATIONS
18327	Transcriptome-Guided Drug Repositioning. <i>Pharmaceutics</i> , 2019, 11, 677.	2.0	26
18328	GenFam: A web application and database for gene family-based classification and functional enrichment analysis. <i>Plant Direct</i> , 2019, 3, e00191.	0.8	16
18329	A novel framework for horizontal and vertical data integration in cancer studies with application to survival time prediction models. <i>Biology Direct</i> , 2019, 14, 22.	1.9	34
18330	Fermentation innovation through complex hybridization of wild and domesticated yeasts. <i>Nature Ecology and Evolution</i> , 2019, 3, 1576-1586.	3.4	76
18331	MicroRNA-related transcription factor regulatory networks in human colorectal cancer. <i>Medicine (United States)</i> , 2019, 98, e15158.	0.4	24
18332	Screening and identification of key biomarkers in nasopharyngeal carcinoma. <i>Medicine (United States)</i> , 2019, 98, e17997.	0.4	18
18333	Brief Normothermic Machine Perfusion Rejuvenates Discarded Human Kidneys. <i>Transplantation Direct</i> , 2019, 5, e502.	0.8	29
18334	Identifying gene-specific subgroups: an alternative to biclustering. <i>BMC Bioinformatics</i> , 2019, 20, 625.	1.2	5
18335	QTL identification for seed weight and size based on a high-density SLAF-seq genetic map in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Plant Biology</i> , 2019, 19, 537.	1.6	54
18336	Comparative analysis of the complete chloroplast genome sequences of six species of <i>Pulsatilla</i> Miller, Ranunculaceae. <i>Chinese Medicine</i> , 2019, 14, 53.	1.6	19
18337	The host jasmonic acid pathway regulates the transcriptomic changes of dodder and host plant under the scenario of caterpillar feeding on dodder. <i>BMC Plant Biology</i> , 2019, 19, 540.	1.6	10
18338	Chromosome-level genome assembly for giant panda provides novel insights into Carnivora chromosome evolution. <i>Genome Biology</i> , 2019, 20, 267.	3.8	31
18339	The genetic diversity and population structure of <i>Sophora alopecuroides</i> (Fabaceae) as determined by microsatellite markers developed from transcriptome. <i>PLoS ONE</i> , 2019, 14, e0226100.	1.1	12
18340	On the possible origin of protein homochirality, structure, and biochemical function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26571-26579.	3.3	30
18341	Mapping the Germline and Somatic Mutation Interaction Landscape in Indolent and Aggressive Prostate Cancers. <i>Journal of Oncology</i> , 2019, 2019, 1-15.	0.6	4
18342	Draft Genome Assembly of a Fouling Barnacle, <i>Amphibalanus amphitrite</i> (Darwin, 1854): The First Reference Genome for Thecostraca. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	24
18343	CircSLNN: Identifying RBP-Binding Sites on circRNAs via Sequence Labeling Neural Networks. <i>Frontiers in Genetics</i> , 2019, 10, 1184.	1.1	47
18344	Transcriptome of Chicken Liver Tissues Reveals the Candidate Genes and Pathways Responsible for Adaptation into Two Different Climatic Conditions. <i>Animals</i> , 2019, 9, 1076.	1.0	10

#	ARTICLE	IF	CITATIONS
18345	DeepMiR2GO: Inferring Functions of Human MicroRNAs Using a Deep Multi-Label Classification Model. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6046.	1.8	7
18346	<p></p>Integrated Analysis To Identify Molecular Biomarkers Of High-Grade Serous Ovarian Cancer</p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 10057-10075.	1.0	4
18347	Differential Proteome Analysis of Hybrid Bamboo (<i>Bambusa pervariabilis</i> — <i>Dendrocalamopsis grandis</i>) Under Fungal Stress (<i>Arthrinium phaeospermum</i>). <i>Scientific Reports</i> , 2019, 9, 18681.	1.6	8
18348	Genetic pathway analysis reveals a major role for extracellular matrix organization in inflammatory and neuropathic pain. <i>Pain</i> , 2019, 160, 932-944.	2.0	53
18349	Undulating changes in human plasma proteome profiles across the lifespan. <i>Nature Medicine</i> , 2019, 25, 1843-1850.	15.2	470
18350	Hypusine biosynthesis in \hat{I}^2 cells links polyamine metabolism to facultative cellular proliferation to maintain glucose homeostasis. <i>Science Signaling</i> , 2019, 12, .	1.6	37
18351	Comparative Network Pharmacology Analysis of Classical TCM Prescriptions for Chronic Liver Disease. <i>Frontiers in Pharmacology</i> , 2019, 10, 1353.	1.6	25
18352	Screening of molecular targets and construction of a ceRNA network for oxaliplatin resistance in colorectal cancer. <i>RSC Advances</i> , 2019, 9, 31413-31424.	1.7	2
18353	OntoPlot: A Novel Visualisation for Non-hierarchical Associations in Large Ontologies. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2019, 26, 1-1.	2.9	0
18354	Genome-Wide Analysis of Whole Human Glycoside Hydrolases by Data-Driven Analysis in Silico. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6290.	1.8	6
18355	Using mechanistic models for the clinical interpretation of complex genomic variation. <i>Scientific Reports</i> , 2019, 9, 18937.	1.6	20
18356	Immunity-related genes and signaling pathways under hypoxic stresses in <i>Haliothis diversicolor</i> : a transcriptome analysis. <i>Scientific Reports</i> , 2019, 9, 19741.	1.6	13
18357	Combination of PPAR \hat{I}^3 Agonist Pioglitazone and Trabectedin Induce Adipocyte Differentiation to Overcome Trabectedin Resistance in Myxoid Liposarcomas. <i>Clinical Cancer Research</i> , 2019, 25, 7565-7575.	3.2	15
18358	Knowledge-Guided Statistical Learning Methods for Analysis of High-Dimensional -Omics Data in Precision Oncology. <i>JCO Precision Oncology</i> , 2019, 3, 1-9.	1.5	8
18359	Identification of Monotonically Differentially Expressed Genes for IFN- \hat{I}^2 -Treated Multiple Sclerosis Patients. <i>BioMed Research International</i> , 2019, 2019, 1-6.	0.9	3
18360	Bioactive Proteins in <i>Channa striata</i> Promote Wound Healing through Angiogenesis and Cell Proliferation. <i>Protein and Peptide Letters</i> , 2019, 27, 48-59.	0.4	5
18361	Inferring gene expression networks with hubs using a degree weighted Lasso approach. <i>Bioinformatics</i> , 2019, 35, 987-994.	1.8	16
18362	Identification of diagnostic biomarker in patients with gestational diabetes mellitus based on transcriptome-wide gene expression and pattern recognition. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 1503-1510.	1.2	9

#	ARTICLE	IF	CITATIONS
18363	Signature-oriented investigation of the efficacy of multicomponent drugs against heart failure. <i>FASEB Journal</i> , 2019, 33, 2187-2198.	0.2	18
18364	Transcriptomic analysis of interactions between <i>Hyphantria cunea</i> larvae and nucleopolyhedrovirus. <i>Pest Management Science</i> , 2019, 75, 1024-1033.	1.7	21
18365	Characterization and sequence analysis of potential biofertilizer and biocontrol agent <i>Bacillus subtilis</i> strain SEM-9 from silkworm excrement. <i>Canadian Journal of Microbiology</i> , 2019, 65, 45-58.	0.8	17
18366	Robust interferon signature and suppressed tissue repair gene expression in synovial tissue from patients with postinfectious, <i>Borrelia burgdorferi</i> -induced Lyme arthritis. <i>Cellular Microbiology</i> , 2019, 21, e12954.	1.1	26
18367	bcGST: an interactive bias-correction method to identify over-represented gene-sets in boutique arrays. <i>Bioinformatics</i> , 2019, 35, 1350-1357.	1.8	1
18368	A comparative system-level analysis of the neurodegenerative diseases. <i>Journal of Cellular Physiology</i> , 2019, 234, 5215-5229.	2.0	6
18369	Gene expression analysis of heat-shock proteins and redox regulators reveals combinatorial prognostic markers in carcinomas of the gastrointestinal tract. <i>Redox Biology</i> , 2019, 25, 101060.	3.9	12
18370	Plasma microRNA expression levels and their targeted pathways in patients with major depressive disorder who are responsive to duloxetine treatment. <i>Journal of Psychiatric Research</i> , 2019, 110, 38-44.	1.5	31
18371	Protein and peptide profiles in neonatal meconium. <i>Journal of Obstetrics and Gynaecology Research</i> , 2019, 45, 556-564.	0.6	9
18372	Exogenous interleukin-1 β signaling negatively impacts acquired chemoresistance and alters cell adhesion molecule expression pattern in colorectal carcinoma cells HCT116. <i>Cytokine</i> , 2019, 114, 38-46.	1.4	4
18373	Benzothiazole inhibits the growth of <i>Phytophthora capsici</i> through inducing apoptosis and suppressing stress responses and metabolic detoxification. <i>Pesticide Biochemistry and Physiology</i> , 2019, 154, 7-16.	1.6	24
18374	Stroke target identification guided by astrocyte transcriptome analysis. <i>Glia</i> , 2019, 67, 619-633.	2.5	77
18375	Conservation of location of several specific inhibitory codon pairs in the <i>Saccharomyces sensu stricto</i> yeasts reveals translational selection. <i>Nucleic Acids Research</i> , 2019, 47, 1164-1177.	6.5	15
18376	Identification of co-located QTLs and genomic regions affecting grapevine cluster architecture. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1159-1177.	1.8	22
18377	Condition-specific series of metabolic sub-networks and its application for gene set enrichment analysis. <i>Bioinformatics</i> , 2019, 35, 2258-2266.	1.8	12
18378	Single-Cell Transcriptomic Analysis of Human Lung Provides Insights into the Pathobiology of Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 199, 1517-1536.	2.5	866
18379	Integrative Approaches for Inference of Genome-Scale Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2019, 1883, 161-194.	0.4	3
18380	Comprehensive analysis of phenotype, microstructure and global transcriptional profiling to unravel the effect of excess copper on the symbiosis between nitrogen-fixing bacteria and <i>Medicago lupulina</i> . <i>Science of the Total Environment</i> , 2019, 656, 1346-1357.	3.9	10

#	ARTICLE	IF	CITATIONS
18381	Genomic variation and strain-specific functional adaptation in the human gut microbiome during early life. <i>Nature Microbiology</i> , 2019, 4, 470-479.	5.9	164
18382	Comparative Analysis of Oomycete Genome Evolution Using the Oomycete Gene Order Browser (OGO). <i>Genome Biology and Evolution</i> , 2019, 11, 189-206.	1.1	17
18383	Comprehensive Transcriptional Profiling of the Gastrointestinal Tract of Ruminants from Birth to Adulthood Reveals Strong Developmental Stage Specific Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 359-373.	0.8	48
18384	Complete genome sequence unveiled cellulose degradation enzymes and secondary metabolic potentials in <i>Streptomyces</i> sp. CC0208. <i>Journal of Basic Microbiology</i> , 2019, 59, 267-276.	1.8	9
18385	Formatting biological big data for modern machine learning in drug discovery. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2019, 9, e1408.	6.2	17
18386	Noncoding rare variants of TBX6 in congenital anomalies of the kidney and urinary tract. <i>Molecular Genetics and Genomics</i> , 2019, 294, 493-500.	1.0	8
18387	MiRNA-target interactions in osteogenic signaling pathways involving zinc via the metal regulatory element. <i>BioMetals</i> , 2019, 32, 111-121.	1.8	6
18388	Candidates responsible for dwarf pear phenotype as revealed by comparative transcriptome analysis. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	32
18389	Extracellular vesicles derived from endometrial human mesenchymal stem cells enhance embryo yield and quality in an aged murine model. <i>Biology of Reproduction</i> , 2019, 100, 1180-1192.	1.2	44
18390	Whole-exome sequencing reveals SALL4 variants in premature ovarian insufficiency: an update on genotype-phenotype correlations. <i>Human Genetics</i> , 2019, 138, 83-92.	1.8	27
18391	Transcriptome-wide analysis of <i>Chlorella</i> reveals auxin-induced carotenogenesis pathway in green microalgae. <i>Algal Research</i> , 2019, 37, 320-335.	2.4	25
18392	Loss of Estrogen-Related Receptor Alpha Facilitates Angiogenesis in Endothelial Cells. <i>Molecular and Cellular Biology</i> , 2019, 39, .	1.1	16
18393	The Major RNA-Binding Protein ProQ Impacts Virulence Gene Expression in <i>Salmonella enterica</i> Serovar Typhimurium. <i>MBio</i> , 2019, 10, .	1.8	81
18394	Identifying Potential Ageing-Modulating Drugs In Silico. <i>Trends in Endocrinology and Metabolism</i> , 2019, 30, 118-131.	3.1	15
18395	Early-onset inflammatory bowel disease as a model disease to identify key regulators of immune homeostasis mechanisms. <i>Immunological Reviews</i> , 2019, 287, 162-185.	2.8	60
18396	Rapid Recapitulation of Nonalcoholic Steatohepatitis upon Loss of Host Cell Factor 1 Function in Mouse Hepatocytes. <i>Molecular and Cellular Biology</i> , 2019, 39, .	1.1	11
18397	Priming integrin $\alpha 5$ promotes human dental pulp stem cells odontogenic differentiation due to extracellular matrix deposition and amplified extracellular matrix-receptor activity. <i>Journal of Cellular Physiology</i> , 2019, 234, 12897-12909.	2.0	12
18398	iTRAQ-based phosphoproteomic analysis reveals host cell's specific responses to <i>Toxoplasma gondii</i> at the phases of invasion and prior to egress. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 202-212.	1.1	10

#	ARTICLE	IF	CITATIONS
18399	HLA-DO Modulates the Diversity of the MHC-II Self-peptidome. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 490-503.	2.5	33
18400	Comparative transcriptome analysis to elucidate the enhanced thermotolerance of tea plants (<i>Camellia sinensis</i>) treated with exogenous calcium. <i>Planta</i> , 2019, 249, 775-786.	1.6	27
18401	The protein interaction networks of mucolipins and two-pore channels. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2019, 1866, 1111-1123.	1.9	28
18402	Human lung epithelial cells cultured in the presence of radon-emitting rock experience gene expression changes similar to those associated with tobacco smoke exposure. <i>Journal of Environmental Radioactivity</i> , 2019, 196, 64-81.	0.9	12
18403	Complete genome and data mining of <i>Aeromicrobium</i> sp. A162 isolated from the Southern Ocean. <i>Marine Genomics</i> , 2019, 45, 5-7.	0.4	2
18404	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	6.5	153
18405	Identification of genes with universally upregulated or downregulated expressions in colorectal cancer. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2019, 34, 880-889.	1.4	16
18406	Blastic plasmacytoid dendritic cell neoplasm: genomics mark epigenetic dysregulation as a primary therapeutic target. <i>Haematologica</i> , 2019, 104, 729-737.	1.7	58
18407	Transcriptome analysis of spleen reveals the signal transduction of toll-like receptors after <i>Aeromonas hydrophila</i> infection in <i>Schizothorax prenanti</i> . <i>Fish and Shellfish Immunology</i> , 2019, 84, 816-824.	1.6	21
18408	High-complexity regions in mammalian genomes are enriched for developmental genes. <i>Bioinformatics</i> , 2019, 35, 1813-1819.	1.8	3
18409	Lineage-Specific Expression Divergence in Grasses Is Associated with Male Reproduction, Host-Pathogen Defense, and Domestication. <i>Genome Biology and Evolution</i> , 2019, 11, 207-219.	1.1	6
18410	MitoMiner v4.0: an updated database of mitochondrial localization evidence, phenotypes and diseases. <i>Nucleic Acids Research</i> , 2019, 47, D1225-D1228.	6.5	97
18411	Chemical Cross-Linking Enables Drafting ClpXP Proximity Maps and Taking Snapshots of In Situ Interaction Networks. <i>Cell Chemical Biology</i> , 2019, 26, 48-59.e7.	2.5	31
18412	SP1, MYC, CTNNB1, CREB1, JUN genes as potential therapy targets for neuropathic pain of brain. <i>Journal of Cellular Physiology</i> , 2019, 234, 6688-6695.	2.0	13
18413	Metabolomics and proteomics identify the toxic form and the associated cellular binding targets of the anti-proliferative drug AICAR. <i>Journal of Biological Chemistry</i> , 2019, 294, 805-815.	1.6	11
18414	SkeletalVis: an exploration and meta-analysis data portal of cross-species skeletal transcriptomics data. <i>Bioinformatics</i> , 2019, 35, 2283-2290.	1.8	18
18415	Identification of hsa-miR-34a, hsa-miR-124, and hsa-miR-204 as signatures for cataract. <i>Journal of Cellular Physiology</i> , 2019, 234, 10709-10717.	2.0	14
18416	Identification of key biomarkers in diabetic nephropathy via bioinformatic analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 8676-8688.	1.2	18

#	ARTICLE	IF	CITATIONS
18417	Importance of flagella in acute and chronic <i>Pseudomonas aeruginosa</i> infections. <i>Environmental Microbiology</i> , 2019, 21, 883-897.	1.8	23
18418	Resequencing of <i>CRL12</i> family reveals haplotype block inheritance and recombination of agronomically important genes in artificial selection. <i>Plant Biotechnology Journal</i> , 2019, 17, 945-955.	4.1	20
18419	OPA2Vec: combining formal and informal content of biomedical ontologies to improve similarity-based prediction. <i>Bioinformatics</i> , 2019, 35, 2133-2140.	1.8	103
18420	IID 2018 update: context-specific physical protein-protein interactions in human, model organisms and domesticated species. <i>Nucleic Acids Research</i> , 2019, 47, D581-D589.	6.5	164
18421	Screening of key candidate genes and pathways for osteocytes involved in the differential response to different types of mechanical stimulation using a bioinformatics analysis. <i>Journal of Bone and Mineral Metabolism</i> , 2019, 37, 614-626.	1.3	6
18422	Assessment of agronomic parameters and gene expression profiling of flax (<i>Linum usitatissimum</i> L.) upon treatment with brassinosteroid and its biosynthetic inhibitor. <i>Industrial Crops and Products</i> , 2019, 128, 270-281.	2.5	4
18423	An important resource for understanding bio-adhesion mechanisms: Cement gland transcriptomes of two goose barnacles, <i>Pollicipes pollicipes</i> and <i>Lepas anatifera</i> (Cirripedia, Thoracica). <i>Marine Genomics</i> , 2019, 45, 16-20.	0.4	11
18424	Bridging the Gap between Connectome and Transcriptome. <i>Trends in Cognitive Sciences</i> , 2019, 23, 34-50.	4.0	245
18425	miRBase: from microRNA sequences to function. <i>Nucleic Acids Research</i> , 2019, 47, D155-D162.	6.5	3,014
18426	Identification of differentially expressed genes and typical fusion genes associated with three subtypes of breast cancer. <i>Breast Cancer</i> , 2019, 26, 305-316.	1.3	2
18427	Progressive behavioural, physiological and transcriptomic shifts over the course of prolonged starvation in ticks. <i>Molecular Ecology</i> , 2019, 28, 49-65.	2.0	39
18428	Phylogenetic, molecular evolution and structural analyses of the WFDC1/prostate stromal protein 20 (ps20). <i>Gene</i> , 2019, 686, 125-140.	1.0	3
18429	Systems Biology and Machine Learning in Plant-Pathogen Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 45-55.	1.4	68
18430	Whole exome sequencing identifies novel predisposing genes in neural tube defects. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e00467.	0.6	25
18431	MicroRNAs profiles of Chinese Perch Brain (CPB) cells infected with <i>Siniperca chuatsi</i> rhabdovirus (SCRV). <i>Fish and Shellfish Immunology</i> , 2019, 84, 1075-1082.	1.6	16
18432	Gel Absorption-Based Sample Preparation Method for Shotgun Analysis of Membrane Proteome. <i>Methods in Molecular Biology</i> , 2019, 1855, 483-490.	0.4	0
18433	Complete genome sequence of marine <i>Bacillus</i> sp. Y-01, isolated from the plastics contamination in the Yellow Sea. <i>Marine Genomics</i> , 2019, 43, 72-74.	0.4	4
18434	Reconstruction of global regulatory network from signaling to cellular functions using phosphoproteomic data. <i>Genes To Cells</i> , 2019, 24, 82-93.	0.5	7

#	ARTICLE	IF	CITATIONS
18435	De novo assembly and comparative transcriptome analysis: novel insights into terpenoid biosynthesis in <i>Chamaemelum nobile</i> L.. <i>Plant Cell Reports</i> , 2019, 38, 101-116.	2.8	20
18436	An optimal kernel-based <i>U</i> -statistic method for quantitative gene-set association analysis. <i>Genetic Epidemiology</i> , 2019, 43, 137-149.	0.6	7
18437	Quantitative Urinary Proteome Reveals Potential Biomarkers for Ureteropelvic Junction Obstruction. <i>Proteomics - Clinical Applications</i> , 2019, 13, 1800101.	0.8	9
18438	Ontology-based semantic mapping of chemical toxicities. <i>Toxicology</i> , 2019, 412, 89-100.	2.0	10
18439	Transcriptome characterization and SSR discovery in <i>Squaliobarbus curriculus</i> . <i>Journal of Oceanology and Limnology</i> , 2019, 37, 235-244.	0.6	6
18440	Identification and characteristics of <i>Stagonosporopsis cucurbitacearum</i> pathogenic factors influencing pumpkin seeding survival in north-east China. <i>Journal of Phytopathology</i> , 2019, 167, 41-55.	0.5	8
18441	Linking Scattered Stem Cell-Based Data to Advance Therapeutic Development. <i>Trends in Molecular Medicine</i> , 2019, 25, 8-19.	3.5	6
18442	Mechanically stimulated osteocytes reduce the bone-metastatic potential of breast cancer cells <i>in vitro</i> by signaling through endothelial cells. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 7590-7601.	1.2	27
18443	Encapsulation of <i>S</i> -nitrosoglutathione: a transcriptomic validation. <i>Drug Development and Industrial Pharmacy</i> , 2019, 45, 423-429.	0.9	1
18444	Elevation in Cell Cycle and Protein Metabolism Gene Transcription in Inactive Colonic Tissue From Icelandic Patients With Ulcerative Colitis. <i>Inflammatory Bowel Diseases</i> , 2019, 25, 317-327.	0.9	5
18445	Assembly of a parts list of the human mitotic cell cycle machinery. <i>Journal of Molecular Cell Biology</i> , 2019, 11, 703-718.	1.5	80
18446	Extracellular Vesicles from Neurosurgical Aspirates Identifies Chaperonin Containing TCP1 Subunit 6A as a Potential Glioblastoma Biomarker with Prognostic Significance. <i>Proteomics</i> , 2019, 19, e1800157.	1.3	59
18447	Benchtop-compatible sample processing workflow for proteome profiling of <math>100\%</math> mammalian cells. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 4587-4596.	1.9	46
18448	Systems biology and gene networks in Alzheimer's disease. <i>Neuroscience and Biobehavioral Reviews</i> , 2019, 96, 31-44.	2.9	17
18449	Unipept 4.0: Functional Analysis of Metaproteome Data. <i>Journal of Proteome Research</i> , 2019, 18, 606-615.	1.8	112
18450	PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. <i>Nucleic Acids Research</i> , 2019, 47, D419-D426.	6.5	2,455
18451	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019, 47, D351-D360.	6.5	1,291
18452	Genomic and transcriptomic insights into the survival of the subaerial cyanobacterium <i>Nostoc flagelliforme</i> in arid and exposed habitats. <i>Environmental Microbiology</i> , 2019, 21, 845-863.	1.8	32

#	ARTICLE	IF	CITATIONS
18453	Comparative metagenomic and metatranscriptomic analyses reveal the breed effect on the rumen microbiome and its associations with feed efficiency in beef cattle. <i>Microbiome</i> , 2019, 7, 6.	4.9	150
18454	Investigation of the Underlying Genes and Mechanism of Macrophage-Enriched Ruptured Atherosclerotic Plaques Using Bioinformatics Method. <i>Journal of Atherosclerosis and Thrombosis</i> , 2019, 26, 636-658.	0.9	25
18455	The complete genome of the antifungal bacterium <i>Pseudomonas</i> sp. strain MS82. <i>Journal of Plant Diseases and Protection</i> , 2019, 126, 153-160.	1.6	8
18456	Rbf Activates the Myogenic Transcriptional Program to Promote Skeletal Muscle Differentiation. <i>Cell Reports</i> , 2019, 26, 702-719.e6.	2.9	26
18457	Integrative Transcriptome and Proteome Analysis Identifies Major Metabolic Pathways Involved in Pepper Fruit Development. <i>Journal of Proteome Research</i> , 2019, 18, 982-994.	1.8	40
18458	Mature IgDlow/- B cells maintain tolerance by promoting regulatory T cell homeostasis. <i>Nature Communications</i> , 2019, 10, 190.	5.8	20
18459	The behavioral origins of novelty: did increased aggression lead to scale-eating in pupfishes?. <i>Behavioral Ecology</i> , 2019, 30, 557-569.	1.0	15
18460	The Evolutionary Traceability of a Protein. <i>Genome Biology and Evolution</i> , 2019, 11, 531-545.	1.1	23
18461	Analysis of transcripts and splice isoforms in <i>Medicago sativa</i> L. by single-molecule long-read sequencing. <i>Plant Molecular Biology</i> , 2019, 99, 219-235.	2.0	38
18462	Quantitative Proteomic Analysis of Small and Large Extracellular Vesicles (EVs) Reveals Enrichment of Adhesion Proteins in Small EVs. <i>Journal of Proteome Research</i> , 2019, 18, 947-959.	1.8	71
18463	Transcriptome-wide identification of differentially expressed genes in <i>Procambarus clarkii</i> in response to chromium challenge. <i>Fish and Shellfish Immunology</i> , 2019, 87, 43-50.	1.6	17
18464	Pathological priming causes developmental gene network heterochronicity in autistic subject-derived neurons. <i>Nature Neuroscience</i> , 2019, 22, 243-255.	7.1	209
18465	Chemically induced vesiculation as a platform for studying TMEM16F activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1309-1318.	3.3	22
18466	Analysis of the distribution of assimilation products and the characteristics of transcriptomes in rice by submergence during the ripening stage. <i>BMC Genomics</i> , 2019, 20, 18.	1.2	7
18467	Multi-omics integration reveals molecular networks and regulators of psoriasis. <i>BMC Systems Biology</i> , 2019, 13, 8.	3.0	37
18468	Precious cargo: Modulation of the mesenteric lymph exosome payload after hemorrhagic shock. <i>Journal of Trauma and Acute Care Surgery</i> , 2019, 86, 52-61.	1.1	12
18469	MAPK ϵ -Targeted Drug Delivered by a pH-Sensitive MSNP Nanocarrier Synergizes with PD ϵ 1 Blockade in Melanoma without T ϵ Cell Suppression. <i>Advanced Functional Materials</i> , 2019, 29, 1806916.	7.8	34
18470	Description and Generalization of Continuous Areal Features. , 2019, , 149-197.		0

#	ARTICLE	IF	CITATIONS
18471	Gene expression changes elicited by a parasitic B chromosome in the grasshopper <i>Eyprepocnemis plorans</i> are consistent with its phenotypic effects. <i>Chromosoma</i> , 2019, 128, 53-67.	1.0	15
18472	Effects of activin A on the transcriptome of mouse oogenesis in vitro. <i>Journal of Cellular Physiology</i> , 2019, 234, 14339-14350.	2.0	4
18473	Description Approaches and Automated Generalization Algorithms for Groups of Map Objects. , 2019, , .		8
18474	<i>Pedobacter paludis</i> sp. nov., isolated from wetland soil. <i>Archives of Microbiology</i> , 2019, 201, 349-355.	1.0	4
18475	Coordinated downregulation of the photosynthetic apparatus as a protective mechanism against UV exposure in the diatom <i>Corethron hystrix</i> . <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1837-1850.	1.7	5
18476	The embryonic transcriptome of <i>Arabidopsis thaliana</i> . <i>Plant Reproduction</i> , 2019, 32, 77-91.	1.3	82
18477	Derivation of Haploid Trophoblast Stem Cells via Conversion In Vitro. <i>IScience</i> , 2019, 11, 508-518.	1.9	24
18478	Comparative transcriptomic analysis reveals different responses of <i>Arabidopsis thaliana</i> roots and shoots to infection by <i>Agrobacterium tumefaciens</i> in a hydroponic co-cultivation system. <i>Physiological and Molecular Plant Pathology</i> , 2019, 106, 109-119.	1.3	4
18479	A scoping review of ontologies related to human behaviour change. <i>Nature Human Behaviour</i> , 2019, 3, 164-172.	6.2	94
18480	Challenges in unsupervised clustering of single-cell RNA-seq data. <i>Nature Reviews Genetics</i> , 2019, 20, 273-282.	7.7	780
18481	miR-142-5p enhances cisplatin-induced apoptosis in ovarian cancer cells by targeting multiple anti-apoptotic genes. <i>Biochemical Pharmacology</i> , 2019, 161, 98-112.	2.0	81
18482	Identification of candidate diagnostic and prognostic biomarkers for pancreatic carcinoma. <i>EBioMedicine</i> , 2019, 40, 382-393.	2.7	93
18483	Identification of key genes and transcription factors in aging mesenchymal stem cells by DNA microarray data. <i>Gene</i> , 2019, 692, 79-87.	1.0	15
18484	15 years of GDR: New data and functionality in the Genome Database for Rosaceae. <i>Nucleic Acids Research</i> , 2019, 47, D1137-D1145.	6.5	285
18485	Meta-analysis of gene expression profiles in long-term non-progressors infected with HIV-1. <i>BMC Medical Genomics</i> , 2019, 12, 3.	0.7	13
18486	Recombination of ecologically and evolutionarily significant loci maintains genetic cohesion in the <i>Pseudomonas syringae</i> species complex. <i>Genome Biology</i> , 2019, 20, 3.	3.8	114
18487	Akt and SGK protein kinases are required for efficient feeding by macropinocytosis. <i>Journal of Cell Science</i> , 2019, 132, .	1.2	26
18488	RCBTB1 Deletion Is Associated with Metastatic Outcome and Contributes to Docetaxel Resistance in Nontranslocation-Related Pleomorphic Sarcomas. <i>Cancers</i> , 2019, 11, 81.	1.7	3

#	ARTICLE	IF	CITATIONS
18489	REDfly: the transcriptional regulatory element database for <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2019, 47, D828-D834.	6.5	59
18490	Genetic and Epigenetic Determinants of Aggressiveness in Cribriform Carcinoma of the Prostate. <i>Molecular Cancer Research</i> , 2019, 17, 446-456.	1.5	44
18491	Complete Genome Sequence of <i>Bacillus cereus</i> CC-1, A Novel Marine Selenate/Selenite Reducing Bacterium Producing Metallic Selenides Nanomaterials. <i>Current Microbiology</i> , 2019, 76, 78-85.	1.0	16
18492	Polysaccharides for tissue engineering: Current landscape and future prospects. <i>Carbohydrate Polymers</i> , 2019, 205, 601-625.	5.1	104
18493	Integration of small RNAs and mRNAs by high-throughput sequencing reveals a complex regulatory network in Chinese sea cucumber, Russian sea cucumber and their hybrids. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 1-13.	0.4	5
18494	Comparison of common machine learning models for classification of tuberculosis using transcriptional biomarkers from integrated datasets. <i>Applied Soft Computing Journal</i> , 2019, 74, 264-273.	4.1	19
18495	A curated gene list for expanding the horizons of pigmentation biology. <i>Pigment Cell and Melanoma Research</i> , 2019, 32, 348-358.	1.5	72
18496	Victors: a web-based knowledge base of virulence factors in human and animal pathogens. <i>Nucleic Acids Research</i> , 2019, 47, D693-D700.	6.5	120
18497	Identification of Potential miRNAs Biomarkers for High-Grade Prostate Cancer by Integrated Bioinformatics Analysis. <i>Pathology and Oncology Research</i> , 2019, 25, 1445-1456.	0.9	20
18498	How crickets become freeze tolerant: The transcriptomic underpinnings of acclimation in <i>Gryllus veletis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 55-66.	0.4	18
18499	Overexpression of <i>Schizosaccharomyces pombe</i> tRNA 3'-end processing enzyme Trz2 leads to an increased cellular iron level and apoptotic cell death. <i>Fungal Genetics and Biology</i> , 2019, 122, 11-20.	0.9	6
18500	Toward the understanding of the role of CDC48, a major component of the protein quality control, in plant immunity. <i>Plant Science</i> , 2019, 279, 34-44.	1.7	20
18501	Computational Analysis of lncRNA Function in Cancer. <i>Methods in Molecular Biology</i> , 2019, 1878, 139-155.	0.4	11
18502	Strategies for Pathway Analysis Using GWAS and WGS Data. <i>Current Protocols in Human Genetics</i> , 2019, 100, e79.	3.5	26
18503	Identification of six miRNAs serving as predictive biomarkers in coronary artery disease. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 1932-1942.	1.2	1
18505	Comparative transcriptome analysis identifies differentially expressed genes between normal and late-blooming Siberian apricot. <i>Journal of Forestry Research</i> , 2019, 30, 2277-2288.	1.7	6
18506	Machine Learning in Human Olfactory Research. <i>Chemical Senses</i> , 2019, 44, 11-22.	1.1	46
18507	PubChem 2019 update: improved access to chemical data. <i>Nucleic Acids Research</i> , 2019, 47, D1102-D1109.	6.5	2,217

#	ARTICLE	IF	CITATIONS
18508	MatrixDB: integration of new data with a focus on glycosaminoglycan interactions. <i>Nucleic Acids Research</i> , 2019, 47, D376-D381.	6.5	93
18509	GaMRed – adaptive filtering of high-throughput biological data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	1.9	9
18510	A Transcriptomic Method to Determine Airway Immune Dysfunction in T2-High and T2-Low Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 199, 465-477.	2.5	98
18511	Hippocampal transcriptome profiling combined with protein-protein interaction analysis elucidates Alzheimer's disease pathways and genes. <i>Neurobiology of Aging</i> , 2019, 74, 225-233.	1.5	30
18512	Translocatome: a novel resource for the analysis of protein translocation between cellular organelles. <i>Nucleic Acids Research</i> , 2019, 47, D495-D505.	6.5	17
18513	The Comparative Toxicogenomics Database: update 2019. <i>Nucleic Acids Research</i> , 2019, 47, D948-D954.	6.5	731
18514	Sequence Alterations of Cortical Genes Linked to Individual Connectivity of the Human Brain. <i>Cerebral Cortex</i> , 2019, 29, 3828-3835.	1.6	10
18515	Transcriptome analysis provides insights into differentially expressed genes and long noncoding RNAs involved in sex-related differences in Amur sturgeon (<i>Acipenser schrenckii</i>). <i>Molecular Reproduction and Development</i> , 2019, 86, 132-144.	1.0	7
18516	Systems vaccinology and big data in the vaccine development chain. <i>Immunology</i> , 2019, 156, 33-46.	2.0	57
18517	Insight into the evolution and functional characteristics of the pan-genome assembly from sesame landraces and modern cultivars. <i>Plant Biotechnology Journal</i> , 2019, 17, 881-892.	4.1	79
18518	SATrans: New Free Available Software for Annotation of Transcriptome and Functional Analysis of Differentially Expressed Genes. <i>Journal of Computational Biology</i> , 2019, 26, 117-123.	0.8	1
18519	Proteomic Analysis of the Initial Oral Pellicle in Caries-Active and Caries-Free Individuals. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1800143.	0.8	27
18520	DeepIsoFun: a deep domain adaptation approach to predict isoform functions. <i>Bioinformatics</i> , 2019, 35, 2535-2544.	1.8	20
18521	Identification of prognostic miRNA biomarkers for predicting overall survival of colon adenocarcinoma and bioinformatics analysis: A study based on The Cancer Genome Atlas database. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 9839-9849.	1.2	10
18522	Differential expression of genes in greenbug (<i>Schizaphis graminum</i> Rondani) treated by imidacloprid and RNA interference. <i>Pest Management Science</i> , 2019, 75, 1726-1733.	1.7	18
18523	Developmental toxicity and apoptosis in zebrafish embryos induced by low-dose I^{137} -ray irradiation. <i>Environmental Science and Pollution Research</i> , 2019, 26, 3869-3881.	2.7	18
18524	Multifactorial Inheritance and Complex Diseases. , 2019, , 323-358.		3
18525	Activation of Nrf2 by Phloretin Attenuates Palmitic Acid-Induced Endothelial Cell Oxidative Stress via AMPK-Dependent Signaling. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 120-131.	2.4	55

#	ARTICLE	IF	CITATIONS
18526	Microgravity-induced hepatogenic differentiation of rBMSCs on board the SJ-10 satellite. <i>FASEB Journal</i> , 2019, 33, 4273-4286.	0.2	19
18527	Integrative analyses of genes associated with idiopathic pulmonary fibrosis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 8648-8660.	1.2	14
18528	In Silico Target Prediction for Small Molecules. <i>Methods in Molecular Biology</i> , 2019, 1888, 273-309.	0.4	19
18530	The Impact of Bioinformatics Tools in the Development of Antimicrobial Drugs and Other Agents. , 2019, , 335-347.		2
18531	ECO, the Evidence & Conclusion Ontology: community standard for evidence information. <i>Nucleic Acids Research</i> , 2019, 47, D1186-D1194.	6.5	67
18532	Building a livestock genetic and genomic information knowledgebase through integrative developments of Animal QTLdb and CorrDB. <i>Nucleic Acids Research</i> , 2019, 47, D701-D710.	6.5	268
18533	An RK/ST C-Terminal Motif is Required for Targeting of OEP7.2 and a Subset of Other Arabidopsis Tail-Anchored Proteins to the Plastid Outer Envelope Membrane. <i>Plant and Cell Physiology</i> , 2019, 60, 516-537.	1.5	16
18534	Altered levels of focal adhesion and extracellular matrix-receptor interacting proteins were identified in Hailey-Hailey disease by quantitative iTRAQ proteome analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 3801-3812.	1.2	6
18535	Identification of tissue-specific tumor biomarker using different optimization algorithms. <i>Genes and Genomics</i> , 2019, 41, 431-443.	0.5	10
18536	Therapeutic effects of rosuvastatin in hypercholesterolemic prediabetic mice in the absence of low density lipoprotein receptor. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 481-490.	1.1	1
18537	The subcellular organisation of <i>Saccharomyces cerevisiae</i> . <i>Current Opinion in Chemical Biology</i> , 2019, 48, 86-95.	2.8	26
18538	Identification of key genes and pathways in diabetic nephropathy by bioinformatics analysis. <i>Journal of Diabetes Investigation</i> , 2019, 10, 972-984.	1.1	52
18539	Transcriptome profiles of soybean leaves and roots in response to zinc deficiency. <i>Physiologia Plantarum</i> , 2019, 167, 330-351.	2.6	27
18540	Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	41
18541	Computational Methods for Drug Repurposing. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	7
18542	Acute Inflammation After Traumatic Brain Injury. , 2019, , 221-239.		1
18543	Differential gene expression profile in monocytic myeloid-derived suppressor cells at maternal-fetal interface in a mouse model of spontaneous abortion. <i>Journal of Cellular Physiology</i> , 2019, 234, 10789-10799.	2.0	5
18544	Construction and analysis of dysregulated lncRNA-associated ceRNA network in colorectal cancer. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 9250-9263.	1.2	30

#	ARTICLE	IF	CITATIONS
18545	Identification of microRNAs related to myocardial ischemic reperfusion injury. <i>Journal of Cellular Physiology</i> , 2019, 234, 11380-11390.	2.0	17
18546	A Nested Genetic Algorithm for feature selection in high-dimensional cancer Microarray datasets. <i>Expert Systems With Applications</i> , 2019, 121, 233-243.	4.4	150
18547	Deuterium induces a distinctive <i>Escherichia coli</i> proteome that correlates with the reduction in growth rate. <i>Journal of Biological Chemistry</i> , 2019, 294, 2279-2292.	1.6	20
18548	Computational Prediction of Drug-Target Interactions via Ensemble Learning. <i>Methods in Molecular Biology</i> , 2019, 1903, 239-254.	0.4	23
18549	The comparative analysis of phenotypic and whole transcriptome gene expression data of ascites susceptible versus ascites resistant chickens. <i>Molecular Biology Reports</i> , 2019, 46, 793-804.	1.0	2
18550	Accurate and efficient estimation of small <i>P</i> -values with the cross-entropy method: applications in genomic data analysis. <i>Bioinformatics</i> , 2019, 35, 2441-2448.	1.8	6
18551	Background on Biology of Ageing and Bioinformatics. <i>Advanced Information and Knowledge Processing</i> , 2019, , 25-43.	0.2	0
18552	Practical considerations on performing and analyzing CLIP-seq experiments to identify transcriptomic-wide RNA-protein interactions. <i>Methods</i> , 2019, 155, 49-57.	1.9	12
18553	Stable-protein Pair Analysis as A Novel Strategy to Identify Proteomic Signatures: Application To Seminal Plasma From Infertile Patients. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S77-S90.	2.5	30
18554	A genome-wide association study identifies new genes associated with developmental dysplasia of the hip. <i>Clinical Genetics</i> , 2019, 95, 345-355.	1.0	7
18555	Computational functional genomics-based reduction of disease-related gene sets to their key components. <i>Bioinformatics</i> , 2019, 35, 2362-2370.	1.8	6
18556	Genome-wide search of nucleosome patterns using visual analytics. <i>Bioinformatics</i> , 2019, 35, 2185-2192.	1.8	1
18557	A systematic screen of conserved <i>Ralstonia solanacearum</i> effectors reveals the role of RipAB, a nuclear-localized effector that suppresses immune responses in potato. <i>Molecular Plant Pathology</i> , 2019, 20, 547-561.	2.0	38
18558	Molecular cross-talk in a unique parasitoid manipulation strategy. <i>Insect Biochemistry and Molecular Biology</i> , 2019, 106, 64-78.	1.2	11
18559	Computational analysis of the <i>Plasmodiophora brassicae</i> genome: mitochondrial sequence description and metabolic pathway database design. <i>Genomics</i> , 2019, 111, 1629-1640.	1.3	27
18561	The Hsp70/J-protein machinery of the African trypanosome, <i>Trypanosoma brucei</i> . <i>Cell Stress and Chaperones</i> , 2019, 24, 125-148.	1.2	12
18563	Identification of eight meta-signature miRNAs as potential biomarkers for oropharyngeal cancers. <i>Cancer Genetics</i> , 2019, 233-234, 75-83.	0.2	5
18564	Transcriptomic analysis of short-term 17 β -ethynylestradiol exposure in two Californian sentinel fish species sardine (<i>Sardinops sagax</i>) and mackerel (<i>Scomber japonicus</i>). <i>Environmental Pollution</i> , 2019, 244, 926-937.	3.7	8

#	ARTICLE	IF	CITATIONS
18565	Deconvoluting essential gene signatures for cancer growth from genomic expression in compound-treated cells. <i>Bioinformatics</i> , 2019, 35, 1167-1173.	1.8	2
18566	The biosynthesis of phenolic acids is positively regulated by the JA-responsive transcription factor ERF115 in <i>Salvia miltiorrhiza</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 243-254.	2.4	120
18567	Novel putative drugs and key initiating genes for neurodegenerative disease determined using network-based genetic integrative analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 5459-5471.	1.2	4
18568	Exploring Protein Conformational Diversity. <i>Methods in Molecular Biology</i> , 2019, 1851, 353-365.	0.4	2
18569	Induction of antibacterial proteins and peptides in the coprophilous mushroom <i>Coprinopsis cinerea</i> in response to bacteria. <i>ISME Journal</i> , 2019, 13, 588-602.	4.4	60
18570	A Roadmap to Domain Based Proteomics. <i>Methods in Molecular Biology</i> , 2019, 1851, 287-300.	0.4	2
18571	Towards region-specific propagation of protein functions. <i>Bioinformatics</i> , 2019, 35, 1737-1744.	1.8	7
18572	Comprehensive analysis of microRNA-messenger RNA regulatory network in gemcitabine-resistant bladder cancer cells. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 6347-6360.	1.2	11
18573	Multiple functions of miR-83p in the development and metamorphosis of the red flour beetle, <i>Tribolium castaneum</i> . <i>Insect Molecular Biology</i> , 2019, 28, 208-221.	1.0	19
18574	Machine learning for integrating data in biology and medicine: Principles, practice, and opportunities. <i>Information Fusion</i> , 2019, 50, 71-91.	11.7	340
18575	Gene ontology enrichment analysis of congenital diaphragmatic hernia-associated genes. <i>Pediatric Research</i> , 2019, 85, 13-19.	1.1	33
18576	Computational Methods in Protein Evolution. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	1
18577	The Bear Giant-Skipper genome suggests genetic adaptations to living inside yucca roots. <i>Molecular Genetics and Genomics</i> , 2019, 294, 211-226.	1.0	10
18578	Identification of a 3' Untranslated Genetic Variant of <i>RARB</i> Associated With Carotid Intima-Media Thickness in Rheumatoid Arthritis: A Genome-Wide Association Study. <i>Arthritis and Rheumatology</i> , 2019, 71, 351-360.	2.9	26
18579	SemGen: a tool for semantics-based annotation and composition of biosimulation models. <i>Bioinformatics</i> , 2019, 35, 1600-1602.	1.8	24
18580	Computational models for lncRNA function prediction and functional similarity calculation. <i>Briefings in Functional Genomics</i> , 2019, 18, 58-82.	1.3	141
18581	TreeGrafter: phylogenetic tree-based annotation of proteins with Gene Ontology terms and other annotations. <i>Bioinformatics</i> , 2019, 35, 518-520.	1.8	22
18582	Single nucleotide polymorphism (SNP) discovery through genotyping-by-sequencing (GBS) and genetic characterization of <i>Dendrobium</i> mutants and cultivars. <i>Scientia Horticulturae</i> , 2019, 244, 225-233.	1.7	14

#	ARTICLE	IF	CITATIONS
18583	Hormonal control and target genes of <i>ftz</i> expression in the honeybee <i>Apis mellifera</i> : a positive loop linking juvenile hormone, <i>ftz</i> , and vitellogenin. <i>Insect Molecular Biology</i> , 2019, 28, 145-159.	1.0	26
18584	Identification of salt stress response genes using the <i>Artemia</i> transcriptome. <i>Aquaculture</i> , 2019, 500, 305-314.	1.7	31
18585	Proteomics and phosphoproteomics in precision medicine: applications and challenges. <i>Briefings in Bioinformatics</i> , 2019, 20, 767-777.	3.2	34
18586	Web-based drug repurposing tools: a survey. <i>Briefings in Bioinformatics</i> , 2019, 20, 299-316.	3.2	38
18587	Network Analysis of MPO and Other Relevant Proteins Involved in Diabetic Foot Ulcer and Other Diabetic Complications. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 180-190.	2.2	5
18588	Analysing Network Models to Make Discoveries about Biological Mechanisms. <i>British Journal for the Philosophy of Science</i> , 2019, 70, 459-484.	1.4	22
18589	Complete Genome Sequence of <i>Pseudomonas Parafulva</i> PRS09-11288, a Biocontrol Strain Produces the Antibiotic Phenazine-1-carboxylic Acid. <i>Current Microbiology</i> , 2019, 76, 1087-1091.	1.0	11
18590	Computational prediction of drug-target interactions using chemogenomic approaches: an empirical survey. <i>Briefings in Bioinformatics</i> , 2019, 20, 1337-1357.	3.2	182
18591	Functional Categorization of Disease Genes Based on Spectral Graph Theory and Integrated Biological Knowledge. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 460-474.	2.2	0
18592	Artificial intelligence in drug combination therapy. <i>Briefings in Bioinformatics</i> , 2019, 20, 1434-1448.	3.2	60
18593	Inferring and analyzing module-specific lncRNA-mRNA causal regulatory networks in human cancer. <i>Briefings in Bioinformatics</i> , 2019, 20, 1403-1419.	3.2	33
18594	Developing a "personalome" for precision medicine: emerging methods that compute interpretable effect sizes from single-subject transcriptomes. <i>Briefings in Bioinformatics</i> , 2019, 20, 789-805.	3.2	24
18595	Classification of Single-Cell Gene Expression Trajectories from Incomplete and Noisy Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 193-207.	1.9	10
18596	Effect of Qinghuang Powder (qinghuang powder) Combined with Bupi Yishen Decoction (bupi yishen decoction) in Treating Patients with Refractory Cytopenia with Multilineage Dysplasia through Regulating DNA Methylation. <i>Chinese Journal of Integrative Medicine</i> , 2019, 25, 354-359.	0.7	4
18597	Community-driven roadmap for integrated disease maps. <i>Briefings in Bioinformatics</i> , 2019, 20, 659-670.	3.2	48
18598	Text mining tools for extracting information about microbial biodiversity in food. <i>Food Microbiology</i> , 2019, 81, 63-75.	2.1	42
18599	iProt-Sub: a comprehensive package for accurately mapping and predicting protease-specific substrates and cleavage sites. <i>Briefings in Bioinformatics</i> , 2019, 20, 638-658.	3.2	166
18600	Non-Negative Matrix Factorizations for Multiplex Network Analysis. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2019, 41, 928-940.	9.7	63

#	ARTICLE	IF	CITATIONS
18601	Identification of microRNA-like RNAs in <i>Ophiocordyceps sinensis</i> . <i>Science China Life Sciences</i> , 2019, 62, 349-356.	2.3	10
18602	Integrating phosphoproteomics into kinase-targeted cancer therapies in precision medicine. <i>Journal of Proteomics</i> , 2019, 191, 68-79.	1.2	30
18603	GPS: Identification of disease genes by rank aggregation of multi-genomic scoring schemes. <i>Genomics</i> , 2019, 111, 612-618.	1.3	5
18604	Molecular subtyping of cancer: current status and moving toward clinical applications. <i>Briefings in Bioinformatics</i> , 2019, 20, 572-584.	3.2	91
18605	Where to search top-K biomedical ontologies?. <i>Briefings in Bioinformatics</i> , 2019, 20, 1477-1491.	3.2	6
18606	Comparison and evaluation of integrative methods for the analysis of multilevel omics data: a study based on simulated and experimental cancer data. <i>Briefings in Bioinformatics</i> , 2019, 20, 671-681.	3.2	23
18607	A review of databases predicting the effects of SNPs in miRNA genes or miRNA-binding sites. <i>Briefings in Bioinformatics</i> , 2019, 20, 1011-1020.	3.2	18
18608	Drug knowledge bases and their applications in biomedical informatics research. <i>Briefings in Bioinformatics</i> , 2019, 20, 1308-1321.	3.2	29
18609	Whole genome sequence of <i>Auricularia heimuer</i> (Basidiomycota, Fungi), the third most important cultivated mushroom worldwide. <i>Genomics</i> , 2019, 111, 50-58.	1.3	61
18610	A combined analysis of genetically correlated traits identifies 187 loci and a role for neurogenesis and myelination in intelligence. <i>Molecular Psychiatry</i> , 2019, 24, 169-181.	4.1	238
18611	Statistical methods for genome-wide association studies. <i>Seminars in Cancer Biology</i> , 2019, 55, 53-60.	4.3	59
18612	Stage-Dependent Gene Expression Profiling in Colorectal Cancer. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1685-1692.	1.9	7
18613	Community Detection in Multi-Layer Networks Using Joint Nonnegative Matrix Factorization. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2019, 31, 273-286.	4.0	111
18614	Drug Target Prediction by Multi-View Low Rank Embedding. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1712-1721.	1.9	17
18615	Essential Protein Detection by Random Walk on Weighted Protein-Protein Interaction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 377-387.	1.9	18
18616	Multitask Protein Function Prediction through Task Dissimilarity. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1550-1560.	1.9	15
18617	Constructing Disease Similarity Networks Based on Disease Module Theory. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 906-915.	1.9	29
18618	NMFGO: Gene Function Prediction via Nonnegative Matrix Factorization with Gene Ontology. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 238-249.	1.9	12

#	ARTICLE	IF	CITATIONS
18619	The Overexpression of CD80 and ISG15 Are Associated with the Progression and Metastasis of Breast Cancer by a Meta-Analysis Integrating Three Microarray Datasets. <i>Pathology and Oncology Research</i> , 2020, 26, 443-452.	0.9	19
18620	Genome-wide analysis reveals extensive genetic overlap between schizophrenia, bipolar disorder, and intelligence. <i>Molecular Psychiatry</i> , 2020, 25, 844-853.	4.1	156
18621	Maternal choline supplementation ameliorates Alzheimer's disease pathology by reducing brain homocysteine levels across multiple generations. <i>Molecular Psychiatry</i> , 2020, 25, 2620-2629.	4.1	54
18622	OBSOLETE: Bioinformatic Platforms for Metagenomics. , 2020, , .		0
18623	Network-based methods for predicting essential genes or proteins: a survey. <i>Briefings in Bioinformatics</i> , 2020, 21, 566-583.	3.2	90
18624	Genome-wide characterization revealed role of NBS-LRR genes during powdery mildew infection in <i>Vitis vinifera</i> . <i>Genomics</i> , 2020, 112, 312-322.	1.3	50
18625	Complete Genome of <i>Bacillus velezensis</i> CMT-6 and Comparative Genome Analysis Reveals Lipopeptide Diversity. <i>Biochemical Genetics</i> , 2020, 58, 1-15.	0.8	14
18626	Transcriptome analysis of <i>Panax ginseng</i> response to high light stress. <i>Journal of Ginseng Research</i> , 2020, 44, 312-320.	3.0	21
18627	Network embedding in biomedical data science. <i>Briefings in Bioinformatics</i> , 2020, 21, 182-197.	3.2	105
18628	Parallel repulsive logic regression with biological adjacency. <i>Biostatistics</i> , 2020, 21, 825-844.	0.9	1
18629	Comprehensive bioinformatics analysis of trabecular meshwork gene expression data to unravel the molecular pathogenesis of primary open-angle glaucoma. <i>Acta Ophthalmologica</i> , 2020, 98, 48-57.	0.6	18
18630	Weighted matrix factorization on multi-relational data for LncRNA-disease association prediction. <i>Methods</i> , 2020, 173, 32-43.	1.9	36
18631	Circular RNA expression profiling in the nucleus accumbens: Effects of electroacupuncture treatment on morphine-induced conditioned place preference. <i>Addiction Biology</i> , 2020, 25, e12794.	1.4	15
18632	Identification of the Apoptosis and Autophagy Bi-functional Proteins. <i>Molecular Informatics</i> , 2020, 39, e1900008.	1.4	0
18633	The rice PLATZ protein SHORT GRAIN6 determines grain size by regulating spikelet hull cell division. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 847-864.	4.1	43
18634	Transcriptome responses to elevated CO ₂ level and <i>Wolbachia</i> infection stress in <i>Hyllyphantes graminicola</i> (Araneae: Linyphiidae). <i>Insect Science</i> , 2020, 27, 908-920.	1.5	1
18635	Elucidating the ecological networks in stone-dwelling microbiomes. <i>Environmental Microbiology</i> , 2020, 22, 1467-1480.	1.8	38
18636	Sole head transcriptomics reveals a coordinated developmental program during metamorphosis. <i>Genomics</i> , 2020, 112, 592-602.	1.3	10

#	ARTICLE	IF	CITATIONS
18637	Characterizing the heterogeneity in 5-aminolevulinic acid-induced fluorescence in glioblastoma. <i>Journal of Neurosurgery</i> , 2020, 132, 1706-1714.	0.9	15
18638	Transcriptome analysis of leg muscles in fast and slow growth Bian chickens. <i>Animal Biotechnology</i> , 2020, 31, 295-305.	0.7	7
18639	Variational Inference for Stochastic Block Models From Sampled Data. <i>Journal of the American Statistical Association</i> , 2020, 115, 455-466.	1.8	15
18640	Identification and Verification of Two Novel Differentially Expressed Proteins from Non-neoplastic Mucosa and Colorectal Carcinoma Via iTRAQ Combined with Liquid Chromatography-Mass Spectrometry. <i>Pathology and Oncology Research</i> , 2020, 26, 967-976.	0.9	4
18641	Comprehensive expression-based isoform biomarkers predictive of drug responses based on isoform co-expression networks and clinical data. <i>Genomics</i> , 2020, 112, 647-658.	1.3	12
18642	Genetic contributions to two special factors of neuroticism are associated with affluence, higher intelligence, better health, and longer life. <i>Molecular Psychiatry</i> , 2020, 25, 3034-3052.	4.1	60
18643	Comparing enrichment analysis and machine learning for identifying gene properties that discriminate between gene classes. <i>Briefings in Bioinformatics</i> , 2020, 21, 803-814.	3.2	15
18644	Meta-GDBP: a high-level stacked regression model to improve anticancer drug response prediction. <i>Briefings in Bioinformatics</i> , 2020, 21, 996-1005.	3.2	63
18645	Ontological representation-oriented term normalization and standardization of the Research Domain Criteria. <i>Health Informatics Journal</i> , 2020, 26, 726-737.	1.1	1
18646	Constructing biomedical domain-specific knowledge graph with minimum supervision. <i>Knowledge and Information Systems</i> , 2020, 62, 317-336.	2.1	45
18647	Shank3 mutation in a mouse model of autism leads to changes in the S-nitroso-proteome and affects key proteins involved in vesicle release and synaptic function. <i>Molecular Psychiatry</i> , 2020, 25, 1835-1848.	4.1	82
18648	Detection of Driver Modules with Rarely Mutated Genes in Cancers. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 390-401.	1.9	9
18649	Application of protein set enrichment analysis to correlation of protein functional sets with mass spectral features and multivariate proteomic tests. <i>Clinical Mass Spectrometry</i> , 2020, 15, 44-53.	1.9	11
18650	Comprehensive characterization of the rRNA metabolism-related genes in human cancer. <i>Oncogene</i> , 2020, 39, 786-800.	2.6	41
18651	Molecular modelling and dynamics of CA2 missense mutations causative to carbonic anhydrase 2 deficiency syndrome. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 4067-4080.	2.0	20
18652	Time-Series Expression Analysis of Epidermal Stem Cells from High Fat Diet Mice. <i>Journal of Computational Biology</i> , 2020, 27, 769-778.	0.8	2
18653	Rapid phenotypic evolution with shallow genomic differentiation during early stages of high elevation adaptation in Eurasian Tree Sparrows. <i>National Science Review</i> , 2020, 7, 113-127.	4.6	36
18654	Protein-Protein Interaction Networks. <i>Methods in Molecular Biology</i> , 2020, , .	0.4	3

#	ARTICLE	IF	CITATIONS
18655	Identification and characterization of long non-coding RNAs in muscle sclerosis of grass carp, <i>Ctenopharyngodon idellus</i> fed with faba bean meal. <i>Aquaculture</i> , 2020, 516, 734521.	1.7	9
18656	Network based analysis of microarray gene expression profiles in response to electroacupuncture. <i>Journal of Traditional and Complementary Medicine</i> , 2020, 10, 471-477.	1.5	1
18657	Epigenome-wide association study of narcolepsy-affected lateral hypothalamic brains, and overlapping DNA methylation profiles between narcolepsy and multiple sclerosis. <i>Sleep</i> , 2020, 43, .	0.6	9
18658	Solute carriers in scallop genome: Gene expansion and expression regulation after exposure to toxic dinoflagellate. <i>Chemosphere</i> , 2020, 241, 124968.	4.2	18
18659	The IBD-associated long noncoding RNA <i>IFNG-AS1</i> regulates the balance between inflammatory and anti-inflammatory cytokine production after T-cell stimulation. <i>American Journal of Physiology - Renal Physiology</i> , 2020, 318, G34-G40.	1.6	23
18660	Identifying candidate genes associated with sperm morphology abnormalities using weighted single-step GWAS in a Duroc boar population. <i>Theriogenology</i> , 2020, 141, 9-15.	0.9	18
18661	Improvements in seismic resolution and current limitations in the Global Seismographic Network. <i>Geophysical Journal International</i> , 2020, 220, 508-521.	1.0	25
18662	Inferring targeting modes of Argonaute-loaded tRNA fragments. <i>RNA Biology</i> , 2020, 17, 1070-1080.	1.5	44
18663	PerMemDB: A database for eukaryotic peripheral membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183076.	1.4	14
18664	pSILAC method coupled with two complementary digestion approaches reveals PRPF39 as a new E7070-dependent DCAF15 substrate. <i>Journal of Proteomics</i> , 2020, 210, 103545.	1.2	15
18665	DeepETC: A deep convolutional neural network architecture for investigating and classifying electron transport chain's complexes. <i>Neurocomputing</i> , 2020, 375, 71-79.	3.5	56
18666	Characterization of immune response against <i>Mycobacterium marinum</i> infection in the main hematopoietic organ of adult zebrafish (<i>Danio rerio</i>). <i>Developmental and Comparative Immunology</i> , 2020, 103, 103523.	1.0	13
18667	Autologous micrograft accelerates endogenous wound healing response through ERK-induced cell migration. <i>Cell Death and Differentiation</i> , 2020, 27, 1520-1538.	5.0	29
18668	Comparative transcriptome analysis of <i>Bambusa pervariabilis</i> – <i>Dendrocalamopsis grandis</i> against <i>Arthrinium phaeospermum</i> under protein AP-toxin induction. <i>Gene</i> , 2020, 725, 144160.	1.0	8
18669	Recent Progress of In Situ Transmission Electron Microscopy for Energy Materials. <i>Advanced Materials</i> , 2020, 32, e1904094.	11.1	59
18670	Construction of a circular RNA–microRNA–messengerRNA regulatory network in stomach adenocarcinoma. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 1317-1331.	1.2	21
18671	Decreased SPTLC1 expression predicts worse outcomes in ccRCC patients. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 1552-1562.	1.2	18
18672	Structural and functional analysis of ‘non-smelly’ proteins. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 2423-2440.	2.4	16

#	ARTICLE	IF	CITATIONS
18673	Mining Myb transcription factors related to wood development in <i>Larix olgensis</i> . <i>Journal of Forestry Research</i> , 2020, 31, 2453-2461.	1.7	3
18674	A chromosome-level genome assembly reveals the genetic basis of cold tolerance in a notorious rice insect pest, <i>Chilo suppressalis</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 268-282.	2.2	51
18675	An <i>in silico</i> Approach for Integrating Phenotypic and Target-based Approaches in Drug Discovery. <i>Molecular Informatics</i> , 2020, 39, e1900096.	1.4	8
18676	Transcriptomic and Proteomic Profiling of Human Mesenchymal Stem Cell Derived from Umbilical Cord in the Study of Preterm Birth. <i>Proteomics - Clinical Applications</i> , 2020, 14, e1900024.	0.8	6
18677	KEGG Mapper for inferring cellular functions from protein sequences. <i>Protein Science</i> , 2020, 29, 28-35.	3.1	791
18678	Differential gene expression in HaCaT cells may account for the various clinical presentation caused by anthropophilic and geophilic dermatophytes infections. <i>Mycoses</i> , 2020, 63, 21-29.	1.8	7
18679	Microbial genomes retrieved from High Arctic lake sediments encode for adaptation to cold and oligotrophic environments. <i>Limnology and Oceanography</i> , 2020, 65, S233.	1.6	20
18680	Knockdown of formin mDia2 alters lamin B1 levels and increases osteogenesis in stem cells. <i>Stem Cells</i> , 2020, 38, 102-117.	1.4	13
18681	Single-sample landscape entropy reveals the imminent phase transition during disease progression. <i>Bioinformatics</i> , 2020, 36, 1522-1532.	1.8	53
18682	Transcriptome analysis of Snow Mountain Garlic for unraveling the organosulfur metabolic pathway. <i>Genomics</i> , 2020, 112, 99-107.	1.3	15
18683	Neurofilament-lysosomal genetic intersections in the cortical network of stuttering. <i>Progress in Neurobiology</i> , 2020, 184, 101718.	2.8	30
18684	Detailed Analysis of Molecular Mechanisms in Primary and Metastatic Melanoma. <i>Journal of Computational Biology</i> , 2020, 27, 9-19.	0.8	5
18685	Current Trends in Biomedical Engineering and Bioimages Analysis. <i>Advances in Intelligent Systems and Computing</i> , 2020, , .	0.5	1
18686	Platelets in myeloproliferative neoplasms have a distinct transcript signature in the presence of marrow fibrosis. <i>British Journal of Haematology</i> , 2020, 188, 272-282.	1.2	18
18687	LAMTOR/Ragulator regulates lipid metabolism in macrophages and foam cell differentiation. <i>FEBS Letters</i> , 2020, 594, 31-42.	1.3	7
18688	The MicroRNA Landscapes Profiling Reveals Potential Signatures of Necrotizing Enterocolitis in Infants. <i>Journal of Computational Biology</i> , 2020, 27, 30-39.	0.8	5
18689	Meta-analysis of genome-wide association studies and functional assays decipher susceptibility genes for gastric cancer in Chinese populations. <i>Gut</i> , 2020, 69, 641-651.	6.1	36
18690	Identification of carbonylated proteins in a bactericidal process induced by curcumin with blue light irradiation on imipenem-resistant <i>Acinetobacter baumannii</i> . <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8548.	0.7	10

#	ARTICLE	IF	CITATIONS
18691	Serial gene co-expression network approach to mine biological meanings from integrated transcriptomes of the porcine endometrium during estrous cycle. <i>Functional and Integrative Genomics</i> , 2020, 20, 117-131.	1.4	1
18692	Exome-Wide Rare Loss-of-Function Variant Enrichment Study of 21,347 Han Chinese Individuals Identifies Four Susceptibility Genes for Psoriasis. <i>Journal of Investigative Dermatology</i> , 2020, 140, 799-805.e1.	0.3	6
18693	Early growth response 1 regulates hematopoietic support and proliferation in human primary bone marrow stromal cells. <i>Haematologica</i> , 2020, 105, 1206-1215.	1.7	11
18694	<i>In silico</i> determination of transposon-derived miRNAs and targets in <i>Aegilops</i> species. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 3098-3109.	2.0	1
18695	Genome-wide analysis sheds light on the high-altitude adaptation of the buff-throated partridge (<i>Tetraophasis szechenyii</i>). <i>Molecular Genetics and Genomics</i> , 2020, 295, 31-46.	1.0	11
18696	Identification of Synthetic Activators of Cancer Cell Migration by Hybrid Deep Learning. <i>ChemBioChem</i> , 2020, 21, 500-507.	1.3	1
18697	Suboptimal Comparison of Partitions. <i>Journal of Classification</i> , 2020, 37, 435-461.	1.2	1
18698	A Novel Genes Signature Associated with the Progression of Polycystic Ovary Syndrome. <i>Pathology and Oncology Research</i> , 2020, 26, 575-582.	0.9	11
18699	Genome-wide functional association networks: background, data & state-of-the-art resources. <i>Briefings in Bioinformatics</i> , 2020, 21, 1224-1237.	3.2	20
18700	The draft genome of a wild barley genotype reveals its enrichment in genes related to biotic and abiotic stresses compared to cultivated barley. <i>Plant Biotechnology Journal</i> , 2020, 18, 443-456.	4.1	45
18701	Contextual Correlation Preserving Multiview Featured Graph Clustering. <i>IEEE Transactions on Cybernetics</i> , 2020, 50, 4318-4331.	6.2	37
18702	IGF2 enhanced the osteoâ€dentinogenic and neurogenic differentiation potentials of stem cells from apical papilla. <i>Journal of Oral Rehabilitation</i> , 2020, 47, 55-65.	1.3	11
18703	Gene expression profiling and identification of hub genes in Nellore cattle with different marbling score levels. <i>Genomics</i> , 2020, 112, 873-879.	1.3	31
18704	Understanding and improving ontology reasoning efficiency through learning and ranking. <i>Information Systems</i> , 2020, 87, 101412.	2.4	7
18705	Identification of <i>Fusarium graminearum</i> -responsive miRNAs and their targets in wheat by sRNA sequencing and degradome analysis. <i>Functional and Integrative Genomics</i> , 2020, 20, 51-61.	1.4	12
18706	Multimapping confounds ribosome profiling analysis: A caseâ€study of the Hsp90 molecular chaperone. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 57-68.	1.5	5
18707	Glioma stages prediction based on machine learning algorithm combined with protein-protein interaction networks. <i>Genomics</i> , 2020, 112, 837-847.	1.3	31
18708	Gene coexpression analysis offers important modules and pathway of human lung adenocarcinomas. <i>Journal of Cellular Physiology</i> , 2020, 235, 454-464.	2.0	14

#	ARTICLE	IF	CITATIONS
18709	The complete genome sequence of <i>Bifidobacterium longum</i> LTBL16, a potential probiotic strain from healthy centenarians with strong antioxidant activity. <i>Genomics</i> , 2020, 112, 769-773.	1.3	22
18710	Complete genome sequence of <i>Paracoccus</i> sp. Arc7-R13, a silver nanoparticles synthesizing bacterium isolated from Arctic Ocean sediments. <i>Marine Genomics</i> , 2020, 50, 100694.	0.4	5
18711	An integrative pan-cancer analysis of biological and clinical impacts underlying ubiquitin-specific-processing proteases. <i>Oncogene</i> , 2020, 39, 587-602.	2.6	11
18712	Protein functional annotation of simultaneously improved stability, accuracy and false discovery rate achieved by a sequence-based deep learning. <i>Briefings in Bioinformatics</i> , 2020, 21, 1437-1447.	3.2	105
18713	Gene Expression Modularity Reveals Footprints of Polygenic Adaptation in <i>Theobroma cacao</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 110-123.	3.5	22
18714	Regulatory annotation of genomic intervals based on tissue-specific expression QTLs. <i>Bioinformatics</i> , 2020, 36, 690-697.	1.8	9
18715	Randomized trial of weight loss in primary breast cancer: Impact on body composition, circulating biomarkers and tumor characteristics. <i>International Journal of Cancer</i> , 2020, 146, 2784-2796.	2.3	36
18716	Statistical genomics in rare cancer. <i>Seminars in Cancer Biology</i> , 2020, 61, 1-10.	4.3	15
18717	Reactive microglia and astrocytes in neonatal intraventricular hemorrhage model are blocked by mesenchymal stem cells. <i>Glia</i> , 2020, 68, 178-192.	2.5	31
18718	Metaproteomics reveal that rapid perturbations in organic matter prioritize functional restructuring over taxonomy in western Arctic Ocean microbiomes. <i>ISME Journal</i> , 2020, 14, 39-52.	4.4	21
18719	Identification of Genes Underlying the Resistance to <i>Melampsora larici-populina</i> in an <i>R</i> Gene Supercluster of the <i>Populus deltoides</i> Genome. <i>Plant Disease</i> , 2020, 104, 1133-1143.	0.7	6
18720	Identification of Potential Gene Signatures Related to Sleep Deprivation. <i>Journal of Computational Biology</i> , 2020, 27, 904-913.	0.8	1
18721	Histidine Phosphorylation. <i>Methods in Molecular Biology</i> , 2020, , .	0.4	2
18722	Comparative gene expression analysis in melanocytes driven by tumor cell-derived exosomes. <i>Experimental Cell Research</i> , 2020, 386, 111690.	1.2	9
18723	Identification of Biomolecular Information in Rotenone-Induced Cellular Model of Parkinson's Disease by Public Microarray Data Analysis. <i>Journal of Computational Biology</i> , 2020, 27, 888-903.	0.8	4
18724	Analysis of Gene Expression in Bladder Cancer: Possible Involvement of Mitosis and Complement and Coagulation Cascades Signaling Pathway. <i>Journal of Computational Biology</i> , 2020, 27, 987-998.	0.8	26
18725	A comprehensive review and evaluation of computational methods for identifying protein complexes from protein-protein interaction networks. <i>Briefings in Bioinformatics</i> , 2020, 21, 1531-1548.	3.2	42
18726	The Dynamic Chromatin Architecture of the Regenerating Liver. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020, 9, 121-143.	2.3	37

#	ARTICLE	IF	CITATIONS
18727	Genetic Contribution of Paleopolyploidy to Adaptive Evolution in Angiosperms. <i>Molecular Plant</i> , 2020, 13, 59-71.	3.9	178
18728	Genomic Resources for Darters (Percidae: Etheostominae) Provide Insight into Postzygotic Barriers Implicated in Speciation. <i>Molecular Biology and Evolution</i> , 2020, 37, 711-729.	3.5	22
18729	Proteomic and phosphoproteomic analyses reveal several events involved in the early stages of bovine herpesvirus 1 infection. <i>Archives of Virology</i> , 2020, 165, 69-85.	0.9	4
18730	Prediction of modes of action of components of traditional medicinal preparations. <i>Physical Sciences Reviews</i> , 2020, 5, .	0.8	3
18731	Antibiotic resistance in <i>Vibrio cholerae</i> El Tor strains isolated during cholera complications in Siberia and the Far East of Russia. <i>Infection, Genetics and Evolution</i> , 2020, 78, 104096.	1.0	16
18732	Complete Genome Sequence of Strain YCSC6, a Marine Bacterium Isolated from Saturated Saltpan with Activity Against <i>Uronema marinum</i> . <i>Current Microbiology</i> , 2020, 77, 129-135.	1.0	2
18733	Screening and Identification of Key Biomarkers in Pancreatic Cancer: Evidence from Bioinformatic Analysis. <i>Journal of Computational Biology</i> , 2020, 27, 1079-1091.	0.8	2
18734	<i>Mesostigma viride</i> Genome and Transcriptome Provide Insights into the Origin and Evolution of Streptophyta. <i>Advanced Science</i> , 2020, 7, 1901850.	5.6	40
18735	NaCl treatment markedly enhanced pollen viability and pollen preservation time of eukaryote <i>Suaeda salsa</i> via up regulation of pollen development-related genes. <i>Journal of Plant Research</i> , 2020, 133, 57-71.	1.2	23
18736	Expression and analysis of zinc finger family gene in <i>Lenzites gibbosa</i> . <i>Journal of Forestry Research</i> , 2020, 31, 1889-1898.	1.7	0
18737	Preferential catabolism of the (S)-enantiomer of the herbicide napropamide mediated by the enantioselective amidohydrolase SnaH and the dioxygenase Snpd in <i>Sphingobium</i> sp. strain B2. <i>Environmental Microbiology</i> , 2020, 22, 286-296.	1.8	19
18738	Genomic analyses reveal selection footprints in rice landraces grown under on-farm conservation conditions during a short-term period of domestication. <i>Evolutionary Applications</i> , 2020, 13, 290-302.	1.5	9
18739	ATM activity in T cells is critical for immune surveillance of lymphoma in vivo. <i>Leukemia</i> , 2020, 34, 771-786.	3.3	13
18740	Predicting bacterial virulence factors – evaluation of machine learning and negative data strategies. <i>Briefings in Bioinformatics</i> , 2020, 21, 1596-1608.	3.2	14
18741	NBS-LRR genes – Plant health sentinels: Structure, roles, evolution and biotechnological applications. , 2020, , 63-120.		9
18742	New developments on the Encyclopedia of DNA Elements (ENCODE) data portal. <i>Nucleic Acids Research</i> , 2020, 48, D882-D889.	6.5	381
18743	Learning complex subcellular distribution patterns of proteins via analysis of immunohistochemistry images. <i>Bioinformatics</i> , 2020, 36, 1908-1914.	1.8	14
18744	Comparative transcriptome profiling of tuberous roots of two sweetpotato lines with contrasting low temperature tolerance during storage. <i>Gene</i> , 2020, 727, 144244.	1.0	21

#	ARTICLE	IF	CITATIONS
18745	Novel Sodium Deoxycholate-Based Chemical Decellularization Method for Peripheral Nerve. <i>Tissue Engineering - Part C: Methods</i> , 2020, 26, 23-36.	1.1	34
18746	Exogenous Treatment with Glutamate Induces Immune Responses in <i>Arabidopsis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 474-487.	1.4	46
18747	<i>Arabidopsis</i> 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
18748	A Comparative Genomic Analysis of the Barley Pathogen <i>Pyrenophora teres</i> f. <i>teres</i> Identifies Subtelomeric Regions as Drivers of Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 173-188.	1.4	28
18749	EnTAP: Bringing faster and smarter functional annotation to non-model eukaryotic transcriptomes. <i>Molecular Ecology Resources</i> , 2020, 20, 591-604.	2.2	111
18750	Impact of left ventricular assist device therapy on the cardiac proteome and metabolome composition in ischemic cardiomyopathy. <i>Artificial Organs</i> , 2020, 44, 257-267.	1.0	6
18751	Plant Regulomics: a data-driven interface for retrieving upstream regulators from plant multi-omics data. <i>Plant Journal</i> , 2020, 101, 237-248.	2.8	75
18752	Screening of significant biomarkers related with prognosis of liver cancer by lncRNA-associated ceRNAs analysis. <i>Journal of Cellular Physiology</i> , 2020, 235, 2464-2477.	2.0	32
18753	The stromal loss of miR-4516 promotes the FOSL1-dependent proliferation and malignancy of triple negative breast cancer. <i>Cancer Letters</i> , 2020, 469, 256-265.	3.2	50
18754	Machine learning techniques for protein function prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 397-413.	1.5	90
18755	Circulating miRNA analysis for cancer diagnostics and therapy. <i>Molecular Aspects of Medicine</i> , 2020, 72, 100825.	2.7	114
18756	Infant Respiratory Syncytial Virus Bronchiolitis and Subsequent Risk of Pneumonia, Otitis Media, and Antibiotic Utilization. <i>Clinical Infectious Diseases</i> , 2020, 71, 211-214.	2.9	8
18757	Complex patterns of dopamine-related gene expression in the ventral tegmental area of male zebra finches relate to dyadic interactions with long-term female partners. <i>Genes, Brain and Behavior</i> , 2020, 19, e12619.	1.1	6
18758	Integrated Analysis of DNA Copy Number Changes and Gene Expression Identifies Key Genes in Gastric Cancer. <i>Journal of Computational Biology</i> , 2020, 27, 877-887.	0.8	11
18759	A genomewide association study in divergently selected lines in rabbits reveals novel genomic regions associated with litter size traits. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 123-138.	0.8	12
18760	THAP11F80L cobalamin disorder-associated mutation reveals normal and pathogenic THAP11 functions in gene expression and cell proliferation. <i>PLoS ONE</i> , 2020, 15, e0224646.	1.1	8
18761	How to Illuminate the Druggable Genome Using Pharos. <i>Current Protocols in Bioinformatics</i> , 2020, 69, e92.	25.8	33
18762	Folate inhibits miR-27a-3p expression during cervical carcinoma progression and oncogenic activity in human cervical cancer cells. <i>Biomedicine and Pharmacotherapy</i> , 2020, 122, 109654.	2.5	9

#	ARTICLE	IF	CITATIONS
18763	Molecular mechanisms associated with macrophage activation by Rhizoma Atractylodis Macrocephalae polysaccharides. <i>International Journal of Biological Macromolecules</i> , 2020, 147, 616-628.	3.6	33
18764	Effect of scrotal insulation on sperm quality and seminal plasma proteome of Brangus bulls. <i>Theriogenology</i> , 2020, 144, 194-203.	0.9	15
18765	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020, 11, 163.	5.8	466
18766	NHC-gold compounds mediate immune suppression through induction of AHR-TGF β 1 signalling in vitro and in scurfy mice. <i>Communications Biology</i> , 2020, 3, 10.	2.0	14
18767	The transcriptional correlates of divergent electric organ discharges in Paramormyrops electric fish. <i>BMC Evolutionary Biology</i> , 2020, 20, 6.	3.2	6
18768	Transcriptome analysis suggests mechanisms for a novel flowering type: Cleistogamous wheat. <i>Crop Journal</i> , 2020, 8, 313-326.	2.3	6
18769	Maternal factor NELFA drives a 2C-like state in mouse embryonic stem cells. <i>Nature Cell Biology</i> , 2020, 22, 175-186.	4.6	72
18770	Leveraging complementary computational models for prioritizing chemicals of developmental and reproductive toxicity concern: an example of food contact materials. <i>Archives of Toxicology</i> , 2020, 94, 485-494.	1.9	20
18771	Developing an effective biclustering technique using an enhanced proximity measure. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2020, 9, 1.	1.2	3
18772	Toxic consequences and oxidative protein carbonylation from chloropicrin exposure in human corneal epithelial cells. <i>Toxicology Letters</i> , 2020, 322, 1-11.	0.4	17
18773	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	120
18774	A proteome-integrated, carbon source dependent genetic regulatory network in <i>Saccharomyces cerevisiae</i> . <i>Molecular Omics</i> , 2020, 16, 59-72.	1.4	11
18775	Differential Expression in Testis and Liver Transcriptomes from Four Species of Peromyscus (Rodentia: Tj ETQq0 0 Q rgBT /Overlock 10 T	1.1	2
18776	miR-149 Suppresses Breast Cancer Metastasis by Blocking Paracrine Interactions with Macrophages. <i>Cancer Research</i> , 2020, 80, 1330-1341.	0.4	41
18777	A comprehensive guide to dynamic analysis of microbial gene expression using the 3D-printed PFibox and a fluorescent reporter library. <i>Nature Protocols</i> , 2020, 15, 575-603.	5.5	2
18778	Presence and structure-activity relationship of intrinsically disordered regions across mucins. <i>FASEB Journal</i> , 2020, 34, 1939-1957.	0.2	7
18779	Computational identification of conserved microRNAs and functional annotation of their target genes in Citrus limon. <i>South African Journal of Botany</i> , 2020, 130, 109-116.	1.2	4
18780	Clonal kinetics and single-cell transcriptional profiling of CAR-T cells in patients undergoing CD19 CAR-T immunotherapy. <i>Nature Communications</i> , 2020, 11, 219.	5.8	167

#	ARTICLE	IF	CITATIONS
18781	Mechanistic insights into transcription factor cooperativity and its impact on protein-phenotype interactions. <i>Nature Communications</i> , 2020, 11, 124.	5.8	54
18782	Systems biology and big data in asthma and allergy: recent discoveries and emerging challenges. <i>European Respiratory Journal</i> , 2020, 55, 1900844.	3.1	22
18783	Schistosomal extracellular vesicle-enclosed miRNAs modulate host T helper cell differentiation. <i>EMBO Reports</i> , 2020, 21, e47882.	2.0	60
18784	Integration of ATAC-Seq and RNA-Seq Identifies Key Genes in Light-Induced Primordia Formation of <i>Sparassis latifolia</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 185.	1.8	21
18785	The Acute Phase Response Is a Prominent Renal Proteome Change in Sepsis in Mice. <i>International Journal of Molecular Sciences</i> , 2020, 21, 200.	1.8	18
18786	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
18787	<i>Malus niedzwetzkyana</i> (Dieck) Langenf transcriptome comparison and phylogenetic analysis with <i>Malus sieversii</i> (Ledeb) Roem. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 313-323.	0.8	3
18788	BcERF070, a novel ERF (ethylene-response factor) transcription factor from non-heading Chinese cabbage, affects the accumulation of ascorbic acid by regulating ascorbic acid-related genes. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	13
18789	Applications of disease pathways in biology and medicine. , 2020, , 629-668.		3
18790	Electrophysiology-based stratification of pancreatic tumorigenicity by label-free single-cell impedance cytometry. <i>Analytica Chimica Acta</i> , 2020, 1101, 90-98.	2.6	43
18791	ZNF143 is dynamically bound to a subset of its interphase sites during mitosis. <i>Biochemical and Biophysical Research Communications</i> , 2020, 523, 293-298.	1.0	4
18792	The atherosclerosis-ameliorating effects and molecular mechanisms of BuYangHuanWu decoction. <i>Biomedicine and Pharmacotherapy</i> , 2020, 123, 109664.	2.5	35
18793	Enhancer jungles establish robust tissue-specific regulatory control in the human genome. <i>Genomics</i> , 2020, 112, 2261-2270.	1.3	4
18794	Identification of microRNAs involved in betalain metabolism in the green and red sectors of amaranth leaves based on Illumina sequencing data. <i>Journal of Horticultural Science and Biotechnology</i> , 2020, 95, 454-469.	0.9	1
18795	ShinyGO: a graphical gene-set enrichment tool for animals and plants. <i>Bioinformatics</i> , 2020, 36, 2628-2629.	1.8	1,793
18796	The Cotton miR477- <i>c</i> CBP60A Module Participates in Plant Defense Against <i>Verticillium dahlia</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 624-636.	1.4	41
18797	Nonspecific expression of fertilization genes in the crown-of-thorns <i>Acanthaster cf. solaris</i> : Unexpected evidence of hermaphroditism in a coral reef predator. <i>Molecular Ecology</i> , 2020, 29, 363-379.	2.0	10
18798	The MathOmics Toolbox: General Analysis Utilities for Dynamic Omics Datasets. <i>Current Protocols in Bioinformatics</i> , 2020, 69, e91.	25.8	4

#	ARTICLE	IF	CITATIONS
18799	Phosphoproteomic profiling reveals a defined genetic program for osteoblastic lineage commitment of human bone marrow-derived stromal stem cells. <i>Genome Research</i> , 2020, 30, 127-137.	2.4	10
18800	Comparative genomics reveals divergent thermal selection in warm- and cold-tolerant marine mussels. <i>Molecular Ecology</i> , 2020, 29, 519-535.	2.0	24
18801	Whole genome sequencing and novel candidate genes for CAKUT and altered nephrogenesis in the HSRA rat. <i>Physiological Genomics</i> , 2020, 52, 56-70.	1.0	5
18802	The dynamics of DNA methylation during epigenetic reprogramming of primordial germ cells in medaka (<i>Oryzias latipes</i>). <i>Epigenetics</i> , 2020, 15, 483-498.	1.3	33
18803	Global variability analysis of mRNA and protein concentrations across and within human tissues. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz010.	1.5	40
18804	Laboratory biases hinder Eco-Evo-Devo integration: Hints from the microbial world. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2020, 334, 14-24.	0.6	4
18805	Several critical genes and microRNAs associated with the development of polycystic ovary syndrome. <i>Annales D'Endocrinologie</i> , 2020, 81, 18-27.	0.6	22
18806	Differential DNA methylation in experienced meditators after an intensive day of mindfulness-based practice: Implications for immune-related pathways. <i>Brain, Behavior, and Immunity</i> , 2020, 84, 36-44.	2.0	44
18807	A network-based predictive gene expression signature for recurrence risks in stage II colorectal cancer. <i>Cancer Medicine</i> , 2020, 9, 179-193.	1.3	16
18808	Screening of Critical Genes Involved in Metastasis and Prognosis of High-Grade Serous Ovarian Cancer by Gene Expression Profile Data. <i>Journal of Computational Biology</i> , 2020, 27, 1104-1114.	0.8	10
18809	Complete genome sequence of the novel alginolytic <i>Psychroserpens</i> sp. NJDZ02 isolated from macroalgae collected from King George Island, Antarctica. <i>Marine Genomics</i> , 2020, 51, 100705.	0.4	1
18810	Genome-wide Transcriptional Analysis of <i>Tetrahymena thermophila</i> Response to Exogenous Cholesterol. <i>Journal of Eukaryotic Microbiology</i> , 2020, 67, 209-222.	0.8	4
18811	Methylation of drug resistance-related genes in chemotherapy-sensitive Epstein-Barr virus-associated gastric cancer. <i>FEBS Open Bio</i> , 2020, 10, 147-157.	1.0	15
18812	Tuning the surface immunomodulatory functions of polyetheretherketone for enhanced osseointegration. <i>Biomaterials</i> , 2020, 230, 119642.	5.7	100
18813	Identifying pseudoenzymes using functional annotation: pitfalls of common practice. <i>FEBS Journal</i> , 2020, 287, 4128-4140.	2.2	19
18814	Single-marker and haplotype-based association analysis of anthracnose (<i>Colletotrichum</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 11	1.0	11
18815	Study on the role of calmodulin in sperm function through the enrichment and identification of calmodulin-binding proteins in bovine ejaculated spermatozoa. <i>Journal of Cellular Physiology</i> , 2020, 235, 5340-5352.	2.0	7
18816	Essential Current Concepts in Stem Cell Biology. <i>Learning Materials in Biosciences</i> , 2020, , .	0.2	2

#	ARTICLE	IF	CITATIONS
18817	Statistical genetic concepts in psychiatric genomics. , 2020, , 103-116.		0
18818	Opportunities and challenges of machine learning approaches for biomarker signature identification in psychiatry. , 2020, , 117-126.		3
18819	Vapor nanobubble is the more reliable photothermal mechanism for inducing endosomal escape of siRNA without disturbing cell homeostasis. Journal of Controlled Release, 2020, 319, 262-275.	4.8	45
18820	Genome and population sequencing of a chromosome-level genome assembly of the Chinese tapertail anchovy (<i>Coilia nasus</i>) provides novel insights into migratory adaptation. GigaScience, 2020, 9, .	3.3	26
18821	Transcriptomic analyses of <i>Pinus koraiensis</i> under different cold stresses. BMC Genomics, 2020, 21, 10.	1.2	29
18822	Tissue-specific gene expression and protein abundance patterns are associated with fractionation bias in maize. BMC Plant Biology, 2020, 20, 4.	1.6	10
18823	Sex-specific and opposite modulatory aspects revealed by PPI network and pathway analysis of ischemic stroke in humans. PLoS ONE, 2020, 15, e0227481.	1.1	3
18824	Identification of microRNAs that Regulate the MAPK Pathway in Human Cumulus Cells from PCOS Women with Insulin Resistance. Reproductive Sciences, 2020, 27, 833-844.	1.1	11
18825	LINC01413/hnRNP-K/ZEB1 Axis Accelerates Cell Proliferation and EMT in Colorectal Cancer via Inducing YAP1/TAZ1 Translocation. Molecular Therapy - Nucleic Acids, 2020, 19, 546-561.	2.3	28
18826	Acute PFOA exposure promotes epigenomic alterations in mouse kidney tissues. Toxicology Reports, 2020, 7, 125-132.	1.6	50
18827	CD155 contributes to the mesenchymal phenotype of triple-negative breast cancer. Cancer Science, 2020, 111, 383-394.	1.7	19
18828	Translation of gastric disease progression at gene level expression. Journal of Cancer, 2020, 11, 520-532.	1.2	7
18829	COL1A1 and MZB1 as the hub genes influenced the proliferation, invasion, migration and apoptosis of rectum adenocarcinoma cells by weighted correlation network analysis. Bioorganic Chemistry, 2020, 95, 103457.	2.0	20
18830	Unravelling the role of long non-coding RNA - LINC01087 in breast cancer. Non-coding RNA Research, 2020, 5, 1-10.	2.4	13
18831	Evolving knowledge graph similarity for supervised learning in complex biomedical domains. BMC Bioinformatics, 2020, 21, 6.	1.2	29
18832	Recommendations for application of the functional evidence PS3/BS3 criterion using the ACMG/AMP sequence variant interpretation framework. Genome Medicine, 2020, 12, 3.	3.6	312
18833	RNA-seq analysis of testes from flurochloridone-treated rats. Toxicology Mechanisms and Methods, 2020, 30, 219-227.	1.3	3
18834	Minimal Cells: Design, Construction, Biotechnological Applications. , 2020, , .		1

#	ARTICLE	IF	CITATIONS
18835	Sirtuin SirD is involved in α -amylase activity and citric acid production in <i>Aspergillus luchuensis</i> mut. kawachii during a solid-state fermentation process. <i>Journal of Bioscience and Bioengineering</i> , 2020, 129, 454-466.	1.1	10
18836	Biochemical and Proteomic Studies of Human Pyridoxal 5 α -Phosphate-Binding Protein (PLPBP). <i>ACS Chemical Biology</i> , 2020, 15, 254-261.	1.6	11
18837	Next-generation hypomethylating agent SGI-110 primes acute myeloid leukemia cells to IAP antagonist by activating extrinsic and intrinsic apoptosis pathways. <i>Cell Death and Differentiation</i> , 2020, 27, 1878-1895.	5.0	8
18838	Systematic evaluation of differential splicing tools for RNA-seq studies. <i>Briefings in Bioinformatics</i> , 2020, 21, 2052-2065.	3.2	124
18839	Semantic persistence of ambiguous biomedical names in the citation network. <i>Bioinformatics</i> , 2020, 36, 2224-2228.	1.8	4
18840	Comparative genomics of six <i>Juglans</i> species reveals disease-associated gene family contractions. <i>Plant Journal</i> , 2020, 102, 410-423.	2.8	25
18841	High-resolution chromosomal microarray analysis for copy-number variations in high-functioning autism reveals large aberration typical for intellectual disability. <i>Journal of Neural Transmission</i> , 2020, 127, 81-94.	1.4	5
18842	Autoantigenomics: Holistic characterization of autoantigen repertoires for a better understanding of autoimmune diseases. <i>Autoimmunity Reviews</i> , 2020, 19, 102450.	2.5	27
18843	High-dimensionality Data Analysis of Pharmacological Systems Associated with Complex Diseases. <i>Pharmacological Reviews</i> , 2020, 72, 191-217.	7.1	17
18844	Draft Genome Sequence of Thermophilic <i>Bacillus</i> sp. TYF-LIM-B05 Directly Producing Ethanol from Various Carbon Sources Including Lignocellulose. <i>Current Microbiology</i> , 2020, 77, 491-499.	1.0	2
18845	Unveiling the genetic etiology of primary ciliary dyskinesia: When standard genetic approach is not enough. <i>Advances in Medical Sciences</i> , 2020, 65, 1-11.	0.9	4
18846	t-Distributed Stochastic Neighbor Embedding (t-SNE): A tool for eco-physiological transcriptomic analysis. <i>Marine Genomics</i> , 2020, 51, 100723.	0.4	113
18847	Co-option of wing-patterning genes underlies the evolution of the treehopper helmet. <i>Nature Ecology and Evolution</i> , 2020, 4, 250-260.	3.4	38
18848	Expression analysis of microRNAs and mRNAs in myofibroblast differentiation of lung resident mesenchymal stem cells. <i>Differentiation</i> , 2020, 112, 10-16.	1.0	13
18849	Population History and Gene Divergence in Native Mexicans Inferred from 76 Human Exomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 994-1006.	3.5	43
18850	Identification of Key Genes and Signaling Pathways Associated with the Progression of Gastric Cancer. <i>Pathology and Oncology Research</i> , 2020, 26, 1903-1919.	0.9	18
18851	Comparative genome and transcriptome analysis of the nematode-trapping fungus <i>Duddingtonia flagrans</i> reveals high pathogenicity during nematode infection. <i>Biological Control</i> , 2020, 143, 104159.	1.4	6
18852	Co-infection with <i>Wolbachia</i> and <i>Cardinium</i> may promote the synthesis of fat and free amino acids in a small spider, <i>Hylyphantes graminicola</i> . <i>Journal of Invertebrate Pathology</i> , 2020, 169, 107307.	1.5	16

#	ARTICLE	IF	CITATIONS
18853	Comparative genomic and metabolic analysis of manganese-oxidizing mechanisms in <i>Celeribacter manganoxidans</i> DY25T: Its adaptation to the environment of polymetallic nodules. <i>Genomics</i> , 2020, 112, 2080-2091.	1.3	18
18854	Preliminary indications that the Attachment and Biobehavioral Catch-up Intervention alters DNA methylation in maltreated children. <i>Development and Psychopathology</i> , 2020, 32, 1486-1494.	1.4	25
18855	Circadian Entrainment Triggers Maturation of Human In Vitro Islets. <i>Cell Stem Cell</i> , 2020, 26, 108-122.e10.	5.2	127
18856	Profiling torpor-responsive microRNAs in muscles of the hibernating primate <i>Microcebus murinus</i> . <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194473.	0.9	14
18857	Loss of the Epigenetic Mark 5-hmC in Psoriasis: Implications for Epidermal Stem Cell Dysregulation. <i>Journal of Investigative Dermatology</i> , 2020, 140, 1266-1275.e3.	0.3	16
18858	Gene Expression Profiling Revealed 2 Types of Bronchial Basal Cell Hyperplasia and Squamous Metaplasia With Different Progression Potentials. <i>Applied Immunohistochemistry and Molecular Morphology</i> , 2020, 28, 477-483.	0.6	6
18859	Differences between KC and KPC pancreatic ductal adenocarcinoma mice models, in terms of their modeling biology and their clinical relevance. <i>Pancreatology</i> , 2020, 20, 79-88.	0.5	24
18860	Nongenetic cancer-risk SNPs affect oncogenes, tumour-suppressor genes, and immune function. <i>British Journal of Cancer</i> , 2020, 122, 569-577.	2.9	22
18861	Integrative Omics Approach to Identifying Genes Associated With Atrial Fibrillation. <i>Circulation Research</i> , 2020, 126, 350-360.	2.0	41
18862	Extracellular Vesicles in the Forebrain Display Reduced miR-346 and miR-331-3p in a Rat Model of Chronic Temporal Lobe Epilepsy. <i>Molecular Neurobiology</i> , 2020, 57, 1674-1687.	1.9	14
18863	Comparative genomics analysis of <i>Nitrospirillum</i> reveals the genomic differences and salt adaptation strategies. <i>Extremophiles</i> , 2020, 24, 249-264.	0.9	8
18864	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	9.0	488
18865	What's the target: understanding two decades of <i>in silico</i> microRNA-target prediction. <i>Briefings in Bioinformatics</i> , 2020, 21, 1999-2010.	3.2	35
18866	Identification and comprehensive characterization of lncRNAs with copy number variations and their driving transcriptional perturbed subpathways reveal functional significance for cancer. <i>Briefings in Bioinformatics</i> , 2020, 21, 2153-2166.	3.2	12
18867	Genetic merit for fertility alters the bovine uterine luminal fluid proteome. <i>Biology of Reproduction</i> , 2020, 102, 730-739.	1.2	10
18868	75-kDa glucose-regulated protein (GRP75) is a novel molecular signature for heat stress response in avian species. <i>American Journal of Physiology - Cell Physiology</i> , 2020, 318, C289-C303.	2.1	12
18869	Physiological and Proteomic Changes in the Apoplast Accompany Leaf Senescence in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1635.	1.7	20
18870	Investigation of PIC1 (permease in chloroplasts 1) gene's role in iron homeostasis: bioinformatics and expression analyses in tomato and sorghum. <i>BioMetals</i> , 2020, 33, 29-44.	1.8	9

#	ARTICLE	IF	CITATIONS
18871	Identification of Long Non-Coding RNA and Circular RNA Expression Profiles in Atrial Fibrillation. <i>Heart Lung and Circulation</i> , 2020, 29, e157-e167.	0.2	22
18872	The pathogenesis of systemic lupus erythematosus: Harnessing big data to understand the molecular basis of lupus. <i>Journal of Autoimmunity</i> , 2020, 110, 102359.	3.0	89
18873	Rare copy number variants in individuals at clinical high risk for psychosis: Enrichment of synaptic/brain-related functional pathways. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 140-151.	1.1	0
18874	Proteomic identification of boar seminal plasma proteins related to sperm resistance to cooling at 17°C. <i>Theriogenology</i> , 2020, 147, 135-145.	0.9	16
18875	Maternal Type-I interferon signaling adversely affects the microglia and the behavior of the offspring accompanied by increased sensitivity to stress. <i>Molecular Psychiatry</i> , 2020, 25, 1050-1067.	4.1	40
18876	Molecular bases of responses to abiotic stress in trees. <i>Journal of Experimental Botany</i> , 2020, 71, 3765-3779.	2.4	65
18877	A comparative analysis of gene expression induced by the embryo in the caprine endometrium. <i>Veterinary Medicine and Science</i> , 2020, 6, 196-203.	0.6	3
18878	Transcriptome analysis of the molecular mechanism of Chrysanthemum flower color change under short-day photoperiods. <i>Plant Physiology and Biochemistry</i> , 2020, 146, 315-328.	2.8	22
18879	Tandem mass tag-based quantitative proteomics reveals the regulators in biofilm formation and biofilm control of <i>Bacillus licheniformis</i> . <i>Food Control</i> , 2020, 110, 107029.	2.8	12
18880	Science behind biostimulant action of seaweed extract on growth and crop yield: insights into transcriptional changes in roots of maize treated with <i>Kappaphycus alvarezii</i> seaweed extract under soil moisture stressed conditions. <i>Journal of Applied Phycology</i> , 2020, 32, 599-613.	1.5	50
18881	2,5-hexanedione-induced deregulation of axon-related microRNA expression in rat nerve tissues. <i>Toxicology Letters</i> , 2020, 320, 95-102.	0.4	8
18882	Candidate lncRNA-miRNA-mRNA network in predicting hepatocarcinogenesis with cirrhosis: an integrated bioinformatics analysis. <i>Journal of Cancer Research and Clinical Oncology</i> , 2020, 146, 87-96.	1.2	33
18883	ATBS1-INTERACTING FACTOR 2 negatively regulates dark- and brassinosteroid-induced leaf senescence through interactions with INDUCER OF CBF EXPRESSION 1. <i>Journal of Experimental Botany</i> , 2020, 71, 1475-1490.	2.4	22
18884	Genome analysis of <i>Crassaminicella</i> sp. SY095, an anaerobic mesophilic marine bacterium isolated from a deep-sea hydrothermal vent on the Southwest Indian Ridge. <i>Marine Genomics</i> , 2020, 52, 100733.	0.4	4
18885	Integrated miRNA-seq analysis reveals the molecular mechanism underlying the effect of acupuncture on endometrial receptivity in patients undergoing fertilization: embryo transplantation. <i>3 Biotech</i> , 2020, 10, 6.	1.1	10
18886	Genetic effects on planum temporale asymmetry and their limited relevance to neurodevelopmental disorders, intelligence or educational attainment. <i>Cortex</i> , 2020, 124, 137-153.	1.1	26
18887	Transcriptomic analysis of oligochaete immune responses to myxosporeans infection: <i>Branchiura sowerbyi</i> infected with <i>Myxobolus cultus</i> . <i>Journal of Invertebrate Pathology</i> , 2020, 169, 107283.	1.5	5
18888	Genomic divergences between the two polyphagous <i>Spodoptera</i> relatives provide cues for successful invasion of the fall armyworm. <i>Insect Science</i> , 2020, 27, 1257-1265.	1.5	8

#	ARTICLE	IF	CITATIONS
18889	CO ₂ -driven ocean acidification weakens mussel shell defense capacity and induces global molecular compensatory responses. <i>Chemosphere</i> , 2020, 243, 125415.	4.2	42
18890	Glycolytic profile shift and antioxidant triggering in symbiont-free and H ₂ O ₂ -resistant <i>Strigomonas culicis</i> . <i>Free Radical Biology and Medicine</i> , 2020, 146, 392-401.	1.3	4
18891	GPR108 Is a Highly Conserved AAV Entry Factor. <i>Molecular Therapy</i> , 2020, 28, 367-381.	3.7	77
18892	Long-read sequencing and de novo assembly of the <i>Luffa cylindrica</i> (L.) Roem. genome. <i>Molecular Ecology Resources</i> , 2020, 20, 511-519.	2.2	27
18893	Anabolism, catabolism and proteomic analysis in the slow-twitch muscle of pacu (<i>Piaractus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2020, 51, 1101-1112.	0.9	1
18894	Transcriptional and Functional Programming of Decidual Innate Lymphoid Cells. <i>Frontiers in Immunology</i> , 2019, 10, 3065.	2.2	21
18895	Single Nucleotide Polymorphism rs6942067 Is a Risk Factor in Young and in Non-Smoking Patients with HPV Negative Head and Neck Squamous Cell Carcinoma. <i>Cancers</i> , 2020, 12, 55.	1.7	14
18896	Transcriptome-Wide Analysis Reveals Key DEGs in Flower Color Regulation of <i>Hosta plantaginea</i> (Lam.) Aschers. <i>Genes</i> , 2020, 11, 31.	1.0	8
18897	RNA-seq and ChIP-seq as Complementary Approaches for Comprehension of Plant Transcriptional Regulatory Mechanism. <i>International Journal of Molecular Sciences</i> , 2020, 21, 167.	1.8	24
18898	Chromosome-Level Comprehensive Genome of Mangrove Sediment-Derived Fungus <i>Penicillium variable</i> HXQ-H-1. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 7.	1.5	6
18899	Complete Genome Sequence of <i>Acidithiobacillus ferrooxidans</i> YNTRS-40, a Strain of the Ferrous Iron- and Sulfur-Oxidizing Acidophile. <i>Microorganisms</i> , 2020, 8, 2.	1.6	21
18900	Identification and study of differentially expressed miRNAs in aged NAFLD rats based on high-throughput sequencing. <i>Annals of Hepatology</i> , 2020, 19, 302-312.	0.6	18
18901	ModEx: A text mining system for extracting mode of regulation of transcription factor-gene regulatory interaction. <i>Journal of Biomedical Informatics</i> , 2020, 102, 103353.	2.5	7
18902	Association of proteome and metabolome signatures with severity in patients with community-acquired pneumonia. <i>Journal of Proteomics</i> , 2020, 214, 103627.	1.2	6
18903	Evolutionary History of Major Chemosensory Gene Families across Panarthropoda. <i>Molecular Biology and Evolution</i> , 2020, 37, 3601-3615.	3.5	10
18904	Sex-specific epigenetic profile of inner cell mass of mice conceived <i>in vivo</i> or by IVF. <i>Molecular Human Reproduction</i> , 2020, 26, 866-878.	1.3	11
18905	Functional networks of co-expressed genes to explore iron homeostasis processes in the pathogenic yeast <i>Candida glabrata</i> . <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa027.	1.5	6
18906	SIFERL Interacts with S-Adenosylmethionine Synthetase to Regulate Fruit Ripening. <i>Plant Physiology</i> , 2020, 184, 2168-2181.	2.3	19

#	ARTICLE	IF	CITATIONS
18907	A Functional Genomic Screen Identifies the Deubiquitinase USP11 as a Novel Transcriptional Regulator of ER α in Breast Cancer. <i>Cancer Research</i> , 2020, 80, 5076-5088.	0.4	18
18908	Identification of Parkinson's disease-related pathways and potential risk factors. <i>Journal of International Medical Research</i> , 2020, 48, 030006052095719.	0.4	6
18909	Transcriptome analysis reveals underlying immune response mechanism of fungal (Penicillium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 445.	1.6	8
18910	Aberration of the modulatory functions of intronic microRNA hsa-miR-933 on its host gene ATF2 results in type II diabetes mellitus and neurodegenerative disease development. <i>Human Genomics</i> , 2020, 14, 34.	1.4	6
18911	Development and Validation of a Novel DNA Methylation-Driven Gene Based Molecular Classification and Predictive Model for Overall Survival and Immunotherapy Response in Patients With Glioblastoma: A Multiomic Analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 576996.	1.8	10
18912	RNAseq Reveals Sensitive, Concentration-Dependent Transcriptional Markers of Copper in Mytilus californianus Larvae and Adults. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	7
18913	Warming Climate Is Reducing the Diversity of Dominant Microbes in the Largest High Arctic Lake. <i>Frontiers in Microbiology</i> , 2020, 11, 561194.	1.5	13
18914	Efficient Propagation of Circulating Tumor Cells: A First Step for Probing Tumor Metastasis. <i>Cancers</i> , 2020, 12, 2784.	1.7	14
18915	Functional Transcription Factor Target Networks Illuminate Control of Epithelial Remodelling. <i>Cancers</i> , 2020, 12, 2823.	1.7	5
18916	Conserved Patterns in Developmental Processes and Phases, Rather than Genes, Unite the Highly Divergent Bilateria. <i>Life</i> , 2020, 10, 182.	1.1	2
18917	Root-Secreted Coumarins and the Microbiota Interact to Improve Iron Nutrition in Arabidopsis. <i>Cell Host and Microbe</i> , 2020, 28, 825-837.e6.	5.1	199
18918	Genetic circuit characterization by inferring RNA polymerase movement and ribosome usage. <i>Nature Communications</i> , 2020, 11, 5001.	5.8	40
18919	Implication of ZNF217 in Accelerating Tumor Development and Therapeutically Targeting ZNF217-Induced PI3K/AKT Signaling for the Treatment of Metastatic Osteosarcoma. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 2528-2541.	1.9	11
18920	DeepAdd: Protein function prediction from k-mer embedding and additional features. <i>Computational Biology and Chemistry</i> , 2020, 89, 107379.	1.1	17
18921	Artificial Intelligence in the Genetic Diagnosis of Rare Disease. <i>Advances in Molecular Pathology</i> , 2020, 3, 143-155.	0.2	0
18922	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. <i>Scientific Data</i> , 2020, 7, 326.	2.4	40
18923	Identification of RNA Transcript Makers Associated With Prognosis of Kidney Renal Clear Cell Carcinoma by a Competing Endogenous RNA Network Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 540094.	1.1	18
18924	A system biological approach to investigate the genetic profiling and comorbidities of type 2 diabetes. <i>Gene Reports</i> , 2020, 21, 100830.	0.4	20

#	ARTICLE	IF	CITATIONS
18925	Antimicrobial susceptibility and genetic features of a heterogeneous vancomycin intermediate-resistant <i>Staphylococcus aureus</i> strain. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104565.	1.0	0
18926	Conjoint Feature Representation of GO and Protein Sequence for PPI Prediction Based on an Inception RNN Attention Network. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 22, 198-208.	2.3	18
18927	MARS: discovering novel cell types across heterogeneous single-cell experiments. <i>Nature Methods</i> , 2020, 17, 1200-1206.	9.0	90
18928	Semantic similarity and machine learning with ontologies. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	73
18929	Resequencing of 296 cultivated and wild lotus accessions unravels its evolution and breeding history. <i>Plant Journal</i> , 2020, 104, 1673-1684.	2.8	21
18930	Influence of the go-based semantic similarity measures in multi-objective gene clustering algorithm performance. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050038.	0.3	1
18931	Identification of the Significant Genes Regulated by Estrogen Receptor in Estrogen Receptor-Positive Breast Cancer and Their Expression Pattern Changes When Tamoxifen or Fulvestrant Resistance Occurs. <i>Frontiers in Genetics</i> , 2020, 11, 538734.	1.1	14
18932	No Assembly Required: Using BTyper3 to Assess the Congruency of a Proposed Taxonomic Framework for the <i>Bacillus cereus</i> Group With Historical Typing Methods. <i>Frontiers in Microbiology</i> , 2020, 11, 580691.	1.5	32
18933	iDRBP_MMC: Identifying DNA-Binding Proteins and RNA-Binding Proteins Based on Multi-Label Learning Model and Motif-Based Convolutional Neural Network. <i>Journal of Molecular Biology</i> , 2020, 432, 5860-5875.	2.0	43
18934	Applications of Genome-Wide Screening and Systems Biology Approaches in Drug Repositioning. <i>Cancers</i> , 2020, 12, 2694.	1.7	14
18935	Paneth Cell-Derived Lysozyme Defines the Composition of Mucolytic Microbiota and the Inflammatory Tone of the Intestine. <i>Immunity</i> , 2020, 53, 398-416.e8.	6.6	97
18936	Osteopontin Expression Identifies a Subset of Recruited Macrophages Distinct from Kupffer Cells in the Fatty Liver. <i>Immunity</i> , 2020, 53, 641-657.e14.	6.6	287
18937	RNA-seq reveals the salt tolerance of <i>Ipomoea pes-caprae</i> , a wild relative of sweet potato. <i>Journal of Plant Physiology</i> , 2020, 255, 153276.	1.6	17
18938	Genetic background dependent modifiers of craniosynostosis severity. <i>Journal of Structural Biology</i> , 2020, 212, 107629.	1.3	9
18939	Intrinsic Endocardial Defects Contribute to Hypoplastic Left Heart Syndrome. <i>Cell Stem Cell</i> , 2020, 27, 574-589.e8.	5.2	89
18940	Î²-HPV 8E6 combined with TERT expression promotes long-term proliferation and genome instability after cytokinesis failure. <i>Virology</i> , 2020, 549, 32-38.	1.1	8
18941	Distinct mRNA and long non-coding RNA expression profiles of decidual natural killer cells in patients with early missed abortion. <i>FASEB Journal</i> , 2020, 34, 14264-14286.	0.2	7
18942	RNA-Seq reveals inflammatory mechanisms of Xiao-Ban-Xia-Tang decoction to ameliorate cisplatin-induced emesis in a rat pica model. <i>Biomedicine and Pharmacotherapy</i> , 2020, 131, 110699.	2.5	13

#	ARTICLE	IF	CITATIONS
18943	Ambient Temperature is A Strong Selective Factor Influencing Human Development and Immunity. Genomics, Proteomics and Bioinformatics, 2020, 18, 489-500.	3.0	5
18944	MEAF6 is essential for cell proliferation and plays a role in the assembly of KAT7 complexes. Experimental Cell Research, 2020, 396, 112279.	1.2	5
18945	Immune response and endocytosis pathways are associated with the resilience against Alzheimer's disease. Translational Psychiatry, 2020, 10, 332.	2.4	33
18946	Expanded Chinese hamster organ and cell line proteomics profiling reveals tissue-specific functionalities. Scientific Reports, 2020, 10, 15841.	1.6	11
18947	Identification of G2 and S Phase-Expressed-1 as a Potential Biomarker in Patients with Prostate Cancer. Cancer Management and Research, 2020, Volume 12, 9259-9269.	0.9	4
18948	Landscape of Exhausted Virus-Specific CD8 ⁺ T Cells in Chronic LCMV Infection. Cell Reports, 2020, 32, 108078.	2.9	45
18949	pS421 huntingtin modulates mitochondrial phenotypes and confers neuroprotection in an HD hiPSC model. Cell Death and Disease, 2020, 11, 809.	2.7	13
18950	The similarity of inherited diseases (II): clinical and biological similarity between the phenotypic series. BMC Medical Genomics, 2020, 13, 139.	0.7	2
18951	Therapeutic mechanism of Toujie Quwen granules in COVID-19 based on network pharmacology. BioData Mining, 2020, 13, 15.	2.2	17
18952	Cancer-associated fibroblasts of the prostate promote a compliant and more invasive phenotype in benign prostate epithelial cells. Materials Today Bio, 2020, 8, 100073.	2.6	7
18953	Identification of the significant pathways of Banxia Houpu decoction in the treatment of depression based on network pharmacology. PLoS ONE, 2020, 15, e0239843.	1.1	7
18954	Expression Profiles of Long Non-coding RNA and Messenger RNA in Human Traumatic Brain Injury. Molecular Therapy - Nucleic Acids, 2020, 22, 99-113.	2.3	19
18955	Integrated phosphoproteomic and metabolomic profiling reveals perturbed pathways in the hippocampus of gut microbiota dysbiosis mice. Translational Psychiatry, 2020, 10, 346.	2.4	24
18956	Bioinformatics-Based Identification of a circRNA-miRNA-mRNA Axis in Esophageal Squamous Cell Carcinomas. Journal of Oncology, 2020, 2020, 1-9.	0.6	7
18957	Differential network analysis of bovine muscle reveals changes in gene coexpression patterns in response to changes in maternal nutrition. BMC Genomics, 2020, 21, 684.	1.2	12
18958	A high-throughput CRISPR interference screen for dissecting functional regulators of GPCR/cAMP signaling. PLoS Genetics, 2020, 16, e1009103.	1.5	15
18959	IurV, Encoded by ORF VCA0231, Is Involved in the Regulation of Iron Uptake Genes in Vibrio cholerae. Genes, 2020, 11, 1184.	1.0	2
18960	Predicting Drug Response and Synergy Using a Deep Learning Model of Human Cancer Cells. Cancer Cell, 2020, 38, 672-684.e6.	7.7	216

#	ARTICLE	IF	CITATIONS
18961	mRNA and miRNA expression profile reveals the role of miR-31 overexpression in neural stem cell. <i>Scientific Reports</i> , 2020, 10, 17537.	1.6	6
18962	Integrative Analyses of Genes Associated with Fulminant Type 1 Diabetes. <i>Journal of Immunology Research</i> , 2020, 2020, 1-10.	0.9	8
18963	Predicted functional interactome of <i>Caenorhabditis elegans</i> and a web tool for the functional interpretation of differentially expressed genes. <i>Biology Direct</i> , 2020, 15, 20.	1.9	3
18964	During bacteremia, <i>Pseudomonas aeruginosa</i> PAO1 adapts by altering the expression of numerous virulence genes including those involved in quorum sensing. <i>PLoS ONE</i> , 2020, 15, e0240351.	1.1	11
18965	Exploration of the Potential Biomarkers of Papillary Thyroid Cancer (PTC) Based on RT-PCR Arrays and Bioinformatics Analysis. <i>Cancer Management and Research</i> , 2020, Volume 12, 9235-9246.	0.9	5
18966	The Lethal(2)-Essential-for-Life [L(2)EFL] Gene Family Modulates Dengue Virus Infection in <i>Aedes aegypti</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 7520.	1.8	9
18967	Dendritic Cells and Microglia Have Non-redundant Functions in the Inflamed Brain with Protective Effects of Type 1 cDCs. <i>Cell Reports</i> , 2020, 33, 108291.	2.9	39
18968	Computational analysis of TP53 vs. CTNNB1 mutations in hepatocellular carcinoma suggests distinct cancer subtypes with differential gene expression profiles and chromatin states. <i>Computational Biology and Chemistry</i> , 2020, 89, 107404.	1.1	1
18969	Common gene signatures and key pathways in hypopharyngeal and esophageal squamous cell carcinoma. <i>Medicine (United States)</i> , 2020, 99, e22434.	0.4	12
18970	A disintegrin and metalloproteinase domain 17-epidermal growth factor receptor signaling contributes to oral cancer pain. <i>Pain</i> , 2020, 161, 2330-2343.	2.0	8
18971	Examining the effector mechanisms of Xuebijing injection on COVID-19 based on network pharmacology. <i>BioData Mining</i> , 2020, 13, 17.	2.2	30
18972	Transcriptome sequencing and screening of genes related to sex determination of <i>Trichosanthes kirilowii</i> Maxim. <i>PLoS ONE</i> , 2020, 15, e0239230.	1.1	9
18973	Cytosolic TaGAPC2 Enhances Tolerance to Drought Stress in Transgenic Arabidopsis Plants. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7499.	1.8	10
18974	LPCAT1 functions as a novel prognostic molecular marker in hepatocellular carcinoma. <i>Genes and Diseases</i> , 2022, 9, 151-164.	1.5	8
18975	RP1, a RAGE antagonist peptide, can improve memory impairment and reduce A β plaque load in the APP/PS1 mouse model of Alzheimer's disease. <i>Neuropharmacology</i> , 2020, 180, 108304.	2.0	18
18976	SWI/SNF inactivation in the endometrial epithelium leads to loss of epithelial integrity. <i>Human Molecular Genetics</i> , 2020, 29, 3412-3430.	1.4	11
18977	Global gene expression profile of periodontal ligament cells submitted to mechanical loading: A systematic review. <i>Archives of Oral Biology</i> , 2020, 118, 104884.	0.8	13
18978	Bioinformatic Identification of Potential Hub Genes in Muscle-Invasive Bladder Urothelial Carcinoma. <i>Cell Transplantation</i> , 2020, 29, 096368972096517.	1.2	2

#	ARTICLE	IF	CITATIONS
18979	Perspective: Linkage Maps, Communities of Geneticists, and Genome Databases. <i>Genetics</i> , 2020, 216, 261-262.	1.2	0
18980	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
18981	RNA sequence analysis of dermal papilla cellsâ€™ regeneration in 3D culture. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 13421-13430.	1.6	6
18982	Development of a Cardiac Sarcomere Functional Genomics Platform to Enable Scalable Interrogation of Human <i>TNNT2</i> Variants. <i>Circulation</i> , 2020, 142, 2262-2275.	1.6	31
18983	On the Logical Design of a Prototypical Data Lake System for Biological Resources. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 553904.	2.0	7
18984	The PD-1 Pathway Regulates Development and Function of Memory CD8+ T Cells following Respiratory Viral Infection. <i>Cell Reports</i> , 2020, 31, 107827.	2.9	72
18985	Protein profile of well-differentiated versus un-differentiated human bronchial/tracheal epithelial cells. <i>Heliyon</i> , 2020, 6, e04243.	1.4	7
18986	In vivo mRNA display enables large-scale proteomics by next generation sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26710-26718.	3.3	9
18987	An empirical bayesian approach for testing gene expression fold change and its application in detecting global dosage effects. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa072.	1.5	0
18988	Functional signatures of evolutionarily young CTCF binding sites. <i>BMC Biology</i> , 2020, 18, 132.	1.7	9
18989	Reconstruction and functional annotation of <i>Ascosphaera apis</i> full-length transcriptome utilizing PacBio long reads combined with Illumina short reads. <i>Journal of Invertebrate Pathology</i> , 2020, 176, 107475.	1.5	6
18990	Interdependent Patterns in Protein-Protein Interaction Networks. <i>IEEE Transactions on Network Science and Engineering</i> , 2020, 7, 3257-3265.	4.1	2
18991	Phenotype-genotype comorbidity analysis of patients with rare disorders provides insight into their pathological and molecular bases. <i>PLoS Genetics</i> , 2020, 16, e1009054.	1.5	14
18992	Improved reproductive growth of euhalophyte <i>Suaeda salsa</i> under salinity is correlated with altered phytohormone biosynthesis and signal transduction. <i>Functional Plant Biology</i> , 2020, 47, 170.	1.1	35
18993	Maximizing cohesion and separation for detecting protein functional modules in protein-protein interaction networks. <i>PLoS ONE</i> , 2020, 15, e0240628.	1.1	4
18994	Argonaut: A Web Platform for Collaborative Multi-omic Data Visualization and Exploration. <i>Patterns</i> , 2020, 1, 100122.	3.1	18
18995	Tumor Cell Attack by Crotalicidin (Ctn) and Its Fragment Ctn[15â€“34]: Insights into Their Dual Membranolytic and Intracellular Targeting Mechanism. <i>ACS Chemical Biology</i> , 2020, 15, 2945-2957.	1.6	10
18996	Analytical Guidelines for co-fractionation Mass Spectrometry Obtained through Global Profiling of Gold Standard <i>Saccharomyces cerevisiae</i> Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1876-1895.	2.5	14

#	ARTICLE	IF	CITATIONS
18997	Differential expression and significance of miRNAs in plasma extracellular vesicles of patients with Parkinson's disease. <i>International Journal of Neuroscience</i> , 2022, 132, 673-688.	0.8	31
18998	Prediction of a competing endogenous RNA co-expression network as a prognostic marker in glioblastoma. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 13346-13355.	1.6	13
18999	Integrative analysis reveals key mRNA and long non-coding RNA interaction in idiopathic pulmonary arterial hypertension. <i>Archives of Medical Science</i> , 2020, , .	0.4	0
19000	Analysis of T lymphocyte-related biomarkers in pancreatic cancer. <i>Pancreatology</i> , 2020, 20, 1502-1510.	0.5	2
19001	A novel tool for standardizing clinical data in a semantically rich model. <i>Journal of Biomedical Informatics</i> , 2020, 112, 100086.	2.5	11
19002	Full-length transcriptome sequencing analysis and development of EST-SSR markers for the endangered species <i>Populus wulianensis</i> . <i>Scientific Reports</i> , 2020, 10, 16249.	1.6	22
19003	Cancer cell-selective modulation of mitochondrial respiration and metabolism by potent organogold(<i>III</i>) dithiocarbamates. <i>Chemical Science</i> , 2020, 11, 10465-10482.	3.7	37
19004	Transcriptome analysis of <i>Actinoplanes utahensis</i> reveals molecular signature of saccharide impact on acarbose biosynthesis. <i>3 Biotech</i> , 2020, 10, 473.	1.1	4
19005	RNA-seq analysis uncovers effects of ammonia on metabolism, oxidant-antioxidant equilibrium and apoptosis in the red swamp crayfish (<i>Procambarus clarkii</i>). <i>Aquaculture Reports</i> , 2020, 18, 100459.	0.7	3
19006	Dihydroartemisinin prevents dextran sodium sulphate-induced colitis through inhibition of the activation of NLRP3 inflammasome and p38 MAPK signaling. <i>International Immunopharmacology</i> , 2020, 88, 106949.	1.7	20
19007	Early-pregnancy transcriptome signatures of preeclampsia: from peripheral blood to placenta. <i>Scientific Reports</i> , 2020, 10, 17029.	1.6	10
19008	Responses to iron oxide and zinc oxide nanoparticles in echinoderm embryos and microalgae: uptake, growth, morphology, and transcriptomic analysis. <i>Nanotoxicology</i> , 2020, 14, 1342-1361.	1.6	15
19009	Mapping scientific landscapes in UMLS research: a scientometric review. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2020, 27, 1612-1624.	2.2	13
19011	Genome-wide identification of low phosphorus responsive microRNAs in two soybean genotypes by high-throughput sequencing. <i>Functional and Integrative Genomics</i> , 2020, 20, 825-838.	1.4	18
19012	Identification of Hub Genes and Key Pathways Associated with Peripheral T-cell Lymphoma. <i>Current Medical Science</i> , 2020, 40, 885-899.	0.7	7
19013	Characteristic antimicrobial resistance of clinically isolated <i>Stenotrophomonas maltophilia</i> CYZ via complete genome sequence. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 23, 186-193.	0.9	9
19014	Integration of genetic variants and gene network for drug repurposing in colorectal cancer. <i>Pharmacological Research</i> , 2020, 161, 105203.	3.1	26
19015	Evaluating the effects of ocean warming and freshening on the physiological energetics and transcriptomic response of the Antarctic limpet <i>Nacella concinna</i> . <i>Science of the Total Environment</i> , 2020, 748, 142448.	3.9	12

#	ARTICLE	IF	CITATIONS
19016	Community curation in PomBase: enabling fission yeast experts to provide detailed, standardized, sharable annotation from research publications. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	19
19017	Pseudohyphal differentiation in <i>Komagataella phaffii</i> : investigating the FLO gene family. FEMS Yeast Research, 2020, 20, .	1.1	5
19018	Potential Prognostic Value and Mechanism of Stromal-Immune Signature in Tumor Microenvironment for Stomach Adenocarcinoma. BioMed Research International, 2020, 2020, 1-15.	0.9	8
19019	Analysis of Transcriptome and miRNAome in the Muscle of Bamei Pigs at Different Developmental Stages. Animals, 2020, 10, 1198.	1.0	11
19020	<i>Falsigemmobacter faecalis</i> gen. nov. sp. nov., isolated from faeces of <i>Rhinopithecus roxellanae</i> , and reclassification of <i>Gemmobacter intermedius</i> as <i>Falsigemmobacter intermedius</i> comb. nov. Archives of Microbiology, 2020, 202, 2599-2606.	1.0	1
19021	Identification of key genes in calcific aortic valve disease by integrated bioinformatics analysis. Medicine (United States), 2020, 99, e21286.	0.4	11
19022	Differential seminal plasma proteome signatures of boars with high and low resistance to hypothermic semen preservation at 5°C. Andrology, 2020, 8, 1907-1922.	1.9	5
19023	Delineation of the Germline and Somatic Mutation Interaction Landscape in Triple-Negative and Non-Triple-Negative Breast Cancer. International Journal of Genomics, 2020, 2020, 1-16.	0.8	1
19024	Development of a Nomogram With Alternative Splicing Signatures for Predicting the Prognosis of Glioblastoma: A Study Based on Large-Scale Sequencing Data. Frontiers in Oncology, 2020, 10, 1257.	1.3	6
19025	The ortholog conjecture revisited: the value of orthologs and paralogs in function prediction. Bioinformatics, 2020, 36, i219-i226.	1.8	47
19026	Ararport Lives: An Updated Framework for Arabidopsis Bioinformatics. Plant Cell, 2020, 32, 2683-2686.	3.1	28
19027	Gold/alpha-lactalbumin nanoprobe for the imaging and treatment of breast cancer. Nature Biomedical Engineering, 2020, 4, 686-703.	11.6	65
19028	Mapping signalling perturbations in myocardial fibrosis via the integrative phosphoproteomic profiling of tissue from diverse sources. Nature Biomedical Engineering, 2020, 4, 889-900.	11.6	17
19029	Investigating higher-order interactions in single-cell data with scHOT. Nature Methods, 2020, 17, 799-806.	9.0	51
19030	Shared up-regulation and contrasting down-regulation of gene expression distinguish desiccation-tolerant from intolerant green algae. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17438-17445.	3.3	22
19031	A-kinase-anchoring protein 1 (dAKAP1)-based signaling complexes coordinate local protein synthesis at the mitochondrial surface. Journal of Biological Chemistry, 2020, 295, 10749-10765.	1.6	15
19032	Chromatin network markers of leukemia. Bioinformatics, 2020, 36, i455-i463.	1.8	8
19033	Factorized embeddings learns rich and biologically meaningful embedding spaces using factorized tensor decomposition. Bioinformatics, 2020, 36, i417-i426.	1.8	5

#	ARTICLE	IF	CITATIONS
19034	Leveraging the Comparative Toxicogenomics Database to Fill in Knowledge Gaps for Environmental Health: A Test Case for Air Pollution-induced Cardiovascular Disease. <i>Toxicological Sciences</i> , 2020, 177, 392-404.	1.4	25
19035	Nonsense-Mediated RNA Decay Factor UPF1 Is Critical for Posttranscriptional and Translational Gene Regulation in Arabidopsis. <i>Plant Cell</i> , 2020, 32, 2725-2741.	3.1	42
19036	A Network Pharmacology Approach to Investigate the Active Compounds and Mechanisms of Musk for Ischemic Stroke. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-14.	0.5	14
19037	The circular RNA landscape in specific peripheral blood mononuclear cells of critically ill patients with sepsis. <i>Critical Care</i> , 2020, 24, 423.	2.5	11
19038	A trafficome-wide RNAi screen reveals deployment of early and late secretory host proteins and the entire late endo-/lysosomal vesicle fusion machinery by intracellular Salmonella. <i>PLoS Pathogens</i> , 2020, 16, e1008220.	2.1	12
19039	Glyceroglycolipid Metabolism Regulations under Phosphate Starvation Revealed by Transcriptome Analysis in <i>Synechococcus elongatus</i> PCC 7942. <i>Marine Drugs</i> , 2020, 18, 360.	2.2	5
19040	Transcriptomic and Ultrastructural Signatures of K ⁺ -Induced Aggregation in <i>Phytophthora parasitica</i> Zoospores. <i>Microorganisms</i> , 2020, 8, 1012.	1.6	7
19041	Hsa_circ_0002320: a novel clinical biomarker for colorectal cancer prognosis. <i>Medicine (United Tj ETQq1 1 0.784314 rgBT /Overlock 10</i>	0.4	10
19042	Deciphering cellular transcriptional alterations in Alzheimer's disease brains. <i>Molecular Neurodegeneration</i> , 2020, 15, 38.	4.4	42
19043	A Guide to Understanding "State-of-the-Art" Basic Research Techniques in Anesthesiology. <i>Anesthesia and Analgesia</i> , 2020, 131, 450-463.	1.1	2
19044	Major Depressive Disorder Is Associated With Differential Expression of Innate Immune and Neutrophil-Related Gene Networks in Peripheral Blood: A Quantitative Review of Whole-Genome Transcriptional Data From Case-Control Studies. <i>Biological Psychiatry</i> , 2020, 88, 625-637.	0.7	43
19045	Interstitial Cell Remodeling Promotes Aberrant Adipogenesis in Dystrophic Muscles. <i>Cell Reports</i> , 2020, 31, 107597.	2.9	64
19046	Distinct Roles of Mitochondrial HIGD1A and HIGD2A in Respiratory Complex and Supercomplex Biogenesis. <i>Cell Reports</i> , 2020, 31, 107607.	2.9	49
19047	Expansion of Adhesion Genes Drives Pathogenic Adaptation of Nematode-Trapping Fungi. <i>IScience</i> , 2020, 23, 101057.	1.9	31
19048	A PEROXO-Tag Enables Rapid Isolation of Peroxisomes from Human Cells. <i>IScience</i> , 2020, 23, 101109.	1.9	26
19049	XPA deficiency affects the ubiquitin-proteasome system function. <i>DNA Repair</i> , 2020, 94, 102937.	1.3	6
19050	Transcriptome studies of the floodwater mosquito, <i>Aedes vexans</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10 Research, 2020, 50, 563-574.	0.6	5
19051	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

#	ARTICLE	IF	CITATIONS
19052	Expanded Phenotypic Definition Identifies Hundreds of Potential Causative Genes for Leukodystrophies and Leukoencephalopathies. <i>Child Neurology Open</i> , 2020, 7, 2329048X2093900.	0.5	8
19053	Optimization of skeletal protein preparation for LC-MS/MS sequencing yields additional coral skeletal proteins in <i>Stylophora pistillata</i> . <i>BMC Materials</i> , 2020, 2, 8.	6.8	19
19054	Unified inference of missense variant effects and gene constraints in the human genome. <i>PLoS Genetics</i> , 2020, 16, e1008922.	1.5	17
19055	A Long-Day Photoperiod and 6-Benzyladenine Promote Runner Formation through Upregulation of Soluble Sugar Content in Strawberry. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4917.	1.8	15
19056	Domain expertise-agnostic feature selection for the analysis of breast cancer data*. <i>Artificial Intelligence in Medicine</i> , 2020, 108, 101928.	3.8	9
19057	Identification of potential blood biomarkers for early diagnosis of Alzheimer's disease through RNA sequencing analysis. <i>Alzheimer's Research and Therapy</i> , 2020, 12, 87.	3.0	48
19058	High-throughput discovery of phage receptors using transposon insertion sequencing of bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18670-18679.	3.3	83
19059	Identification of potential crucial genes in atrial fibrillation: a bioinformatic analysis. <i>BMC Medical Genomics</i> , 2020, 13, 104.	0.7	20
19060	Aberrant DNA methylation results in altered gene expression in non-alcoholic steatohepatitis-related hepatocellular carcinomas. <i>Journal of Cancer Research and Clinical Oncology</i> , 2020, 146, 2461-2477.	1.2	27
19061	Prioritizing positive feature values: a new hierarchical feature selection method. <i>Applied Intelligence</i> , 2020, 50, 4412-4433.	3.3	4
19062	A bioinformatics investigation into molecular mechanism of Yinzhihuang granules for treating hepatitis B by network pharmacology and molecular docking verification. <i>Scientific Reports</i> , 2020, 10, 11448.	1.6	27
19063	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
19064	Transcriptome sequencing and expression profiling of genes involved in daylily (<i>Hemerocallis citrina</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.5	5
19065	Identification of tumor-infiltrating immune cells and prognostic validation of tumor-infiltrating mast cells in adrenocortical carcinoma: results from bioinformatics and real-world data. <i>Oncolmmunology</i> , 2020, 9, 1784529.	2.1	27
19066	Exploring the Molecular Mechanisms of Pterygium by Constructing lncRNA-miRNA-mRNA Regulatory Network. , 2020, 61, 12.		13
19067	Are we better off with just one ontology on the Web?. <i>Semantic Web</i> , 2020, 11, 87-99.	1.1	6
19068	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	13.5	273
19069	ID1 As a Prognostic Biomarker and Promising Drug Target Plays a Pivotal Role in Deterioration of Clear Cell Renal Cell Carcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	1

#	ARTICLE	IF	CITATIONS
19070	Avian Immunome DB: an example of a user-friendly interface for extracting genetic information. <i>BMC Bioinformatics</i> , 2020, 21, 502.	1.2	8
19071	Virtual screening and network pharmacology-based synergistic mechanism identification of multiple components contained in Guanxin V against coronary artery disease. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 345.	1.2	24
19072	Comparative Genomics Analysis Provides New Strategies for Bacteriostatic Ability of <i>Bacillus velezensis</i> HAB-2. <i>Frontiers in Microbiology</i> , 2020, 11, 594079.	1.5	12
19073	Inflammatory Response of Ischemic Tolerance in Circulating Plasma: Preconditioning-Induced by Transient Ischemic Attack (TIA) Phenomena in Acute Ischemia Patients (AIS). <i>Frontiers in Neurology</i> , 2020, 11, 552470.	1.1	7
19074	Transcriptional Effects of Psychoactive Drugs on Genes Involved in Neurogenesis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8333.	1.8	7
19075	Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact. <i>Cell</i> , 2020, 183, 1185-1201.e20.	13.5	161
19076	Functional Specialization of Human Salivary Glands and Origins of Proteins Intrinsic to Human Saliva. <i>Cell Reports</i> , 2020, 33, 108402.	2.9	54
19077	A Selective Autophagy Pathway for Phase-Separated Endocytic Protein Deposits. <i>Molecular Cell</i> , 2020, 80, 764-778.e7.	4.5	82
19078	Ensemble dimensionality reduction and feature gene extraction for single-cell RNA-seq data. <i>Nature Communications</i> , 2020, 11, 5853.	5.8	23
19079	Widespread regulation of gene expression by glucocorticoids in chondrocytes from patients with osteoarthritis as determined by RNA-Seq. <i>Arthritis Research and Therapy</i> , 2020, 22, 271.	1.6	23
19080	Gene Expression Signatures in AML-12 Hepatocyte Cells upon Dengue virus Infection and Acetaminophen Treatment. <i>Viruses</i> , 2020, 12, 1284.	1.5	4
19081	Urinary glycoproteins associated with aggressive prostate cancer. <i>Theranostics</i> , 2020, 10, 11892-11907.	4.6	22
19082	Demyelination Regulates the Circadian Transcription Factor BMAL1 to Signal Adult Neural Stem Cells to Initiate Oligodendrogenesis. <i>Cell Reports</i> , 2020, 33, 108394.	2.9	19
19083	Discovering lethal alleles across the turkey genome using a transmission ratio distortion approach. <i>Animal Genetics</i> , 2020, 51, 876-889.	0.6	12
19084	Pathway mapping reveals antiretroviral treatments' targeted cell cycle regulation in lung cancer. <i>Informatics in Medicine Unlocked</i> , 2020, 21, 100426.	1.9	1
19085	Identification of Monotonically Differentially Expressed Genes across Pathologic Stages for Cancers. <i>Journal of Oncology</i> , 2020, 2020, 1-9.	0.6	1
19086	Identification of Tumor Microenvironment-Related Prognostic Biomarkers in Luminal Breast Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 555865.	1.1	16
19087	Physiological Changes in Barley mlo-11 Powdery Mildew Resistance Conditioned by Tandem Repeat Copy Number. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8769.	1.8	5

#	ARTICLE	IF	CITATIONS
19088	Haematopoietic stem cell-dependent Notch transcription is mediated by p53 through the Histone chaperone Supt16h. <i>Nature Cell Biology</i> , 2020, 22, 1411-1422.	4.6	9
19089	Chicken cecal DNA methylome alteration in the response to <i>Salmonella enterica</i> serovar Enteritidis inoculation. <i>BMC Genomics</i> , 2020, 21, 814.	1.2	5
19090	Spatial profiling of gastric cancer patient-matched primary and locoregional metastases reveals principles of tumour dissemination. <i>Gut</i> , 2021, 70, 1823-1832.	6.1	38
19091	Comprehensive proteomic atlas of skin biomatrix scaffolds reveals a supportive microenvironment for epidermal development. <i>Journal of Tissue Engineering</i> , 2020, 11, 204173142097231.	2.3	17
19092	A Machine Learning Approach for Tracing Tumor Original Sites With Gene Expression Profiles. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 607126.	2.0	6
19093	Comprehensive Transcriptomic Analysis Reveals Dysregulated Competing Endogenous RNA Network in Endocrine Resistant Breast Cancer Cells. <i>Frontiers in Oncology</i> , 2020, 10, 600487.	1.3	10
19094	The human EV membranome. <i>Advances in Biomembranes and Lipid Self-Assembly</i> , 2020, , 53-82.	0.3	0
19095	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	13.5	177
19096	The potential biomarkers for the formation and development of intracranial aneurysm. <i>Journal of Clinical Neuroscience</i> , 2020, 81, 270-278.	0.8	8
19097	ClusterM: a scalable algorithm for computational prediction of conserved protein complexes across multiple protein interaction networks. <i>BMC Genomics</i> , 2020, 21, 615.	1.2	4
19098	iTRAQ-Based Phosphoproteomic Analysis of <i>Toxoplasma gondii</i> Tachyzoites Provides Insight Into the Role of Phosphorylation for its Invasion and Egress. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 586466.	1.8	6
19099	A review of protein-protein interaction network alignment: From pathway comparison to global alignment. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2647-2656.	1.9	17
19100	RNA-mediated control of cell shape modulates antibiotic resistance in <i>Vibrio cholerae</i> . <i>Nature Communications</i> , 2020, 11, 6067.	5.8	22
19101	CD74, a novel predictor for bronchopulmonary dysplasia in preterm infants. <i>Medicine (United States)</i> , 2020, 99, e23477.	0.4	3
19102	Integrated computational approach toward discovery of multi-targeted natural products from <i>Thumbai (Leucas aspera)</i> for attuning NKT cells. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 2893-2907.	2.0	5
19103	The Mediation of miR-34a/miR-449c for Immune Cytokines in Acute Cold/Heat-Stressed Broiler Chicken. <i>Animals</i> , 2020, 10, 2168.	1.0	5
19104	Identification of hsa-miR-1275 as a Novel Biomarker Targeting MECP2 for Human Epilepsy of Unknown Etiology. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 19, 398-410.	1.8	5
19105	Quorum Sensing System in <i>Bacteroides thetaiotaomicron</i> Strain Identified by Genome Sequence Analysis. <i>ACS Omega</i> , 2020, 5, 27502-27513.	1.6	1

#	ARTICLE	IF	CITATIONS
19106	Recent evolution of a TET-controlled and DPPA3/STELLA-driven pathway of passive DNA demethylation in mammals. <i>Nature Communications</i> , 2020, 11, 5972.	5.8	38
19107	What Can Machine Learning Approaches in Genomics Tell Us about the Molecular Basis of Amyotrophic Lateral Sclerosis?. <i>Journal of Personalized Medicine</i> , 2020, 10, 247.	1.1	14
19108	Dataset of full-length transcriptome assembly and annotation of <i>apocynum venetum</i> using pacbio sequel II. <i>Data in Brief</i> , 2020, 33, 106494.	0.5	4
19109	Regulators of TNF \pm mediated insulin resistance elucidated by quantitative proteomics. <i>Scientific Reports</i> , 2020, 10, 20878.	1.6	33
19110	MiR-215-5p Reduces Liver Metastasis in an Experimental Model of Colorectal Cancer through Regulation of ECM-Receptor Interactions and Focal Adhesion. <i>Cancers</i> , 2020, 12, 3518.	1.7	32
19111	Reprogramming to recover youthful epigenetic information and restore vision. <i>Nature</i> , 2020, 588, 124-129.	13.7	424
19112	Wide-ranging transcriptomic analysis of <i>Poncirus trifoliata</i> , <i>Citrus sunki</i> , <i>Citrus sinensis</i> and contrasting hybrids reveals HLB tolerance mechanisms. <i>Scientific Reports</i> , 2020, 10, 20865.	1.6	22
19113	Systematic Analysis of Protein-Protein and Gene-Environment Interactions to Decipher the Cognitive Mechanisms of Autism Spectrum Disorder. <i>Cellular and Molecular Neurobiology</i> , 2022, 42, 1091-1103.	1.7	5
19114	Functional, Morphological, and Evolutionary Characterization of Hearing in Subterranean, Eusocial African Mole-Rats. <i>Current Biology</i> , 2020, 30, 4329-4341.e4.	1.8	19
19115	Prognostic Implication of a Metabolism-Associated Gene Signature in Lung Adenocarcinoma. <i>Molecular Therapy - Oncolytics</i> , 2020, 19, 265-277.	2.0	38
19116	Establishment of immune prognostic signature and analysis of prospective molecular mechanisms in childhood osteosarcoma patients. <i>Medicine (United States)</i> , 2020, 99, e23251.	0.4	5
19117	Dedifferentiation and neuronal repression define familial Alzheimer's disease. <i>Science Advances</i> , 2020, 6, .	4.7	44
19118	Transcriptome analysis of genes related to cadmium absorption and transportation in pepper. <i>Israel Journal of Ecology and Evolution</i> , 2020, 67, 29-38.	0.2	0
19119	Leaf shape in <i>Populus tremula</i> is a complex, omnigenic trait. <i>Ecology and Evolution</i> , 2020, 10, 11922-11940.	0.8	19
19120	Transcriptome Sequencing and Comparative Analysis of Amphoteric ESCs and PGCs in Chicken (<i>Gallus</i>) Tj ETQq0 0.0rgBT /Oyerlock 10	1.0	2
19121	Identification of biomarkers in colon cancer based on bioinformatic analysis. <i>Translational Cancer Research</i> , 2020, 9, 4879-4895.	0.4	5
19122	Ubiquitin-Like Modifier Activating Enzyme 1 as a Novel Diagnostic and Prognostic Indicator That Correlates With Ferroptosis and the Malignant Phenotypes of Liver Cancer Cells. <i>Frontiers in Oncology</i> , 2020, 10, 592413.	1.3	36
19123	Deep learning suggests that gene expression is encoded in all parts of a co-evolving interacting gene regulatory structure. <i>Nature Communications</i> , 2020, 11, 6141.	5.8	83

#	ARTICLE	IF	CITATIONS
19124	Informatics Inference of Exercise-Induced Modulation of Brain Pathways Based on Cerebrospinal Fluid Micro-RNAs in Myalgic Encephalomyelitis/Chronic Fatigue Syndrome. <i>Network and Systems Medicine</i> , 2020, 3, 142-158.	2.7	2
19125	Transcriptome and proteome profiling reveal complementary scavenger and immune features of rat liver sinusoidal endothelial cells and liver macrophages. <i>BMC Molecular and Cell Biology</i> , 2020, 21, 85.	1.0	21
19126	Comparative Analysis of the Global Transcriptomic Response to Oxidative Stress of <i>Bacillus anthracis</i> htrA-Disrupted and Parental Wild Type Strains. <i>Microorganisms</i> , 2020, 8, 1896.	1.6	4
19127	A human ESC-based screen identifies a role for the translated lncRNA LINC00261 in pancreatic endocrine differentiation. <i>ELife</i> , 2020, 9, .	2.8	25
19128	Mathematical and Computational Oncology. <i>Lecture Notes in Computer Science</i> , 2020, , .	1.0	0
19129	Integrated Analysis of Gene Expression and Metabolite Data Reveals Candidate Molecular Markers in Colorectal Carcinoma. <i>Cancer Biotherapy and Radiopharmaceuticals</i> , 2020, , .	0.7	5
19130	Increased M1 Macrophages Infiltration Correlated With Poor Survival Outcomes and Radiation Response in Gliomas. <i>Dose-Response</i> , 2020, 18, 155932582096499.	0.7	5
19131	Network Pharmacology Identifies the Mechanisms of Action of Tongxie Anchang Decoction in the Treatment of Irritable Bowel Syndrome with Diarrhea Predominant. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-10.	0.5	2
19132	A Novel Proximity Biotinylation Assay Based on the Self-Associating Split GFP1â€™10/11. <i>Proteomes</i> , 2020, 8, 37.	1.7	3
19133	Conserved Epigenetic Regulatory Logic Infers Genes Governing Cell Identity. <i>Cell Systems</i> , 2020, 11, 625-639.e13.	2.9	31
19134	Donkey genomes provide new insights into domestication and selection for coat color. <i>Nature Communications</i> , 2020, 11, 6014.	5.8	63
19135	TTK, CDC25A, and ESPL1 as Prognostic Biomarkers for Endometrial Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	12
19136	Network Pharmacology-Based Study on the Mechanism of Gegen Qinlian Decoction against Colorectal Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-14.	0.5	6
19137	Transcriptome Remodeling in Gradual Development of Inverse Resistance between Paclitaxel and Cisplatin in Ovarian Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9218.	1.8	9
19138	Transferrin Receptor Functionally Marks Thermogenic Adipocytes. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 572459.	1.8	11
19139	Systematic expression analysis of EAF family reveals the importance of EAF2 in melanoma. <i>International Immunopharmacology</i> , 2020, 88, 106958.	1.7	2
19140	Maternal physical activity significantly alters the placental transcriptome. <i>Placenta</i> , 2020, 100, 111-121.	0.7	4
19141	FunRes: resolving tissue-specific functional cell states based on a cellâ€™cell communication network model. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7

#	ARTICLE	IF	CITATIONS
19142	Lung transcriptome of a COVID-19 patient and systems biology predictions suggest impaired surfactant production which may be druggable by surfactant therapy. <i>Scientific Reports</i> , 2020, 10, 19395.	1.6	75
19143	The ZSWIM8 ubiquitin ligase mediates target-directed microRNA degradation. <i>Science</i> , 2020, 370, .	6.0	138
19144	Investigation of the Potential Mechanism Governing the Effect of the Shen Zhu San on COVID-19 by Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-23.	0.5	6
19145	A Phylogenetic Rate Parameter Indicates Different Sequence Divergence Patterns in Orthologs and Paralogs. <i>Journal of Molecular Evolution</i> , 2020, 88, 720-730.	0.8	3
19146	RNA Sequencing of Formalin-Fixed and Paraffin-Embedded Tissue as a Complementary Method in Ophthalmopathology. <i>Klinische Monatsblätter Fur Augenheilkunde</i> , 2020, 237, 860-866.	0.3	4
19147	Screening of T Cell-Related Long Noncoding RNA-MicroRNA-mRNA Regulatory Networks in Non-Small-Cell Lung Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	6
19148	Effects of febrile seizures in mesial temporal lobe epilepsy with hippocampal sclerosis on gene expression using bioinformatical analysis. <i>Acta Epileptologica</i> , 2020, 2, .	0.4	4
19149	Boosting gene expression clustering with system-wide biological information: a robust autoencoder approach. <i>International Journal of Computational Biology and Drug Design</i> , 2020, 13, 98.	0.3	4
19150	Epidermal Growth Factor Is Essential for the Maintenance of Novel Prostate Epithelial Cells Isolated From Patient-Derived Organoids. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 571677.	1.8	14
19151	Transcriptomic Data Analyses Reveal a Reprogrammed Lipid Metabolism in HCV-Derived Hepatocellular Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 581863.	1.8	6
19152	Proteomic Analysis of Exosome-Like Vesicles Isolated From Saliva of the Tick <i>Haemaphysalis longicornis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 542319.	1.8	21
19153	Identification of Potential Core Genes Associated With the Progression of Stomach Adenocarcinoma Using Bioinformatic Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 517362.	1.1	11
19154	Recurrent Drought Conditions Enhance the Induction of Drought Stress Memory Genes in <i>Glycine max</i> L. <i>Frontiers in Genetics</i> , 2020, 11, 576086.	1.1	26
19155	Molecular estimation of neurodegeneration pseudotime in older brains. <i>Nature Communications</i> , 2020, 11, 5781.	5.8	26
19156	Singular manifolds of proteomic drivers to model the evolution of inflammatory bowel disease status. <i>Scientific Reports</i> , 2020, 10, 19066.	1.6	2
19157	Protamine-2 Deficiency Initiates a Reactive Oxygen Species (ROS)-Mediated Destruction Cascade during Epididymal Sperm Maturation in Mice. <i>Cells</i> , 2020, 9, 1789.	1.8	21
19158	Bioinformatics analysis of microRNA profiles and identification of microRNA-mRNA network and biological markers in intracranial aneurysm. <i>Medicine (United States)</i> , 2020, 99, e21186.	0.4	9
19159	Identification and comparison of proteomic and peptide profiles of mung bean seeds and sprouts. <i>BMC Chemistry</i> , 2020, 14, 46.	1.6	10

#	ARTICLE	IF	CITATIONS
19160	Circuits Regulating Superoxide and Nitric Oxide Production and Neutralization in Different Cell Types: Expression of Participating Genes and Changes Induced by Ionizing Radiation. <i>Antioxidants</i> , 2020, 9, 701.	2.2	4
19161	Metastasis of Uveal Melanoma with Monosomy-3 Is Associated with a Less Glycogenetic Gene Expression Profile and the Dysregulation of Glycogen Storage. <i>Cancers</i> , 2020, 12, 2101.	1.7	10
19162	Tousled-Like Kinases Suppress Innate Immune Signaling Triggered by Alternative Lengthening of Telomeres. <i>Cell Reports</i> , 2020, 32, 107983.	2.9	23
19163	Variants in SCAF4 Cause a Neurodevelopmental Disorder and Are Associated with Impaired mRNA Processing. <i>American Journal of Human Genetics</i> , 2020, 107, 544-554.	2.6	13
19164	MicroRNA Profiling in Paired Left and Right Eyes, Lungs, and Testes of Normal Mice. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 21, 687-695.	2.3	3
19165	Mutant p53 induces Golgi tubulo-vesiculation driving a prometastatic secretome. <i>Nature Communications</i> , 2020, 11, 3945.	5.8	52
19166	Differential proteomics study of postharvest <i>Volvariella volvacea</i> during storage at 4°C. <i>Scientific Reports</i> , 2020, 10, 13134.	1.6	4
19167	The effect of Jiedu Huoxue decoction on rat model of experimental nonbacterial prostatitis via regulation of miRNAs. <i>Pharmaceutical Biology</i> , 2020, 58, 745-759.	1.3	7
19168	A review of auditing techniques for the Unified Medical Language System. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2020, 27, 1625-1638.	2.2	7
19169	Big data in epilepsy: Clinical and research considerations. Report from the Epilepsy Big Data Task Force of the International League Against Epilepsy. <i>Epilepsia</i> , 2020, 61, 1869-1883.	2.6	23
19170	An interspecies translation model implicates integrin signaling in infliximab-resistant inflammatory bowel disease. <i>Science Signaling</i> , 2020, 13, .	1.6	19
19171	Causal mutations from adaptive laboratory evolution are outlined by multiple scales of genome annotations and condition-specificity. <i>BMC Genomics</i> , 2020, 21, 514.	1.2	23
19172	De novo assembly and Transcriptome characterization of an endemic species of Vietnam, <i>Panax vietnamensis</i> Ha et Grushv., including the development of EST-SSR markers for population genetics. <i>BMC Plant Biology</i> , 2020, 20, 358.	1.6	23
19173	Gut transcriptomic changes during hibernation in the greater horseshoe bat (<i>Rhinolophus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.9	4
19174	Bioinformatics analysis of differentially expressed genes in subchondral bone in early experimental osteoarthritis using microarray data. <i>Journal of Orthopaedic Surgery and Research</i> , 2020, 15, 310.	0.9	2
19175	Transcriptomic analysis reveals differential gene expression, alternative splicing, and novel exons during mouse trophoblast stem cell differentiation. <i>Stem Cell Research and Therapy</i> , 2020, 11, 342.	2.4	11
19176	Genomics and Virulence of <i>Fonsecaea pugnacius</i> , Agent of Disseminated Chromoblastomycosis. <i>Frontiers in Genetics</i> , 2020, 11, 822.	1.1	5
19177	iPS-Derived Early Oligodendrocyte Progenitor Cells from SPMS Patients Reveal Deficient In Vitro Cell Migration Stimulation. <i>Cells</i> , 2020, 9, 1803.	1.8	11

#	ARTICLE	IF	CITATIONS
19178	Transcriptome Analysis and Expression of Selected Cationic Amino Acid Transporters in the Liver of Broiler Chicken Fed Diets with Varying Concentrations of Lysine. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5594.	1.8	4
19179	The chromosome-level wintersweet (<i>Chimonanthus praecox</i>) genome provides insights into floral scent biosynthesis and flowering in winter. <i>Genome Biology</i> , 2020, 21, 200.	3.8	69
19180	Identification of key differentially expressed genes between ER-positive/HER2-negative breast cancer and ER-negative/HER2-negative breast cancer using integrated bioinformatics analysis. <i>Gland Surgery</i> , 2020, 9, 661-675.	0.5	2
19181	De novo assembly and annotation of transcriptomes from two cultivars of <i>Cannabis sativa</i> with different cannabinoid profiles. <i>Gene</i> , 2020, 762, 145026.	1.0	11
19182	Draft genome sequence of <i>Actinomadura</i> sp. K4S16 and elucidation of the nonthmicin biosynthetic pathway. <i>Journal of Genomics</i> , 2020, 8, 53-61.	0.6	4
19183	A knowledge-based approach to hierarchical classification: A voting metaphor. <i>Expert Systems With Applications</i> , 2020, 161, 113737.	4.4	3
19184	An autophagy-related model of 4 key genes for predicting prognosis of patients with laryngeal cancer. <i>Medicine (United States)</i> , 2020, 99, e21163.	0.4	6
19185	iTRAQ protein profile analysis of sugar beet under salt stress: different coping mechanisms in leaves and roots. <i>BMC Plant Biology</i> , 2020, 20, 347.	1.6	12
19186	Aging-associated decrease in the histone acetyltransferase KAT6B is linked to altered hematopoietic stem cell differentiation. <i>Experimental Hematology</i> , 2020, 82, 43-52.e4.	0.2	18
19187	Ontology based conceptual models for predicting fundamental organic reactivity. <i>Journal of Molecular Graphics and Modelling</i> , 2020, 100, 107691.	1.3	1
19188	Sustained immune activation is associated with susceptibility to the amphibian chytrid fungus. <i>Molecular Ecology</i> , 2020, 29, 2889-2903.	2.0	24
19189	Transcriptome Analysis Provides Insights into Grain Filling in Foxtail Millet (<i>Setaria italica</i> L.). <i>International Journal of Molecular Sciences</i> , 2020, 21, 5031.	1.8	10
19190	Leveraging computational genomics to understand the molecular basis of metal homeostasis. <i>New Phytologist</i> , 2020, 228, 1472-1489.	3.5	4
19191	Prognostic implication and functional annotations of APOBEC3G expression in patients with Melanoma. <i>Journal of Cancer</i> , 2020, 11, 5245-5256.	1.2	7
19192	Retene, pyrene and phenanthrene cause distinct molecular-level changes in the cardiac tissue of rainbow trout (<i>Oncorhynchus mykiss</i>) larvae, part 1 – Transcriptomics. <i>Science of the Total Environment</i> , 2020, 745, 141031.	3.9	16
19193	Comparison of gene regulatory networks to identify pathogenic genes for lymphoma. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050029.	0.3	0
19194	The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. <i>BMC Biology</i> , 2020, 18, 90.	1.7	40
19195	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

#	ARTICLE	IF	CITATIONS
19196	Scalable phylogenetic profiling using MinHash uncovers likely eukaryotic sexual reproduction genes. <i>PLoS Computational Biology</i> , 2020, 16, e1007553.	1.5	19
19197	Calmodulin-binding transcription activator (CAMTA) genes family: Genome-wide survey and phylogenetic analysis in flax (<i>Linum usitatissimum</i>). <i>PLoS ONE</i> , 2020, 15, e0236454.	1.1	20
19198	Identification of a Recurrence Signature and Validation of Cell Infiltration Level of Thyroid Cancer Microenvironment. <i>Frontiers in Endocrinology</i> , 2020, 11, 467.	1.5	12
19199	Analysis of the Antifungal Properties of <i>Bacillus velezensis</i> B-4 Through a Bioassay and Complete-Genome Sequencing. <i>Frontiers in Genetics</i> , 2020, 11, 703.	1.1	11
19200	Shedding the Light on <i>Litopenaeus vannamei</i> Differential Muscle and Hepatopancreas Immune Responses in White Spot Syndrome Virus (WSSV) Exposure. <i>Genes</i> , 2020, 11, 805.	1.0	12
19201	A Genomic Perspective on the Potential of Wild-Type Rumen Bacterium <i>Enterobacter</i> sp. LU1 as an Industrial Platform for Bio-Based Succinate Production. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4835.	1.8	3
19202	Genome-wide association study of corneal biomechanical properties identifies over 200 loci providing insight into the genetic etiology of ocular diseases. <i>Human Molecular Genetics</i> , 2020, 29, 3154-3164.	1.4	26
19203	<i>dhx36</i> , <i>bax</i> , and <i>arpc1b</i> May Be Critical for the Diagnosis and Treatment of Tuberculosis. <i>Canadian Respiratory Journal</i> , 2020, 2020, 1-11.	0.8	4
19204	Irradiation-Induced Upregulation of miR-711 Inhibits DNA Repair and Promotes Neurodegeneration Pathways. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5239.	1.8	7
19205	An Activity-Guided Map of Electrophile-Cysteine Interactions in Primary Human T Cells. <i>Cell</i> , 2020, 182, 1009-1026.e29.	13.5	194
19206	RNA-seq of aboveground sporophyte's transcriptome of <i>Huperzia serrata</i> and transcriptional understanding of early steps associated with huperzine biosynthesis in forest. <i>Current Plant Biology</i> , 2020, 24, 100159.	2.3	2
19207	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	13.7	257
19208	Draft Genome Sequence of the Bacterium <i>Paraburkholderia aromaticivorans</i> AR20-38, a Gram-Negative, Cold-Adapted Degrader of Aromatic Compounds. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	5
19209	Integrated transcriptomic and metabolomic analyses of yellow horn (<i>Xanthoceras sorbifolia</i>) in response to cold stress. <i>PLoS ONE</i> , 2020, 15, e0236588.	1.1	14
19210	Modeling Secondary Iron Overload Cardiomyopathy with Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes. <i>Cell Reports</i> , 2020, 32, 107886.	2.9	27
19211	Integrated bioinformatics analysis to decipher molecular mechanism of compound Kushen injection for esophageal cancer by combining WGCNA with network pharmacology. <i>Scientific Reports</i> , 2020, 10, 12745.	1.6	19
19212	Systematic analysis of miRNAs in patients with postmenopausal osteoporosis. <i>Gynecological Endocrinology</i> , 2020, 36, 997-1001.	0.7	7
19213	Network-principled deep generative models for designing drug combinations as graph sets. <i>Bioinformatics</i> , 2020, 36, i445-i454.	1.8	24

#	ARTICLE	IF	CITATIONS
19214	Identification of the Key Regulatory Genes Involved in Elaborate Petal Development and Specialized Character Formation in <i>Nigella damascena</i> (Ranunculaceae). <i>Plant Cell</i> , 2020, 32, 3095-3112.	3.1	27
19215	Polyphosphate Functions <i>In Vivo</i> as an Iron Chelator and Fenton Reaction Inhibitor. <i>MBio</i> , 2020, 11, .	1.8	36
19216	Circulating miRNA-3552 as a Potential Biomarker for Ischemic Stroke in Rats. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	8
19217	Identification of Immune-Related Prognostic Biomarkers Based on the Tumor Microenvironment in 20 Malignant Tumor Types With Poor Prognosis. <i>Frontiers in Oncology</i> , 2020, 10, 1008.	1.3	11
19218	Parental Selenium Nutrition Affects the One-Carbon Metabolism and the Hepatic DNA Methylation Pattern of Rainbow Trout (<i>Oncorhynchus mykiss</i>) in the Progeny. <i>Life</i> , 2020, 10, 121.	1.1	9
19219	Proteome-wide Prediction of Lysine Methylation Leads to Identification of H2BK43 Methylation and Outlines the Potential Methyllysine Proteome. <i>Cell Reports</i> , 2020, 32, 107896.	2.9	17
19220	PAK5 promotes the cell stemness ability by phosphorylating SOX2 in lung squamous cell carcinomas. <i>Experimental Cell Research</i> , 2020, 395, 112187.	1.2	3
19221	A novel <i>in silico</i> antimicrobial peptide DP7 combats MDR <i>Pseudomonas aeruginosa</i> and related biofilm infections. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3248-3259.	1.3	24
19222	ClusterMine: A knowledge-integrated clustering approach based on expression profiles of gene sets. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2040009.	0.3	3
19223	The Spruce Genome. <i>Compendium of Plant Genomes</i> , 2020, , .	0.3	0
19224	Identification of the aberrantly methylated differentially expressed genes in proliferative diabetic retinopathy. <i>Experimental Eye Research</i> , 2020, 199, 108141.	1.2	7
19225	Identification of Key Genes for the Ultrahigh Yield of Rice Using Dynamic Cross-tissue Network Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 256-270.	3.0	9
19226	Developing an automated mechanism to identify medical articles from wikipedia for knowledge extraction. <i>International Journal of Medical Informatics</i> , 2020, 141, 104234.	1.6	1
19227	Genome reanalysis to decipher resistome, virulome, and attenuated characters of attenuated <i>Streptococcus agalactiae</i> strain HZAUSC001. <i>Microbial Pathogenesis</i> , 2020, 147, 104416.	1.3	3
19228	Ribosome profiling reveals the effects of nitrogen application translational regulation of yield recovery after abrupt drought-flood alternation in rice. <i>Plant Physiology and Biochemistry</i> , 2020, 155, 42-58.	2.8	24
19229	Transcriptional mechanism of differential sugar accumulation in pulp of two contrasting mango (<i>Mangifera indica</i> L.) cultivars. <i>Genomics</i> , 2020, 112, 4505-4515.	1.3	18
19230	IL-15 Preconditioning Augments CAR T Cell Responses to Checkpoint Blockade for Improved Treatment of Solid Tumors. <i>Molecular Therapy</i> , 2020, 28, 2379-2393.	3.7	49
19231	Transcriptional Changes in the Ovaries of Perch from Chernobyl. <i>Environmental Science & Technology</i> , 2020, 54, 10078-10087.	4.6	8

#	ARTICLE	IF	CITATIONS
19232	Formal axioms in biomedical ontologies improve analysis and interpretation of associated data. <i>Bioinformatics</i> , 2020, 36, 2229-2236.	1.8	13
19233	Breed Differences in Dog Cognition Associated with Brain-Expressed Genes and Neurological Functions. <i>Integrative and Comparative Biology</i> , 2020, 60, 976-990.	0.9	24
19234	Genome-Wide Screen for Context-Dependent Tumor Suppressors Identified Using in Vivo Models for Neoplasia in <i>Drosophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2999-3008.	0.8	3
19235	Changes in porcine cauda epididymal fluid proteome by disrupting the HPT axis: Unveiling potential mechanisms of male infertility. <i>Molecular Reproduction and Development</i> , 2020, 87, 952-965.	1.0	2
19236	Genome-wide effect of tetracycline, doxycycline and 4-epidoxycycline on gene expression in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2020, 37, 389-396.	0.8	8
19237	Identification of biomarkers associated with extracellular vesicles based on an integrative pan-cancer bioinformatics analysis. <i>Medical Oncology</i> , 2020, 37, 79.	1.2	5
19238	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. <i>Cell</i> , 2020, 182, 1419-1440.e23.	13.5	1,162
19239	Pathogenic Tau Causes a Toxic Depletion of Nuclear Calcium. <i>Cell Reports</i> , 2020, 32, 107900.	2.9	23
19240	Network based study to explore genetic linkage between diabetes mellitus and myocardial ischemia: Bioinformatics approach. <i>Gene Reports</i> , 2020, 21, 100809.	0.4	4
19241	Analysis of Menstrual Blood Stromal Cells Reveals SOX15 Triggers Oocyte-Based Human Cell Reprogramming. <i>IScience</i> , 2020, 23, 101376.	1.9	9
19242	Full-length transcriptome sequences of ridgetail white prawn <i>Exopalaemon carinicauda</i> provide insight into gene expression dynamics during thermal stress. <i>Science of the Total Environment</i> , 2020, 747, 141238.	3.9	13
19243	Effects of silver nanoparticles on T98G human glioblastoma cells. <i>Toxicology and Applied Pharmacology</i> , 2020, 404, 115178.	1.3	14
19244	Genome sequencing and flavor compound biosynthesis pathway analyses of <i>Bacillus licheniformis</i> isolated from Chinese Maotai-flavor liquor-brewing microbiome. <i>Food Biotechnology</i> , 2020, 34, 193-211.	0.6	14
19245	Co-occurrence of cohesin complex and Ras signaling mutations during progression from myelodysplastic syndromes to secondary acute myeloid leukemia. <i>Haematologica</i> , 2021, 106, 2215-2223.	1.7	12
19246	A Neural Network Framework for Predicting the Tissue-of-Origin of 15 Common Cancer Types Based on RNA-Seq Data. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 737.	2.0	39
19247	Differently Expression Analysis and Function Prediction of Long Non-coding RNAs in Duck Embryo Fibroblast Cells Infected by Duck Tembusu Virus. <i>Frontiers in Immunology</i> , 2020, 11, 1729.	2.2	15
19248	Analysis of Metabolites and Gene Expression Changes Relative to Apricot (<i>Prunus armeniaca</i> L.) Fruit Quality During Development and Ripening. <i>Frontiers in Plant Science</i> , 2020, 11, 1269.	1.7	36
19249	Embedding-based Silhouette community detection. <i>Machine Learning</i> , 2020, 109, 2161-2193.	3.4	11

#	ARTICLE	IF	CITATIONS
19250	Inducers of the endothelial cell barrier identified through chemogenomic screening in genome-edited hPSC-endothelial cells. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19854-19865.	3.3	35
19251	Predicted yeast interactome and network-based interpretation of transcriptionally changed genes. Yeast, 2020, 37, 573-583.	0.8	1
19252	Mitochondrial DNA drives abscopal responses to radiation that are inhibited by autophagy. Nature Immunology, 2020, 21, 1160-1171.	7.0	214
19253	Transcriptomic differences between male and female <i>Trachycarpus fortunei</i> . Scientific Reports, 2020, 10, 12338.	1.6	5
19254	SINGLE FLOWER TRUSS and SELF-PRUNING signal developmental and metabolic networks to guide cotton architectures. Journal of Experimental Botany, 2020, 71, 5911-5923.	2.4	5
19255	Zonal regulation of collagen-type proteins and posttranslational modifications in prostatic benign and cancer tissues by imaging mass spectrometry. Prostate, 2020, 80, 1071-1086.	1.2	21
19256	Bioinformatics resources, databases, and tools for human mtDNA. , 2020, , 277-304.		0
19257	The type of dietary nanoparticles influences salivary protein corona composition. NanoImpact, 2020, 19, 100238.	2.4	10
19258	Ribosomal Protein uL11 as a Regulator of Metabolic Circuits Related to Aging and Cell Cycle. Cells, 2020, 9, 1745.	1.8	7
19259	A unified framework for integrative study of heterogeneous gene regulatory mechanisms. Nature Machine Intelligence, 2020, 2, 447-456.	8.3	6
19260	Common neural and transcriptional correlates of inhibitory control underlie emotion regulation and memory control. Social Cognitive and Affective Neuroscience, 2020, 15, 523-536.	1.5	16
19261	Aberrant lncRNA Profiles Are Associated With Chronic Benzene Poisoning and Acute Myelocytic Leukemia. Journal of Occupational and Environmental Medicine, 2020, 62, e308-e317.	0.9	5
19262	A review of computational drug repositioning: strategies, approaches, opportunities, challenges, and directions. Journal of Cheminformatics, 2020, 12, 46.	2.8	194
19263	Graph2GO: a multi-modal attributed network embedding method for inferring protein functions. GigaScience, 2020, 9, .	3.3	22
19264	SOX10-regulated promoter use defines isoform-specific gene expression in Schwann cells. BMC Genomics, 2020, 21, 549.	1.2	13
19265	RNAAgeCalc: A multi-tissue transcriptional age calculator. PLoS ONE, 2020, 15, e0237006.	1.1	40
19266	Gonad-Specific Transcriptomes Reveal Differential Expression of Gene and miRNA Between Male and Female of the Discus Fish (<i>Symphysodon aequifasciatus</i>). Frontiers in Physiology, 2020, 11, 754.	1.3	10
19267	De novo transcriptome assembly and functional annotation for Y-organs of the blue crab (<i>Callinectes</i>) Tj ETQq1 1 0.784314 rgBT /Ove Endocrinology, 2020, 298, 113567.	0.8	7

#	ARTICLE	IF	CITATIONS
19268	Bacterial polyphosphates interfere with the innate host defense to infection. <i>Nature Communications</i> , 2020, 11, 4035.	5.8	65
19269	<i>Mycoplasma hyopneumoniae</i> J elicits an antioxidant response and decreases the expression of ciliary genes in infected swine epithelial cells. <i>Scientific Reports</i> , 2020, 10, 13707.	1.6	6
19270	A comparative pan-genomic analysis of 53 <i>C. pseudotuberculosis</i> strains based on functional domains. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 6974-6986.	2.0	6
19271	Absence of AGPAT2 impairs brown adipogenesis, increases IFN stimulated gene expression and alters mitochondrial morphology. <i>Metabolism: Clinical and Experimental</i> , 2020, 111, 154341.	1.5	14
19272	Analysis on the virulomes and resistomes of multi-drug resistance clinical <i>Escherichia coli</i> isolates, as well as the interactome with gut microbiome. <i>Microbial Pathogenesis</i> , 2020, 148, 104423.	1.3	2
19274	Transcriptome Profile Analysis of Resistance Inoculated by <i>Dryopteris crassirhizoma</i> Dryocrassin ABBA in Potato Tubers. <i>American Journal of Potato Research</i> , 2020, 97, 325-335.	0.5	1
19275	A methodology for multilayer networks analysis in the context of open and private data: biological application. <i>Applied Network Science</i> , 2020, 5, .	0.8	4
19276	Capturing Multicellular System Designs Using Synthetic Biology Open Language (SBOL). <i>ACS Synthetic Biology</i> , 2020, 9, 2410-2417.	1.9	1
19277	Genome-wide identification and characterization of bHLH family genes from <i>Ginkgo biloba</i> . <i>Scientific Reports</i> , 2020, 10, 13723.	1.6	34
19278	Combining Gene-Disease Associations with Single-Cell Gene Expression Data Provides Anatomy-Specific Subnetworks in Age-Related Macular Degeneration. <i>Network and Systems Medicine</i> , 2020, 3, 105-121.	2.7	13
19279	Targeted cyclooxygenase-2 inhibiting nanomedicine results in pain-relief and differential expression of the RNA transcriptome in the dorsal root ganglia of injured male rats. <i>Molecular Pain</i> , 2020, 16, 174480692094330.	1.0	5
19280	NPF:network propagation for protein function prediction. <i>BMC Bioinformatics</i> , 2020, 21, 355.	1.2	11
19281	Computational Methods for Predicting Functions at the mRNA Isoform Level. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5686.	1.8	4
19282	Whole Transcriptome RNA Sequencing Identified circ_022743, circ_052666, and circ_004452 Were Associated with Colon Cancer Development. <i>DNA and Cell Biology</i> , 2020, 39, 1825-1837.	0.9	2
19283	Transcriptome Profiling-Based Analysis of Carbohydrate-Active Enzymes in <i>Aspergillus terreus</i> Involved in Plant Biomass Degradation. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 564527.	2.0	12
19284	β-Catenin signaling dynamics regulate cell fate in differentiating neural stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28828-28837.	3.3	29
19285	Impact of the Continuous Evolution of Gene Ontology on the Performance of Similarity Measures for Scoring Confidence of Protein Interactions. <i>SN Computer Science</i> , 2020, 1, 1.	2.3	1
19286	A Novel Proteomic Method Reveals NLS Tagging of T-DM1 Contravenes Classical Nuclear Transport in a Model of HER2-Positive Breast Cancer. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 19, 99-119.	1.8	8

#	ARTICLE	IF	CITATIONS
19287	Proximity labeling in mammalian cells with TurboID and split-TurboID. <i>Nature Protocols</i> , 2020, 15, 3971-3999.	5.5	171
19288	Term Matrix: a novel Gene Ontology annotation quality control system based on ontology term co-annotation patterns. <i>Open Biology</i> , 2020, 10, 200149.	1.5	7
19289	CYP27B1 Downregulation: A New Molecular Mechanism Regulating EZH2 in Ovarian Cancer Tumorigenicity. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 561804.	1.8	7
19290	A Systems Biology Approach to Identifying a Master Regulator That Can Transform the Fast Growing Cellular State to a Slowly Growing One in Early Colorectal Cancer Development Model. <i>Frontiers in Genetics</i> , 2020, 11, 570546.	1.1	12
19291	Transcriptomic Profiling of Mouse Brain During Acute and Chronic Infections by <i>Toxoplasma gondii</i> Oocysts. <i>Frontiers in Microbiology</i> , 2020, 11, 570903.	1.5	10
19292	Prolonged Targeted Cardiovascular Epidural Stimulation Improves Immunological Molecular Profile: A Case Report in Chronic Severe Spinal Cord Injury. <i>Frontiers in Systems Neuroscience</i> , 2020, 14, 571011.	1.2	8
19293	Genome Sequencing of <i>Paecilomyces Penicillatus</i> Provides Insights into Its Phylogenetic Placement and Mycoparasitism Mechanisms on Morel Mushrooms. <i>Pathogens</i> , 2020, 9, 834.	1.2	19
19294	Feedback enrichment analysis for transcription factor-target genes in signaling pathways. <i>BioSystems</i> , 2020, 198, 104262.	0.9	3
19295	The structural variation landscape in 492 Atlantic salmon genomes. <i>Nature Communications</i> , 2020, 11, 5176.	5.8	60
19296	Comparative morphological and transcriptomic analyses reveal chemosensory genes in the poultry red mite, <i>Dermanyssus gallinae</i> . <i>Scientific Reports</i> , 2020, 10, 17923.	1.6	7
19297	DIA (Data Independent Acquisition) proteomic based study on maize filling-kernel stage drought stress-responsive proteins and metabolic pathways. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 1198-1214.	0.5	2
19298	Benchmarking gene ontology function predictions using negative annotations. <i>Bioinformatics</i> , 2020, 36, i210-i218.	1.8	12
19299	Exploration in the Mechanism of Kaempferol for the Treatment of Gastric Cancer Based on Network Pharmacology. <i>BioMed Research International</i> , 2020, 2020, 1-11.	0.9	15
19300	De novo transcriptome assembly from the gonads of a scleractinian coral, <i>Euphyllia ancora</i> : molecular mechanisms underlying scleractinian gametogenesis. <i>BMC Genomics</i> , 2020, 21, 732.	1.2	14
19301	Plasma Proteome Responses in Salmonid Fish Following Immunization. <i>Frontiers in Immunology</i> , 2020, 11, 581070.	2.2	9
19302	iODA: An integrated tool for analysis of cancer pathway consistency from heterogeneous multi-omics data. <i>Journal of Biomedical Informatics</i> , 2020, 112, 103605.	2.5	10
19303	Computational Identification of Human Biological Processes and Protein Sequence Motifs Putatively Targeted by SARS-CoV-2 Proteins Using Protein-Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2020, 19, 4553-4566.	1.8	13
19304	Systematic Investigation of Resistance Evolution to Common Antibiotics Reveals Conserved Collateral Responses across Common Human Pathogens. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	1.4	9

#	ARTICLE	IF	CITATIONS
19305	Plasmatic Membrane Expression of Adhesion Molecules in Human Cardiac Progenitor/Stem Cells Might Explain Their Superior Cell Engraftment after Cell Transplantation. <i>Stem Cells International</i> , 2020, 2020, 1-13.	1.2	3
19306	A curated list of genes that affect the plant ionome. <i>Plant Direct</i> , 2020, 4, e00272.	0.8	23
19307	Brain-Enriched Coding and Long Non-coding RNA Genes Are Overrepresented in Recurrent Neurodevelopmental Disorder CNVs. <i>Cell Reports</i> , 2020, 33, 108307.	2.9	20
19308	Network pharmacology-based investigation on the mechanisms of action of <i>Morinda officinalis</i> How. in the treatment of osteoporosis. <i>Computers in Biology and Medicine</i> , 2020, 127, 104074.	3.9	26
19309	Dynamics of protein synthesis in the initial steps of strobilation in the model cestode parasite <i>Mesocestoides corti</i> (syn. <i>vogae</i>). <i>Journal of Proteomics</i> , 2020, 228, 103939.	1.2	2
19310	Increased RNA editing in maternal immune activation model of neurodevelopmental disease. <i>Nature Communications</i> , 2020, 11, 5236.	5.8	24
19311	Differential gene regulatory pattern in the human brain from schizophrenia using transcriptomic-causal network. <i>BMC Bioinformatics</i> , 2020, 21, 469.	1.2	14
19312	Identification of key genes and pathways for melanoma in the TRIM family. <i>Cancer Medicine</i> , 2020, 9, 8989-9005.	1.3	15
19313	Transcriptome and proteome mapping in the sheep atria reveal molecular features of atrial fibrillation progression. <i>Cardiovascular Research</i> , 2021, 117, 1760-1775.	1.8	14
19314	High Expression of UBB, RAC1, and ITGB1 Predicts Worse Prognosis among Nonsmoking Patients with Lung Adenocarcinoma through Bioinformatics Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-14.	0.9	10
19315	Characteristic and Phylogenetic Analysis of the Complete Chloroplast Genomes of Three Medicinal Plants of Schisandraceae. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	1
19316	Evolutionary Biology – A Transdisciplinary Approach. , 2020, , .		5
19317	Higher miR-543 levels correlate with lower <i>STK31</i> expression and longer pancreatic cancer survival. <i>Cancer Medicine</i> , 2020, 9, 9632-9640.	1.3	12
19318	Nuclear gene proximity and protein interactions shape transcript covariations in mammalian single cells. <i>Nature Communications</i> , 2020, 11, 5445.	5.8	20
19319	Murine interfollicular epidermal differentiation is gradualistic with GRHL3 controlling progression from stem to transition cell states. <i>Nature Communications</i> , 2020, 11, 5434.	5.8	33
19320	Electricity from lignocellulosic substrates by thermophilic <i>Geobacillus</i> species. <i>Scientific Reports</i> , 2020, 10, 17047.	1.6	8
19321	Agasicles hygrophila attack increases nerolidol synthase gene expression in <i>Alternanthera philoxeroides</i> , facilitating host finding. <i>Scientific Reports</i> , 2020, 10, 16994.	1.6	2
19322	Graph-based exploitation of gene ontology using COxploreR for scrutinizing biological significance. <i>Scientific Reports</i> , 2020, 10, 16672.	1.6	19

#	ARTICLE	IF	CITATIONS
19323	Rewiring of gene expression in circulating white blood cells is associated with pregnancy outcome in heifers (<i>Bos taurus</i>). <i>Scientific Reports</i> , 2020, 10, 16786.	1.6	14
19324	Quantifying the distribution of protein oligomerization degree reflects cellular information capacity. <i>Scientific Reports</i> , 2020, 10, 17689.	1.6	13
19325	Maximized quantitative phosphoproteomics allows high confidence dissection of the DNA damage signaling network. <i>Scientific Reports</i> , 2020, 10, 18056.	1.6	9
19326	Transcriptomic profile of Pea3 family members reveal regulatory codes for axon outgrowth and neuronal connection specificity. <i>Scientific Reports</i> , 2020, 10, 18162.	1.6	6
19327	A Coordinated Approach by Public Domain Bioinformatics Resources to Aid the Fight Against Alzheimer's Disease Through Expert Curation of Key Protein Targets. <i>Journal of Alzheimer's Disease</i> , 2020, 77, 257-273.	1.2	7
19328	Systematic Identification of Hub Genes in Placenta Accreta Spectrum Based on Integrated Transcriptomic and Proteomic Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 551495.	1.1	6
19329	Divergent Resistance Mechanisms to Immunotherapy Explain Responses in Different Skin Cancers. <i>Cancers</i> , 2020, 12, 2946.	1.7	6
19330	Meta-analysis of Transcriptomic Data Reveals Pathophysiological Modules Involved with Atrial Fibrillation. <i>Molecular Diagnosis and Therapy</i> , 2020, 24, 737-751.	1.6	9
19331	A proposal for score assignment to characterize biological processes from mass spectral analysis of serum. <i>Clinical Mass Spectrometry</i> , 2020, 18, 13-26.	1.9	2
19332	iMDA-BN: Identification of miRNA-disease associations based on the biological network and graph embedding algorithm. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2391-2400.	1.9	11
19333	Hierarchical Community Detection by Recursive Partitioning. <i>Journal of the American Statistical Association</i> , 2022, 117, 951-968.	1.8	25
19334	Fungal heavy metal adaptation through single nucleotide polymorphisms and copy number variation. <i>Molecular Ecology</i> , 2020, 29, 4157-4169.	2.0	24
19335	Systemic Mesenchymal Stem Cell Treatment Mitigates Structural and Functional Retinal Ganglion Cell Degeneration in a Mouse Model of Multiple Sclerosis. <i>Translational Vision Science and Technology</i> , 2020, 9, 16.	1.1	19
19336	binomialRF: interpretable combinatoric efficiency of random forests to identify biomarker interactions. <i>BMC Bioinformatics</i> , 2020, 21, 374.	1.2	3
19337	Comprehensive analysis of key genes associated with ceRNA networks in nasopharyngeal carcinoma based on bioinformatics analysis. <i>Cancer Cell International</i> , 2020, 20, 408.	1.8	11
19338	Experimental Evolution of <i>Bacillus subtilis</i> Reveals the Evolutionary Dynamics of Horizontal Gene Transfer and Suggests Adaptive and Neutral Effects. <i>Genetics</i> , 2020, 216, 543-558.	1.2	20
19339	The Phoebe genome sheds light on the evolution of magnoliids. <i>Horticulture Research</i> , 2020, 7, 146.	2.9	41
19340	Inference and multiscale model of epithelial-to-mesenchymal transition via single-cell transcriptomic data. <i>Nucleic Acids Research</i> , 2020, 48, 9505-9520.	6.5	45

#	ARTICLE	IF	CITATIONS
19341	Multivariate gene expression-based survival predictor model in esophageal adenocarcinoma. <i>Thoracic Cancer</i> , 2020, 11, 2896-2908.	0.8	8
19342	Screening and identification of miRNAs related to sexual differentiation of strobili in <i>Ginkgo biloba</i> by integration analysis of small RNA, RNA, and degradome sequencing. <i>BMC Plant Biology</i> , 2020, 20, 387.	1.6	12
19343	Identification of circular RNA hsa_circ_0044556 and its effect on the progression of colorectal cancer. <i>Cancer Cell International</i> , 2020, 20, 427.	1.8	13
19344	Genomic landscape of the immune microenvironments of brain metastases in breast cancer. <i>Journal of Translational Medicine</i> , 2020, 18, 327.	1.8	14
19345	Proteomic and Transcriptomic Analyses Indicate Metabolic Changes and Reduced Defense Responses in Mycorrhizal Roots of <i>Oeceoclades maculata</i> (Orchidaceae) Collected in Nature. <i>Journal of Fungi</i> (Basel, Switzerland), 2020, 6, 148.	1.5	13
19346	Changes in MicroRNA Expression during Rabbit Hemorrhagic Disease Virus (RHDV) Infection. <i>Viruses</i> , 2020, 12, 965.	1.5	5
19347	Genomic Analysis for Antioxidant Property of <i>Lactobacillus plantarum</i> FLPL05 from Chinese Longevity People. <i>Probiotics and Antimicrobial Proteins</i> , 2020, 12, 1451-1458.	1.9	14
19348	Pathogenic impact of transcript isoform switching in 1,209 cancer samples covering 27 cancer types using an isoform-specific interaction network. <i>Scientific Reports</i> , 2020, 10, 14453.	1.6	27
19349	The impact of transcription inhibition during in vitro maturation on the proteome of bovine oocytes. <i>Biology of Reproduction</i> , 2020, 103, 1000-1011.	1.2	13
19350	Transcriptome Profiling of Gold Queen Hami Melons under Cold Stress. <i>Russian Journal of Plant Physiology</i> , 2020, 67, 888-897.	0.5	4
19351	Analysis of key genes and pathways associated with the pathogenesis of intervertebral disc degeneration. <i>Journal of Orthopaedic Surgery and Research</i> , 2020, 15, 371.	0.9	13
19352	Genome Wide Analysis Reveals the Role of VadA in Stress Response, Germination, and Sterigmatocystin Production in <i>Aspergillus nidulans</i> Conidia. <i>Microorganisms</i> , 2020, 8, 1319.	1.6	12
19353	Active Packaging of Immobilized Zinc Oxide Nanoparticles Controls <i>Campylobacter jejuni</i> in Raw Chicken Meat. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	28
19354	Tumor-Infiltrating Regulatory T-cell Accumulation in the Tumor Microenvironment Is Mediated by IL33/ST2 Signaling. <i>Cancer Immunology Research</i> , 2020, 8, 1393-1406.	1.6	28
19355	Cancer cell line-specific protein profiles in extracellular vesicles identified by proteomics. <i>PLoS ONE</i> , 2020, 15, e0238591.	1.1	23
19356	Haplotype Block Analysis Reveals Candidate Genes and QTLs for Meat Quality and Disease Resistance in Chinese Jiangquhai Pig Breed. <i>Frontiers in Genetics</i> , 2020, 11, 752.	1.1	6
19357	Screening and Identification of Key Biomarkers in Acquired Lapatinib-Resistant Breast Cancer. <i>Frontiers in Pharmacology</i> , 2020, 11, 577150.	1.6	4
19358	Dissecting Transcription Factor-Target Interaction in Bovine Coronavirus Infection. <i>Microorganisms</i> , 2020, 8, 1323.	1.6	5

#	ARTICLE	IF	CITATIONS
19359	Differential processing and localization of human Nocturnin controls metabolism of mRNA and nicotinamide adenine dinucleotide cofactors. <i>Journal of Biological Chemistry</i> , 2020, 295, 15112-15133.	1.6	6
19360	Adaptive Unsupervised Feature Learning for Gene Signature Identification in Non-Small-Cell Lung Cancer. <i>IEEE Access</i> , 2020, 8, 154354-154362.	2.6	6
19361	iASIS Open Data Graph: Automated Semantic Integration of Disease-Specific Knowledge. , 2020, , .		4
19362	Microbial regulation of a lincRNA-miRNA-mRNA network in the mouse hippocampus. <i>Epigenomics</i> , 2020, 12, 1377-1387.	1.0	13
19363	Secretome Proteomic Approaches for Biomarker Discovery: An Update on Colorectal Cancer. <i>Medicina (Lithuania)</i> , 2020, 56, 443.	0.8	7
19364	De novo transcriptome sequencing of <i>Rhododendron molle</i> and identification of genes involved in the biosynthesis of secondary metabolites. <i>BMC Plant Biology</i> , 2020, 20, 414.	1.6	9
19365	Creating Neuroscientific Knowledge Organization System Based on Word Representation and Agglomerative Clustering Algorithm. <i>Frontiers in Neuroinformatics</i> , 2020, 14, 38.	1.3	2
19366	Unveiling Sex-Based Differences in the Effects of Alcohol Abuse: A Comprehensive Functional Meta-Analysis of Transcriptomic Studies. <i>Genes</i> , 2020, 11, 1106.	1.0	19
19367	Identification of Significant Genes and Pathways in Acute Pancreatitis via Bioinformatical Analysis. <i>Digestive Diseases and Sciences</i> , 2021, 66, 3045-3053.	1.1	9
19368	An unanticipated tumor-suppressive role of the SUMO pathway in the intestine unveiled by Ubc9 haploinsufficiency. <i>Oncogene</i> , 2020, 39, 6692-6703.	2.6	10
19369	A high-quality chromosome-level genome assembly reveals genetics for important traits in eggplant. <i>Horticulture Research</i> , 2020, 7, 153.	2.9	85
19370	Pseudo2GO: A Graph-Based Deep Learning Method for Pseudogene Function Prediction by Borrowing Information From Coding Genes. <i>Frontiers in Genetics</i> , 2020, 11, 807.	1.1	3
19371	Bioinformatics Data Mining Repurposes the JAK2 (Janus Kinase 2) Inhibitor Fedratinib for Treating Pancreatic Ductal Adenocarcinoma by Reversing the KRAS (Kirsten Rat Sarcoma 2 Viral Oncogene) Tj ETQq0 0 0 rg811/Overlook 10 Tf 50		
19372	SPT6-driven error-free DNA repair safeguards genomic stability of glioblastoma cancer stem-like cells. <i>Nature Communications</i> , 2020, 11, 4709.	5.8	17
19373	Systematic Elucidation of the Mechanism of Quercetin against Gastric Cancer via Network Pharmacology Approach. <i>BioMed Research International</i> , 2020, 2020, 1-11.	0.9	18
19374	Identification of hub genes in colon cancer via bioinformatics analysis. <i>Journal of International Medical Research</i> , 2020, 48, 030006052095323.	0.4	6
19375	Identification of hub genes in diabetic kidney disease via multiple-microarray analysis. <i>Annals of Translational Medicine</i> , 2020, 8, 997-997.	0.7	16
19376	Aldh inhibitor restores auditory function in a mouse model of human deafness. <i>PLoS Genetics</i> , 2020, 16, e1009040.	1.5	8

#	ARTICLE	IF	CITATIONS
19377	Single-Cell RNA-Sequencing From Mouse Incisor Reveals Dental Epithelial Cell-Type Specific Genes. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 841.	1.8	39
19378	Review on the Computational Genome Annotation of Sequences Obtained by Next-Generation Sequencing. <i>Biology</i> , 2020, 9, 295.	1.3	45
19379	Identifying Risk Genes and Interpreting Pathogenesis for Parkinson's Disease by a Multiomics Analysis. <i>Genes</i> , 2020, 11, 1100.	1.0	13
19380	Genome-wide identification and expression analysis of bZIP gene family in <i>Carthamus tinctorius</i> L.. <i>Scientific Reports</i> , 2020, 10, 15521.	1.6	20
19381	PTEN status determines chemosensitivity to proteasome inhibition in cholangiocarcinoma. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	23
19382	Cardiac glycosides inhibit cancer through Na/K-ATPase-dependent cell death induction. <i>Biochemical Pharmacology</i> , 2020, 182, 114226.	2.0	16
19383	Designing custom CRISPR libraries for hypothesis-driven drug target discovery. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2237-2246.	1.9	10
19384	Transcriptomic analysis of the orchestrated molecular mechanisms underlying fruiting body initiation in Chinese cordyceps. <i>Gene</i> , 2020, 763, 145061.	1.0	8
19385	Identification of immune-related biomarkers in adrenocortical carcinoma. <i>International Immunopharmacology</i> , 2020, 88, 106930.	1.7	6
19386	Network pharmacology analysis of the therapeutic mechanisms of the traditional Chinese herbal formula Lian Hua Qing Wen in Corona virus disease 2019 (COVID-19), gives fundamental support to the clinical use of LHQW. <i>Phytomedicine</i> , 2020, 79, 153336.	2.3	64
19387	Multi-layered Spatial Transcriptomics Identify Secretory Factors Promoting Human Hematopoietic Stem Cell Development. <i>Cell Stem Cell</i> , 2020, 27, 822-839.e8.	5.2	51
19388	Human Pluripotent Stem Cell-Derived Neural Cells and Brain Organoids Reveal SARS-CoV-2 Neurotropism Predominates in Choroid Plexus Epithelium. <i>Cell Stem Cell</i> , 2020, 27, 937-950.e9.	5.2	314
19389	Proteomics reveals the effect of type I interferon on the pathogenicity of duck hepatitis A virus genotype 3 in Pekin ducks. <i>Veterinary Microbiology</i> , 2020, 248, 108813.	0.8	10
19390	Identification of a prognostic signature of epithelial ovarian cancer based on tumor immune microenvironment exploration. <i>Genomics</i> , 2020, 112, 4827-4841.	1.3	41
19391	Molecular Characterization of the Coproduced Extracellular Vesicles in HEK293 during Virus-Like Particle Production. <i>Journal of Proteome Research</i> , 2020, 19, 4516-4532.	1.8	15
19392	The extent of cyclin C promoter occupancy directs changes in stress-dependent transcription. <i>Journal of Biological Chemistry</i> , 2020, 295, 16280-16291.	1.6	6
19393	Identification, Validation, and Functional Annotations of Genome-Wide Profile Variation between Melanocytic Nevus and Malignant Melanoma. <i>BioMed Research International</i> , 2020, 2020, 1-19.	0.9	7
19394	PAWER: protein array web exploreR. <i>BMC Bioinformatics</i> , 2020, 21, 411.	1.2	4

#	ARTICLE	IF	CITATIONS
19395	Long-read sequencing and de novo genome assembly of marine medaka (<i>Oryzias melastigma</i>). <i>BMC Genomics</i> , 2020, 21, 640.	1.2	7
19396	Rps27a might act as a controller of microglia activation in triggering neurodegenerative diseases. <i>PLoS ONE</i> , 2020, 15, e0239219.	1.1	27
19397	Transcriptomics predicts compound synergy in drug and natural product treated glioblastoma cells. <i>PLoS ONE</i> , 2020, 15, e0239551.	1.1	15
19398	Transcript Isoforms of SLC7A11-AS1 Are Associated With Varicocele-Related Male Infertility. <i>Frontiers in Genetics</i> , 2020, 11, 1015.	1.1	11
19399	Whole-Genome Sequencing Analysis of Quorum Quenching Bacterial Strain <i>Acinetobacter lactucae</i> QL-1 Identifies the FadY Enzyme for Degradation of the Diffusible Signal Factor. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6729.	1.8	13
19400	Modelling kidney disease using ontology: insights from the Kidney Precision Medicine Project. <i>Nature Reviews Nephrology</i> , 2020, 16, 686-696.	4.1	45
19401	Hepatopancreas immune response during molt cycle in the mud crab, <i>Scylla paramamosain</i> . <i>Scientific Reports</i> , 2020, 10, 13102.	1.6	23
19402	Systems biology reveals reprogramming of the S-nitroso-proteome in the cortical and striatal regions of mice during aging process. <i>Scientific Reports</i> , 2020, 10, 13913.	1.6	19
19403	Transcriptional analysis of cleft palate in TGF β 3 mutant mice. <i>Scientific Reports</i> , 2020, 10, 14940.	1.6	4
19404	Transcription factor expression defines subclasses of developing projection neurons highly similar to single-cell RNA-seq subtypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25074-25084.	3.3	23
19405	Complement C7 (C7), a Potential Tumor Suppressor, Is an Immune-Related Prognostic Biomarker in Prostate Cancer (PC). <i>Frontiers in Oncology</i> , 2020, 10, 1532.	1.3	13
19406	Matrisome Provides a Supportive Microenvironment for Skin Functions of Diverse Species. <i>ACS Biomaterials Science and Engineering</i> , 2020, 6, 5720-5733.	2.6	10
19407	Transcriptome analysis reveals key signature genes involved in the oncogenesis of lung cancer. <i>Cancer Biomarkers</i> , 2020, 29, 475-482.	0.8	5
19408	A framework for pathway knowledge driven prioritization in genome-wide association studies. <i>Genetic Epidemiology</i> , 2020, 44, 841-853.	0.6	2
19409	The NK cell granule protein NKG7 regulates cytotoxic granule exocytosis and inflammation. <i>Nature Immunology</i> , 2020, 21, 1205-1218.	7.0	110
19410	ChIP-seq Profiling Identifies Histone Deacetylase 2 Targeting Genes Involved in Immune and Inflammatory Regulation Induced by Calcitonin Gene-Related Peptide in Microglial Cells. <i>Journal of Immunology Research</i> , 2020, 2020, 1-10.	0.9	8
19411	Complete Genome Sequence and Biodegradation Characteristics of Benzoic Acid-Degrading Bacterium <i>Pseudomonas</i> sp. SCB32. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	8
19412	Physiological Characterization and Transcriptome Analysis of <i>Camellia oleifera</i> Abel. during Leaf Senescence. <i>Forests</i> , 2020, 11, 812.	0.9	10

#	ARTICLE	IF	CITATIONS
19413	Transcriptomic Analysis of Short-Term Salt Stress Response in Watermelon Seedlings. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6036.	1.8	24
19414	Third-generation sequencing found LncRNA associated with heat shock protein response to heat stress in <i>Populus qionghdaoensis</i> seedlings. <i>BMC Genomics</i> , 2020, 21, 572.	1.2	15
19415	Experimental and Biological Insights from Proteomic Analyses of Extracellular Vesicle Cargos in Normalcy and Disease. <i>Advanced Biology</i> , 2020, 4, e2000069.	3.0	8
19416	Comparative Analysis of the Extracellular Matrix Proteome across the Myotendinous Junction. <i>Journal of Proteome Research</i> , 2020, 19, 3955-3967.	1.8	39
19417	An epigenome-wide association study of early-onset major depression in monozygotic twins. <i>Translational Psychiatry</i> , 2020, 10, 301.	2.4	30
19418	Study of Osteoarthritis-Related Hub Genes Based on Bioinformatics Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	11
19419	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
19420	Identification, Expression and Co-Expression Analysis of R2R3-MYB Family Genes Involved in Graft Union Formation in Pecan (<i>Carya illinoensis</i>). <i>Forests</i> , 2020, 11, 917.	0.9	14
19421	CIPHER-SC: Disease-Gene Association Inference Using Graph Convolution on a Context-Aware Network with Single-Cell Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	1.9	8
19422	A Bioinformatics Research on Novel Mechanism of Compound Kushen Injection for Treating Breast Cancer by Network Pharmacology and Molecular Docking Verification. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-14.	0.5	8
19423	Newly identified Gon4l/Udu-interacting proteins implicate novel functions. <i>Scientific Reports</i> , 2020, 10, 14213.	1.6	4
19424	Predicting Gram-Positive Bacterial Protein Subcellular Location by Using Combined Features. <i>BioMed Research International</i> , 2020, 2020, 1-8.	0.9	2
19425	In silico analysis reveals interrelation of enriched pathways and genes in type 1 diabetes. <i>Immunogenetics</i> , 2020, 72, 399-412.	1.2	5
19426	Semantic Tree-Based 3D Scene Model Recognition. , 2020, , .		1
19427	Transcriptomic and anatomic profiling reveal the germination process of different wheat varieties in response to waterlogging stress. <i>BMC Genetics</i> , 2020, 21, 93.	2.7	22
19428	Functional Identification of the Dextranucrase Gene of <i>Leuconostoc mesenteroides</i> DRP105. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6596.	1.8	4
19429	Compounds with multitarget activity: structure-based analysis and machine learning. <i>Future Drug Discovery</i> , 2020, 2, .	0.8	7
19430	Complete Genome Sequence of <i>Pseudomonas aeruginosa</i> XN-1, Isolated from the Sputum of a Severe Pneumonia Patient. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	5

#	ARTICLE	IF	CITATIONS
19431	Tunica-Specific Transcriptome of Abdominal Aortic Aneurysm and the Effect of Intraluminal Thrombus, Smoking, and Diameter Growth Rate. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 40, 2700-2713.	1.1	18
19432	<i>Drosophila</i> Voltage-Gated Sodium Channels Are Only Expressed in Active Neurons and Are Localized to Distal Axonal Initial Segment-like Domains. <i>Journal of Neuroscience</i> , 2020, 40, 7999-8024.	1.7	50
19433	Circadian GLP-1 Secretion in Mice Is Dependent on the Intestinal Microbiome for Maintenance of Diurnal Metabolic Homeostasis. <i>Diabetes</i> , 2020, 69, 2589-2602.	0.3	33
19434	FLUTE: Fast and reliable knowledge retrieval from biomedical literature. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	13
19435	Grad-seq shines light on unrecognized RNA and protein complexes in the model bacterium <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2020, 48, 9301-9319.	6.5	30
19436	Revealing the full-length transcriptome of caucasian clover rhizome development. <i>BMC Plant Biology</i> , 2020, 20, 429.	1.6	13
19437	Differential Transcription and Alternative Splicing in Cotton Underly Specialized Defense Responses Against Pests. <i>Frontiers in Plant Science</i> , 2020, 11, 573131.	1.7	10
19438	A Pilot Study on MicroRNA Profile in Tear Fluid to Predict Response to Anti-VEGF Treatments for Diabetic Macular Edema. <i>Journal of Clinical Medicine</i> , 2020, 9, 2920.	1.0	10
19439	Dynamic transcriptome profiling toward understanding the development of the human embryonic heart during different Carnegie stages. <i>FEBS Letters</i> , 2020, 594, 4307-4319.	1.3	3
19440	Single-Cell NGS-Based Analysis of Copy Number Alterations Reveals New Insights in Circulating Tumor Cells Persistence in Early-Stage Breast Cancer. <i>Cancers</i> , 2020, 12, 2490.	1.7	25
19441	Identification of a metabolism-related gene expression prognostic model in endometrial carcinoma patients. <i>BMC Cancer</i> , 2020, 20, 864.	1.1	21
19442	Transcriptomic analysis links diverse hypothalamic cell types to fibroblast growth factor 1-induced sustained diabetes remission. <i>Nature Communications</i> , 2020, 11, 4458.	5.8	34
19443	De novo transcriptome assembly and population genetic analyses of an important coastal shrub, <i>Apocynum venetum</i> L. <i>BMC Plant Biology</i> , 2020, 20, 408.	1.6	10
19444	In vivo antiviral host transcriptional response to SARS-CoV-2 by viral load, sex, and age. <i>PLoS Biology</i> , 2020, 18, e3000849.	2.6	225
19445	Telomere-to-telomere assembled and centromere annotated genomes of the two main subspecies of the button mushroom <i>Agaricus bisporus</i> reveal especially polymorphic chromosome ends. <i>Scientific Reports</i> , 2020, 10, 14653.	1.6	12
19446	Differential contribution of bone marrow-derived infiltrating monocytes and resident macrophages to persistent lung inflammation in chronic air pollution exposure. <i>Scientific Reports</i> , 2020, 10, 14348.	1.6	16
19447	A bilateral tumor model identifies transcriptional programs associated with patient response to immune checkpoint blockade. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23684-23694.	3.3	32
19448	DEAD-Box Helicase 4 (Ddx4)+ Stem Cells Sustain Tumor Progression in Non-Serous Ovarian Cancers. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6096.	1.8	2

#	ARTICLE	IF	CITATIONS
19449	Transcriptional signatures in histologic structures within glioblastoma tumors may predict personalized drug sensitivity and survival. <i>Neuro-Oncology Advances</i> , 2020, 2, vdaa093.	0.4	5
19450	Transcriptomic signatures across human tissues identify functional rare genetic variation. <i>Science</i> , 2020, 369, .	6.0	89
19451	Cancer-Testis Gene Expression in Hepatocellular Carcinoma: Identification of Prognostic Markers and Potential Targets for Immunotherapy. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303382094427.	0.8	4
19452	Bioinformatics Analysis of Key Genes and circRNA-miRNA-mRNA Regulatory Network in Gastric Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-16.	0.9	25
19453	Identification of Biomarkers to Construct a Competing Endogenous RNA Network and Establishment of a Genomic-Clinicopathologic Nomogram to Predict Survival for Children with Rhabdoid Tumors of the Kidney. <i>BioMed Research International</i> , 2020, 2020, 1-27.	0.9	1
19454	Single-molecule real-time sequencing of the full-length transcriptome of loquat under low-temperature stress. <i>PLoS ONE</i> , 2020, 15, e0238942.	1.1	6
19455	Finding semantic patterns in omics data using concept rule learning with an ontology-based refinement operator. <i>BioData Mining</i> , 2020, 13, 13.	2.2	1
19456	Innate immune response in neuronopathic forms of Gaucher disease confers resistance against viral-induced encephalitis. <i>Acta Neuropathologica Communications</i> , 2020, 8, 144.	2.4	8
19457	Identification of Hidradenitis Suppurativa-Related mRNA Expression Patterns Through Analysis of Gene Expression Omnibus. <i>Dose-Response</i> , 2020, 18, 155932582094264.	0.7	3
19458	Piperlongumine inhibits head and neck squamous cell carcinoma proliferation by docking to Akt. <i>Phytotherapy Research</i> , 2020, 34, 3345-3358.	2.8	8
19459	Large-scale tethered function assays identify factors that regulate mRNA stability and translation. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 989-1000.	3.6	51
19460	Discovery of small molecules that normalize the transcriptome and enhance cysteine cathepsin activity in progranulin-deficient microglia. <i>Scientific Reports</i> , 2020, 10, 13688.	1.6	13
19461	Deregulated High Affinity Copper Transport Alters Iron Homeostasis in Arabidopsis. <i>Frontiers in Plant Science</i> , 2020, 11, 1106.	1.7	14
19462	Weighted single-step genomic best linear unbiased prediction integrating variants selected from sequencing data by association and bioinformatics analyses. <i>Genetics Selection Evolution</i> , 2020, 52, 48.	1.2	11
19463	Paired Box 9 (PAX9), the RNA polymerase II transcription factor, regulates human ribosome biogenesis and craniofacial development. <i>PLoS Genetics</i> , 2020, 16, e1008967.	1.5	9
19464	Integrated Framework of the Immune-Defense Transcriptional Signatures in the Arabidopsis Shoot Apical Meristem. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5745.	1.8	0
19465	CRISPR interference of nucleotide biosynthesis improves production of a single-domain antibody in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2020, 117, 3835-3848.	1.7	13
19466	Characterization of a Protease Hyper-Productive Mutant of <i>Bacillus pumilus</i> by Comparative Genomic and Transcriptomic Analysis. <i>Current Microbiology</i> , 2020, 77, 3612-3622.	1.0	4

#	ARTICLE	IF	CITATIONS
19467	An Overview of Utilizing Knowledge Bases in Neural Networks for Question Answering. <i>Information Systems Frontiers</i> , 2020, 22, 1095-1111.	4.1	10
19468	A cosmopolitan fungal pathogen of dicots adopts an endophytic lifestyle on cereal crops and protects them from major fungal diseases. <i>ISME Journal</i> , 2020, 14, 3120-3135.	4.4	57
19469	HIF-1 α and HIF-2 α differently regulate tumour development and inflammation of clear cell renal cell carcinoma in mice. <i>Nature Communications</i> , 2020, 11, 4111.	5.8	141
19470	The chromosome-level draft genome of <i>Dalbergia odorifera</i> . <i>GigaScience</i> , 2020, 9, .	3.3	21
19471	Network Pharmacology-Based Strategy for Predicting Active Ingredients and Potential Targets of Gegen Qinlian Decoction for Rotavirus Enteritis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-12.	0.5	6
19472	Construction and Investigation of MicroRNA-mRNA Regulatory Network of Gastric Cancer with <i>Helicobacter pylori</i> Infection. <i>Biochemistry Research International</i> , 2020, 2020, 1-10.	1.5	2
19473	Risuteganib Protects against Hydroquinone-induced Injury in Human RPE Cells. , 2020, 61, 35.		11
19474	The current landscape of coronavirus-host protein-protein interactions. <i>Journal of Translational Medicine</i> , 2020, 18, 319.	1.8	66
19475	Pregnancy-associated changes in cervical noncoding RNA. <i>Epigenomics</i> , 2020, 12, 1013-1025.	1.0	3
19476	Computational Identification and Characterization of New microRNAs in Human Platelets Stored in a Blood Bank. <i>Biomolecules</i> , 2020, 10, 1173.	1.8	4
19477	STAT3 and GR Cooperate to Drive Gene Expression and Growth of Basal-Like Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2020, 80, 4355-4370.	0.4	17
19478	The Integrated Analyses of Driver Genes Identify Key Biomarkers in Thyroid Cancer. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303382094044.	0.8	4
19479	Analyzing the lncRNA, miRNA, and mRNA-associated ceRNA networks to reveal potential prognostic biomarkers for glioblastoma multiforme. <i>Cancer Cell International</i> , 2020, 20, 393.	1.8	19
19480	Associations between dietary patterns and gene expression pattern in peripheral blood mononuclear cells: A cross-sectional study. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2020, 30, 2111-2122.	1.1	7
19481	Extreme Phenotype Approach Suggests Taste Transduction Pathway for Carotid Plaque in a Multi-Ethnic Cohort. <i>Stroke</i> , 2020, 51, 2761-2769.	1.0	4
19482	Metalloproteins and apolipoprotein C: candidate plasma biomarkers of T2DM screened by comparative proteomics and lipidomics in ZDF rats. <i>Nutrition and Metabolism</i> , 2020, 17, 66.	1.3	6
19483	Word embeddings for biomedical natural language processing: A survey. <i>Language and Linguistics Compass</i> , 2020, 14, e12402.	1.3	10
19484	Analysis of readability and structural accuracy in SNOMED CT. <i>BMC Medical Informatics and Decision Making</i> , 2020, 20, 284.	1.5	2

#	ARTICLE	IF	CITATIONS
19485	Outlier concepts auditing methodology for a large family of biomedical ontologies. BMC Medical Informatics and Decision Making, 2020, 20, 296.	1.5	1
19486	Missing lateral relationships in top-level concepts of an ontology. BMC Medical Informatics and Decision Making, 2020, 20, 305.	1.5	2
19487	Towards semantic interoperability: finding and repairing hidden contradictions in biomedical ontologies. BMC Medical Informatics and Decision Making, 2020, 20, 311.	1.5	10
19488	CD8+ T Cell Co-Expressed Genes Correlate With Clinical Phenotype and Microenvironments of Urothelial Cancer. Frontiers in Oncology, 2020, 10, 553399.	1.3	26
19489	Genetic Determinants of Gating Functions: Do We Get Closer to Understanding Schizophrenia Etiopathogenesis?. Frontiers in Psychiatry, 2020, 11, 550225.	1.3	5
19490	The identification of co-expressed gene modules in Streptococcus pneumonia from colonization to infection to predict novel potential virulence genes. BMC Microbiology, 2020, 20, 376.	1.3	0
19491	Functional in vivo and in vitro effects of 20q11.21 genetic aberrations on hPSC differentiation. Scientific Reports, 2020, 10, 18582.	1.6	17
19492	Loss of PHF6 leads to aberrant development of human neuron-like cells. Scientific Reports, 2020, 10, 19030.	1.6	3
19493	Integrative genomic meta-analysis reveals novel molecular insights into cystic fibrosis and $\hat{F}508$ -CFTR rescue. Scientific Reports, 2020, 10, 20553.	1.6	7
19494	Machine learning approaches reveal genomic regions associated with sugarcane brown rust resistance. Scientific Reports, 2020, 10, 20057.	1.6	19
19495	Functional characterisation of the transcriptome from leaf tissue of the fluoroacetate-producing plant, Dichapetalum cymosum, in response to mechanical wounding. Scientific Reports, 2020, 10, 20539.	1.6	7
19496	Neural Network and Random Forest Models in Protein Function Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1772-1781.	1.9	11
19497	Clustering of Cancer Attributed Networks via Integration of Graph Embedding and Matrix Factorization. IEEE Access, 2020, 8, 197463-197472.	2.6	3
19498	Towards the Understanding of the Human Genome: A Holistic Conceptual Modeling Approach. IEEE Access, 2020, 8, 197111-197123.	2.6	12
19499	Identification of Hub Genes of Mesio Temporal Lobe Epilepsy and Prognostic Biomarkers of Brain Low-grade Gliomas Based on Bioinformatics Analysis. Cell Transplantation, 2020, 29, 096368972097872.	1.2	4
19500	Distinct genomic profiles of gestational choriocarcinoma, a unique cancer of pregnant tissues. Experimental and Molecular Medicine, 2020, 52, 2046-2054.	3.2	12
19501	Identification of Key Modules and Hub Genes Involved in Esophageal Squamous Cell Carcinoma Tumorigenesis Using WCGNA. Cancer Control, 2020, 27, 107327482097881.	0.7	15
19502	ideal: an R/Bioconductor package for interactive differential expression analysis. BMC Bioinformatics, 2020, 21, 565.	1.2	23

#	ARTICLE	IF	CITATIONS
19503	Machine Learning Models to Predict Primary Sites of Metastatic Cervical Carcinoma From Unknown Primary. <i>Frontiers in Genetics</i> , 2020, 11, 614823.	1.1	1
19504	Comprehensive Profiling of Gene Expression in the Cerebral Cortex and Striatum of BTBRTF/ArtRbrc Mice Compared to C57BL/6J Mice. <i>Frontiers in Cellular Neuroscience</i> , 2020, 14, 595607.	1.8	8
19505	Screening and Identification of Prognostic Tumor-Infiltrating Immune Cells and Genes of Endometrioid Endometrial Adenocarcinoma: Based on The Cancer Genome Atlas Database and Bioinformatics. <i>Frontiers in Oncology</i> , 2020, 10, 554214.	1.3	9
19506	First identification of dopamine receptors in pikeperch, <i>Sander lucioperca</i> , during the pre-ovulatory period. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 36, 100747.	0.4	0
19507	Micronutrient supplementation affects transcriptional and epigenetic regulation of lipid metabolism in a dose-dependent manner. <i>Epigenetics</i> , 2021, 16, 1217-1234.	1.3	25
19508	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
19509	Genome Sequence of <i>Klebsiella pneumoniae</i> YBQ, a Clinical Strain Isolated from the Sputum of a Patient with Severe Pneumonia. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
19510	Role of COL3A1 and POSTN on Pathologic Stages of Esophageal Cancer. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303382097748.	0.8	13
19511	miR-140-5p in Small Extracellular Vesicles From Human Papilla Cells Stimulates Hair Growth by Promoting Proliferation of Outer Root Sheath and Hair Matrix Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 593638.	1.8	18
19512	Episodic Decrease in Temperature Increases <i>mcy</i> Gene Transcription and Cellular Microcystin in Continuous Cultures of <i>Microcystis aeruginosa</i> PCC 7806. <i>Frontiers in Microbiology</i> , 2020, 11, 601864.	1.5	23
19513	GAS2L1 Is a Potential Biomarker of Circulating Tumor Cells in Pancreatic Cancer. <i>Cancers</i> , 2020, 12, 3774.	1.7	9
19514	First Draft Genome Assembly of the Malaysian Stingless Bee, <i>Heterotrigona itama</i> (Apidae, Meliponinae). <i>Data</i> , 2020, 5, 112.	1.2	0
19515	A bioinformatics analysis on the potential role of ACE2 in cardiac impairment of patients with coronavirus disease 2019. <i>Annals of Translational Medicine</i> , 2020, 8, 1403-1403.	0.7	1
19516	A Novel Family of <i>Acinetobacter</i> Mega-Plasmids Are Disseminating Multi-Drug Resistance Across the Globe While Acquiring Location-Specific Accessory Genes. <i>Frontiers in Microbiology</i> , 2020, 11, 605952.	1.5	18
19517	Platelet microparticles load a repertory of miRNAs programmed to drive osteogenic phenotype. <i>Journal of Biomedical Materials Research - Part A</i> , 2021, 109, 1502-1511.	2.1	6
19518	Identifying Important Nodes in Bio-Molecular Networks. , 2020, , 315-396.		0
19519	Creation of bladder assembloids mimicking tissue regeneration and cancer. <i>Nature</i> , 2020, 588, 664-669.	13.7	133
19520	Characterization of the TyrR Regulon in the Rhizobacterium <i>Enterobacter ludwigii</i> UW5 Reveals Overlap with the CpxR Envelope Stress Response. <i>Journal of Bacteriology</i> , 2020, 203, .	1.0	2

#	ARTICLE	IF	CITATIONS
19521	Tumors Widely Express Hundreds of Embryonic Germline Genes. <i>Cancers</i> , 2020, 12, 3812.	1.7	12
19522	Selective Sweeps Lead to Evolutionary Success in an Amazonian Hyperdominant Palm. <i>Frontiers in Genetics</i> , 2020, 11, 596662.	1.1	4
19523	Analysis of Crucial Genes and Pathways Associated with Spared Nerve Injury-Induced Neuropathic Pain. <i>Neural Plasticity</i> , 2020, 2020, 1-12.	1.0	0
19524	Digital gene expression profiling analysis of A549 cells cultured with PM10 in moxa smoke. <i>Journal of Traditional Chinese Medical Sciences</i> , 2020, 7, 404-412.	0.1	0
19525	Proteomic analysis reveals dexamethasone rescues matrix breakdown but not anabolic dysregulation in a cartilage injury model. <i>Osteoarthritis and Cartilage Open</i> , 2020, 2, 100099.	0.9	9
19526	A Lightweight Approach to the Multi-perspective Modeling of Processes and Objects. <i>Procedia Computer Science</i> , 2020, 176, 1053-1062.	1.2	2
19527	Immunogenetic and tolerance strategies against a novel parasitoid of wild field crickets. <i>Ecology and Evolution</i> , 2020, 10, 13312-13326.	0.8	0
19528	Modeling and Analysis of Bio-molecular Networks. , 2020, , .		6
19529	NLRP3 inflammasome deficiency attenuates metabolic disturbances involving alterations in the gut microbial profile in mice exposed to high fat diet. <i>Scientific Reports</i> , 2020, 10, 21006.	1.6	21
19530	Olfactomedin 4 mediation of prostate stem/progenitor-like cell proliferation and differentiation via MYC. <i>Scientific Reports</i> , 2020, 10, 21924.	1.6	7
19531	Transcriptomic Profiling of Human Pluripotent Stem Cell-derived Retinal Pigment Epithelium over Time. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 223-242.	3.0	25
19532	A chromosome-scale reference genome of <i>Lobularia maritima</i> , an ornamental plant with high stress tolerance. <i>Horticulture Research</i> , 2020, 7, 197.	2.9	6
19533	Trans- and cis-acting effects of Firre on epigenetic features of the inactive X chromosome. <i>Nature Communications</i> , 2020, 11, 6053.	5.8	33
19534	Nuclear numbers in syncytial muscle fibers promote size but limit the development of larger myonuclear domains. <i>Nature Communications</i> , 2020, 11, 6287.	5.8	57
19535	Improving existing analysis pipeline to identify and analyze cancer driver genes using multi-omics data. <i>Scientific Reports</i> , 2020, 10, 20521.	1.6	10
19536	An Integrated Bioinformatic Analysis of the S100 Gene Family for the Prognosis of Colorectal Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-15.	0.9	10
19537	Identification of an RNA binding protein-related gene signature in hepatocellular carcinoma patients. <i>Molecular Medicine</i> , 2020, 26, 125.	1.9	9
19538	Comparative transcriptome analysis of three gonadal development stages reveals potential genes involved in gametogenesis of the fluted giant clam (<i>Tridacna squamosa</i>). <i>BMC Genomics</i> , 2020, 21, 872.	1.2	12

#	ARTICLE	IF	CITATIONS
19539	GCNG: graph convolutional networks for inferring gene interaction from spatial transcriptomics data. <i>Genome Biology</i> , 2020, 21, 300.	3.8	83
19540	Identification of key factors associated with early- and late-onset ovarian serous cystadenocarcinoma. <i>Future Oncology</i> , 2020, 16, 2821-2833.	1.1	2
19541	Integrated Physiological and Transcriptomic Analyses Reveal a Regulatory Network of Anthocyanin Metabolism Contributing to the Ornamental Value in a Novel Hybrid Cultivar of <i>Camellia japonica</i> . <i>Plants</i> , 2020, 9, 1724.	1.6	8
19542	Gene set inference from single-cell sequencing data using a hybrid of matrix factorization and variational autoencoders. <i>Nature Machine Intelligence</i> , 2020, 2, 800-809.	8.3	5
19543	Expression patterns and prognostic values of the cyclin-dependent kinase 1 and cyclin A2 gene cluster in pancreatic adenocarcinoma. <i>Journal of International Medical Research</i> , 2020, 48, 030006052093011.	0.4	4
19544	Genetic insights into the evolution of genera with the eastern Asia-eastern North America floristic disjunction: a transcriptomics analysis. <i>American Journal of Botany</i> , 2020, 107, 1736-1748.	0.8	6
19545	Systematic Data Analysis and Diagnostic Machine Learning Reveal Differences between Compounds with Single- and Multitarget Activity. <i>Molecular Pharmaceutics</i> , 2020, 17, 4652-4666.	2.3	14
19546	Systematic elucidation of neuron-astrocyte interaction in models of amyotrophic lateral sclerosis using multi-modal integrated bioinformatics workflow. <i>Nature Communications</i> , 2020, 11, 5579.	5.8	28
19547	Transcriptomic profiling of feline teeth highlights the role of matrix metalloproteinase 9 (MMP9) in tooth resorption. <i>Scientific Reports</i> , 2020, 10, 18958.	1.6	8
19548	Functional Contexts of Adipose and Gluteal Muscle Tissue Gene Co-expression Networks in the Domestic Horse. <i>Integrative and Comparative Biology</i> , 2023, 63, 238-249.	0.9	1
19549	smORFunction: a tool for predicting functions of small open reading frames and microproteins. <i>BMC Bioinformatics</i> , 2020, 21, 455.	1.2	12
19550	A Framework for Enhancing Big Data Integration in Biological Domain Using Distributed Processing. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 7092.	1.3	2
19551	TMEA: A Thermodynamically Motivated Framework for Functional Characterization of Biological Responses to System Acclimation. <i>Entropy</i> , 2020, 22, 1030.	1.1	5
19552	Hybrid and Environmental Effects on Gene Expression in Poplar Clones in Pure and Mixed with Black Locust Stands. <i>Forests</i> , 2020, 11, 1075.	0.9	3
19553	The Role of Salmonella Genomic Island 4 in Metal Tolerance of Salmonella enterica Serovar I 4,[5],12:i:-Pork Outbreak Isolate USDA15WA-1. <i>Genes</i> , 2020, 11, 1291.	1.0	14
19554	Integrated Analysis of the Transcriptome and Metabolome of <i>Cecropia obtusifolia</i> : A Plant with High Chlorogenic Acid Content Traditionally Used to Treat Diabetes Mellitus. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7572.	1.8	10
19555	Comparative Proteomic Profiling of Marine and Freshwater Synechocystis Strains Using Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Marine Science and Engineering</i> , 2020, 8, 790.	1.2	4
19556	Circulating miR-1246 in the Progression of Chronic Obstructive Pulmonary Disease (COPD) in Patients from the BODE Cohort. <i>International Journal of COPD</i> , 2020, Volume 15, 2727-2737.	0.9	7

#	ARTICLE	IF	CITATIONS
19557	OsteoBLAST: Computational Routine of Global Molecular Analysis Applied to Biomaterials Development. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 565901.	2.0	4
19558	The Cyclically Seasonal <i>Drosophila subobscura</i> Inversion O7 Originated From Fragile Genomic Sites and Relocated Immunity and Metabolic Genes. <i>Frontiers in Genetics</i> , 2020, 11, 565836.	1.1	4
19559	Transcriptome Analyses of β -Thalassemia α^2 (A&G) Mutation Using Isogenic Cell Models Generated by CRISPR/Cas9 and Asymmetric Single-Stranded Oligodeoxynucleotides (assODNs). <i>Frontiers in Genetics</i> , 2020, 11, 577053.	1.1	5
19560	Genomic and transcriptomic landscapes and evolutionary dynamics of molluscan glycoside hydrolase families with implications for algae-feeding biology. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2744-2756.	1.9	2
19561	The Transcriptome of <i>Cunninghamia lanceolata</i> male/female cone reveal the association between MIKC MADS-box genes and reproductive organs development. <i>BMC Plant Biology</i> , 2020, 20, 508.	1.6	15
19562	Wildlife Population Genomics: Applications and Approaches. <i>Population Genomics</i> , 2020, , 3-59.	0.2	7
19563	A proteomics approach to further highlight the altered inflammatory condition in Rett syndrome. <i>Archives of Biochemistry and Biophysics</i> , 2020, 696, 108660.	1.4	5
19564	Mitochondrial-Y chromosome epistasis in <i>Drosophila melanogaster</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200469.	1.2	4
19565	Full function of exon junction complex factor, Rbm8a, is critical for interneuron development. <i>Translational Psychiatry</i> , 2020, 10, 379.	2.4	16
19566	A realism-based approach to an ontological representation of symbiotic interactions. <i>BMC Medical Informatics and Decision Making</i> , 2020, 20, 258.	1.5	1
19567	Investigation of hub genes involved in diabetic nephropathy using biological informatics methods. <i>Annals of Translational Medicine</i> , 2020, 8, 1087-1087.	0.7	10
19568	<p></p>Desmoglein 3 and Keratin 14 for Distinguishing Between Lung Adenocarcinoma and Lung Squamous Cell Carcinoma</p>. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 11111-11124.	1.0	10
19569	The Differential Composition of Whey Proteomes in Hu Sheep Colostrum and Milk during Different Lactation Periods. <i>Animals</i> , 2020, 10, 1784.	1.0	3
19570	The draft genome of the blood pheasant (<i>Ithaginis cruentus</i>): Phylogeny and high altitude adaptation. <i>Ecology and Evolution</i> , 2020, 10, 11440-11452.	0.8	1
19571	G protein-coupled receptor Gpr115 (Adgrf4) is required for enamel mineralization mediated by ameloblasts. <i>Journal of Biological Chemistry</i> , 2020, 295, 15328-15341.	1.6	12
19572	Deep learning approach for predicting functional Z-DNA regions using omics data. <i>Scientific Reports</i> , 2020, 10, 19134.	1.6	29
19573	Bioinformatics-based identification of miRNA-, lncRNA-, and mRNA-associated ceRNA networks and potential biomarkers for preeclampsia. <i>Medicine (United States)</i> , 2020, 99, e22985.	0.4	12
19574	String of PURLs " frugal migration and maintenance of persistent identifiers. <i>Data Science</i> , 2020, 3, 3-13.	0.7	3

#	ARTICLE	IF	CITATIONS
19576	Epitope prediction and identification- adaptive T cell responses in humans. <i>Seminars in Immunology</i> , 2020, 50, 101418.	2.7	36
19577	The Model of <i>PPARδ</i> -Downregulated Signaling in Psoriasis. <i>PPAR Research</i> , 2020, 2020, 1-11.	1.1	9
19578	Container-aided integrative QTL and RNA-seq analysis of Collaborative Cross mice supports distinct sex-oriented molecular modes of response in obesity. <i>BMC Genomics</i> , 2020, 21, 761.	1.2	7
19579	Bioinformatic Analysis Identifies Potential Key Genes in the Pathogenesis of Melanoma. <i>Frontiers in Oncology</i> , 2020, 10, 581985.	1.3	9
19580	Entropic Ranks: A Methodology for Enhanced, Threshold-Free, Information-Rich Data Partition and Interpretation. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 7077.	1.3	0
19581	Network Building with the Cytoscape BioGateway App Explained in Five Use Cases. <i>Current Protocols in Bioinformatics</i> , 2020, 72, e106.	25.8	4
19582	Finding reusable structured resources for the integration of environmental research data. <i>Environmental Modelling and Software</i> , 2020, 133, 104813.	1.9	4
19583	Ubiquitinome Profiling Reveals the Landscape of Ubiquitination Regulation in Rice Young Panicles. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 305-320.	3.0	18
19584	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
19585	ABC Efflux Transporters and the Circuitry of miRNAs: Kinetics of Expression in Cancer Drug Resistance. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2985.	1.8	12
19586	Negative binomial additive model for RNA-Seq data analysis. <i>BMC Bioinformatics</i> , 2020, 21, 171.	1.2	18
19587	Partners of wild type Grb7 and a mutant lacking its calmodulin-binding domain. <i>Archives of Biochemistry and Biophysics</i> , 2020, 687, 108386.	1.4	3
19588	Comprehensive Immunoprofiling of Pediatric Zika Reveals Key Role for Monocytes in the Acute Phase and No Effect of Prior Dengue Virus Infection. <i>Cell Reports</i> , 2020, 31, 107569.	2.9	43
19589	BrainMap Elucidates the Macromolecular Connectivity Landscape of Mammalian Brain. <i>Cell Systems</i> , 2020, 10, 333-350.e14.	2.9	48
19590	Genome-wide association study of MRI markers of cerebral small vessel disease in 42,310 participants. <i>Nature Communications</i> , 2020, 11, 2175.	5.8	93
19591	Human adipose-derived mesenchymal stem cell-conditioned medium ameliorates polyneuropathy and foot ulceration in diabetic BKS db/db mice. <i>Stem Cell Research and Therapy</i> , 2020, 11, 168.	2.4	60
19592	A single-cell transcriptomic landscape of primate arterial aging. <i>Nature Communications</i> , 2020, 11, 2202.	5.8	95
19593	Shared genetic architecture and casual relationship between leptin levels and type 2 diabetes: large-scale cross-trait meta-analysis and Mendelian randomization analysis. <i>BMJ Open Diabetes Research and Care</i> , 2020, 8, e001140.	1.2	13

#	ARTICLE	IF	CITATIONS
19594	OntoPowSys: A power system ontology for cross domain interactions in an eco industrial park. Energy and AI, 2020, 1, 100008.	5.8	31
19595	A high-quality reference genome of wild Cannabis sativa. Horticulture Research, 2020, 7, 73.	2.9	73
19596	Activation of a Subset of Evolutionarily Young Transposable Elements and Innate Immunity Are Linked to Clinical Responses to 5-Azacytidine. Cancer Research, 2020, 80, 2441-2450.	0.4	33
19597	Identification of key genes, pathways and potential therapeutic agents for IgA nephropathy using an integrated bioinformatics analysis. JRAAS - Journal of the Renin-Angiotensin-Aldosterone System, 2020, 21, 147032032091963.	1.0	7
19598	Identification of differentially expressed genes in actinic keratosis samples treated with ingenol mebutate gel. PLoS ONE, 2020, 15, e0232146.	1.1	4
19599	WormCat: An Online Tool for Annotation and Visualization of <i>Caenorhabditis elegans</i> Genome-Scale Data. Genetics, 2020, 214, 279-294.	1.2	125
19600	Label-Free Quantitative Proteomic Profiling Identifies Potential Active Components to Exert Pharmacological Effects in the Fruit of <i>Alpinia oxyphylla</i> by Mass Spectrometry. Journal of Plant Biology, 2020, 63, 297-310.	0.9	2
19601	Integrated multi-omics approaches to improve classification of chronic kidney disease. Nature Reviews Nephrology, 2020, 16, 657-668.	4.1	99
19602	Gene Ontology Curation of Neuroinflammation Biology Improves the Interpretation of Alzheimer's Disease Gene Expression Data. Journal of Alzheimer's Disease, 2020, 75, 1417-1435.	1.2	18
19603	Identification of Prognostic miRNA Signature and Lymph Node Metastasis-Related Key Genes in Cervical Cancer. Frontiers in Pharmacology, 2020, 11, 544.	1.6	29
19604	Comprehensive analysis reveals a six-gene signature and associated drugs in mimic inguinal hernia model. Hernia: the Journal of Hernias and Abdominal Wall Surgery, 2020, 24, 1211-1219.	0.9	3
19605	Large-scale network analysis captures biological features of bacterial plasmids. Nature Communications, 2020, 11, 2452.	5.8	78
19606	Quantifying genetic effects on disease mediated by assayed gene expression levels. Nature Genetics, 2020, 52, 626-633.	9.4	191
19607	Identification of Pannexin 2 as a Novel Marker Correlating with Ferroptosis and Malignant Phenotypes of Prostate Cancer Cells. OncoTargets and Therapy, 2020, Volume 13, 4411-4421.	1.0	24
19608	The long-term environmental risks from the aging of organochlorine pesticide lindane. Environment International, 2020, 141, 105778.	4.8	16
19609	The genome of Mekong tiger perch (<i>Datnioides undecimradiatus</i>) provides insights into the phylogenetic position of Lobotiformes and biological conservation. Scientific Reports, 2020, 10, 8164.	1.6	3
19610	Molecular Signatures of Placentation and Secretion Uncovered in <i>Poeciliopsis</i> Maternal Follicles. Molecular Biology and Evolution, 2020, 37, 2679-2690.	3.5	21
19611	Tropomyosin 1 genetically constrains in vitro hematopoiesis. BMC Biology, 2020, 18, 52.	1.7	8

#	ARTICLE	IF	CITATIONS
19612	Identification of significant genes with prognostic influence in clear cell renal cell carcinoma via bioinformatics analysis. <i>Translational Andrology and Urology</i> , 2020, 9, 452-461.	0.6	7
19613	Polygenic risk scores indicates genetic overlap between peripheral pain syndromes and chronic postsurgical pain. <i>Neurogenetics</i> , 2020, 21, 205-215.	0.7	10
19614	Comparative transcriptome analysis reveals the genes and pathways involved in terminal drought tolerance in pearl millet. <i>Plant Molecular Biology</i> , 2020, 103, 639-652.	2.0	34
19615	Connecting MetaProteomeAnalyzer and PeptideShaker to Unipept for Seamless End-to-End Metaproteomics Data Analysis. <i>Journal of Proteome Research</i> , 2020, 19, 3562-3566.	1.8	11
19616	Myocardial micro-biopsy procedure for molecular characterization with increased precision and reduced trauma. <i>Scientific Reports</i> , 2020, 10, 8029.	1.6	11
19617	A potential prognostic model based on miRNA expression profile in The Cancer Genome Atlas for bladder cancer patients. <i>Journal of Biological Research</i> , 2020, 27, 6.	2.2	3
19618	<p>Arsenic Disulfide Promoted Hypomethylation by Increasing DNA Methyltransferases Expression in Myelodysplastic Syndrome</p>. <i>Drug Design, Development and Therapy</i> , 2020, Volume 14, 1641-1650.	2.0	6
19619	Characterization of Stem-like Circulating Tumor Cells in Pancreatic Cancer. <i>Diagnostics</i> , 2020, 10, 305.	1.3	7
19620	Ageing Neuro-Behavior Ontology. <i>Applied Ontology</i> , 2020, 15, 219-239.	1.0	4
19621	A Single-Cell Transcriptional Roadmap of the Mouse and Human Lymph Node Lymphatic Vasculature. <i>Frontiers in Cardiovascular Medicine</i> , 2020, 7, 52.	1.1	97
19622	SZDB2.0: an updated comprehensive resource for schizophrenia research. <i>Human Genetics</i> , 2020, 139, 1285-1297.	1.8	35
19623	Transcriptome profiling reveals insertional mutagenesis suppressed the expression of candidate pathogenicity genes in honeybee fungal pathogen, <i>Ascosphaera apis</i> . <i>Scientific Reports</i> , 2020, 10, 7532.	1.6	4
19624	Proteomic Profiling of Small Extracellular Vesicles Secreted by Human Pancreatic Cancer Cells Implicated in Cellular Transformation. <i>Scientific Reports</i> , 2020, 10, 7713.	1.6	19
19625	Tomato Atypical Receptor Kinase1 Is Involved in the Regulation of Preinvasion Defense. <i>Plant Physiology</i> , 2020, 183, 1306-1318.	2.3	13
19626	Functional genomics analysis of human colon organoids identifies key transcription factors. <i>Physiological Genomics</i> , 2020, 52, 234-244.	1.0	16
19627	Third-Generation Sequencing Reveals LncRNA-Regulated HSP Genes in the <i>Populus x canadensis</i> Moench Heat Stress Response. <i>Frontiers in Genetics</i> , 2020, 11, 249.	1.1	10
19628	Shared Regulatory Pathways Reveal Novel Genetic Correlations Between Grip Strength and Neuromuscular Disorders. <i>Frontiers in Genetics</i> , 2020, 11, 393.	1.1	5
19629	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

#	ARTICLE	IF	CITATIONS
19630	CK14 Expression Identifies a Basal/Squamous-Like Type of Papillary Non-Muscle-Invasive Upper Tract Urothelial Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 623.	1.3	9
19631	Comparative Transcriptome Analysis Combining SMRT- and Illumina-Based RNA-Seq Identifies Potential Candidate Genes Involved in Betalain Biosynthesis in Pitaya Fruit. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3288.	1.8	23
19632	Bioinformatics Resources for Plant Abiotic Stress Responses: State of the Art and Opportunities in the Fast Evolving -Omics Era. <i>Plants</i> , 2020, 9, 591.	1.6	25
19633	Darkâ€rearing uncovers novel gene expression patterns in an obligate caveâ€dwelling fish. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2020, 334, 518-529.	0.6	6
19634	The Genetic Basis of Morphological Diversity in Domesticated Goldfish. <i>Current Biology</i> , 2020, 30, 2260-2274.e6.	1.8	52
19635	CoCoCoNet: conserved and comparative co-expression across a diverse set of species. <i>Nucleic Acids Research</i> , 2020, 48, W566-W571.	6.5	35
19636	Suppression of Endothelial AGO1 Promotes Adipose Tissue Browning and Improves Metabolic Dysfunction. <i>Circulation</i> , 2020, 142, 365-379.	1.6	44
19637	A multiple genomic data fused SF2 prediction model, signature identification, and gene regulatory network inference for personalized radiotherapy. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303382090911.	0.8	8
19638	Identifying <i>Candida albicans</i> Gene Networks Involved in Pathogenicity. <i>Frontiers in Genetics</i> , 2020, 11, 375.	1.1	5
19639	Chromosome-scale assembly of the <i>Kandelia obovata</i> genome. <i>Horticulture Research</i> , 2020, 7, 75.	2.9	38
19640	The Change of Interleukin-6 Level-Related Genes and Pathways Induced by Exercise in Sedentary Individuals. <i>Journal of Interferon and Cytokine Research</i> , 2020, 40, 236-244.	0.5	4
19641	New insights into the potential mechanisms of spermatogenic failure in patients with idiopathic azoospermia. <i>Molecular Human Reproduction</i> , 2020, 26, 469-484.	1.3	5
19642	Lower oxygen consumption and Complex I activity in mitochondria isolated from skeletal muscle of fetal sheep with intrauterine growth restriction. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2020, 319, E67-E80.	1.8	29
19643	Transcriptional Sequencing and Gene Expression Analysis of Various Genes in Fruit Development of Three Different Black Pepper (<i>Piper nigrum</i>) Varieties. <i>International Journal of Genomics</i> , 2020, 1-18.	0.8	8
19644	STAT5 is required for lipid breakdown and beta-adrenergic responsiveness of brown adipose tissue. <i>Molecular Metabolism</i> , 2020, 40, 101026.	3.0	15
19645	Functional insights from the GC-poor genomes of two aphid parasitoids, <i>Aphidius ervi</i> and <i>Lysiphlebus fabarum</i> . <i>BMC Genomics</i> , 2020, 21, 376.	1.2	19
19646	Genetic Underpinnings of Host Manipulation by <i>Ophiocordyceps</i> as Revealed by Comparative Transcriptomics. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2275-2296.	0.8	33
19647	Zebrafish brain RNA sequencing reveals that cell adhesion molecules are critical in brain aging. <i>Neurobiology of Aging</i> , 2020, 94, 164-175.	1.5	7

#	ARTICLE	IF	CITATIONS
19648	Unraveling tumor-immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. <i>Nature Genetics</i> , 2020, 52, 582-593.	9.4	136
19649	Systematic mapping of genetic interactions for de novo fatty acid synthesis identifies C12orf49 as a regulator of lipid metabolism. <i>Nature Metabolism</i> , 2020, 2, 499-513.	5.1	72
19650	Database Mining of Genes of Prognostic Value for the Prostate Adenocarcinoma Microenvironment Using the Cancer Gene Atlas. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	16
19651	APEX2S: A two-layer machine learning model for discovery of host-pathogen protein-protein interactions on cloud-based multiomics data. <i>Concurrency Computation Practice and Experience</i> , 2020, 32, e5846.	1.4	3
19652	Elevated maternal androgen is associated with dysfunctional placenta and lipid disorder in newborns of mothers with polycystic ovary syndrome. <i>Fertility and Sterility</i> , 2020, 113, 1275-1285.e2.	0.5	18
19653	Quantitative proteomics analysis of tomato growth inhibition by ammonium nitrogen. <i>Plant Physiology and Biochemistry</i> , 2020, 154, 129-141.	2.8	15
19654	A strategy for large-scale comparison of evolutionary- and reaction-based classifications of enzyme function. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	5
19655	Trade-offs, Pleiotropy, and Shared Molecular Pathways: A Unified View of Constraints on Adaptation. <i>Integrative and Comparative Biology</i> , 2020, 60, 332-347.	0.9	30
19656	Medical Text Annotation Tool based on IBM Watson Platform. , 2020, , .		4
19657	Comprehensive RNA-Seq profiling of the lung transcriptome of Argali hybrid sheep in response to experimental <i>Mycoplasma ovipneumoniae</i> infection. <i>Research in Veterinary Science</i> , 2020, 132, 57-68.	0.9	3
19658	Unipept CLI 2.0: adding support for visualizations and functional annotations. <i>Bioinformatics</i> , 2020, 36, 4220-4221.	1.8	9
19659	A bibliometric analysis and visualization of medical data mining research. <i>Medicine (United States)</i> , 2020, 99, e20338.	0.4	27
19660	Integrated Analysis of mRNA and microRNA Elucidates the Regulation of Glycyrrhizic Acid Biosynthesis in <i>Glycyrrhiza uralensis</i> Fisch. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3101.	1.8	10
19661	Transcriptomics in Toxicogenomics, Part II: Preprocessing and Differential Expression Analysis for High Quality Data. <i>Nanomaterials</i> , 2020, 10, 903.	1.9	31
19662	CARD9-Associated Dectin-1 and Dectin-2 Are Required for Protective Immunity of a Multivalent Vaccine against <i>Coccidioides posadasii</i> Infection. <i>Journal of Immunology</i> , 2020, 204, 3296-3306.	0.4	19
19663	Draft genome of the famous ornamental plant <i>Paeonia suffruticosa</i> . <i>Ecology and Evolution</i> , 2020, 10, 4518-4530.	0.8	34
19664	Regulation by fungal endophyte of <i>Rhodiola crenulata</i> from enzyme genes to metabolites based on combination of transcriptome and metabolome. <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 4483-4494.	1.7	3
19665	Therapeutic potential of lipids obtained from β -irradiated PBMCs in dendritic cell-mediated skin inflammation. <i>EBioMedicine</i> , 2020, 55, 102774.	2.7	18

#	ARTICLE	IF	CITATIONS
19666	Alternative splicing of LSD1+8a in neuroendocrine prostate cancer is mediated by SRRM4. <i>Neoplasia</i> , 2020, 22, 253-262.	2.3	19
19667	Absolute yeast mitochondrial proteome quantification reveals trade-off between biosynthesis and energy generation during diauxic shift. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7524-7535.	3.3	92
19668	Ewastools: Infinium Human Methylation BeadChip pipeline for population epigenetics integrated into Galaxy. <i>GigaScience</i> , 2020, 9, .	3.3	12
19669	Integrated small RNA and mRNA expression profiles reveal miRNAs and their target genes in response to <i>Aspergillus flavus</i> growth in peanut seeds. <i>BMC Plant Biology</i> , 2020, 20, 215.	1.6	17
19670	De novo transcriptome sequence of <i>Senna tora</i> provides insights into anthraquinone biosynthesis. <i>PLoS ONE</i> , 2020, 15, e0225564.	1.1	14
19671	Comparative analysis of tissue-specific transcriptomic responses to nitrogen stress in spinach (<i>Spinacia oleracea</i>). <i>PLoS ONE</i> , 2020, 15, e0232011.	1.1	15
19672	A Novel Computational Approach for Identifying Essential Proteins From Multiplex Biological Networks. <i>Frontiers in Genetics</i> , 2020, 11, 343.	1.1	6
19673	Expression Quantitative Trait Loci (eQTL) Mapping in Korean Patients With Crohn's Disease and Identification of Potential Causal Genes Through Integration With Disease Associations. <i>Frontiers in Genetics</i> , 2020, 11, 486.	1.1	15
19674	Bioinformatics Analysis Identifying Key Biomarkers in Bladder Cancer. <i>Data</i> , 2020, 5, 38.	1.2	3
19675	Potential Molecular Mechanism and Biomarker Investigation for Spinal Cord Injury Based on Bioinformatics Analysis. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 1345-1353.	1.1	3
19676	Lactic acid biosynthesis pathways and important genes of <i>Lactobacillus panis</i> L7 isolated from the Chinese liquor brewing microbiome. <i>Food Bioscience</i> , 2020, 36, 100627.	2.0	18
19677	Compensatory combination of romidepsin with gemcitabine and cisplatin to effectively and safely control urothelial carcinoma. <i>British Journal of Cancer</i> , 2020, 123, 226-239.	2.9	10
19678	A MicroRNA Signature Identifies Pancreatic Ductal Adenocarcinoma Patients at Risk for Lymph Node Metastases. <i>Gastroenterology</i> , 2020, 159, 562-574.	0.6	33
19679	Revenant: a database of resurrected proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	6
19680	Comprehensive analysis of mutations of renal cell carcinoma in an autosomal dominant polycystic kidney disease patient. <i>Medicine (United States)</i> , 2020, 99, e20071.	0.4	3
19681	Genome Sequencing and Analysis of the Fungal Symbiont of <i>Sirex noctilio</i> , <i>Amylostereum areolatum</i> : Revealing the Biology of Fungus-Insect Mutualism. <i>MSphere</i> , 2020, 5, .	1.3	11
19682	Global Transcriptional Profiling Reveals Novel Autocrine Functions of Interleukin 6 in Human Vascular Endothelial Cells. <i>Mediators of Inflammation</i> , 2020, 2020, 1-12.	1.4	8
19683	A Network Pharmacology-Based Study on the Anti-Lung Cancer Effect of <i>Dipsaci Radix</i> . <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-9.	0.5	7

#	ARTICLE	IF	CITATIONS
19684	The complete genome sequence of the archaeal isolate Halomicrobium sp. ZPS1 reveals the nitrogen metabolism characteristics under hypersaline conditions. <i>Annals of Microbiology</i> , 2020, 70, .	1.1	4
19685	Phenotypic Associations Among Cell Cycle Genes in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2345-2351.	0.8	3
19686	The Influence of Methylating Mutations on Acute Myeloid Leukemia: Preliminary Analysis on 56 Patients. <i>Diagnostics</i> , 2020, 10, 263.	1.3	3
19687	In Vitro Evaluation of the Effects of Commercial Prebiotic GOS and FOS Products on Human Colonic Caco-2 Cells. <i>Nutrients</i> , 2020, 12, 1281.	1.7	13
19688	Protein biomarkers associated with frozen Japanese puffer fish (<i>Takifugu rubripes</i>) quality traits. <i>Food Chemistry</i> , 2020, 327, 127002.	4.2	22
19689	Identification of co-expression modules and potential biomarkers of breast cancer by WGCNA. <i>Gene</i> , 2020, 750, 144757.	1.0	36
19690	Zonation of Ribosomal DNA Transcription Defines a Stem Cell Hierarchy in Colorectal Cancer. <i>Cell Stem Cell</i> , 2020, 26, 845-861.e12.	5.2	59
19691	SPEED2: inferring upstream pathway activity from differential gene expression. <i>Nucleic Acids Research</i> , 2020, 48, W307-W312.	6.5	28
19692	Complete Genome of <i>Vibrio neocaledonicus</i> CGJ02-2, An active Compounds Producing Bacterium Isolated from South China Sea. <i>Current Microbiology</i> , 2020, 77, 2665-2673.	1.0	3
19693	Draft genome sequence of the termite, <i>Coptotermes formosanus</i> : Genetic insights into the pyruvate dehydrogenase complex of the termite. <i>Journal of Asia-Pacific Entomology</i> , 2020, 23, 666-674.	0.4	24
19694	Evaluation of Poly(I:C) and combination of CpG ODN plus Montanide ISA adjuvants to enhance the efficacy of outer membrane vesicles as an acellular vaccine against <i>Brucella melitensis</i> infection in mice. <i>International Immunopharmacology</i> , 2020, 84, 106573.	1.7	10
19695	DNF: A differential network flow method to identify rewiring drivers for gene regulatory networks. <i>Neurocomputing</i> , 2020, 410, 202-210.	3.5	9
19696	SemanticGO: a tool for gene functional similarity analysis in <i>Arabidopsis thaliana</i> and rice. <i>Plant Science</i> , 2020, 297, 110527.	1.7	3
19697	Inferring Virus-Host relationship between HPV and its host <i>Homo sapiens</i> using protein interaction network. <i>Scientific Reports</i> , 2020, 10, 8719.	1.6	15
19698	Replicated umbilical cord blood DNA methylation loci associated with gestational age at birth. <i>Epigenetics</i> , 2020, 15, 1243-1258.	1.3	10
19699	ASAP 2020 update: an open, scalable and interactive web-based portal for (single-cell) omics analyses. <i>Nucleic Acids Research</i> , 2020, 48, W403-W414.	6.5	17
19700	Family-specific analysis of variant pathogenicity prediction tools. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa014.	1.5	8
19701	Minor DNA methylation changes are observed in spermatozoa prepared using different protocols. <i>Andrology</i> , 2020, 8, 1312-1323.	1.9	5

#	ARTICLE	IF	CITATIONS
19702	Whole blood transcriptional variations between responders and nonresponders in asthma patients receiving omalizumab. <i>Clinical and Experimental Allergy</i> , 2020, 50, 1017-1034.	1.4	10
19703	Deep belief network-Based Matrix Factorization Model for MicroRNA-Disease Associations Prediction. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432091970.	0.6	16
19704	Multipathway synergy promotes testicular transition from growth to spermatogenesis in early-puberty goats. <i>BMC Genomics</i> , 2020, 21, 372.	1.2	19
19705	Epigenetic deregulation of lamina-associated domains in Hutchinson-Gilford progeria syndrome. <i>Genome Medicine</i> , 2020, 12, 46.	3.6	40
19706	Identification of Hub Genes in Type 2 Diabetes Mellitus Using Bioinformatics Analysis. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2020, Volume 13, 1793-1801.	1.1	14
19707	Pituispheres Contain Genetic Variants Characteristic to Pituitary Adenoma Tumor Tissue. <i>Frontiers in Endocrinology</i> , 2020, 11, 313.	1.5	5
19708	Molecular signature of eutopic endometrium in endometriosis based on the multi-omics integrative synthesis. <i>Journal of Assisted Reproduction and Genetics</i> , 2020, 37, 1593-1611.	1.2	14
19709	Research Techniques Made Simple: Whole-Transcriptome Sequencing by RNA-Seq for Diagnosis of Monogenic Disorders. <i>Journal of Investigative Dermatology</i> , 2020, 140, 1117-1126.e1.	0.3	46
19710	Draft Genome Assembly of <i>Floccularia luteovirens</i> , an Edible and Symbiotic Mushroom on Qinghai-Tibet Plateau. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1167-1173.	0.8	5
19711	Construction of an Immunogenomic Risk Score for Prognostication in Colon Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 499.	1.1	9
19712	Itch attenuates CD4 cell proliferation in mice by limiting WBP2 protein stability. <i>European Journal of Immunology</i> , 2020, 50, 1468-1483.	1.6	5
19714	Next generation sequencing and microbiome's taxonomical characterization of frozen soil of north western Himalayas of Jammu and Kashmir, India. <i>Electronic Journal of Biotechnology</i> , 2020, 45, 30-37.	1.2	4
19715	Uterine disorders affecting female fertility: what are the molecular functions altered in endometrium?. <i>Fertility and Sterility</i> , 2020, 113, 1261-1274.	0.5	26
19716	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
19717	Transcript expression-aware annotation improves rare variant interpretation. <i>Nature</i> , 2020, 581, 452-458.	13.7	142
19718	Remethylation of <i>Dnmt3a</i> hematopoietic cells is associated with partial correction of gene dysregulation and reduced myeloid skewing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3123-3134.	3.3	27
19719	A memory of eS25 loss drives resistance phenotypes. <i>Nucleic Acids Research</i> , 2020, 48, 7279-7297.	6.5	4
19720	ARTDeco: automatic readthrough transcription detection. <i>BMC Bioinformatics</i> , 2020, 21, 214.	1.2	21

#	ARTICLE	IF	CITATIONS
19721	De novo identification of toxicants that cause irreparable damage to parasitic nematode intestinal cells. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007942.	1.3	10
19722	Proteomics of intracellular freezing survival. <i>PLoS ONE</i> , 2020, 15, e0233048.	1.1	1
19723	Integrative meta-analysis for the identification of hub genes in chemoresistant colorectal cancer. <i>Biomarkers in Medicine</i> , 2020, 14, 525-537.	0.6	3
19724	Comparative Analyses of Five Complete Chloroplast Genomes from the Genus <i>Pterocarpus</i> (Fabaceae). <i>International Journal of Molecular Sciences</i> , 2020, 21, 3758.	1.8	52
19725	Transcriptional dynamics of Zn-accumulation in developing kernels of maize reveals important Zn-uptake mechanisms. <i>Genomics</i> , 2020, 112, 3435-3447.	1.3	9
19726	Screening and functional identification of lncRNAs in antler mesenchymal and cartilage tissues using high-throughput sequencing. <i>Scientific Reports</i> , 2020, 10, 9492.	1.6	5
19727	PINOT: an intuitive resource for integrating protein-protein interactions. <i>Cell Communication and Signaling</i> , 2020, 18, 92.	2.7	21
19728	Novel Insights Into Triple-Negative Breast Cancer Prognosis by Comprehensive Characterization of Aberrant Alternative Splicing. <i>Frontiers in Genetics</i> , 2020, 11, 534.	1.1	10
19729	Characterization of <i>Hemerocallis citrina</i> Transcriptome and Development of EST-SSR Markers for Evaluation of Genetic Diversity and Population Structure of <i>Hemerocallis</i> Collection. <i>Frontiers in Plant Science</i> , 2020, 11, 686.	1.7	14
19730	Whole-genome sequencing provides insights into the genetic diversity and domestication of bitter melon (<i>Momordica charantia</i> L.). <i>Horticulture Research</i> , 2020, 7, 85.	2.9	41
19731	mTADA is a framework for identifying risk genes from de novo mutations in multiple traits. <i>Nature Communications</i> , 2020, 11, 2929.	5.8	10
19732	A Novel Feature Selection Method for Uncertain Features: An Application to the Prediction of Pro-/Anti-Longevity Genes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2230-2238.	1.9	10
19733	Exploring the potential microRNA sponge interactions of breast cancer based on some known interactions. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050007.	0.3	1
19734	Cell Type- and Stimulation-Dependent Transcriptional Programs Regulated by Atg16L1 and Its Crohn's Disease Risk Variant T300A. <i>Journal of Immunology</i> , 2020, 205, 414-424.	0.4	7
19735	Transcriptome profiling of <i>Plumbago auriculata</i> Lam. in response to cold stress. <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	1.0	5
19736	Comparative transcriptome analysis of normal and CD44-deleted mouse brain under chronic infection with <i>Toxoplasma gondii</i> . <i>Acta Tropica</i> , 2020, 210, 105589.	0.9	2
19737	Single-cell ATAC sequencing analysis: From data preprocessing to hypothesis generation. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1429-1439.	1.9	91
19738	Transcriptional regulation of strigolactone signalling in <i>Arabidopsis</i> . <i>Nature</i> , 2020, 583, 277-281.	13.7	188

#	ARTICLE	IF	CITATIONS
19739	CIDO, a community-based ontology for coronavirus disease knowledge and data integration, sharing, and analysis. <i>Scientific Data</i> , 2020, 7, 181.	2.4	70
19740	Identification of a Robust Five-Gene Risk Model in Prostate Cancer: A Robust Likelihood-Based Survival Analysis. <i>International Journal of Genomics</i> , 2020, 2020, 1-23.	0.8	15
19741	Novel Insights Into the Effects of Interleukin 6 Antagonism in Non-ST-Segment Elevation Myocardial Infarction Employing the SOMAScan Proteomics Platform. <i>Journal of the American Heart Association</i> , 2020, 9, e015628.	1.6	16
19742	Identification of a competing endogenous RNA network associated with prognosis of pancreatic adenocarcinoma. <i>Cancer Cell International</i> , 2020, 20, 231.	1.8	27
19743	Platelet-derived growth factor receptor β^2 activation and regulation in murine myelofibrosis. <i>Haematologica</i> , 2020, 105, 2083-2094.	1.7	20
19744	PDGFD induces ibrutinib resistance of diffuse large B-cell lymphoma through activation of EGFR. <i>Molecular Medicine Reports</i> , 2020, 21, 2209-2219.	1.1	7
19745	Machine learning analyses of methylation profiles uncovers tissue-specific gene expression patterns in wheat. <i>Plant Genome</i> , 2020, 13, e20027.	1.6	13
19746	The Number of Transcription Factors at an Enhancer Determines Switch-like Gene Expression. <i>Cell Reports</i> , 2020, 31, 107724.	2.9	25
19747	What kind of novelties can machine learning possibly generate? The case of genomics. <i>Studies in History and Philosophy of Science Part A</i> , 2020, 83, 86-96.	0.6	5
19748	Functional genomics of parental care of insects. <i>Hormones and Behavior</i> , 2020, 122, 104756.	1.0	5
19749	Gaussian embedding for large-scale gene set analysis. <i>Nature Machine Intelligence</i> , 2020, 2, 387-395.	8.3	7
19750	The MYCL and MXD1 transcription factors regulate the fitness of murine dendritic cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4885-4893.	3.3	16
19751	A selective inference approach for false discovery rate control using multiomics covariates yields insights into disease risk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15028-15035.	3.3	16
19752	RNA-GPS Predicts SARS-CoV-2 RNA Residency to Host Mitochondria and Nucleolus. <i>Cell Systems</i> , 2020, 11, 102-108.e3.	2.9	119
19753	Identification of new protein biomarkers associated with the boar fertility using iTRAQ-based quantitative proteomic analysis. <i>International Journal of Biological Macromolecules</i> , 2020, 162, 50-59.	3.6	17
19754	Transcriptomic analysis of interferon- β -regulated genes in endometrial explants and their possible role in regulating maternal endometrial immunity during the implantation period in pigs, a true epitheliochorial placentation species. <i>Theriogenology</i> , 2020, 155, 114-124.	0.9	18
19755	Manumycin polyketides act as molecular glues between UBR7 and P53. <i>Nature Chemical Biology</i> , 2020, 16, 1189-1198.	3.9	79
19756	RNA Sequencing for Gene Expression Profiles in Peripheral Blood Mononuclear Cells with Ankylosing Spondylitis RNA. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	3

#	ARTICLE	IF	CITATIONS
19757	Identification, characterization and functional differentiation of the NAC gene family and its roles in response to cold stress in ginseng, <i>Panax ginseng</i> A.C. Meyer. <i>PLoS ONE</i> , 2020, 15, e0234423.	1.1	16
19758	Ustiloxin A is Produced Early in Experimental <i>Ustilagoidea virens</i> Infection and Affects Transcription in Rice. <i>Current Microbiology</i> , 2020, 77, 2766-2774.	1.0	13
19759	Genomic analysis of <i>Brevundimonas mediterranea</i> D151-2-6 isolated from hadal sediment of the Pacific Ocean. <i>Marine Genomics</i> , 2020, 54, 100787.	0.4	1
19760	TBtools: An Integrative Toolkit Developed for Interactive Analyses of Big Biological Data. <i>Molecular Plant</i> , 2020, 13, 1194-1202.	3.9	7,081
19761	The role of rare compound heterozygous events in autism spectrum disorder. <i>Translational Psychiatry</i> , 2020, 10, 204.	2.4	2
19762	Bioinformatics analysis of different candidate genes involved in hepatocellular carcinoma induced by HepG2 cells or tumor cells of patients. <i>Journal of International Medical Research</i> , 2020, 48, 030006052093211.	0.4	1
19763	Transcriptomic microRNA Profiling of Dendritic Cells in Response to Gut Microbiota-Secreted Vesicles. <i>Cells</i> , 2020, 9, 1534.	1.8	15
19764	A Knowledge-Based Machine Learning Approach to Gene Prioritisation in Amyotrophic Lateral Sclerosis. <i>Genes</i> , 2020, 11, 668.	1.0	16
19765	Optimization for Sequencing and Analysis of Degraded FFPE-RNA Samples. <i>Journal of Visualized Experiments</i> , 2020, , .	0.2	6
19766	Identification and characterization of male reproduction-related genes in pig (<i>Sus scrofa</i>) using transcriptome analysis. <i>BMC Genomics</i> , 2020, 21, 381.	1.2	7
19767	Urban air particulate matter induces mitochondrial dysfunction in human olfactory mucosal cells. <i>Particle and Fibre Toxicology</i> , 2020, 17, 18.	2.8	36
19768	Proteomic signatures of metronidazole-resistant <i>Trichomonas vaginalis</i> reveal novel proteins associated with drug resistance. <i>Parasites and Vectors</i> , 2020, 13, 274.	1.0	12
19769	Cadmium, Smoking, and Human Blood DNA Methylation Profiles in Adults from the Strong Heart Study. <i>Environmental Health Perspectives</i> , 2020, 128, 67005.	2.8	57
19770	Multiplexed relative and absolute quantitative immunopeptidomics reveals MHC I repertoire alterations induced by CDK4/6 inhibition. <i>Nature Communications</i> , 2020, 11, 2760.	5.8	61
19771	Similar Disease Prediction With Heterogeneous Disease Information Networks. <i>IEEE Transactions on Nanobioscience</i> , 2020, 19, 571-578.	2.2	12
19772	Assembly and Function of a Bioengineered Human Liver for Transplantation Generated Solely from Induced Pluripotent Stem Cells. <i>Cell Reports</i> , 2020, 31, 107711.	2.9	81
19773	Genome sequence and comparative analysis of reindeer (<i>Rangifer tarandus</i>) in northern Eurasia. <i>Scientific Reports</i> , 2020, 10, 8980.	1.6	30
19774	Network Pharmacology-Based Identification of the Mechanisms of Shen-Qi Compound Formula in Treating Diabetes Mellitus. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-15.	0.5	6

#	ARTICLE	IF	CITATIONS
19775	A tissue level atlas of the healthy human virome. <i>BMC Biology</i> , 2020, 18, 55.	1.7	50
19776	Developmental alterations in the transcriptome of three distinct rodent models of schizophrenia. <i>PLoS ONE</i> , 2020, 15, e0232200.	1.1	9
19777	Defining Critical Genes During Spherule Remodeling and Endospore Development in the Fungal Pathogen, <i>Coccidioides posadasii</i> . <i>Frontiers in Genetics</i> , 2020, 11, 483.	1.1	23
19778	GC-AG Introns Features in Long Non-coding and Protein-Coding Genes Suggest Their Role in Gene Expression Regulation. <i>Frontiers in Genetics</i> , 2020, 11, 488.	1.1	17
19779	Transcriptome Analysis Reveals Potential Genes Involved in Digestive Enzyme Function in a Mudflat Crab <i>Helice tientsinensis</i> . <i>Thalassas</i> , 2020, 36, 573-583.	0.1	1
19780	Excessive Homeostatic Gain in Spinal Motoneurons in a Mouse Model of Amyotrophic Lateral Sclerosis. <i>Scientific Reports</i> , 2020, 10, 9049.	1.6	10
19781	The Intruding <i>Wolbachia</i> Strain from the Moth Fails to Establish Itself in the Fruit Fly Due to Immune and Exclusion Reactions. <i>Current Microbiology</i> , 2020, 77, 2441-2448.	1.0	0
19782	Draft genome sequence data of <i>Microbacterium</i> sp. strain Be9 isolated from uranium-mill tailings porewaters. <i>Data in Brief</i> , 2020, 31, 105732.	0.5	4
19783	The core SWI/SNF catalytic subunit Brg1 regulates nephron progenitor cell proliferation and differentiation. <i>Developmental Biology</i> , 2020, 464, 176-187.	0.9	14
19784	Interpreting molecular similarity between patients as a determinant of disease comorbidity relationships. <i>Nature Communications</i> , 2020, 11, 2854.	5.8	20
19785	ThETA: transcriptome-driven efficacy estimates for gene-based TARGET discovery. <i>Bioinformatics</i> , 2020, 36, 4214-4216.	1.8	5
19786	A New TTZ Feature Extracting Algorithm to Decipher Tobacco Related Mutation Signature Genes for the Personalized Lung Adenocarcinoma Treatment. <i>IEEE Access</i> , 2020, 8, 89031-89040.	2.6	7
19787	Transcriptomic plasticity of mesophotic corals among natural populations and transplants of <i>Montastraea cavernosa</i> in the Gulf of Mexico and Belize. <i>Molecular Ecology</i> , 2020, 29, 2399-2415.	2.0	6
19788	Population-Specific Genetic and Expression Differentiation in Europeans. <i>Genome Biology and Evolution</i> , 2020, 12, 358-369.	1.1	4
19789	Genome-wide CRISPR synthetic lethality screen identifies a role for the ADP-ribosyltransferase PARP14 in DNA replication dynamics controlled by ATR. <i>Nucleic Acids Research</i> , 2020, 48, 7252-7264.	6.5	15
19790	CT Irradiation-induced Changes of Gene Expression within Peripheral Blood Cells. <i>Health Physics</i> , 2020, 119, 44-51.	0.3	9
19791	Dynamic rewiring of the human interactome by interferon signaling. <i>Genome Biology</i> , 2020, 21, 140.	3.8	25
19792	Transcriptome Analysis of Maternal Gene Transcripts in Unfertilized Eggs of <i>Misgurnus anguillicaudatus</i> and Identification of Immune-Related Maternal Genes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3872.	1.8	4

#	ARTICLE	IF	CITATIONS
19793	Single molecule real-time sequencing and RNA-seq unravel the role of long non-coding and circular RNA in the regulatory network during Nile tilapia (<i>Oreochromis niloticus</i>) infection with <i>Streptococcus agalactiae</i> . <i>Fish and Shellfish Immunology</i> , 2020, 104, 640-653.	1.6	13
19794	MIPPIE: the mouse integrated protein-protein interaction reference. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	14
19795	DNA methylation-based diagnostic and prognostic biomarkers of nasopharyngeal carcinoma patients. <i>Medicine (United States)</i> , 2020, 99, e20682.	0.4	11
19796	Impact of Regulatory T Cells on Type 2 Alveolar Epithelial Cell Transcriptomes during Resolution of Acute Lung Injury and Contributions of IFN- β . <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2020, 63, 464-477.	1.4	22
19797	RNA Binding Proteins as Drivers and Therapeutic Target Candidates in Pancreatic Ductal Adenocarcinoma. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4190.	1.8	16
19798	Long-term Changes in the Central Amygdala Proteome in Rats with a History of Chronic Cocaine Self-administration. <i>Neuroscience</i> , 2020, 443, 93-109.	1.1	6
19799	Cold priming uncouples light- and cold-regulation of gene expression in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2020, 20, 281.	1.6	15
19800	Multiple Forms of Multifunctional Proteins in Health and Disease. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 451.	1.8	25
19801	Relative Abundance of SARS-CoV-2 Entry Genes in the Enterocytes of the Lower Gastrointestinal Tract. <i>Genes</i> , 2020, 11, 645.	1.0	57
19802	Transcriptome, Spliceosome and Editome Expression Patterns of the Porcine Endometrium in Response to a Single Subclinical Dose of Salmonella Enteritidis Lipopolysaccharide. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4217.	1.8	9
19803	Increased density of endosymbiotic <i>Buchnera</i> related to pesticide resistance in yellow morph of melon aphid. <i>Journal of Pest Science</i> , 2020, 93, 1281-1294.	1.9	17
19804	Data of de novo assembly and annotation of transcriptome from <i>Aspidistra fenghuangensis</i> (Asparagaceae: Nolinoideae). <i>Data in Brief</i> , 2020, 31, 105738.	0.5	1
19805	The evolution of sex-biased gene expression in the <i>Drosophila</i> brain. <i>Genome Research</i> , 2020, 30, 874-884.	2.4	24
19806	Upregulation of cGMP-dependent Protein Kinase (PRKG1) in the Development of Adolescent Idiopathic Scoliosis. <i>Orthopaedic Surgery</i> , 2020, 12, 1261-1269.	0.7	5
19807	Genome-Scale Metabolic Model Driven Design of a Defined Medium for <i>Campylobacter jejuni</i> M1cam. <i>Frontiers in Microbiology</i> , 2020, 11, 1072.	1.5	8
19808	Unraveling the Genomic-Epigenomic Interaction Landscape in Triple Negative and Non-Triple Negative Breast Cancer. <i>Cancers</i> , 2020, 12, 1559.	1.7	13
19809	Gene Expression Profiling in Fibromyalgia Indicates an Autoimmune Origin of the Disease and Opens New Avenues for Targeted Therapy. <i>Journal of Clinical Medicine</i> , 2020, 9, 1814.	1.0	20
19810	An integrated analysis of testis miRNA and mRNA transcriptome reveals important functional miRNA-targets in reproduction traits of roosters. <i>Reproductive Biology</i> , 2020, 20, 433-440.	0.9	6

#	ARTICLE	IF	CITATIONS
19811	System-wide analyses of the fission yeast poly(A) RNA interactome reveal insights into organization and function of RNA-protein complexes. <i>Genome Research</i> , 2020, 30, 1012-1026.	2.4	6
19812	Transcriptome-Wide Regulation of Key Developmental Pathways in the Mouse Neural Tube by Prenatal Alcohol Exposure. <i>Alcoholism: Clinical and Experimental Research</i> , 2020, 44, 1540-1550.	1.4	6
19813	Optimized low pH formulation of niacinamide enhances induction of autophagy marker ATG5 gene expression and protein levels in human epidermal keratinocytes. <i>Journal of the European Academy of Dermatology and Venereology</i> , 2020, 34, 3-11.	1.3	7
19814	Multilayered VBC score predicts sgRNAs that efficiently generate loss-of-function alleles. <i>Nature Methods</i> , 2020, 17, 708-716.	9.0	77
19815	Transcriptome-wide organization of subcellular microenvironments revealed by ATLAS-Seq. <i>Nucleic Acids Research</i> , 2020, 48, 5859-5872.	6.5	9
19816	Phen2Gene: rapid phenotype-driven gene prioritization for rare diseases. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa032.	1.5	45
19817	Comparative Target Analysis of Chlorinated Biphenyl Antimicrobials Highlights MenG as a Molecular Target of Triclocarban. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	7
19818	Gene regulation could be attributed to TCF3 and other key transcription factors in the muscle of pubertal heifers. <i>Veterinary Medicine and Science</i> , 2020, 6, 695-710.	0.6	6
19819	Expression of SARS-CoV-2 receptor ACE2 and coincident host response signature varies by asthma inflammatory phenotype. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 315-324.e7.	1.5	90
19820	A survey on automatically constructed universal knowledge bases. <i>Journal of Information Science</i> , 2021, 47, 551-574.	2.0	2
19821	An improved clear cell renal cell carcinoma stage prediction model based on gene sets. <i>BMC Bioinformatics</i> , 2020, 21, 232.	1.2	17
19822	Bioinformatics Analysis of Prognostic miRNA Signature and Potential Critical Genes in Colon Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 478.	1.1	30
19823	A Photo-clickable ATP-Mimetic Reveals Nucleotide Interactors in the Membrane Proteome. <i>Cell Chemical Biology</i> , 2020, 27, 1073-1083.e12.	2.5	13
19824	Polymorphisms in miRNA binding sites involved in metabolic diseases in mice and humans. <i>Scientific Reports</i> , 2020, 10, 7202.	1.6	8
19825	Phenotypic Responses to and Genetic Architecture of Sterility Following Exposure to Sub-Lethal Temperature During Development. <i>Frontiers in Genetics</i> , 2020, 11, 573.	1.1	31
19826	Differentially Regulated Transcription Factors and ABC Transporters in a Mitochondrial Dynamics Mutant Can Alter Azole Susceptibility of <i>Aspergillus fumigatus</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1017.	1.5	12
19827	Ontology-Based Graphs of Research Communities: A Tool for Understanding Threat Reduction Networks. <i>Frontiers in Research Metrics and Analytics</i> , 2020, 5, 3.	0.9	4
19828	Transcriptome Profiling of <i>Toxoplasma gondii</i> -Infected Human Cerebrovascular Endothelial Cell Response to Treatment with Monensin. <i>Microorganisms</i> , 2020, 8, 842.	1.6	12

#	ARTICLE	IF	CITATIONS
19829	Identification of miRNA-mRNA-TFs Regulatory Network and Crucial Pathways Involved in Tetralogy of Fallot. <i>Frontiers in Genetics</i> , 2020, 11, 552.	1.1	17
19830	Comparative profiles of DNA methylation and differential gene expression in osteocytic areas from aged and young mice. <i>Cell Biochemistry and Function</i> , 2020, 38, 721-732.	1.4	5
19831	Anti-infective nitazoxanide disrupts transcription of ribosome biogenesis-related genes in yeast. <i>Genes and Genomics</i> , 2020, 42, 915-926.	0.5	6
19832	Establishment and validation of an immune-based prognostic score model in glioblastoma. <i>International Immunopharmacology</i> , 2020, 85, 106636.	1.7	34
19833	An age-independent gene signature for monitoring acute rejection in kidney transplantation. <i>Theranostics</i> , 2020, 10, 6977-6986.	4.6	9
19834	The Long Noncoding RNA NEAT1 Promotes Sarcoma Metastasis by Regulating RNA Splicing Pathways. <i>Molecular Cancer Research</i> , 2020, 18, 1534-1544.	1.5	16
19835	Sequencing of RNA in single cells reveals a distinct transcriptome signature of hematopoiesis in GATA2 deficiency. <i>Blood Advances</i> , 2020, 4, 2702-2716.	2.5	23
19836	Identification of lncRNAs Involved in PCV2 Infection of PK-15 Cells. <i>Pathogens</i> , 2020, 9, 479.	1.2	6
19837	Gill transcriptomes reveal expression changes of genes related with immune and ion transport under salinity stress in silvery pomfret (<i>Pampus argenteus</i>). <i>Fish Physiology and Biochemistry</i> , 2020, 46, 1255-1277.	0.9	19
19838	Sjögren syndrome/scleroderma autoantigen 1 is a direct Tankyrase binding partner in cancer cells. <i>Communications Biology</i> , 2020, 3, 123.	2.0	5
19839	GSA: an alternative to enrichment analysis for annotating gene sets. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa017.	1.5	18
19840	Whole transcriptome expression profiles in placenta samples from women with gestational diabetes mellitus. <i>Journal of Diabetes Investigation</i> , 2020, 11, 1307-1317.	1.1	42
19841	Isolation of <i>Bacillus subtilis</i> strain SEM-2 from silkworm excrement and characterisation of its antagonistic effect against <i>Fusarium</i> spp.. <i>Canadian Journal of Microbiology</i> , 2020, 66, 401-412.	0.8	10
19842	Systematical Analysis of the Cancer Genome Atlas Database Reveals EMCN/MUC15 Combination as a Prognostic Signature for Gastric Cancer. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 19.	1.6	16
19843	Test of Arabidopsis Space Transcriptome: A Discovery Environment to Explore Multiple Plant Biology Spaceflight Experiments. <i>Frontiers in Plant Science</i> , 2020, 11, 147.	1.7	23
19844	C-terminal binding proteins 1 and 2 in traumatic brain injury-induced inflammation and their inhibition as an approach for anti-inflammatory treatment. <i>International Journal of Biological Sciences</i> , 2020, 16, 1107-1120.	2.6	11
19845	Identification of key genes and pathways of diagnosis and prognosis in cervical cancer by bioinformatics analysis. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1200.	0.6	29
19846	FKBP10 Regulates Protein Translation to Sustain Lung Cancer Growth. <i>Cell Reports</i> , 2020, 30, 3851-3863.e6.	2.9	19

#	ARTICLE	IF	CITATIONS
19847	A Dual Workflow to Improve the Proteomic Coverage in Plasma Using Data-Independent Acquisition-MS. <i>Journal of Proteome Research</i> , 2020, 19, 2828-2837.	1.8	11
19848	Integrated miRNA/mRNA Counter-Expression Analysis Highlights Oxidative Stress-Related Genes CCR7 and FOXO1 as Blood Markers of Coronary Arterial Disease. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1943.	1.8	13
19849	Systems toxicology assessment revealed the impact of graphene-based materials on cell cycle regulators. <i>Journal of Biomedical Materials Research - Part A</i> , 2020, 108, 1520-1533.	2.1	8
19850	OPAL: An extensible framework for ontology-based program analysis. <i>Software - Practice and Experience</i> , 2020, 50, 1425-1462.	2.5	6
19851	Transcriptomic and metabolomic analyses of <i>Lycium ruthenicum</i> and <i>Lycium barbarum</i> fruits during ripening. <i>Scientific Reports</i> , 2020, 10, 4354.	1.6	17
19852	CuAS: a database of annotated transcripts generated by alternative splicing in cucumbers. <i>BMC Plant Biology</i> , 2020, 20, 119.	1.6	8
19853	Comprehensive Analysis of Differentially Expressed Profiles of mRNA, lncRNA, and circRNA in the Uterus of Seasonal Reproduction Sheep. <i>Genes</i> , 2020, 11, 301.	1.0	24
19854	Comprehensive Phosphoproteomic Analysis of Pepper Fruit Development Provides Insight into Plant Signaling Transduction. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1962.	1.8	11
19855	Sexual-biased gene expression of olfactory-related genes in the antennae of <i>Conogethes pinicolalis</i> (Lepidoptera: Crambidae). <i>BMC Genomics</i> , 2020, 21, 244.	1.2	12
19856	Immune-related prognosis biomarkers associated with osteosarcoma microenvironment. <i>Cancer Cell International</i> , 2020, 20, 83.	1.8	45
19857	Aralar Sequesters GABA into Hyperactive Mitochondria, Causing Social Behavior Deficits. <i>Cell</i> , 2020, 180, 1178-1197.e20.	13.5	62
19858	Brassinosteroid signaling may regulate the germination of axillary buds in ratoon rice. <i>BMC Plant Biology</i> , 2020, 20, 76.	1.6	10
19859	Pairwise Versus Multiple Global Network Alignment. <i>IEEE Access</i> , 2020, 8, 41961-41974.	2.6	7
19860	Quantitative analysis of protein crotonylation identifies its association with immunoglobulin A nephropathy. <i>Molecular Medicine Reports</i> , 2020, 21, 1242-1250.	1.1	8
19861	Characterization of genetic variation and antioxidant properties in strawberry (<i>Fragaria ananassa</i>) Tj ETQqO 0 0 rgBT /Overl 0.81	0.81	8
19862	Expression profiles of miRNAs in giant cell tumor of bone showed miR-187-5p and miR-1323 can regulate biological functions through inhibiting FRS2. <i>Cancer Medicine</i> , 2020, 9, 3163-3173.	1.3	9
19863	Bioinformatical Analysis of Gene Expression Omnibus Database Associates TAF7/CCNB1, TAF7/CCNA2, and GTF2E2/CDC20 Pathways with Glioblastoma Development and Prognosis. <i>World Neurosurgery</i> , 2020, 138, e492-e514.	0.7	22
19864	Temporal changes in the gene expression heterogeneity during brain development and aging. <i>Scientific Reports</i> , 2020, 10, 4080.	1.6	34

#	ARTICLE	IF	CITATIONS
19865	DNA methylation QTL analysis identifies new regulators of human longevity. <i>Human Molecular Genetics</i> , 2020, 29, 1154-1167.	1.4	15
19866	The recent progress and therapy in endometriosis-associated ovarian cancer. <i>Journal of the Chinese Medical Association</i> , 2020, 83, 227-232.	0.6	23
19867	Comparative proteomics analysis of Tibetan hull-less barley under osmotic stress via data-independent acquisition mass spectrometry. <i>GigaScience</i> , 2020, 9, .	3.3	20
19868	The draft genome of a new <i>Verminephrobacter eiseniae</i> strain: a nephridial symbiont of earthworms. <i>Annals of Microbiology</i> , 2020, 70, .	1.1	3
19869	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
19870	Context-dependent genetic architecture of <i>Drosophila</i> life span. <i>PLoS Biology</i> , 2020, 18, e3000645.	2.6	47
19871	Effect of VCP modulators on gene expression profiles of retinal ganglion cells in an acute injury mouse model. <i>Scientific Reports</i> , 2020, 10, 4251.	1.6	4
19872	Wnt Signaling Drives Ectopic Gene Expression and Larval Arrest in the Absence of the <i>Caenorhabditis elegans</i> DREAM Repressor Complex. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 863-874.	0.8	0
19874	Cost-sensitive hierarchical classification for imbalance classes. <i>Applied Intelligence</i> , 2020, 50, 2328-2338.	3.3	23
19875	Differential metabolic and hepatic transcriptome responses of two miniature pig breeds to high dietary cholesterol. <i>Life Sciences</i> , 2020, 250, 117514.	2.0	3
19876	Comprehensive RNA Sequencing in Adenoma-Cancer Transition Identified Predictive Biomarkers and Therapeutic Targets of Human CRC. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 20, 25-33.	2.3	29
19877	Skeletal Toxicity of Coplanar Polychlorinated Biphenyl Congener 126 in the Rat Is Aryl Hydrocarbon Receptor Dependent. <i>Toxicological Sciences</i> , 2020, 175, 113-125.	1.4	9
19878	Genome Sequence Resource for <i>Elsinoë ampelina</i> , the Causal Organism of Grapevine Anthracnose. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 576-579.	1.4	13
19879	Drp1 modulates mitochondrial stress responses to mitotic arrest. <i>Cell Death and Differentiation</i> , 2020, 27, 2620-2634.	5.0	18
19880	A roadmap for research in octoploid strawberry. <i>Horticulture Research</i> , 2020, 7, 33.	2.9	47
19881	CircRNA Expression Profiles and the Potential Role of CircZFP644 in Mice With Severe Acute Pancreatitis via Sponging miR-21-3p. <i>Frontiers in Genetics</i> , 2020, 11, 206.	1.1	20
19882	A Gene-Set Enrichment and Protein-Protein Interaction Network-Based GWAS with Regulatory SNPs Identifies Candidate Genes and Pathways Associated with Carcass Traits in Hanwoo Cattle. <i>Genes</i> , 2020, 11, 316.	1.0	39
19883	Genome-Wide Analysis and Function Prediction of Long Noncoding RNAs in Sheep Pituitary Gland Associated with Sexual Maturation. <i>Genes</i> , 2020, 11, 320.	1.0	16

#	ARTICLE	IF	CITATIONS
19884	Standard machine learning approaches outperform deep representation learning on phenotype prediction from transcriptomics data. <i>BMC Bioinformatics</i> , 2020, 21, 119.	1.2	41
19885	Linking reaction mechanisms and quantum chemistry: An ontological approach. <i>Computers and Chemical Engineering</i> , 2020, 137, 106813.	2.0	20
19886	Preoperative plasma biomarkers associated with atrial fibrillation after coronary artery bypass surgery. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2021, 162, 851-863.e3.	0.4	15
19887	Readthrough Errors Purge Deleterious Cryptic Sequences, Facilitating the Birth of Coding Sequences. <i>Molecular Biology and Evolution</i> , 2020, 37, 1761-1774.	3.5	11
19888	<i>Sergentomyia schwetzi</i> : Salivary gland transcriptome, proteome and enzymatic activities in two lineages adapted to different blood sources. <i>PLoS ONE</i> , 2020, 15, e0230537.	1.1	7
19889	A Computational Approach for Mapping Heme Biology in the Context of Hemolytic Disorders. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 74.	2.0	16
19890	Metadata Analysis of mcr-1-Bearing Plasmids Inspired by the Sequencing Evidence for Horizontal Transfer of Antibiotic Resistance Genes Between Polluted River and Wild Birds. <i>Frontiers in Microbiology</i> , 2020, 11, 352.	1.5	18
19891	Genome sequence of the fungus <i>Pycnoporus sanguineus</i> , which produces cinnabarinic acid and pH- and thermo- stable laccases. <i>Gene</i> , 2020, 742, 144586.	1.0	8
19892	Comparative transcriptome analysis digs out genes related to antifreeze between fresh and frozen-thawed rooster sperm. <i>Poultry Science</i> , 2020, 99, 2841-2851.	1.5	9
19893	Integrative differential expression and gene set enrichment analysis using summary statistics for scRNA-seq studies. <i>Nature Communications</i> , 2020, 11, 1585.	5.8	43
19894	SSIF: Subsumption-based Sub-term Inference Framework to audit Gene Ontology. <i>Bioinformatics</i> , 2020, 36, 3207-3214.	1.8	7
19895	CLING: Candidate Cancer-Related lncRNA Prioritization via Integrating Multiple Biological Networks. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 138.	2.0	1
19896	Dataset for de novo transcriptome assembly of the African bullfrog <i>Pyxicephalus adspersus</i> . <i>Data in Brief</i> , 2020, 30, 105388.	0.5	2
19897	Traditional Chinese Medicine Containing Arsenic Treated MDS Patients Effectively through Regulating Aberrant Hypomethylation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-9.	0.5	4
19898	Transcriptome Analysis of the Cytokinin Response in <i>Medicago truncatula</i> . <i>Journal of Plant Biology</i> , 2020, 63, 189-202.	0.9	2
19899	Gene correlation networks reveal the transcriptomic response to elevated nitrogen in a photosynthetic sponge. <i>Molecular Ecology</i> , 2020, 29, 1452-1462.	2.0	4
19900	Network Pharmacology-Based Strategy for Predicting Therapy Targets of Traditional Chinese Medicine Xihuang Pill on Liver Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-12.	0.5	6
19901	Systems Pharmacology-Based Strategy to Investigate Pharmacological Mechanisms of <i>Radix Puerariae</i> for Treatment of Hypertension. <i>Frontiers in Pharmacology</i> , 2020, 11, 345.	1.6	18

#	ARTICLE	IF	CITATIONS
19902	A high-quality genome provides insights into the new taxonomic status and genomic characteristics of <i>Cladopus chinensis</i> (Podostemaceae). <i>Horticulture Research</i> , 2020, 7, 46.	2.9	11
19903	EpiMOLAS: an intuitive web-based framework for genome-wide DNA methylation analysis. <i>BMC Genomics</i> , 2020, 21, 163.	1.2	0
19904	An efficient gene bigdata analysis using machine learning algorithms. <i>Multimedia Tools and Applications</i> , 2020, 79, 9847-9870.	2.6	6
19905	Functional genomics by integrated analysis of transcriptome of sweet potato (<i>Ipomoea batatas</i> (L.) Tj ETQq1 1 0.784314 rgBT /Over 0.5	0.5	0
19906	Identification of Key Genes and Pathways for Enchondromas by Bioinformatics Analysis. <i>Dose-Response</i> , 2020, 18, 155932582090753.	0.7	0
19907	Emergence of an evolutionary innovation: Gene expression differences associated with the transition between oviparity and viviparity. <i>Molecular Ecology</i> , 2020, 29, 1315-1327.	2.0	16
19908	Functional colour genes and signals of selection in colour polymorphic salamanders. <i>Molecular Ecology</i> , 2020, 29, 1284-1299.	2.0	15
19909	Identification of a Plasma MicroRNA Profile Associated With Venous Thrombosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 40, 1392-1399.	1.1	21
19910	Genes associated with inflammation may serve as biomarkers for the diagnosis of coronary artery disease and ischaemic stroke. <i>Lipids in Health and Disease</i> , 2020, 19, 37.	1.2	15
19911	Identification of molecules associated with response to abatacept in patients with rheumatoid arthritis. <i>Arthritis Research and Therapy</i> , 2020, 22, 46.	1.6	19
19912	Genome Sequence, Assembly, and Characterization of the Antagonistic Yeast <i>Candida oleophila</i> Used as a Biocontrol Agent Against Post-harvest Diseases. <i>Frontiers in Microbiology</i> , 2020, 11, 295.	1.5	26
19913	Transcriptome Analyses of <i>Diaphorina citri</i> Midgut Responses to <i>Candidatus Liberibacter Asiaticus</i> Infection. <i>Insects</i> , 2020, 11, 171.	1.0	33
19914	Knowledge representation and data sharing to unlock crop variation for nutritional food security. <i>Crop Science</i> , 2020, 60, 516-529.	0.8	7
19915	A bioinformatics approach for identification lncRNA-miRNA-protein interactions for SNHG1 and SNHG5. <i>Gene Reports</i> , 2020, 19, 100643.	0.4	0
19916	Identification of the core ontologies and signature genes of polycystic ovary syndrome (PCOS): A bioinformatics analysis. <i>Informatics in Medicine Unlocked</i> , 2020, 18, 100304.	1.9	13
19917	Acid ceramidase of macrophages traps herpes simplex virus in multivesicular bodies and protects from severe disease. <i>Nature Communications</i> , 2020, 11, 1338.	5.8	32
19918	Hierarchy and levels: analysing networks to study mechanisms in molecular biology. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190320.	1.8	10
19919	Survival in the Tropics despite isolation, inbreeding and asexual reproduction: insights from the genome of the world's southernmost poplar (<i>Populus ilicifolia</i>). <i>Plant Journal</i> , 2020, 103, 430-442.	2.8	23

#	ARTICLE	IF	CITATIONS
19920	Hepatic transcriptome of the freeze-tolerant <i>Copeia</i> 's gray treefrog, <i>Dryophytes chrysoscelis</i> : responses to cold acclimation and freezing. <i>BMC Genomics</i> , 2020, 21, 226.	1.2	17
19921	Myeloid-specific deficiency of pregnane X receptor decreases atherosclerosis in LDL receptor-deficient mice. <i>Journal of Lipid Research</i> , 2020, 61, 696-706.	2.0	18
19922	Bioinformatic Analysis Identifies Potential Key Genes in the Pathogenesis of Turner Syndrome. <i>Frontiers in Endocrinology</i> , 2020, 11, 104.	1.5	35
19923	Comparative Transcriptome-Based Mining and Expression Profiling of Transcription Factors Related to Cold Tolerance in Peanut. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1921.	1.8	29
19924	&integrated Gene Expression Profiling Analysis Reveals Probable Molecular Mechanism and Candidate Biomarker in Anti-TNF± Non-Response IBD Patients&. <i>Journal of Inflammation Research</i> , 2020, Volume 13, 81-95.	1.6	18
19925	Evaluation of Pathway Activation for a Single Sample Toward Inflammatory Bowel Disease Classification. <i>Frontiers in Genetics</i> , 2019, 10, 1401.	1.1	9
19926	Pathogenic Gene Prediction Algorithm Based on Heterogeneous Information Fusion. <i>Frontiers in Genetics</i> , 2020, 11, 5.	1.1	5
19927	An Anti-inflammatory microRNA Signature Distinguishes Group 3 Innate Lymphoid Cells From Natural Killer Cells in Human Decidua. <i>Frontiers in Immunology</i> , 2020, 11, 133.	2.2	15
19928	Comparative Insights Into the Complete Genome Sequence of Highly Metal Resistant <i>Cupriavidus metallidurans</i> Strain BS1 Isolated From a Goldâ€Copper Mine. <i>Frontiers in Microbiology</i> , 2020, 11, 47.	1.5	27
19929	Comparative Transcriptomic Response of Two <i>Pinus</i> Species to Infection with the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> . <i>Forests</i> , 2020, 11, 204.	0.9	19
19930	Sustainable engineering technologies to promote activities of beneficial microbiome. , 2020, , 231-275.		1
19931	<i>Micromonospora zhangzhouensis</i> sp. nov., a Novel Actinobacterium Isolated from Mangrove Soil, Exerts a Cytotoxic Activity in vitro. <i>Scientific Reports</i> , 2020, 10, 3889.	1.6	8
19932	Equivalent change enrichment analysis: assessing equivalent and inverse change in biological pathways between diverse experiments. <i>BMC Genomics</i> , 2020, 21, 180.	1.2	2
19933	Supervised learning is an accurate method for network-based gene classification. <i>Bioinformatics</i> , 2020, 36, 3457-3465.	1.8	28
19934	Predicted <i>Drosophila</i> Interactome Resource and web tool for functional interpretation of differentially expressed genes. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	8
19935	Whole Transcriptome Analysis of Mesenchyme Tissue in Sika Deer Antler Revealed the CeRNAs Regulatory Network Associated With Antler Development. <i>Frontiers in Genetics</i> , 2019, 10, 1403.	1.1	16
19936	CRb and PbBa8.1 Synergically Increases Resistant Genes Expression upon Infection of <i>Plasmodiophora brassicae</i> in <i>Brassica napus</i> . <i>Genes</i> , 2020, 11, 202.	1.0	15
19937	Identification of the Molecular Mechanisms of Peimine in the Treatment of Cough Using Computational Target Fishing. <i>Molecules</i> , 2020, 25, 1105.	1.7	10

#	ARTICLE	IF	CITATIONS
19938	Studying human and nonhuman primate evolutionary biology with powerful in vitro and in vivo functional genomics tools. <i>Evolutionary Anthropology</i> , 2020, 29, 143-158.	1.7	9
19939	New Aspects of VEGF, GABA, and Glutamate Signaling in the Neocortex of Human Temporal Lobe Pharmacoresistant Epilepsy Revealed by RT-qPCR Arrays. <i>Journal of Molecular Neuroscience</i> , 2020, 70, 916-929.	1.1	7
19940	Integrative transcriptomics and proteomics analysis constructs a new molecular model for ovule abortion in the female-sterile line of <i>Pinus tabuliformis</i> Carr.. <i>Plant Science</i> , 2020, 294, 110462.	1.7	8
19941	Pigment variation and transcriptional response of the pigment synthesis pathway in the S2309 triple-color ornamental kale (<i>Brassica oleracea</i> L. var. <i>acephala</i>) line. <i>Genomics</i> , 2020, 112, 2658-2665.	1.3	10
19942	Transcriptional diversity and bioenergetic shift in human breast cancer metastasis revealed by single-cell RNA sequencing. <i>Nature Cell Biology</i> , 2020, 22, 310-320.	4.6	189
19943	A pathway coordinated by DELE1 relays mitochondrial stress to the cytosol. <i>Nature</i> , 2020, 579, 433-437.	13.7	276
19944	Functionally Enigmatic Genes in Cancer: Using TCGA Data to Map the Limitations of Annotations. <i>Scientific Reports</i> , 2020, 10, 4106.	1.6	14
19945	Nuclear Respiratory Factor 1 (NRF1) Transcriptional Activity-Driven Gene Signature Association with Severity of Astrocytoma and Poor Prognosis of Glioblastoma. <i>Molecular Neurobiology</i> , 2020, 57, 3827-3845.	1.9	18
19946	De novo assembly and comparative transcriptome analysis of contrasting pearl millet (<i>Pennisetum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 63, 341-352.	0.9	9
19947	Inferring essential proteins from centrality in interconnected multilayer networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2020, 557, 124853.	1.2	5
19948	Quantitative analysis of proteins which are members of the same protein complex but cause locus heterogeneity in disease. <i>Scientific Reports</i> , 2020, 10, 10423.	1.6	3
19949	Time-resolved mRNA and miRNA expression profiling reveals crucial coregulation of molecular pathways involved in epithelial-pneumococcal interactions. <i>Immunology and Cell Biology</i> , 2020, 98, 726-742.	1.0	3
19950	Searching and inferring colorful topological motifs in vertex-colored graphs. <i>Journal of Combinatorial Optimization</i> , 2020, 40, 379-411.	0.8	0
19951	Transcriptome analysis of testis reveals the effects of developmental exposure to bisphenol a or 17 β -ethinylestradiol in medaka (<i>Oryzias latipes</i>). <i>Aquatic Toxicology</i> , 2020, 225, 105553.	1.9	11
19952	Enhancement of phenol biodegradation: Metabolic division of labor in co-culture of <i>Stenotrophomonas</i> sp. N5 and <i>Advenella</i> sp. B9. <i>Journal of Hazardous Materials</i> , 2020, 400, 123214.	6.5	40
19953	An integrated chemical environment with tools for chemical safety testing. <i>Toxicology in Vitro</i> , 2020, 67, 104916.	1.1	37
19954	NF- κ B/TWIST1 Mediates Migration and Phagocytosis of Macrophages in the Mice Model of Implant-Associated <i>Staphylococcus aureus</i> Osteomyelitis. <i>Frontiers in Microbiology</i> , 2020, 11, 1301.	1.5	15
19955	Identification of Cell-Surface Proteins Endocytosed by Human Brain Microvascular Endothelial Cells In Vitro. <i>Pharmaceutics</i> , 2020, 12, 579.	2.0	12

#	ARTICLE	IF	CITATIONS
19956	Gene signatures of SARS-CoV/SARS-CoV-2-infected ferret lungs in short- and long-term models. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104438.	1.0	50
19957	Comparative analysis of full-length transcriptomes based on hybrid population reveals regulatory mechanisms of anthocyanin biosynthesis in sweet potato (<i>Ipomoea batatas</i> (L.) Lam). <i>BMC Plant Biology</i> , 2020, 20, 299.	1.6	6
19958	A Literature Review of Gene Function Prediction by Modeling Gene Ontology. <i>Frontiers in Genetics</i> , 2020, 11, 400.	1.1	53
19959	The Construction and Comprehensive Prognostic Analysis of the LncRNA-Associated Competitive Endogenous RNAs Network in Colorectal Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 583.	1.1	17
19960	Comparative Pathway Integrator: A Framework of Meta-Analytic Integration of Multiple Transcriptomic Studies for Consensual and Differential Pathway Analysis. <i>Genes</i> , 2020, 11, 696.	1.0	7
19961	Cardiac Transcriptome Analysis Reveals Nr4a1 Mediated Glucose Metabolism Dysregulation in Response to High-Fat Diet. <i>Genes</i> , 2020, 11, 720.	1.0	7
19962	Insights into the mechanism of cyanobacteria removal by the algicidal fungi <i>Bjerkandera adusta</i> and <i>Trametes versicolor</i> . <i>MicrobiologyOpen</i> , 2020, 9, e1042.	1.2	12
19963	Physiological blood-brain transport is impaired with age by a shift in transcytosis. <i>Nature</i> , 2020, 583, 425-430.	13.7	243
19964	<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
19965	Genetic colocalization atlas points to common regulatory sites and genes for hematopoietic traits and hematopoietic contributions to disease phenotypes. <i>BMC Medical Genomics</i> , 2020, 13, 89.	0.7	10
19966	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. <i>PLoS ONE</i> , 2020, 15, e0233311.	1.1	7
19967	Transcriptome Profiling of Pacu (<i>Piaractus mesopotamicus</i>) Challenged With Pathogenic <i>Aeromonas hydrophila</i> : Inference on Immune Gene Response. <i>Frontiers in Genetics</i> , 2020, 11, 604.	1.1	8
19968	PSIONplusm Server for Accurate Multi-Label Prediction of Ion Channels and Their Types. <i>Biomolecules</i> , 2020, 10, 876.	1.8	7
19969	X-ray Structure-Based Chemoinformatic Analysis Identifies Promiscuous Ligands Binding to Proteins from Different Classes with Varying Shapes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3782.	1.8	7
19970	Identification of Prognostic Organic Cation and Anion Transporters in Different Cancer Entities by In Silico Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4491.	1.8	8
19971	Experimentally Determined Long Intrinsically Disordered Protein Regions Are Now Abundant in the Protein Data Bank. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4496.	1.8	25
19972	Identification of Novel microRNA Profiles Dysregulated in Plasma and Tissue of Abdominal Aortic Aneurysm Patients. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4600.	1.8	20
19973	Transcriptome Analysis of Wounding in the Model Grass <i>Lolium temulentum</i> . <i>Plants</i> , 2020, 9, 780.	1.6	5

#	ARTICLE	IF	CITATIONS
19974	Adaptation to Extreme Antarctic Environments Revealed by the Genome of a Sea Ice Green Alga. <i>Current Biology</i> , 2020, 30, 3330-3341.e7.	1.8	48
19975	Development of an immune gene prognostic classifier for survival prediction and respond to immuncheckpoint inhibitor therapy/chemotherapy in endometrial cancer. <i>International Immunopharmacology</i> , 2020, 86, 106735.	1.7	16
19976	Association study based on topological constraints of protein-protein interaction networks. <i>Scientific Reports</i> , 2020, 10, 10797.	1.6	3
19977	Fulvic acid increases forage legume growth inducing preferential up-regulation of nodulation and signalling-related genes. <i>Journal of Experimental Botany</i> , 2020, 71, 5689-5704.	2.4	19
19978	An Integrative Framework of Heterogeneous Genomic Data for Cancer Dynamic Modules Based on Matrix Decomposition. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 305-316.	1.9	26
19979	Identification of vital candidate microRNA/mRNA pairs regulating ovule development using high-throughput sequencing in hazel. <i>BMC Developmental Biology</i> , 2020, 20, 13.	2.1	11
19980	Proteomic Profiling of <i>Emiliana huxleyi</i> Using a Three-Dimensional Separation Method Combined with Tandem Mass Spectrometry. <i>Molecules</i> , 2020, 25, 3028.	1.7	5
19981	Generation of High Yielding and Fragrant Rice (<i>Oryza sativa</i> L.) Lines by CRISPR/Cas9 Targeted Mutagenesis of Three Homoeologs of Cytochrome P450 Gene Family and OsBADH2 and Transcriptome and Proteome Profiling of Revealed Changes Triggered by Mutations. <i>Plants</i> , 2020, 9, 788.	1.6	57
19982	Dietary genistein supplementation protects against lipopolysaccharide-induced intestinal injury through altering transcriptomic profile. <i>Poultry Science</i> , 2020, 99, 3411-3427.	1.5	20
19983	Data-driven network alignment. <i>PLoS ONE</i> , 2020, 15, e0234978.	1.1	11
19984	Enterovirus A71 Oncolysis of Malignant Gliomas. <i>Molecular Therapy</i> , 2020, 28, 1533-1546.	3.7	10
19985	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
19986	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
19987	Comparison of the transcriptomes of different life history stages of the freshwater Rhodophyte <i>Thorea hispida</i> . <i>Genomics</i> , 2020, 112, 3978-3990.	1.3	3
19988	A systems biology-driven approach to construct a comprehensive protein interaction network of influenza A virus with its host. <i>BMC Infectious Diseases</i> , 2020, 20, 480.	1.3	7
19989	Transcriptome Analyses of <i>Candida albicans</i> Biofilms, Exposed to Arachidonic Acid and Fluconazole, Indicates Potential Drug Targets. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3099-3108.	0.8	11
19990	Low Oxygen Stress During Early Development Influences Regulation of Hypoxia-Response Genes in Farmed Atlantic Salmon (<i>Salmo salar</i>). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3179-3188.	0.8	13
19991	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

#	ARTICLE	IF	CITATIONS
19992	Comparative analysis of single-cell transcriptomics in human and zebrafish oocytes. <i>BMC Genomics</i> , 2020, 21, 471.	1.2	14
19993	An expanded cell wall damage signaling network is comprised of the transcription factors Rlm1 and Sko1 in <i>Candida albicans</i> . <i>PLoS Genetics</i> , 2020, 16, e1008908.	1.5	19
19994	Epigenetic Regulator miRNA Pattern Differences Among SARS-CoV, SARS-CoV-2, and SARS-CoV-2 World-Wide Isolates Delineated the Mystery Behind the Epic Pathogenicity and Distinct Clinical Characteristics of Pandemic COVID-19. <i>Frontiers in Genetics</i> , 2020, 11, 765.	1.1	144
19995	A Cancer Gene Module Mining Method Based on Bio-Network of Multi-Omics Gene Groups. <i>Frontiers in Oncology</i> , 2020, 10, 1159.	1.3	3
19996	Silencing trust: confidence and familiarity in re-engineering knowledge infrastructures. <i>Medicine, Health Care and Philosophy</i> , 2020, 23, 471-484.	0.9	4
19997	Single-Cell RNA Sequencing for Precision Oncology: Current State-of-Art. <i>Journal of the Indian Institute of Science</i> , 2020, 100, 579-588.	0.9	9
19998	Lymphocyte cytosolic protein 1 (LCP1) is a novel TRAF3 dysregulation biomarker with potential prognostic value in multiple myeloma. <i>Genome Instability & Disease</i> , 2020, 1, 286-299.	0.5	5
19999	Altered hemodynamics during arteriovenous fistula remodeling leads to reduced fistula patency in female mice. <i>JVS Vascular Science</i> , 2020, 1, 42-56.	0.4	15
20000	Research Note: Circular RNA expressing in different developmental stages of the chicken bursa of Fabricius. <i>Poultry Science</i> , 2020, 99, 3846-3852.	1.5	6
20001	Two hierarchical LuxR-LuxI type quorum sensing systems in <i>Novosphingobium</i> activate microcystin degradation through transcriptional regulation of the mlr pathway. <i>Water Research</i> , 2020, 183, 116092.	5.3	27
20002	Genome sequencing and transcriptome analysis of <i>Geotrichum citri-aurantii</i> on citrus reveal the potential pathogenic- and guazatine-resistance related genes. <i>Genomics</i> , 2020, 112, 4063-4071.	1.3	15
20003	Immune-related genes in tumor-specific CD4+ and CD8+ T cells in colon cancer. <i>BMC Cancer</i> , 2020, 20, 585.	1.1	17
20004	Transcription Analysis of the Chemerin Impact on Gene Expression Profile in the Luteal Cells of Gilts. <i>Genes</i> , 2020, 11, 651.	1.0	8
20005	Identification of Conserved Proteomic Networks in Neurodegenerative Dementia. <i>Cell Reports</i> , 2020, 31, 107807.	2.9	49
20006	Deletion of the Dishevelled family of genes disrupts anterior-posterior axis specification and selectively prevents mesoderm differentiation. <i>Developmental Biology</i> , 2020, 464, 161-175.	0.9	8
20007	Comparative and Phylogenetic Analyses of the Complete Chloroplast Genomes of Six Almond Species (<i>Prunus</i> spp. L.). <i>Scientific Reports</i> , 2020, 10, 10137.	1.6	18
20008	In silico identification of therapeutic compounds against microRNA targets in drug-resistant pancreatic ductal adenocarcinoma. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 39, 1-9.	2.0	3
20009	Functional surface proteomic profiling reveals the host heat shock protein α A8 as a mediator of <i>Lichtheimia corymbifera</i> recognition by murine alveolar macrophages. <i>Environmental Microbiology</i> , 2020, 22, 3722-3740.	1.8	5

#	ARTICLE	IF	CITATIONS
20010	Drosophila models of pathogenic copy-number variant genes show global and non-neuronal defects during development. <i>PLoS Genetics</i> , 2020, 16, e1008792.	1.5	9
20011	Proteomic analyses unraveling water stress response in two Eucalyptus species originating from contrasting environments for aridity. <i>Molecular Biology Reports</i> , 2020, 47, 5191-5205.	1.0	5
20012	Beta-amyloid deposition around hepatic bile ducts is a novel pathobiological and diagnostic feature of biliary atresia. <i>Journal of Hepatology</i> , 2020, 73, 1391-1403.	1.8	31
20013	Detecting and correcting misclassified sequences in the large-scale public databases. <i>Bioinformatics</i> , 2020, 36, 4699-4705.	1.8	18
20014	Molecular atlas of the adult mouse brain. <i>Science Advances</i> , 2020, 6, eabb3446.	4.7	183
20015	Redox States of Protein Cysteines in Pathways of Protein Turnover and Cytoskeleton Dynamics Are Changed with Aging and Reversed by Slc7a11 Restoration in Mouse Lung Fibroblasts. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-17.	1.9	10
20016	Transcriptomic Analysis of Extracellular RNA Governed by the Endocytic Adaptor Protein Cin1 of <i>Cryptococcus deneoformans</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 256.	1.8	12
20017	Platelet-Released Growth Factors and Platelet-Rich Fibrin Induce Expression of Factors Involved in Extracellular Matrix Organization in Human Keratinocytes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4404.	1.8	12
20018	PRC2-mediated H3K27me3 modulates shoot iron homeostasis in <i>Arabidopsis thaliana</i> . <i>Plant Signaling and Behavior</i> , 2020, 15, 1784549.	1.2	10
20019	FOBI: an ontology to represent food intake data and associate it with metabolomic data. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	29
20020	protein2vec: Predicting Protein-Protein Interactions Based on LSTM. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	1.9	5
20021	Semantic Access Control for Privacy Management of Personal Sensing in Smart Cities. <i>IEEE Transactions on Emerging Topics in Computing</i> , 2022, 10, 199-210.	3.2	6
20022	Expansions of chemosensory gene orthologs among selected tsetse fly species and their expressions in <i>Glossina morsitans morsitans</i> tsetse fly. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008341.	1.3	9
20023	Identification of hub genes involved in apparent metabolizable energy of chickens. <i>Animal Biotechnology</i> , 2022, 33, 242-249.	0.7	3
20024	The Lyme disease bacterium, <i>Borrelia burgdorferi</i> , stimulates an inflammatory response in human choroid plexus epithelial cells. <i>PLoS ONE</i> , 2020, 15, e0234993.	1.1	13
20025	Complete Genome Sequencing and Transcriptome Analysis of Nitrogen Metabolism of <i>Succinivibrio dextrinosolvens</i> Strain Z6 Isolated From Dairy Cow Rumen. <i>Frontiers in Microbiology</i> , 2020, 11, 1826.	1.5	22
20026	Screening and identification of key gene in sepsis development. <i>Medicine (United States)</i> , 2020, 99, e20759.	0.4	6
20027	Breathing fresh air into respiratory research with single-cell RNA sequencing. <i>European Respiratory Review</i> , 2020, 29, 200060.	3.0	11

#	ARTICLE	IF	CITATIONS
20028	Discovery, identification, and functional characterization of long noncoding RNAs in <i>Arachis hypogaea</i> L.. <i>BMC Plant Biology</i> , 2020, 20, 308.	1.6	12
20029	Salivary gland transcriptome of the Asiatic <i>Triatoma rubrofasciata</i> . <i>Acta Tropica</i> , 2020, 210, 105473.	0.9	4
20030	Transcriptomic analysis identifies early cellular and molecular events by which estrogen disrupts testis differentiation and causes feminization in <i>Xenopus laevis</i> . <i>Aquatic Toxicology</i> , 2020, 226, 105557.	1.9	9
20031	Investigation of spectroscopic and proteomic alterations underlying prostate carcinogenesis. <i>Journal of Proteomics</i> , 2020, 226, 103888.	1.2	7
20032	Differential expression of microRNA in exosomes derived from endometrial stromal cells of women with endometriosis-associated infertility. <i>Reproductive BioMedicine Online</i> , 2020, 41, 170-181.	1.1	19
20033	Screening and identification of key biomarkers in alimentary tract cancers: A bioinformatic analysis. <i>Cancer Biomarkers</i> , 2020, 29, 221-233.	0.8	2
20034	Using Language Representation Learning Approach to Efficiently Identify Protein Complex Categories in Electron Transport Chain. <i>Molecular Informatics</i> , 2020, 39, e2000033.	1.4	4
20035	Quantitative Translation of Dog-to-Human Aging by Conserved Remodeling of the DNA Methylome. <i>Cell Systems</i> , 2020, 11, 176-185.e6.	2.9	67
20036	RNA is essential for PRC2 chromatin occupancy and function in human pluripotent stem cells. <i>Nature Genetics</i> , 2020, 52, 931-938.	9.4	99
20037	Evolutionary History of the Globin Gene Family in Annelids. <i>Genome Biology and Evolution</i> , 2020, 12, 1719-1733.	1.1	8
20038	Signatures of adaptation to a monocot host in the plant-parasitic cyst nematode <i>Heterodera sacchari</i> . <i>Plant Journal</i> , 2020, 103, 1263-1274.	2.8	9
20039	OASL as a Diagnostic Marker for Influenza Infection Revealed by Integrative Bioinformatics Analysis With XGBoost. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 729.	2.0	7
20040	The IUPHAR Guide to Immunopharmacology: connecting immunology and pharmacology. <i>Immunology</i> , 2020, 160, 10-23.	2.0	7
20041	Integration of genome-wide association study and expression quantitative trait loci data identifies <i>AIM2</i> as a risk gene of periodontitis. <i>Journal of Clinical Periodontology</i> , 2020, 47, 583-593.	2.3	14
20042	PANEV: an R package for a pathway-based network visualization. <i>BMC Bioinformatics</i> , 2020, 21, 46.	1.2	15
20043	Identification of transcriptome and fluralaner responsive genes in the common cutworm <i>Spodoptera litura</i> Fabricius, based on RNA-seq. <i>BMC Genomics</i> , 2020, 21, 120.	1.2	20
20044	PlaPPISite: a comprehensive resource for plant protein-protein interaction sites. <i>BMC Plant Biology</i> , 2020, 20, 61.	1.6	25
20045	Whole Genome Sequencing and Comparative Genomics of Two Nematicidal <i>Bacillus</i> Strains Reveals a Wide Range of Possible Virulence Factors. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 881-890.	0.8	12

#	ARTICLE	IF	CITATIONS
20046	Automated Methods Enable Direct Computation on Phenotypic Descriptions for Novel Candidate Gene Prediction. <i>Frontiers in Plant Science</i> , 2019, 10, 1629.	1.7	10
20047	Complete transcriptome assembly and annotation of a critically important amphipod species in freshwater ecotoxicological risk assessment: <i>Gammarus fossarum</i> . <i>Environment International</i> , 2020, 137, 105319.	4.8	8
20048	Local adaptation across a complex bioclimatic landscape in two montane bumble bee species. <i>Molecular Ecology</i> , 2020, 29, 920-939.	2.0	41
20049	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
20050	IGF1-mediated human embryonic stem cell self-renewal recapitulates the embryonic niche. <i>Nature Communications</i> , 2020, 11, 764.	5.8	41
20051	Right Singular Vector Projection Graphs: Fast High Dimensional Covariance Matrix Estimation under Latent Confounding. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2020, 82, 361-389.	1.1	8
20052	Screening of Prognostic Factors in Early-Onset Breast Cancer. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303381989367.	0.8	9
20053	Altered Hippocampal Epigenetic Regulation Underlying Reduced Cognitive Development in Response to Early Life Environmental Insults. <i>Genes</i> , 2020, 11, 162.	1.0	8
20054	EHMT2 Inhibition Induces Cell Death in Human Non-Small Cell Lung Cancer by Altering the Cholesterol Biosynthesis Pathway. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1002.	1.8	12
20055	Formal Ontologies in Information Systems Development: A Systematic Review. <i>Information (Switzerland)</i> , 2020, 11, 66.	1.7	20
20056	Transcriptome-Wide Identification, Evolutionary Analysis, and GA Stress Response of the GRAS Gene Family in <i>Panax ginseng</i> C. A. Meyer. <i>Plants</i> , 2020, 9, 190.	1.6	13
20057	The hornwort genome and early land plant evolution. <i>Nature Plants</i> , 2020, 6, 107-118.	4.7	203
20058	Quantifying Gene Essentiality Based on the Context of Cellular Components. <i>Frontiers in Genetics</i> , 2019, 10, 1342.	1.1	1
20059	Comparative genomics and association analysis identifies virulence genes of <i>Cercospora soja</i> in soybean. <i>BMC Genomics</i> , 2020, 21, 172.	1.2	13
20060	microRNA-137 downregulates MCL1 in ovarian cancer cells and mediates cisplatin-induced apoptosis. <i>Pharmacogenomics</i> , 2020, 21, 195-207.	0.6	12
20061	Genomic diversity analysis and identification of novel SSR markers in four tobacco varieties by high-throughput resequencing. <i>Plant Physiology and Biochemistry</i> , 2020, 150, 80-89.	2.8	8
20062	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
20063	Integrative analysis suggests cell type-specific decoding of NF- κ B dynamics. <i>Science Signaling</i> , 2020, 13, .	1.6	33

#	ARTICLE	IF	CITATIONS
20064	Gene interaction network studies to decipher the multi-drug resistance mechanism in <i>Salmonella enterica</i> serovar Typhi CT18 reveal potential drug targets. <i>Microbial Pathogenesis</i> , 2020, 142, 104096.	1.3	43
20065	Pan-cancer mapping of differential protein-protein interactions. <i>Scientific Reports</i> , 2020, 10, 3272.	1.6	36
20066	Data libraries – the missing element for modeling biological systems. <i>FEBS Journal</i> , 2020, 287, 4594-4601.	2.2	3
20067	Exploring Integrative Analysis Using the BioMedical Evidence Graph. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 147-159.	1.0	4
20068	Comparative Proteomic Analysis of Wild-Type <i>Physcomitrella Patens</i> and an OPDA-Deficient <i>Physcomitrella Patens</i> Mutant with Disrupted PpAOS1 and PpAOS2 Genes after Wounding. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1417.	1.8	8
20069	Neutrophil-like HL-60 cells expressing only GFP-tagged β -actin exhibit nearly normal motility. <i>Cytoskeleton</i> , 2020, 77, 181-196.	1.0	16
20070	Bioinformatic framework for analysis of transcription factor changes as the molecular link between replicative cellular senescence signaling pathways and carcinogenesis. <i>Biogerontology</i> , 2020, 21, 357-366.	2.0	0
20071	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. <i>Nature Communications</i> , 2020, 11, 1106.	5.8	125
20072	Elevated SLC2A1 Expression Correlates with Poor Prognosis in Patients with Surgically Resected Lung Adenocarcinoma: A Study Based on Immunohistochemical Analysis and Bioinformatics. <i>DNA and Cell Biology</i> , 2020, 39, 631-644.	0.9	15
20073	Tripal EUtils: a Tripal module to increase exchange and reuse of genome assembly metadata. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	0
20074	Building a pipeline to solicit expert knowledge from the community to aid gene summary curation. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	5
20075	A Survey of Systematic Evidence Mapping Practice and the Case for Knowledge Graphs in Environmental Health and Toxicology. <i>Toxicological Sciences</i> , 2020, 175, 35-49.	1.4	19
20076	RNA-Seq Analysis of Genetic and Transcriptome Network Effects of Dual-Trait Selection for Ethanol Preference and Withdrawal Using SOT and NOT Genetic Models. <i>Alcoholism: Clinical and Experimental Research</i> , 2020, 44, 820-830.	1.4	9
20077	Endogenous Retrovirus Activation as a Key Mechanism of Anti-Tumor Immune Response in Radiotherapy. <i>Radiation Research</i> , 2020, 193, 305.	0.7	33
20078	Transcriptome profiling reveals multiple pathways responsible for the beneficial metabolic effects of <i>Smilax glabra</i> flavonoids in mouse 3T3-L1 adipocytes. <i>Biomedicine and Pharmacotherapy</i> , 2020, 125, 110011.	2.5	2
20079	Proteomic investigation of interhyphal interactions between strains of <i>Agaricus bisporus</i> . <i>Fungal Biology</i> , 2020, 124, 579-591.	1.1	4
20080	Integrated transcriptomic correlation network analysis identifies COPD molecular determinants. <i>Scientific Reports</i> , 2020, 10, 3361.	1.6	35
20081	Genome Sequence of <i>Micromonospora terminaliae</i> TMS7 ^T , a New Endophytic Actinobacterium Isolated from the Medicinal Plant <i>Terminalia mucronata</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 721-723.	1.4	5

#	ARTICLE	IF	CITATIONS
20082	informatics Approaches for Harmonized Intelligent Integration of Stem Cell Research. Stem Cells and Cloning: Advances and Applications, 2020, Volume 13, 1-20.	2.3	5
20083	Transcriptome Analysis and Identification of Genes Associated with Starch Metabolism in <i>Castanea henryi</i> Seed (Fagaceae). International Journal of Molecular Sciences, 2020, 21, 1431.	1.8	19
20085	Gene regulatory network analysis with drug sensitivity reveals synergistic effects of combinatory chemotherapy in gastric cancer. Scientific Reports, 2020, 10, 3932.	1.6	9
20086	A deep neural network based hierarchical multi-label classification method. Review of Scientific Instruments, 2020, 91, 024103.	0.6	8
20087	Identification and characterization of <i>NAC</i> genes in response to abiotic stress conditions in <i>Picea wilsonii</i> using transcriptome sequencing. Biotechnology and Biotechnological Equipment, 2020, 34, 93-103.	0.5	7
20088	Comparison of Pseudoknotted RNA Secondary Structures by Topological Centroid Identification and Tree Edit Distance. Journal of Computational Biology, 2020, 27, 1443-1451.	0.8	6
20089	Topologically Guided Prioritization of Candidate Gene Transcripts Coexpressed with the 5-HT1A Receptor by Combining In Vivo PET and Allen Human Brain Atlas Data. Cerebral Cortex, 2020, 30, 3771-3780.	1.6	10
20090	Biomarkers for Traumatic Brain Injury: Data Standards and Statistical Considerations. Journal of Neurotrauma, 2021, 38, 2514-2529.	1.7	23
20091	SurfaceGenie: a web-based application for prioritizing cell-type-specific marker candidates. Bioinformatics, 2020, 36, 3447-3456.	1.8	37
20092	Identification and validation of key genes with prognostic value in non-small cell lung cancer via integrated bioinformatics analysis. Thoracic Cancer, 2020, 11, 851-866.	0.8	22
20093	LncRNA PCAT6 predicts poor prognosis in hepatocellular carcinoma and promotes proliferation through the regulation of cell cycle arrest and apoptosis. Cell Biochemistry and Function, 2020, 38, 895-904.	1.4	34
20094	A census of pathway maps in cancer systems biology. Nature Reviews Cancer, 2020, 20, 233-246.	12.8	60
20095	FUNMarker: Fusion Network-Based Method to Identify Prognostic and Heterogeneous Breast Cancer Biomarkers. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2483-2491.	1.9	10
20096	The modular nature of protein evolution: domain rearrangement rates across eukaryotic life. BMC Evolutionary Biology, 2020, 20, 30.	3.2	33
20097	Transcriptome profiles of <i>Quercus rubra</i> responding to increased O ₃ stress. BMC Genomics, 2020, 21, 160.	1.2	11
20098	Somatic mutations and T-cell clonality in patients with immunodeficiency. Haematologica, 2020, 105, 2757-2768.	1.7	18
20099	Whole-exome sequencing of 81 individuals from 27 multiply affected bipolar disorder families. Translational Psychiatry, 2020, 10, 57.	2.4	23
20100	Machine Learning and Bioinformatics Models to Identify Pathways that Mediate Influences of Welding Fumes on Cancer Progression. Scientific Reports, 2020, 10, 2795.	1.6	23

#	ARTICLE	IF	CITATIONS
20101	An initial comparative genomic autopsy of wasting disease in sea stars. <i>Molecular Ecology</i> , 2020, 29, 1087-1102.	2.0	22
20102	Network Pharmacology-Based Strategy to Investigate the Pharmacologic Mechanisms of <i>Atractylodes macrocephala</i> Koidz. for the Treatment of Chronic Gastritis. <i>Frontiers in Pharmacology</i> , 2019, 10, 1629.	1.6	59
20103	Epigenomic analysis of 5-hydroxymethylcytosine (5hmC) reveals novel DNA methylation markers for lung cancers. <i>Neoplasia</i> , 2020, 22, 154-161.	2.3	15
20104	Predicting clinical benefit of immunotherapy by antigenic or functional mutations affecting tumour immunogenicity. <i>Nature Communications</i> , 2020, 11, 951.	5.8	34
20105	The Adipocyte Acquires a Fibroblast-Like Transcriptional Signature in Response to a High Fat Diet. <i>Scientific Reports</i> , 2020, 10, 2380.	1.6	49
20107	Dual Eigen-modules of Cis-Element Regulation Profiles and Selection of Cognition-Language Eigen-direction along Evolution in Hominidae. <i>Molecular Biology and Evolution</i> , 2020, 37, 1679-1693.	3.5	5
20108	In Vitro Zika Virus Infection of Human Neural Progenitor Cells: Meta-Analysis of RNA-Seq Assays. <i>Microorganisms</i> , 2020, 8, 270.	1.6	15
20109	Plant Epigenetics and Epigenomics. <i>Methods in Molecular Biology</i> , 2020, , .	0.4	1
20110	Analysis of testis metabolome and transcriptome from the oriental river prawn (<i>Macrobrachium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4 and Physiology Part D: Genomics and Proteomics, 2020, 34, 100662.	0.4	25
20111	Radiogenomic-Based Survival Risk Stratification of Tumor Habitat on Gd-T1w MRI Is Associated with Biological Processes in Glioblastoma. <i>Clinical Cancer Research</i> , 2020, 26, 1866-1876.	3.2	67
20112	Identification of Candidate Chemosensory Receptors in the Antennae of the Variegated Cutworm, <i>Peridroma saucia</i> H&A, Based on a Transcriptome Analysis. <i>Frontiers in Physiology</i> , 2020, 11, 39.	1.3	11
20113	liWRKY34 positively regulates yield, lignan biosynthesis and stress tolerance in <i>Isatis indigotica</i> . <i>Acta Pharmaceutica Sinica B</i> , 2020, 10, 2417-2432.	5.7	26
20114	Multiple protein and mRNA expression correlations in the rat cerebral cortex after ischemic injury and repair due to buchang naoxintong jiaonang (BNJ) intervention. <i>Biomedicine and Pharmacotherapy</i> , 2020, 125, 109917.	2.5	6
20115	Indirectly stimulation of DCs by <i>Ganoderma atrum</i> polysaccharide in intestinal-like Caco-2/DCs co-culture model based on RNA-seq. <i>Journal of Functional Foods</i> , 2020, 67, 103850.	1.6	21
20116	Plant regeneration in leaf culture of <i>Centaurium erythraea</i> Rafn. Part 3: de novo transcriptome assembly and validation of housekeeping genes for studies of in vitro morphogenesis. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 141, 417-433.	1.2	9
20117	Identification, quantification and bioinformatic analysis of RNA-dependent proteins by RNase treatment and density gradient ultracentrifugation using R-DeeP. <i>Nature Protocols</i> , 2020, 15, 1338-1370.	5.5	16
20118	Feature selection for hierarchical classification via joint semantic and structural information of labels. <i>Knowledge-Based Systems</i> , 2020, 195, 105655.	4.0	19
20119	Analysis of histological and microRNA profiles changes in rabbit skin development. <i>Scientific Reports</i> , 2020, 10, 454.	1.6	7

#	ARTICLE	IF	CITATIONS
20120	A rare subpopulation of melanoma cells with low expression of metastasis suppressor NME1 is highly metastatic in vivo. <i>Scientific Reports</i> , 2020, 10, 1971.	1.6	11
20121	Controllability analysis of molecular pathways points to proteins that control the entire interaction network. <i>Scientific Reports</i> , 2020, 10, 2943.	1.6	7
20122	The genetics of situs inversus without primary ciliary dyskinesia. <i>Scientific Reports</i> , 2020, 10, 3677.	1.6	37
20123	The power and limitations of gene expression pathway analyses toward predicting population response to environmental stressors. <i>Evolutionary Applications</i> , 2020, 13, 1166-1182.	1.5	11
20124	Genomic insight into the origins and evolution of symbiosis genes in <i>Phaseolus vulgaris</i> microsymbionts. <i>BMC Genomics</i> , 2020, 21, 186.	1.2	24
20125	Transcriptome differences in adipose stromal cells derived from pre- and postmenopausal women. <i>Stem Cell Research and Therapy</i> , 2020, 11, 92.	2.4	2
20126	Transcriptome Changes of <i>Mycobacterium marinum</i> in the Process of Resuscitation From Hypoxia-Induced Dormancy. <i>Frontiers in Genetics</i> , 2019, 10, 1359.	1.1	7
20127	Genetic Modifiers and Rare Mendelian Disease. <i>Genes</i> , 2020, 11, 239.	1.0	96
20128	In-Depth Understanding of <i>Camellia oleifera</i> Self-Incompatibility by Comparative Transcriptome, Proteome and Metabolome. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1600.	1.8	24
20129	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
20130	MicroRNA-based recombinant AAV vector assembly improves efficiency of suicide gene transfer in a murine model of lymphoma. <i>Cancer Medicine</i> , 2020, 9, 3188-3201.	1.3	4
20131	Comparative characterization and functional genomic analysis of two <i>Comamonas</i> sp. strains for biodegradation of quinoline. <i>Journal of Chemical Technology and Biotechnology</i> , 2020, 95, 2017-2026.	1.6	13
20132	Integrated bioinformatics analyses identified SCL3-induced regulatory network in <i>Arabidopsis thaliana</i> roots. <i>Biotechnology Letters</i> , 2020, 42, 1019-1033.	1.1	6
20133	A Collagenolytic Aspartic Protease from <i>Thermomucor indicae-seudaticae</i> Expressed in <i>Escherichia coli</i> and <i>Pichia pastoris</i> . <i>Applied Biochemistry and Biotechnology</i> , 2020, 191, 1258-1270.	1.4	7
20134	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. <i>American Journal of Human Genetics</i> , 2020, 106, 389-404.	2.6	118
20135	Transcriptome analysis of near-isogenic lines for glume hairiness of wheat. <i>Gene</i> , 2020, 739, 144517.	1.0	7
20136	Comparative proteomic analysis of host responses to <i>Plasmodiophora brassicae</i> infection in susceptible and resistant <i>Brassica oleracea</i> . <i>Plant Biotechnology Reports</i> , 2020, 14, 263-274.	0.9	11
20137	VisBicluster: A Matrix-Based Bicluster Visualization of Expression Data. <i>Journal of Computational Biology</i> , 2020, 27, 1384-1396.	0.8	5

#	ARTICLE	IF	CITATIONS
20138	Biocontrol Potential of a Novel Endophytic Bacterium From Mulberry (Morus) Tree. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 488.	2.0	23
20139	Classification of Trispanins: A Diverse Group of Proteins That Function in Membrane Synthesis and Transport Mechanisms. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 386.	1.8	0
20140	The Personalisation of Glioblastoma Treatment Using Whole Exome Sequencing: A Pilot Study. <i>Genes</i> , 2020, 11, 173.	1.0	3
20141	Microglial A20 Protects the Brain from CD8 T-Cell-Mediated Immunopathology. <i>Cell Reports</i> , 2020, 30, 1585-1597.e6.	2.9	36
20142	Early-life trauma endophenotypes and brain circuitâ€“gene expression relationships in functional neurological (conversion) disorder. <i>Molecular Psychiatry</i> , 2021, 26, 3817-3828.	4.1	53
20143	Genetic Mapping Combined with a Transcriptome Analysis to Screen for Candidate Genes Responsive to Abscisic Acid Treatment in <i>Brassica napus</i> Embryos During Seed Germination. <i>DNA and Cell Biology</i> , 2020, 39, 533-547.	0.9	4
20144	IGFBP6 Is Downregulated in Unstable Carotid Atherosclerotic Plaques According to an Integrated Bioinformatics Analysis and Experimental Verification. <i>Journal of Atherosclerosis and Thrombosis</i> , 2020, 27, 1068-1085.	0.9	19
20145	Restricted immunological and cellular pathways are shared by murine models of chronic alcohol consumption. <i>Scientific Reports</i> , 2020, 10, 2451.	1.6	8
20146	Characterization and whole genome sequencing of a novel strain of <i>Bergeyella cardium</i> related to infective endocarditis. <i>BMC Microbiology</i> , 2020, 20, 32.	1.3	2
20147	Robustness and applicability of transcription factor and pathway analysis tools on single-cell RNA-seq data. <i>Genome Biology</i> , 2020, 21, 36.	3.8	216
20148	Selection in Australian Thoroughbred horses acts on a locus associated with early two-year old speed. <i>PLoS ONE</i> , 2020, 15, e0227212.	1.1	11
20149	Metabolome and Transcriptome Analysis of Hexaploid <i>Solidago canadensis</i> Roots Reveals its Invasive Capacity Related to Polyploidy. <i>Genes</i> , 2020, 11, 187.	1.0	15
20150	Identification of key genes and pathways associated with esophageal squamous cell carcinoma development based on weighted gene correlation network analysis. <i>Journal of Cancer</i> , 2020, 11, 1393-1402.	1.2	10
20151	A chromosome-level reference genome of the hornbeam, <i>Carpinus fangiana</i> . <i>Scientific Data</i> , 2020, 7, 24.	2.4	8
20152	Data mining powered by the gene ontology. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2020, 10, e1359.	4.6	6
20153	Identification of drought resistant miRNA in <i>Macleaya cordata</i> by high-throughput sequencing. <i>Archives of Biochemistry and Biophysics</i> , 2020, 684, 108300.	1.4	9
20154	A systems approach to infectious disease. <i>Nature Reviews Genetics</i> , 2020, 21, 339-354.	7.7	72
20155	Poly-Enrich: count-based methods for gene set enrichment testing with genomic regions. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa006.	1.5	13

#	ARTICLE	IF	CITATIONS
20156	Electroacupuncture Alleviates Experimental Chronic Inflammatory Pain by Inhibiting Calcium Voltage-Gated Channel-Mediated Inflammation. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-10.	0.5	5
20157	Proteomic profiling of proteins in the dorsal horn of the spinal cord in dairy cows with chronic lameness. PLoS ONE, 2020, 15, e0228134.	1.1	2
20158	Towards an ontological cross-disciplinary solution for multidisciplinary data: VI-SEEM data management and the FAIR principles. International Journal on Digital Libraries, 2021, 22, 297-307.	1.1	4
20159	DDAPRED: a computational method for predicting drug repositioning using regularized logistic matrix factorization. Journal of Molecular Modeling, 2020, 26, 60.	0.8	5
20160	The genome sequence of celery (<i>Apium graveolens</i> L.), an important leaf vegetable crop rich in apigenin in the Apiaceae family. Horticulture Research, 2020, 7, 9.	2.9	61
20161	Transcriptome analyses identify hub genes and potential mechanisms in adenoid cystic carcinoma. Medicine (United States), 2020, 99, e18676.	0.4	4
20162	Divergent northern and southern populations and demographic history of the pearl oyster in the western Pacific revealed with genomic SNPs. Evolutionary Applications, 2020, 13, 837-853.	1.5	24
20163	Brief communication: Long-term absence of Langerhans cells alters the gene expression profile of keratinocytes and dendritic epidermal T cells. PLoS ONE, 2020, 15, e0223397.	1.1	11
20165	Environmental arginine controls multinuclear giant cell metabolism and formation. Nature Communications, 2020, 11, 431.	5.8	37
20166	Transcriptome meta-analysis reveals differences of immune profile between eutopic endometrium from stage I-II and III-IV endometriosis independently of hormonal milieu. Scientific Reports, 2020, 10, 313.	1.6	54
20167	Single-cell morphology encodes metastatic potential. Science Advances, 2020, 6, eaaw6938.	4.7	112
20168	Accumulation of genetic variants associated with immunity in the selective breeding of broilers. BMC Genetics, 2020, 21, 5.	2.7	13
20169	Knowledge-guided analysis of "omics" data using the KnowEnG cloud platform. PLoS Biology, 2020, 18, e3000583.	2.6	34
20170	Water Deficit Transcriptomic Responses Differ in the Invasive <i>Tamarix chinensis</i> and <i>T. ramosissima</i> Established in the Southern and Northern United States. Plants, 2020, 9, 86.	1.6	10
20171	Tentacle Transcriptomes of the Speckled Anemone (<i>Actiniaria: Actiniidae: Oulactis</i> sp.): Venom-Related Components and Their Domain Structure. Marine Biotechnology, 2020, 22, 207-219.	1.1	19
20172	Impact of an Antifungal Insect Defensin on the Proteome of the Phytopathogenic Fungus <i>Botrytis cinerea</i> . Journal of Proteome Research, 2020, 19, 1131-1146.	1.8	15
20173	Maternal transcription profiles at different stages for the development of early embryo in buffalo. Reproduction in Domestic Animals, 2020, 55, 503-514.	0.6	1
20174	A competency question-oriented approach for the transformation of semi-structured bioinformatics data into linked open data. Engineering Applications of Artificial Intelligence, 2020, 90, 103495.	4.3	1

#	ARTICLE	IF	CITATIONS
20175	Dipeptidyl peptidase-4 is increased in the abdominal aortic aneurysm vessel wall and is associated with aneurysm disease processes. <i>PLoS ONE</i> , 2020, 15, e0227889.	1.1	6
20176	Biofilm formation displays intrinsic offensive and defensive features of <i>Bacillus cereus</i> . <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 3.	2.9	34
20177	Parallel evolutionary paths to produce more than one <i>Pseudomonas aeruginosa</i> biofilm phenotype. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 2.	2.9	36
20178	A high-quality chromosomal genome assembly of <i>Diospyros oleifera</i> Cheng. <i>GigaScience</i> , 2020, 9, .	3.3	37
20180	Enhanced genome assembly and a new official gene set for <i>Tribolium castaneum</i> . <i>BMC Genomics</i> , 2020, 21, 47.	1.2	84
20181	De novo variants in exomes of congenital heart disease patients identify risk genes and pathways. <i>Genome Medicine</i> , 2020, 12, 9.	3.6	43
20182	Distinct but Intertwined Evolutionary Histories of Multiple <i>Salmonella enterica</i> Subspecies. <i>MSystems</i> , 2020, 5, .	1.7	24
20183	Enhanced cardiomyocyte reactive oxygen species signaling promotes ibrutinib-induced atrial fibrillation. <i>Redox Biology</i> , 2020, 30, 101432.	3.9	36
20184	ISOGO: Functional annotation of protein-coding splice variants. <i>Scientific Reports</i> , 2020, 10, 1069.	1.6	6
20185	An operon consisting of a P-type ATPase gene and a transcriptional regulator gene responsible for cadmium resistances in <i>Bacillus vietnamensis</i> 151 and <i>Bacillus marisflavi</i> 151. <i>BMC Microbiology</i> , 2020, 20, 18.	1.3	22
20186	Ontology engineering: Current state, challenges, and future directions. <i>Semantic Web</i> , 2020, 11, 125-138.	1.1	26
20187	Imputation of Gene Expression Data in Blood Cancer and Its Significance in Inferring Biological Pathways. <i>Frontiers in Oncology</i> , 2020, 9, 1442.	1.3	13
20188	Survival-Associated Metabolic Genes in Human Papillomavirus-Positive Head and Neck Cancers. <i>Cancers</i> , 2020, 12, 253.	1.7	40
20189	Growth Mode and Physiological State of Cells Prior to Biofilm Formation Affect Immune Evasion and Persistence of <i>Staphylococcus aureus</i> . <i>Microorganisms</i> , 2020, 8, 106.	1.6	18
20190	Multiplexed Quantitative Proteomic Analysis of HEK293 Provides Insights into Molecular Changes Associated with the Cell Density Effect, Transient Transfection, and Virus-Like Particle Production. <i>Journal of Proteome Research</i> , 2020, 19, 1085-1099.	1.8	23
20191	Pro-efferocytic nanoparticles are specifically taken up by lesional macrophages and prevent atherosclerosis. <i>Nature Nanotechnology</i> , 2020, 15, 154-161.	15.6	173
20192	A Deep Learning Framework for Gene Ontology Annotations With Sequence- and Network-Based Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2208-2217.	1.9	21
20193	Proteomic Analysis of Brain Region and Sex-Specific Synaptic Protein Expression in the Adult Mouse Brain. <i>Cells</i> , 2020, 9, 313.	1.8	20

#	ARTICLE	IF	CITATIONS
20194	Identification of Key Biomarkers in Bladder Cancer: Evidence from a Bioinformatics Analysis. <i>Diagnostics</i> , 2020, 10, 66.	1.3	24
20195	An Algorithm of Inductively Identifying Clusters from Attributed Graphs. <i>IEEE Transactions on Big Data</i> , 2020, , 1-1.	4.4	36
20196	Folic acid supplementation regulates milk production variables, metabolic associated genes and pathways in perinatal Holsteins. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2020, 104, 483-492.	1.0	19
20197	Role of Secreted Frizzled-Related Protein 1 in Early Mammary Gland Tumorigenesis and Its Regulation in Breast Microenvironment. <i>Cells</i> , 2020, 9, 208.	1.8	14
20198	Genetic studies of urinary metabolites illuminate mechanisms of detoxification and excretion in humans. <i>Nature Genetics</i> , 2020, 52, 167-176.	9.4	101
20199	A human ciliopathy reveals essential functions for NEK10 in airway mucociliary clearance. <i>Nature Medicine</i> , 2020, 26, 244-251.	15.2	45
20200	Lag penalized weighted correlation for time series clustering. <i>BMC Bioinformatics</i> , 2020, 21, 21.	1.2	9
20201	Differential expression of microRNAs in tomato leaves treated with different light qualities. <i>BMC Genomics</i> , 2020, 21, 37.	1.2	14
20202	Novel Approaches for Identifying the Molecular Background of Schizophrenia. <i>Cells</i> , 2020, 9, 246.	1.8	13
20203	Immune gene signatures for predicting durable clinical benefit of anti-PD-1 immunotherapy in patients with non-small cell lung cancer. <i>Scientific Reports</i> , 2020, 10, 643.	1.6	124
20204	Gene expression changes in arterial and venous endothelial cells exposed to gestational diabetes mellitus. <i>Gynecological Endocrinology</i> , 2020, 36, 791-795.	0.7	10
20205	Profiling of the muscle-specific dystroglycan interactome reveals the role of Hippo signaling in muscular dystrophy and age-dependent muscle atrophy. <i>BMC Medicine</i> , 2020, 18, 8.	2.3	20
20206	Transcriptional analysis of THP-1 cells infected with <i>Leishmania infantum</i> indicates no activation of the inflammasome platform. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007949.	1.3	18
20207	Probiotic <i>Bacillus subtilis</i> Protects against α -Synuclein Aggregation in <i>C.Âlegans</i> . <i>Cell Reports</i> , 2020, 30, 367-380.e7.	2.9	114
20208	Systematic metadata analysis of brown rot fungi gene expression data reveals the genes involved in Fentonâ€™s reaction and wood decay process. <i>Mycology</i> , 2020, 11, 22-37.	2.0	9
20209	Construction of asthma related competing endogenous RNA network revealed novel long non-coding RNAs and potential new drugs. <i>Respiratory Research</i> , 2020, 21, 14.	1.4	18
20210	Comparative genomics of the aconidial <i>Aspergillus niger</i> strain LDM3 predicts genes associated with its high protein secretion capacity. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 2623-2637.	1.7	9
20211	Zika virus targets the human thymic epithelium. <i>Scientific Reports</i> , 2020, 10, 1378.	1.6	16

#	ARTICLE	IF	CITATIONS
20212	Molecular and expression characterization of Toll-like receptor family genes from the <i>Anadara sativa</i> (Bivalvia, Arcidae) transcriptome. <i>Developmental and Comparative Immunology</i> , 2020, 106, 103630.	1.0	7
20213	Visualization and analysis of the interaction network of proteins associated with blood-cell targeting autoimmune diseases. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165714.	1.8	3
20214	Functional and transcriptomic analyses of the NF-Y family provide insights into the defense mechanisms of honeybees under adverse circumstances. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 4977-4995.	2.4	6
20215	Astrocyte-Derived Exosomal microRNA miR-200a-3p Prevents MPP+-Induced Apoptotic Cell Death Through Down-Regulation of MKK4. <i>Neurochemical Research</i> , 2020, 45, 1020-1033.	1.6	43
20216	Electronic health records for the diagnosis of rare diseases. <i>Kidney International</i> , 2020, 97, 676-686.	2.6	37
20217	Integrative pathway enrichment analysis of multivariate omics data. <i>Nature Communications</i> , 2020, 11, 735.	5.8	125
20218	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020, 11, 729.	5.8	73
20219	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020, 578, 129-136.	13.7	280
20220	<i>APOE</i> genotype regulates pathology and disease progression in synucleinopathy. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	102
20221	Combining lexical and context features for automatic ontology extension. <i>Journal of Biomedical Semantics</i> , 2020, 11, 1.	0.9	14
20222	Q-Cell Glioblastoma Resource: Proteomics Analysis Reveals Unique Cell-States Are Maintained in 3D Culture. <i>Cells</i> , 2020, 9, 267.	1.8	12
20223	Comparative Transcriptome Analysis of Different <i>Dendrobium</i> Species Reveals Active Ingredients-Related Genes and Pathways. <i>International Journal of Molecular Sciences</i> , 2020, 21, 861.	1.8	23
20224	CDK1 serves as a potential prognostic biomarker and target for lung cancer. <i>Journal of International Medical Research</i> , 2020, 48, 030006051989750.	0.4	46
20225	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
20226	Transcriptome Analysis Reveals the Resistance Mechanism of <i>Pseudomonas aeruginosa</i> to Tachyplesin I. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 155-169.	1.1	5
20227	Establishment and Characterisation by Expression Microarray of Patient-Derived Xenograft Panel of Human Pancreatic Adenocarcinoma Patients. <i>International Journal of Molecular Sciences</i> , 2020, 21, 962.	1.8	12
20228	Wnt/Catenin Preserves the Stem State of Murine Bone Marrow Stromal Cells Through Activation of EZH2. <i>Journal of Bone and Mineral Research</i> , 2020, 35, 1149-1162.	3.1	42
20229	Coordinating dissent as an alternative to consensus classification: insights from systematics for bio-ontologies. <i>History and Philosophy of the Life Sciences</i> , 2020, 42, 8.	0.6	17

#	ARTICLE	IF	CITATIONS
20230	A comparative chemogenic analysis for predicting Drug-Target Pair via Machine Learning Approaches. <i>Scientific Reports</i> , 2020, 10, 6870.	1.6	12
20231	RadAtlas 1.0: a knowledgebase focusing on radiation-associated genes. <i>International Journal of Radiation Biology</i> , 2020, 96, 980-987.	1.0	7
20232	Prostate cancer cellâ€intrinsic interferon signaling regulates dormancy and metastatic outgrowth in bone. <i>EMBO Reports</i> , 2020, 21, e50162.	2.0	58
20233	Key genes of renal tubular necrosis: a bioinformatics analysis. <i>Translational Andrology and Urology</i> , 2020, 9, 654-664.	0.6	3
20234	Co-regularized nonnegative matrix factorization for evolving community detection in dynamic networks. <i>Information Sciences</i> , 2020, 528, 265-279.	4.0	16
20235	Complete genome sequence of <i>Bacillus</i> sp. N1-1, a \hat{e} -selenocarrageenan degrading bacterium isolated from the cold seep in the South China Sea. <i>Marine Genomics</i> , 2020, 54, 100771.	0.4	10
20236	Gene expression profiles for low-dose exposure to diethyl phthalate in rodents and humans: a translational study with implications for breast carcinogenesis. <i>Scientific Reports</i> , 2020, 10, 7067.	1.6	19
20237	Genetic variants and underlying mechanisms influencing variance heterogeneity in maize. <i>Plant Journal</i> , 2020, 103, 1089-1102.	2.8	7
20238	Comparative mitochondrial proteomics of <i>Leishmania tropica</i> clinical isolates resistant and sensitive to meglumine antimoniate. <i>Parasitology Research</i> , 2020, 119, 1857-1871.	0.6	9
20239	Non-contiguous finished genome sequence and description of <i>Bartonella sahelensis</i> sp. nov. from the blood of <i>Gerbilliscus gambianus</i> from Senegal. <i>New Microbes and New Infections</i> , 2020, 35, 100667.	0.8	3
20240	Contribution of common and rare damaging variants in familial forms of bipolar disorder and phenotypic outcome. <i>Translational Psychiatry</i> , 2020, 10, 124.	2.4	5
20241	Plasma MicroRNA Expression Profiles in Psoriasis. <i>Journal of Immunology Research</i> , 2020, 2020, 1-12.	0.9	9
20242	Screening and Identification of Differentially Expressed Genes Expressed among Left and Right Colon Adenocarcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-16.	0.9	4
20243	Comparative Transcriptome Analyses of <i>Schistosoma japonicum</i> Derived From SCID Mice and BALB/c Mice: Clues to the Abnormality in Parasite Growth and Development. <i>Frontiers in Microbiology</i> , 2020, 11, 274.	1.5	5
20244	An APETALA2/ethylene responsive factor, OsEBP89 knockout enhances adaptation to direct-seeding on wet land and tolerance to drought stress in rice. <i>Molecular Genetics and Genomics</i> , 2020, 295, 941-956.	1.0	27
20245	Identification of a conserved set of cytokinin-responsive genes expressed in the fruits of <i>Prunus persica</i> . <i>Plant Growth Regulation</i> , 2020, 92, 65-80.	1.8	1
20246	Reactive oxygen species and antimicrobial peptides are sequentially produced in silkworm midgut in response to bacterial infection. <i>Developmental and Comparative Immunology</i> , 2020, 110, 103720.	1.0	10
20247	Comprehensive analysis of the SLC16A gene family in pancreatic cancer via integrated bioinformatics. <i>Scientific Reports</i> , 2020, 10, 7315.	1.6	37

#	ARTICLE	IF	CITATIONS
20248	Hypoxia-induced alterations of transcriptome and chromatin accessibility in HL cells. <i>IUBMB Life</i> , 2020, 72, 1737-1746.	1.5	13
20249	The negative regulator SMAX1 controls mycorrhizal symbiosis and strigolactone biosynthesis in rice. <i>Nature Communications</i> , 2020, 11, 2114.	5.8	101
20250	A novel method to predict essential proteins based on tensor and HITS algorithm. <i>Human Genomics</i> , 2020, 14, 14.	1.4	11
20251	Exercise Training in Obese Rats Does Not Induce Browning at Thermoneutrality and Induces a Muscle-Like Signature in Brown Adipose Tissue. <i>Frontiers in Endocrinology</i> , 2020, 11, 97.	1.5	28
20252	Uncovering Prognosis-Related Genes and Pathways by Multi-Omics Analysis in Lung Cancer. <i>Biomolecules</i> , 2020, 10, 524.	1.8	33
20253	Genomic Features of <i>Cladobotryum dendroides</i> , Which Causes Cobweb Disease in Edible Mushrooms, and Identification of Genes Related to Pathogenicity and Mycoparasitism. <i>Pathogens</i> , 2020, 9, 232.	1.2	15
20254	Immunotoxicities of microplastics and sertraline, alone and in combination, to a bivalve species: size-dependent interaction and potential toxication mechanism. <i>Journal of Hazardous Materials</i> , 2020, 396, 122603.	6.5	109
20255	GOMCL: a toolkit to cluster, evaluate, and extract non-redundant associations of Gene Ontology-based functions. <i>BMC Bioinformatics</i> , 2020, 21, 139.	1.2	37
20256	Genome-wide DNA polymorphisms in four <i>Actinidia arguta</i> genotypes based on whole-genome re-sequencing. <i>PLoS ONE</i> , 2020, 15, e0219884.	1.1	3
20257	Loci associated with conception rate in crossbred beef heifers. <i>PLoS ONE</i> , 2020, 15, e0230422.	1.1	4
20258	Cell type-specific transcriptomics of esophageal adenocarcinoma as a scalable alternative for single cell transcriptomics. <i>Molecular Oncology</i> , 2020, 14, 1170-1184.	2.1	8
20259	LncRNA SNHG6 plays an oncogenic role in colorectal cancer and can be used as a prognostic biomarker for solid tumors. <i>Journal of Cellular Physiology</i> , 2020, 235, 7620-7634.	2.0	27
20260	A macroscopic theory for predicting catastrophic phenomena in both biological and mechanical chemical reactions. <i>Artificial Life and Robotics</i> , 2020, 25, 178-188.	0.7	0
20261	Prognostic medication: prediction by a macroscopic equation model for actual medical histories of illness with various recovery speeds. <i>Artificial Life and Robotics</i> , 2020, 25, 189-198.	0.7	0
20262	Genetic Architecture of Gene Expression in European and African Americans: An eQTL Mapping Study in GENOA. <i>American Journal of Human Genetics</i> , 2020, 106, 496-512.	2.6	56
20263	Histologic examination and transcriptome analysis uncovered liver damage in largemouth bass from formulated diets. <i>Aquaculture</i> , 2020, 526, 735329.	1.7	15
20264	Cell Type-Specific Intralocus Interactions Reveal Oligodendrocyte Mechanisms in MS. <i>Cell</i> , 2020, 181, 382-395.e21.	13.5	39
20265	Rewilding Nod2 and Atg16l1 Mutant Mice Uncovers Genetic and Environmental Contributions to Microbial Responses and Immune Cell Composition. <i>Cell Host and Microbe</i> , 2020, 27, 830-840.e4.	5.1	62

#	ARTICLE	IF	CITATIONS
20266	Ontologies in radiation oncology. <i>Physica Medica</i> , 2020, 72, 103-113.	0.4	13
20267	Identification and comparison of exosomal microRNAs in the milk and colostrum of two different cow breeds. <i>Gene</i> , 2020, 743, 144609.	1.0	34
20268	De novo leaf transcriptome assembly of <i>Bougainvillea spectabilis</i> for the identification of genes involves in the secondary metabolite pathways. <i>Gene</i> , 2020, 746, 144660.	1.0	5
20269	Study on the virulome and resistome of a vancomycin intermediate-resistance <i>Staphylococcus aureus</i> . <i>Microbial Pathogenesis</i> , 2020, 145, 104187.	1.3	5
20270	Transcriptional and Spatial Resolution of Cell Types in the Mammalian Habenula. <i>Neuron</i> , 2020, 106, 743-758.e5.	3.8	99
20271	Ultrastructure observation and transcriptome analysis of <i>Penicillium expansum</i> invasion in postharvest pears. <i>Postharvest Biology and Technology</i> , 2020, 165, 111198.	2.9	27
20272	Microbiome structure and function in rhizosphere of Jerusalem artichoke grown in saline land. <i>Science of the Total Environment</i> , 2020, 724, 138259.	3.9	44
20273	Chromosome doubling mediates superior drought tolerance in <i>Lycium ruthenicum</i> via abscisic acid signaling. <i>Horticulture Research</i> , 2020, 7, 40.	2.9	48
20274	Genome sequence of <i>Gossypium herbaceum</i> and genome updates of <i>Gossypium arboreum</i> and <i>Gossypium hirsutum</i> provide insights into cotton A-genome evolution. <i>Nature Genetics</i> , 2020, 52, 516-524.	9.4	240
20275	The transcriptome of the newt <i>Cynops orientalis</i> provides new insights into evolution and function of sexual gene networks in sarcopterygians. <i>Scientific Reports</i> , 2020, 10, 5445.	1.6	11
20276	WeiBI (web-based platform): Enriching integrated interaction network with increased coverage and functional proteins from genome-wide experimental OMICS data. <i>Scientific Reports</i> , 2020, 10, 5618.	1.6	3
20277	Cell Cycle Profiling Reveals Protein Oscillation, Phosphorylation, and Localization Dynamics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 608-623.	2.5	22
20278	A Similar Genetic Architecture Underlies the Convergent Evolution of the Selfing Syndrome in <i>Capsella</i> . <i>Plant Cell</i> , 2020, 32, 935-949.	3.1	19
20279	To construct a ceRNA regulatory network as prognostic biomarkers for bladder cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 5375-5386.	1.6	51
20280	Hemagglutinin Stability Regulates H1N1 Influenza Virus Replication and Pathogenicity in Mice by Modulating Type I Interferon Responses in Dendritic Cells. <i>Journal of Virology</i> , 2020, 94, .	1.5	18
20281	Integrated Analysis to Evaluate the Prognostic Value of Signature mRNAs in Glioblastoma Multiforme. <i>Frontiers in Genetics</i> , 2020, 11, 253.	1.1	11
20282	Capital Breeding in a Diapausing Copepod: A Transcriptomics Analysis. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	10
20283	Cellular Analysis and Comparative Transcriptomics Reveal the Tolerance Mechanisms of <i>Candida tropicalis</i> Toward Phenol. <i>Frontiers in Microbiology</i> , 2020, 11, 544.	1.5	10

#	ARTICLE	IF	CITATIONS
20284	Genome and Transcriptome Analyses Provide Insight Into the Omega-3 Long-Chain Polyunsaturated Fatty Acids Biosynthesis of <i>Schizochytrium limacinum</i> SR21. <i>Frontiers in Microbiology</i> , 2020, 11, 687.	1.5	20
20285	Astrocyte-Derived Small Extracellular Vesicles Regulate Dendritic Complexity through miR-26a-5p Activity. <i>Cells</i> , 2020, 9, 930.	1.8	42
20286	Transcriptomic Prediction of Pig Liver-Enriched Gene 1 Functions in a Liver Cell Line. <i>Genes</i> , 2020, 11, 412.	1.0	1
20287	De Novo Transcriptome Assembly and Annotation of Liver and Brain Tissues of Common Brushtail Possums (<i>Trichosurus vulpecula</i>) in New Zealand: Transcriptome Diversity after Decades of Population Control. <i>Genes</i> , 2020, 11, 436.	1.0	8
20288	HIV-1 and Amyloid Beta Remodel Proteome of Brain Endothelial Extracellular Vesicles. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2741.	1.8	11
20289	Independent analysis reveals PDK4 as independent predictor of recurrence in prostate cancer. <i>Molecular Systems Biology</i> , 2020, 16, e9247.	3.2	38
20290	Association of Proteins Modulating Immune Response and Insulin Clearance during Gestation with Antenatal Complications in Patients with Gestational or Type 2 Diabetes Mellitus. <i>Cells</i> , 2020, 9, 1032.	1.8	7
20291	A comprehensive review of computational techniques for the prediction of drug side effects. <i>Drug Development Research</i> , 2020, 81, 650-670.	1.4	27
20292	Biomechanical stimulation effects on the metabolism of adipocyte. <i>Journal of Cellular Physiology</i> , 2020, 235, 8702-8713.	2.0	8
20293	Bioinformatics analysis and verification of gene targets for benign tracheal stenosis. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1245.	0.6	3
20294	Single-cell analysis of a mutant library generated using CRISPR-guided deaminase in human melanoma cells. <i>Communications Biology</i> , 2020, 3, 154.	2.0	25
20295	RA-map: building a state-of-the-art interactive knowledge base for rheumatoid arthritis. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	25
20296	Protein Synthesis by Day 16 Bovine Conceptuses during the Time of Maternal Recognition of Pregnancy. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2870.	1.8	10
20297	Red Chinese Cabbage Transcriptome Analysis Reveals Structural Genes and Multiple Transcription Factors Regulating Reddish Purple Color. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2901.	1.8	21
20298	Identification of AfIR Binding Sites in the Genome of <i>Aspergillus flavus</i> by ChIP-Seq. <i>Journal of Fungi</i> (Basel, Switzerland), 2020, 6, 52.	1.5	9
20299	Time Course of Changes in Sorafenib-Treated Hepatocellular Carcinoma Cells Suggests Involvement of Phospho-Regulated Signaling in Ferroptosis Induction. <i>Proteomics</i> , 2020, 20, 2000006.	1.3	21
20300	CRISPR-mediated gene targeting of CK1 β leads to enhanced understanding of their role in endocytosis via phosphoregulation of GAPVD1. <i>Scientific Reports</i> , 2020, 10, 6797.	1.6	8
20301	Transcriptomic profiling and discovery of key genes involved in adventitious root formation from green cuttings of highbush blueberry (<i>Vaccinium corymbosum</i> L.). <i>BMC Plant Biology</i> , 2020, 20, 182.	1.6	22

#	ARTICLE	IF	CITATIONS
20302	Identification and integrated analysis of hepatocellular carcinoma-related circular RNA signature. <i>Annals of Translational Medicine</i> , 2020, 8, 294-294.	0.7	16
20303	Genome Sequencing and Analysis of the Hypocrellin-Producing Fungus <i>Shiraia bambusicola</i> S4201. <i>Frontiers in Microbiology</i> , 2020, 11, 643.	1.5	7
20304	Microbiota Characterization of Agricultural Green Waste-Based Suppressive Composts Using Omics and Classic Approaches. <i>Agriculture (Switzerland)</i> , 2020, 10, 61.	1.4	21
20305	Identification of Novel Targets of RBM5 in the Healthy and Injured Brain. <i>Neuroscience</i> , 2020, 440, 299-315.	1.1	7
20306	Pathogenic and antimicrobial resistance genes in <i>Streptococcus oralis</i> strains revealed by comparative genome analysis. <i>Genomics</i> , 2020, 112, 3783-3793.	1.3	6
20307	The phylogenetic landscape and nosocomial spread of the multidrug-resistant opportunist <i>Stenotrophomonas maltophilia</i> . <i>Nature Communications</i> , 2020, 11, 2044.	5.8	76
20308	Electronic Cigarette (E-Cigarette) Vapor Exposure Alters the <i>Streptococcus pneumoniae</i> Transcriptome in a Nicotine-Dependent Manner without Affecting Pneumococcal Virulence. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	13
20309	Comparative Genomic Analysis of Closely Related <i>Acetobacter pasteurianus</i> Strains Provides Evidence of Horizontal Gene Transfer and Reveals Factors Necessary for Thermotolerance. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	17
20310	Growth and elongation of axons through mechanical tension mediated by fluorescent-magnetic bifunctional Fe ₃ O ₄ -Rhodamine 6G@PDA superparticles. <i>Journal of Nanobiotechnology</i> , 2020, 18, 64.	4.2	15
20311	GATA2 and Progesterone Receptor Interaction in Endometrial Stromal Cells Undergoing Decidualization. <i>Endocrinology</i> , 2020, 161, .	1.4	12
20312	Comparison of Transcriptome Profiles of the Fungus <i>Botrytis cinerea</i> and Insect Pest <i>Bradysia odoriphaga</i> in Response to Benzothiazole. <i>Frontiers in Microbiology</i> , 2020, 11, 1043.	1.5	9
20313	Analysis of differentially expressed genes and pathways associated with male sterility lines in watermelon via bulked segregant RNA-seq. <i>3 Biotech</i> , 2020, 10, 222.	1.1	9
20314	Investigating global gene expression changes in a murine model of cherubism. <i>Bone</i> , 2020, 135, 115315.	1.4	0
20315	Stress-mediated convergence of splicing landscapes in male and female rock doves. <i>BMC Genomics</i> , 2020, 21, 251.	1.2	5
20316	Comparative molecular cell-of-origin classification of diffuse large B-cell lymphoma based on liquid and tissue biopsies. <i>Translational Medicine Communications</i> , 2020, 5, .	0.5	11
20317	Regulation of intrinsic polarity establishment by a differentiation-type MAPK pathway. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	11
20318	Draft Genome Assembly for the Tibetan Black Bear (<i>Ursus thibetanus thibetanus</i>). <i>Frontiers in Genetics</i> , 2020, 11, 231.	1.1	8
20319	Deep Proteomic Insights into the Individual Short-Term Pellicle Formation on Enamel—An In Situ Pilot Study. <i>Proteomics - Clinical Applications</i> , 2020, 14, e1900090.	0.8	15

#	ARTICLE	IF	CITATIONS
20320	Learning-induced mRNA alterations in olfactory bulb mitral cells in neonatal rats. <i>Learning and Memory</i> , 2020, 27, 209-221.	0.5	3
20321	SDN2GO: An Integrated Deep Learning Model for Protein Function Prediction. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 391.	2.0	38
20322	Fold-Change-Specific Enrichment Analysis (FSEA): Quantification of Transcriptional Response Magnitude for Functional Gene Groups. <i>Genes</i> , 2020, 11, 434.	1.0	7
20323	Differential Transcriptome Analysis of <i>Cervus elaphus songaricus</i> and <i>Cervus elaphus yarkandensis</i> Reveals Candidate Genes for Antler Regeneration. <i>Russian Journal of Genetics</i> , 2020, 56, 324-332.	0.2	1
20324	Identification of genes and signaling pathways associated with immune response of <i>Hemibarbus maculatus</i> (Bleeker, 1871) to ammonia stress. <i>Aquaculture</i> , 2020, 524, 735265.	1.7	9
20325	Identification and validation of metformin protects against PM2.5-induced macrophages cytotoxicity by targeting toll like receptor pathway. <i>Chemosphere</i> , 2020, 251, 126526.	4.2	6
20326	Mutational landscape and genetic signatures of cell-free DNA in tumour-induced osteomalacia. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 4931-4943.	1.6	4
20327	Genome of extreme halophyte <i>Puccinellia tenuiflora</i> . <i>BMC Genomics</i> , 2020, 21, 311.	1.2	8
20328	Full-length transcriptome sequencing and comparative transcriptomic analysis to uncover genes involved in early gametogenesis in the gonads of Amur sturgeon (<i>Acipenser schrenckii</i>). <i>Frontiers in Zoology</i> , 2020, 17, 11.	0.9	21
20329	Fifteen Years of Gene Set Analysis for High-Throughput Genomic Data: A Review of Statistical Approaches and Future Challenges. <i>Entropy</i> , 2020, 22, 427.	1.1	34
20330	Whole genome sequence analysis of the mosquitocidal <i>Bacillus thuringiensis</i> LLP29. <i>Archives of Microbiology</i> , 2020, 202, 1693-1700.	1.0	5
20331	Pleiotropy-Based Decomposition of Genetic Risk Scores: Association and Interaction Analysis for Type 2 Diabetes and CAD. <i>American Journal of Human Genetics</i> , 2020, 106, 646-658.	2.6	17
20332	Characterization of aerobic denitrification genome sequencing of <i>Vibrio parahaemolyticus</i> strain HA2 from recirculating mariculture system in China. <i>Aquaculture</i> , 2020, 526, 735295.	1.7	13
20333	Insulin-Like Growth Factors Are Key Regulators of T Helper 17 Regulatory T Cell Balance in Autoimmunity. <i>Immunity</i> , 2020, 52, 650-667.e10.	6.6	84
20334	Transcriptomic analysis of pepper plants provides insights into host responses to <i>Fusarium solani</i> infestation. <i>Journal of Biotechnology</i> , 2020, 314-315, 53-62.	1.9	9
20335	A network pharmacology approach to investigate the mechanism of Shuxuening injection in the treatment of ischemic stroke. <i>Journal of Ethnopharmacology</i> , 2020, 257, 112891.	2.0	61
20336	Complete genome sequence data of multidrug-resistant <i>Stenotrophomonas</i> sp. strain SXG-1. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 206-209.	0.9	4
20337	Schwann Cell Migration through Magnetic Actuation Mediated by Fluorescent Magnetic Bifunctional Fe ₃ O ₄ -Rhodamine 6G@Polydopamine Superparticles. <i>ACS Chemical Neuroscience</i> , 2020, 11, 1359-1370.	1.7	5

#	ARTICLE	IF	CITATIONS
20338	Adaptive Shifts in Gene Regulation Underlie a Developmental Delay in Thermogenesis in High-Altitude Deer Mice. <i>Molecular Biology and Evolution</i> , 2020, 37, 2309-2321.	3.5	18
20339	<i>Camellia</i> Plant Resistance and Susceptibility to Petal Blight Disease Are Defined by the Timing of Defense Responses. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 982-995.	1.4	2
20340	Transcriptomics at Maize Embryo/Endosperm Interfaces Identifies a Transcriptionally Distinct Endosperm Subdomain Adjacent to the Embryo Scutellum. <i>Plant Cell</i> , 2020, 32, 833-852.	3.1	60
20341	Comparison of the transcriptional profile in the decidua of early-onset and late-onset pre-eclampsia. <i>Journal of Obstetrics and Gynaecology Research</i> , 2020, 46, 1055-1066.	0.6	13
20342	Protein modification with ISG15 blocks coxsackievirus pathology by antiviral and metabolic reprogramming. <i>Science Advances</i> , 2020, 6, eaay1109.	4.7	27
20343	<i>Clostridioies difficile</i> -Associated Antibiotics Alter Human Mucosal Barrier Functions by Microbiome-Independent Mechanisms. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	7
20344	A Five-Genes-Based Prognostic Signature for Cervical Cancer Overall Survival Prediction. <i>International Journal of Genomics</i> , 2020, 2020, 1-13.	0.8	23
20345	miR-29a Is Repressed by MYC in Pancreatic Cancer and Its Restoration Drives Tumor-Suppressive Effects via Downregulation of LOXL2. <i>Molecular Cancer Research</i> , 2020, 18, 311-323.	1.5	27
20346	Dual Relief of T-lymphocyte Proliferation and Effector Function Underlies Response to PD-1 Blockade in Epithelial Malignancies. <i>Cancer Immunology Research</i> , 2020, 8, 869-882.	1.6	16
20347	Transcriptomic diversity in seedling roots of European flint maize in response to cold. <i>BMC Genomics</i> , 2020, 21, 300.	1.2	14
20348	Common gene expression signatures in Parkinson's disease are driven by changes in cell composition. <i>Acta Neuropathologica Communications</i> , 2020, 8, 55.	2.4	38
20349	Immune Suppressive Extracellular Vesicle Proteins of <i>Leptopilina heterotoma</i> Are Encoded in the Wasp Genome. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1-12.	0.8	12
20350	Divergence of Peroxisome Membrane Gene Sequence and Expression Between Yeast Species. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2079-2085.	0.8	3
20351	Knowledge-Based Biomedical Data Science. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 23-41.	2.8	34
20352	PSF Promotes ER-Positive Breast Cancer Progression via Posttranscriptional Regulation of <i>ESR1</i> and <i>SCFD2</i> . <i>Cancer Research</i> , 2020, 80, 2230-2242.	0.4	50
20353	Diversity of peripheral blood human NK cells identified by single-cell RNA sequencing. <i>Blood Advances</i> , 2020, 4, 1388-1406.	2.5	125
20354	Highly multiplexed proteomic assessment of human bone marrow in acute myeloid leukemia. <i>Blood Advances</i> , 2020, 4, 367-379.	2.5	29
20355	Transcriptome Ortholog Alignment Sequence Tools (TOAST) for phylogenomic dataset assembly. <i>BMC Evolutionary Biology</i> , 2020, 20, 41.	3.2	9

#	ARTICLE	IF	CITATIONS
20356	Stable intronic sequence RNAs (sisRNAs) are selected regions in introns with distinct properties. <i>BMC Genomics</i> , 2020, 21, 287.	1.2	3
20357	Inactivation of <i>Zeb1</i> in GRHL2-deficient mouse embryos rescues mid-gestation viability and secondary palate closure. <i>DMM Disease Models and Mechanisms</i> , 2020, 13, .	1.2	16
20358	Hydra: A mixture modeling framework for subtyping pediatric cancer cohorts using multimodal gene expression signatures. <i>PLoS Computational Biology</i> , 2020, 16, e1007753.	1.5	1
20359	eXplainable Artificial Intelligence (XAI) for the identification of biologically relevant gene expression patterns in longitudinal human studies, insights from obesity research. <i>PLoS Computational Biology</i> , 2020, 16, e1007792.	1.5	44
20360	Draft genome of multiple resistance donor plant <i>Sinapis alba</i> : An insight into SSRs, annotations and phylogenetics. <i>PLoS ONE</i> , 2020, 15, e0231002.	1.1	17
20361	Unveiling new disease, pathway, and gene associations via multi-scale neural network. <i>PLoS ONE</i> , 2020, 15, e0231059.	1.1	18
20362	Modulator-Dependent RBPs Changes Alternative Splicing Outcomes in Kidney Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 265.	1.1	22
20363	Identification of Co-expressed Genes Between Atrial Fibrillation and Stroke. <i>Frontiers in Neurology</i> , 2020, 11, 184.	1.1	15
20364	Integrated Analysis of Long Non-coding RNAs (lncRNAs) and mRNAs Reveals the Regulatory Role of lncRNAs Associated With Salt Resistance in <i>Camellia sinensis</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 218.	1.7	28
20365	Cardiac miRNA Expression and their mRNA Targets in a Rat Model of Prediabetes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2128.	1.8	9
20366	Cytoplasm Types Affect DNA Methylation among Different Cytoplasmic Male Sterility Lines and Their Maintainer Line in Soybean (<i>Glycine max</i> L.). <i>Plants</i> , 2020, 9, 385.	1.6	2
20367	Development of IFN-Stimulated Gene Expression from Embryogenesis through Adulthood, with and without Constitutive MDA5 Pathway Activation. <i>Journal of Immunology</i> , 2020, 204, 2791-2807.	0.4	0
20368	Decreased Expression of NUSAP1 Predicts Poor Overall Survival in Cervical Cancer. <i>Journal of Cancer</i> , 2020, 11, 2852-2863.	1.2	19
20369	Majority of cerebrospinal fluid-contacting neurons in the spinal cord of <i>C57Bl/6N</i> mice is present in ectopic position unlike in other studied experimental mice strains and mammalian species. <i>Journal of Comparative Neurology</i> , 2020, 528, 2523-2550.	0.9	13
20370	Genetic diagnosis of autoinflammatory disease patients using clinical exome sequencing. <i>European Journal of Medical Genetics</i> , 2020, 63, 103920.	0.7	15
20371	Genomic analysis of a hop-resistance <i>Lactobacillus brevis</i> strain responsible for food spoilage and capable of entering into the VBNC state. <i>Microbial Pathogenesis</i> , 2020, 145, 104186.	1.3	7
20372	The morphology, molecular development and ecological function of pseudonectaries on <i>Nigella damascena</i> (Ranunculaceae) petals. <i>Nature Communications</i> , 2020, 11, 1777.	5.8	18
20373	Interactive semi-supervised learning for microarray analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, , 1-1.	1.9	0

#	ARTICLE	IF	CITATIONS
20374	Integrating multi-network topology for gene function prediction using deep neural networks. Briefings in Bioinformatics, 2021, 22, 2096-2105.	3.2	73
20375	Genome-wide identification and expression analysis of detoxification efflux carriers (DTX) genes family under abiotic stresses in flax. Physiologia Plantarum, 2021, 171, 483-501.	2.6	21
20376	Identification of Potential Hub Genes of Atherosclerosis Through Bioinformatic Analysis. Journal of Computational Biology, 2021, 28, 60-78.	0.8	4
20377	Short-term transcriptomic responses of Populus euphratica roots and leaves to drought stress. Journal of Forestry Research, 2021, 32, 841-853.	1.7	32
20378	Dynamical patterning modules and network motifs as joint determinants of development: Lessons from an aggregative bacterium. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2021, 336, 300-314.	0.6	3
20379	Emerging Methods and Resources for Biological Interrogation of Neuropsychiatric Polygenic Signal. Biological Psychiatry, 2021, 89, 41-53.	0.7	38
20380	Using Reactome to build an autophagy mechanism knowledgebase. Autophagy, 2021, 17, 1543-1554.	4.3	5
20381	Associations Between <i>IFI44L</i> Gene Variants and Rates of Respiratory Tract Infections During Early Childhood. Journal of Infectious Diseases, 2021, 223, 157-165.	1.9	7
20382	Dissecting the phenotypic components and genetic architecture of maize stem vascular bundles using high-throughput phenotypic analysis. Plant Biotechnology Journal, 2021, 19, 35-50.	4.1	25
20383	Inflammatory macrophage memory in nonsteroidal anti-inflammatory drug-exacerbated respiratory disease. Journal of Allergy and Clinical Immunology, 2021, 147, 587-599.	1.5	25
20384	Using conceptual modeling to improve genome data management. Briefings in Bioinformatics, 2021, 22, 45-54.	3.2	12
20385	Survey and comparative assessments of computational multi-omics integrative methods with multiple regulatory networks identifying distinct tumor compositions across pan-cancer data sets. Briefings in Bioinformatics, 2021, 22, .	3.2	9
20386	The Minimum Information about a Molecular Interaction CAusal STATEment (MI2CAST). Bioinformatics, 2021, 36, 5712-5718.	1.8	14
20387	Improvements in Genomic Technologies: Applications to Crop Research. , 2021, , 113-126.		0
20388	Structured sparsity regularization for analyzing high-dimensional omics data. Briefings in Bioinformatics, 2021, 22, 77-87.	3.2	27
20389	idenPC-MIIP: identify protein complexes from weighted PPI networks using mutual important interacting partner relation. Briefings in Bioinformatics, 2021, 22, 1972-1983.	3.2	15
20390	Making AI meaningful again. Synthèse, 2021, 198, 2061-2081.	0.6	16
20391	System-level analyses of keystone genes required for mammalian tooth development. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2021, 336, 7-17.	0.6	27

#	ARTICLE	IF	CITATIONS
20392	Bacterial–fungal interactions revealed by genome-wide analysis of bacterial mutant fitness. <i>Nature Microbiology</i> , 2021, 6, 87-102.	5.9	49
20393	Common Adaptive Strategies Underlie Within-Host Evolution of Bacterial Pathogens. <i>Molecular Biology and Evolution</i> , 2021, 38, 1101-1121.	3.5	28
20394	Genome sequence of a Vietnamese <i>Bacillus thuringiensis</i> strain TH19 reveals two potential insecticidal crystal proteins against <i>Etiella zinckenella</i> larvae. <i>Biological Control</i> , 2021, 152, 104473.	1.4	4
20395	CLAVATA Signaling Ensures Reproductive Development in Plants across Thermal Environments. <i>Current Biology</i> , 2021, 31, 220-227.e5.	1.8	19
20396	TCRD and Pharos 2021: mining the human proteome for disease biology. <i>Nucleic Acids Research</i> , 2021, 49, D1334-D1346.	6.5	109
20397	Elevated rates of positive selection drive the evolution of pestiferousness in the Colorado potato beetle (<i>Leptinotarsa decemlineata</i> , Say). <i>Molecular Ecology</i> , 2021, 30, 237-254.	2.0	16
20398	Blocking IL1 Beta Promotes Tumor Regression and Remodeling of the Myeloid Compartment in a Renal Cell Carcinoma Model: Multidimensional Analyses. <i>Clinical Cancer Research</i> , 2021, 27, 608-621.	3.2	73
20399	DrugCentral 2021 supports drug discovery and repositioning. <i>Nucleic Acids Research</i> , 2021, 49, D1160-D1169.	6.5	129
20400	Expression Changes in Epigenetic Gene Pathways Associated With One-Carbon Nutritional Metabolites in Maternal Blood From Pregnancies Resulting in Autism and Non-typical Neurodevelopment. <i>Autism Research</i> , 2021, 14, 11-28.	2.1	8
20401	CSF1R inhibition depletes tumor-associated macrophages and attenuates tumor progression in a mouse sonic Hedgehog-Medulloblastoma model. <i>Oncogene</i> , 2021, 40, 396-407.	2.6	35
20402	Sugar accumulation and characterization of metabolizing enzyme genes in leafy head of Chinese cabbage (<i>Brassica campestris</i> L. ssp. <i>pekinensis</i>). <i>Horticulture Environment and Biotechnology</i> , 2021, 62, 17-29.	0.7	8
20403	Deciphering cell–cell interactions and communication from gene expression. <i>Nature Reviews Genetics</i> , 2021, 22, 71-88.	7.7	575
20404	Marmoset Brain ISH Data Revealed Molecular Difference Between Cortical Folding Patterns. <i>Cerebral Cortex</i> , 2021, 31, 1660-1674.	1.6	2
20405	Clinical trait-connected network analysis reveals transcriptional markers of active psoriasis treatment with Liangxue-Jiedu decoction. <i>Journal of Ethnopharmacology</i> , 2021, 268, 113551.	2.0	14
20406	An <i>in silico</i> approach to identification, categorization and prediction of nucleic acid binding proteins. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	69
20407	Exploration of DNA Methylation-Driven Genes in Papillary Thyroid Carcinoma Based on the Cancer Genome Atlas. <i>Journal of Computational Biology</i> , 2021, 28, 99-114.	0.8	4
20408	Prevalence of Colistin Resistance in <i>Escherichia coli</i> in Eastern Turkey and Genomic Characterization of an <i>mcr-1</i> Positive Strain from Retail Chicken Meat. <i>Microbial Drug Resistance</i> , 2021, 27, 424-432.	0.9	10
20409	Characterization of left-handed beta helix domains, and identification and functional annotation of proteins containing such domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 6-20.	1.5	1

#	ARTICLE	IF	CITATIONS
20410	Complex landscape of alternative splicing in myeloid neoplasms. <i>Leukemia</i> , 2021, 35, 1108-1120.	3.3	39
20411	VRmol: an integrative web-based virtual reality system to explore macromolecular structure. <i>Bioinformatics</i> , 2021, 37, 1029-1031.	1.8	16
20412	Integrative biomarker detection on high-dimensional gene expression data sets: a survey on prior knowledge approaches. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	12
20413	Rumen metaproteomics: Closer to linking rumen microbial function to animal productivity traits. <i>Methods</i> , 2021, 186, 42-51.	1.9	21
20414	Analysis and identification of novel biomarkers involved in neuroblastoma via integrated bioinformatics. <i>Investigational New Drugs</i> , 2021, 39, 52-65.	1.2	8
20415	Proteomic Characterization of Circulating Molecular Perturbations Associated With Pancreatic Adenocarcinoma Following Intravenous 1% Fatty Acid and Gemcitabine Administration: A Pilot Study. <i>Journal of Parenteral and Enteral Nutrition</i> , 2021, 45, 738-750.	1.3	1
20416	Predicting disease-associated genes: Computational methods, databases, and evaluations. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2021, 11, e1383.	4.6	4
20417	Comparative transcriptome analysis of abalone <i>Haliotis discus hannai</i> with green and gray egg colors. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 350-361.	0.6	0
20418	Immune cell infiltration features and related marker genes in lung cancer based on single-cell RNA-seq. <i>Clinical and Translational Oncology</i> , 2021, 23, 405-417.	1.2	33
20419	Inhibition of the catalytic subunit of DNA-dependent protein kinase (DNA-PKcs) stimulates osteoblastogenesis by potentiating bone morphogenetic protein 2 (BMP2) responses. <i>Journal of Cellular Physiology</i> , 2021, 236, 1195-1213.	2.0	4
20420	Semantic Technologies in Drug Discovery. , 2021, , 129-144.		4
20421	Mass spectrometry-based protein identification in proteomics—a review. <i>Briefings in Bioinformatics</i> , 2021, 22, 1620-1638.	3.2	55
20422	Transcriptome differential expression analysis reveals the activated genes in <i>Litopenaeus vannamei</i> shrimp families of superior growth performance. <i>Aquaculture</i> , 2021, 531, 735871.	1.7	22
20423	Inducible Deletion of YAP and TAZ in Adult Mouse Smooth Muscle Causes Rapid and Lethal Colonic Pseudo-Obstruction. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 11, 623-637.	2.3	14
20424	Screening and Identification of Key Biomarkers in Melanoma: Evidence from Bioinformatic Analyses. <i>Journal of Computational Biology</i> , 2021, 28, 317-329.	0.8	3
20425	Unsupervised protein embeddings outperform hand-crafted sequence and structure features at predicting molecular function. <i>Bioinformatics</i> , 2021, 37, 162-170.	1.8	73
20426	Genome-Wide Association Analysis of Neonatal White Matter Microstructure. <i>Cerebral Cortex</i> , 2021, 31, 933-948.	1.6	3
20427	Mycobacterium tuberculosis Raf kinase inhibitor protein (RKIP) Rv2140c is involved in cell wall arabinogalactan biosynthesis via phosphorylation. <i>Microbiological Research</i> , 2021, 242, 126615.	2.5	3

#	ARTICLE	IF	CITATIONS
20428	High-throughput meta-analysis and validation of differentially expressed genes as potential biomarkers of ionizing radiation-response. <i>Radiotherapy and Oncology</i> , 2021, 154, 21-28.	0.3	7
20429	Mouse Genetic Reference Populations: Cellular Platforms for Integrative Systems Genetics. <i>Trends in Genetics</i> , 2021, 37, 251-265.	2.9	12
20430	The ModelSEED Biochemistry Database for the integration of metabolic annotations and the reconstruction, comparison and analysis of metabolic models for plants, fungi and microbes. <i>Nucleic Acids Research</i> , 2021, 49, D575-D588.	6.5	119
20431	Functional Genomics Platform, A Cloud-Based Platform for Studying Microbial Life at Scale. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 940-952.	1.9	18
20432	Predicting candidate genes from phenotypes, functions and anatomical site of expression. <i>Bioinformatics</i> , 2021, 37, 853-860.	1.8	23
20433	Transcriptomic analysis of gene expression in normal goat ovary and intersex goat gonad. <i>Reproduction in Domestic Animals</i> , 2021, 56, 12-25.	0.6	2
20434	Transcriptomic Analysis Reveals Common Adaptation Mechanisms Under Different Stresses for Moderately Piezophilic Bacteria. <i>Microbial Ecology</i> , 2021, 81, 617-629.	1.4	26
20435	Proteomics reveals sex-specific heat shock response of Baikal amphipod <i>Eulimnogammarus cyaneus</i> . <i>Science of the Total Environment</i> , 2021, 763, 143008.	3.9	4
20436	Comparative Toxicogenomics Database (CTD): update 2021. <i>Nucleic Acids Research</i> , 2021, 49, D1138-D1143.	6.5	625
20437	Computational prediction and analysis of histone H3k27me1-associated miRNAs. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140539.	1.1	4
20438	Early transcriptional changes after UVB treatment in atopic dermatitis include inverse regulation of IL-36 β and IL-37. <i>Experimental Dermatology</i> , 2021, 30, 249-261.	1.4	14
20439	OGEE v3: Online GENE Essentiality database with increased coverage of organisms and human cell lines. <i>Nucleic Acids Research</i> , 2021, 49, D998-D1003.	6.5	42
20440	A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. <i>European Respiratory Journal</i> , 2021, 57, 2002693.	3.1	15
20441	Kernelized fuzzy rough sets based online streaming feature selection for large-scale hierarchical classification. <i>Applied Intelligence</i> , 2021, 51, 1602-1615.	3.3	17
20442	Identification of potential key genes and miRNAs involved in Hepatoblastoma pathogenesis and prognosis. <i>Journal of Cell Communication and Signaling</i> , 2021, 15, 131-142.	1.8	8
20443	Transcriptome analysis of unsaturated fatty acids biosynthesis shows essential genes in sprouting of <i>Acer truncatum</i> Bunge seeds. <i>Food Bioscience</i> , 2021, 41, 100739.	2.0	5
20444	Addition of genistein to the fermentation process reduces citrinin production by <i>Monascus</i> via changes at the transcription level. <i>Food Chemistry</i> , 2021, 343, 128410.	4.2	21
20445	Nano-Al ₂ O ₃ can mediate transduction-like transformation of antibiotic resistance genes in water. <i>Journal of Hazardous Materials</i> , 2021, 405, 124224.	6.5	29

#	ARTICLE	IF	CITATIONS
20446	A genome-wide association study identifies a gene network associated with paranoid schizophrenia and antipsychotics-induced tardive dyskinesia. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2021, 105, 110134.	2.5	4
20447	Sexually dimorphic radiogenomic models identify distinct imaging and biological pathways that are prognostic of overall survival in glioblastoma. <i>Neuro-Oncology</i> , 2021, 23, 251-263.	0.6	24
20448	Novel loss-of-function variants in <i>DNAH17</i> cause multiple morphological abnormalities of the sperm flagella in humans and mice. <i>Clinical Genetics</i> , 2021, 99, 176-186.	1.0	26
20449	Cell populations in neonatal rat peripheral nerves identified by single-cell transcriptomics. <i>Glia</i> , 2021, 69, 765-778.	2.5	22
20450	Compartment-specific transcriptomics of ozone-exposed murine lungs reveals sex- and cell type-associated perturbations relevant to mucoinflammatory lung diseases. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2021, 320, L99-L125.	1.3	19
20451	Multi-ethnic GWAS and meta-analysis of sleep quality identify MPP6 as a novel gene that functions in sleep center neurons. <i>Sleep</i> , 2021, 44, .	0.6	5
20452	Analysis of the circRNAs expression profile in mouse lung with H7N9 influenza A virus infection. <i>Genomics</i> , 2021, 113, 716-727.	1.3	9
20453	Complete Genome Sequence of Zearalenone Degrading Bacteria <i>Bacillus velezensis</i> A2. <i>Current Microbiology</i> , 2021, 78, 347-350.	1.0	3
20454	Decoding the wheat awn transcriptome and overexpressing TaRca1 ¹² in rice for heat stress tolerance. <i>Plant Molecular Biology</i> , 2021, 105, 133-146.	2.0	16
20455	Melatonergic systems of AANAT, melatonin, and its receptor MT2 in the corpus luteum are essential for reproductive success in mammals. <i>Biology of Reproduction</i> , 2021, 104, 430-444.	1.2	10
20456	The Bgee suite: integrated curated expression atlas and comparative transcriptomics in animals. <i>Nucleic Acids Research</i> , 2021, 49, D831-D847.	6.5	112
20457	COVID-KOP: integrating emerging COVID-19 data with the ROBOKOP database. <i>Bioinformatics</i> , 2021, 37, 586-587.	1.8	15
20458	Expression Profiling and Functional Characterization of MicroRNAs in Apical Periodontitis. <i>Journal of Endodontics</i> , 2021, 47, 263-271.	1.4	14
20459	DeepPSP: A Global-Local Information-Based Deep Neural Network for the Prediction of Protein Phosphorylation Sites. <i>Journal of Proteome Research</i> , 2021, 20, 346-356.	1.8	25
20460	Identification of novel mRNA isoforms associated with meat tenderness using RNA sequencing data in beef cattle. <i>Meat Science</i> , 2021, 173, 108378.	2.7	17
20461	Quantitative Proteomics Reveals UGA-Independent Misincorporation of Selenocysteine throughout the <i>Escherichia coli</i> Proteome. <i>Journal of Proteome Research</i> , 2021, 20, 212-221.	1.8	8
20462	RNA Sequencing Reveals Diverse Functions of Amniotic Fluid Neutrophils and Monocytes/Macrophages in Intra-Amniotic Infection. <i>Journal of Innate Immunity</i> , 2021, 13, 63-82.	1.8	29
20463	Integration of the Drug-Gene Interaction Database (DGIdb 4.0) with open crowdsource efforts. <i>Nucleic Acids Research</i> , 2021, 49, D1144-D1151.	6.5	439

#	ARTICLE	IF	CITATIONS
20464	The transcriptional repressors VAL1 and VAL2 recruit PRC2 for genome-wide Polycomb silencing in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2021, 49, 98-113.	6.5	50
20465	Targeted inhibition of ER α signaling and PIP5K1 α /Akt pathways in castration-resistant prostate cancer. <i>Molecular Oncology</i> , 2021, 15, 968-986.	2.1	14
20466	Novel reference transcriptomes for the sponges <i>Carteriospongia foliascens</i> and <i>Cliona orientalis</i> and associated algal symbiont <i>Gerakladium endoclonium</i> . <i>Coral Reefs</i> , 2021, 40, 9-13.	0.9	3
20467	Intercellular Mitochondria Transfer to Macrophages Regulates White Adipose Tissue Homeostasis and Is Impaired in Obesity. <i>Cell Metabolism</i> , 2021, 33, 270-282.e8.	7.2	160
20468	Bioinformatics analysis of correlation between protein function and intrinsic disorder. <i>International Journal of Biological Macromolecules</i> , 2021, 167, 446-456.	3.6	6
20469	Identification of the interactomes associated with SCD6 and RBP42 proteins in <i>Leishmania braziliensis</i> . <i>Journal of Proteomics</i> , 2021, 233, 104066.	1.2	2
20470	Low-pass whole genome bisulfite sequencing of neonatal dried blood spots identifies a role for RUNX1 in Down syndrome DNA methylation profiles. <i>Human Molecular Genetics</i> , 2021, 29, 3465-3476.	1.4	32
20471	Assembly of the non-heading pak choi genome and comparison with the genomes of heading Chinese cabbage and the oilseed yellow sarson. <i>Plant Biotechnology Journal</i> , 2021, 19, 966-976.	4.1	28
20472	Hypoxic conditioned promotes the proliferation of human olfactory mucosa mesenchymal stem cells and relevant lncRNA and mRNA analysis. <i>Life Sciences</i> , 2021, 265, 118861.	2.0	6
20473	Whole genome sequencing and genome annotation of <i>Dermacoccus abyssi</i> strain HZAU 226 isolated from spoiled eggs. <i>Genomics</i> , 2021, 113, 1199-1206.	1.3	5
20474	RBP2GO: a comprehensive pan-species database on RNA-binding proteins, their interactions and functions. <i>Nucleic Acids Research</i> , 2021, 49, D425-D436.	6.5	41
20475	Transcriptomic responses from improved murine sepsis models can better mimic human surgical sepsis. <i>FASEB Journal</i> , 2021, 35, e21156.	0.2	5
20476	Insulin-promoted mobilization of GLUT4 from a perinuclear storage site requires RAB10. <i>Molecular Biology of the Cell</i> , 2021, 32, 57-73.	0.9	21
20477	Vascular neutrophilic inflammation and immunothrombosis distinguish severe COVID-19 from influenza pneumonia. <i>Journal of Thrombosis and Haemostasis</i> , 2021, 19, 574-581.	1.9	80
20478	Cancer/Testis Antigens into mitochondria: a hub between spermatogenesis, tumorigenesis and mitochondrial physiology adaptation. <i>Mitochondrion</i> , 2021, 56, 73-81.	1.6	7
20480	Alterations of 5-hydroxymethylcytosines in circulating cell-free DNA reflect retinopathy in type 2 diabetes. <i>Genomics</i> , 2021, 113, 79-87.	1.3	12
20481	Insights into amphicarp from the compact genome of the legume <i>Amphicarpaea edgeworthii</i> . <i>Plant Biotechnology Journal</i> , 2021, 19, 952-965.	4.1	22
20483	Quantitative Interactomics of Lck-TurboID in Living Human T Cells Unveils T Cell Receptor Stimulation-Induced Proximal Lck Interactors. <i>Journal of Proteome Research</i> , 2021, 20, 715-726.	1.8	16

#	ARTICLE	IF	CITATIONS
20484	Identification of Natural CRISPR Systems and Targets in the Human Microbiome. <i>Cell Host and Microbe</i> , 2021, 29, 94-106.e4.	5.1	20
20485	Global Inventory of ClpP- and ClpX-Regulated Proteins in <i>Staphylococcus aureus</i> . <i>Journal of Proteome Research</i> , 2021, 20, 867-879.	1.8	21
20486	The Integrin Interactome. <i>Methods in Molecular Biology</i> , 2021, , .	0.4	0
20487	NONCODEV6: an updated database dedicated to long non-coding RNA annotation in both animals and plants. <i>Nucleic Acids Research</i> , 2021, 49, D165-D171.	6.5	166
20488	Responses of the sugarcane rhizosphere microbiota to different levels of water stress. <i>Applied Soil Ecology</i> , 2021, 159, 103817.	2.1	12
20489	FunRich enables enrichment analysis of OMICs datasets. <i>Journal of Molecular Biology</i> , 2021, 433, 166747.	2.0	144
20490	Differential expression of lncRNAs in hypertension-induced pericytes. <i>Scandinavian Cardiovascular Journal</i> , 2021, 55, 102-105.	0.4	0
20491	NECAB1 and NECAB2 are Prevalent Calcium-Binding Proteins of CB1/CCK-Positive GABAergic Interneurons. <i>Cerebral Cortex</i> , 2021, 31, 1786-1806.	1.6	18
20492	Genome-wide investigation of the dynamic changes of epigenome modifications after global DNA methylation editing. <i>Nucleic Acids Research</i> , 2021, 49, 158-176.	6.5	20
20493	DeepMAge: A Methylation Aging Clock Developed with Deep Learning. , 2021, 12, 1252.		72
20494	Hypoxic naked mole-rat brains use microRNA to coordinate hypometabolic fuels and neuroprotective defenses. <i>Journal of Cellular Physiology</i> , 2021, 236, 5080-5097.	2.0	16
20495	Hidden in plain sight: The effects of BCG vaccination in the COVID-19 pandemic. <i>Journal of Medical Virology</i> , 2021, 93, 1950-1966.	2.5	13
20496	COPD patients with chronic bronchitis and higher sputum eosinophil counts show increased type-2 and PDE4 gene expression in sputum. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 905-918.	1.6	16
20497	Replaying the evolutionary tape to investigate subgenome dominance in allopolyploid <i>Brassica napus</i> . <i>New Phytologist</i> , 2021, 230, 354-371.	3.5	57
20498	<i>Dioscorea Alata</i> Tuber Proteome Analysis Uncovers Differentially Regulated Growth-associated Pathways of Tuber Development. <i>Plant and Cell Physiology</i> , 2021, 62, 191-204.	1.5	5
20499	Circulating microRNAs Associated With Reversible Cerebral Vasoconstriction Syndrome. <i>Annals of Neurology</i> , 2021, 89, 459-473.	2.8	23
20500	Specific MiRNAs in naïve T cells associated with Hepatitis C Virus-induced Hepatocellular Carcinoma. <i>Journal of Cancer</i> , 2021, 12, 1-9.	1.2	7
20501	Hearing impairment due to <i>Mir183/96/182</i> mutations suggests both loss-of-function and gain-of-function effects. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	1.2	14

#	ARTICLE	IF	CITATIONS
20502	Chronic circadian shift leads to adipose tissue inflammation and fibrosis. <i>Molecular and Cellular Endocrinology</i> , 2021, 521, 111110.	1.6	28
20503	Reduced lipolysis in lipoma phenocopies lipid accumulation in obesity. <i>International Journal of Obesity</i> , 2021, 45, 565-576.	1.6	14
20504	Chromosome-level reference genome assembly provides insights into aroma biosynthesis in passion fruit (<i>Passiflora edulis</i>). <i>Molecular Ecology Resources</i> , 2021, 21, 955-968.	2.2	31
20505	Transcriptome analysis of <i>Macrobrachium rosenbergii</i> hepatopancreas in response to <i>Vibrio harveyi</i> infection. <i>Aquaculture Research</i> , 2021, 52, 1855-1875.	0.9	3
20506	Full exome sequencing of 11 families with Hidradenitis suppurativa. <i>Journal of the European Academy of Dermatology and Venereology</i> , 2021, 35, 1203-1211.	1.3	17
20507	Ancient microRNA profiles of 14,300-yr-old canid samples confirm taxonomic origin and provide glimpses into tissue-specific gene regulation from the Pleistocene. <i>Rna</i> , 2021, 27, 324-334.	1.6	7
20508	Characterization and analysis of the transcriptome in <i>Opisina arenosella</i> from different developmental stages using single-molecule real-time transcript sequencing and RNA-seq. <i>International Journal of Biological Macromolecules</i> , 2021, 169, 216-227.	3.6	10
20509	Systematic review and meta-analysis of human transcriptomics reveals neuroinflammation, deficient energy metabolism, and proteostasis failure across neurodegeneration. <i>Neurobiology of Disease</i> , 2021, 149, 105225.	2.1	54
20510	Fully Automated Sample Processing and Analysis Workflow for Low-Input Proteome Profiling. <i>Analytical Chemistry</i> , 2021, 93, 1658-1666.	3.2	72
20511	Restoration of Î²-Globin Expression with Optimally Designed Lentiviral Vector for Î²-Thalassemia Treatment in Chinese Patients. <i>Human Gene Therapy</i> , 2021, 32, 481-494.	1.4	6
20512	Proteomics analysis of <i>Cyclobalanopsis gilva</i> provides new insights of low seed germination. <i>Biochimie</i> , 2021, 180, 68-78.	1.3	14
20513	Immunological Role and Prognostic Value of APBB1IP in Pan-Cancer Analysis. <i>Journal of Cancer</i> , 2021, 12, 595-610.	1.2	24
20514	Comparative genomics reveals dynamic genome evolution in host specialist ectomycorrhizal fungi. <i>New Phytologist</i> , 2021, 230, 774-792.	3.5	37
20515	Transcriptomic response of brain tissue to focused ultrasound-mediated blood-brain barrier disruption depends strongly on anesthesia. <i>Bioengineering and Translational Medicine</i> , 2021, 6, e10198.	3.9	12
20516	Urinary vitronectin identifies patients with high levels of fibrosis in kidney grafts. <i>Journal of Nephrology</i> , 2021, 34, 861-874.	0.9	20
20517	Competition between PRC2.1 and 2.2 subcomplexes regulates PRC2 chromatin occupancy in human stem cells. <i>Molecular Cell</i> , 2021, 81, 488-501.e9.	4.5	38
20518	Possible immune regulation mechanisms for the progression of chronic thromboembolic pulmonary hypertension. <i>Thrombosis Research</i> , 2021, 198, 122-131.	0.8	11
20519	Haldane's rule in the placenta: Sex-biased misregulation of the <i>Kcnq1</i> imprinting cluster in hybrid mice. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 86-100.	1.1	10

#	ARTICLE	IF	CITATIONS
20520	TOA: A software package for automated functional annotation in non-model plant species. <i>Molecular Ecology Resources</i> , 2021, 21, 621-636.	2.2	10
20521	The whole-genome sequencing and analysis of a <i>Ganoderma lucidum</i> strain provide insights into the genetic basis of its high triterpene content. <i>Genomics</i> , 2021, 113, 840-849.	1.3	19
20522	Transcriptome expression profiles between diploid and triploid Pacific abalone (<i>Haliotis discus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667. <i>100820</i> .	0.4	7
20523	CNS genomic profiling in the mouse chronic social stress model implicates a novel category of candidate genes integrating affective pathogenesis. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2021, 105, 110086.	2.5	6
20524	RUNX3 methylation drives hypoxia-induced cell proliferation and antiapoptosis in early tumorigenesis. <i>Cell Death and Differentiation</i> , 2021, 28, 1251-1269.	5.0	16
20525	Paternal reprogramming-escape histone H3K4me3 marks located within promoters of RNA splicing genes. <i>Bioinformatics</i> , 2021, 37, 1039-1044.	1.8	6
20526	Multiple transcriptomic profiling: p53 signaling pathway is involved in DEHP-induced prepubertal testicular injury via promoting cell apoptosis and inhibiting cell proliferation of Leydig cells. <i>Journal of Hazardous Materials</i> , 2021, 406, 124316.	6.5	39
20527	Microarray Profiling and Functional Identification of LncRNA in Mice Intestinal Mucosa Following Intestinal Ischemia/Reperfusion. <i>Journal of Surgical Research</i> , 2021, 258, 389-404.	0.8	3
20528	Stem lodging resistance in hullless barley: Transcriptome and metabolome analysis of lignin biosynthesis pathways in contrasting genotypes. <i>Genomics</i> , 2021, 113, 935-943.	1.3	20
20529	Transcriptome analysis of porcine endometrium after LPS-induced inflammation: effects of the PPAR-gamma ligands in vitro. <i>Biology of Reproduction</i> , 2021, 104, 130-143.	1.2	4
20530	MolluscDB: an integrated functional and evolutionary genomics database for the hyper-diverse animal phylum Mollusca. <i>Nucleic Acids Research</i> , 2021, 49, D988-D997.	6.5	54
20531	Third-Generation Sequencing Indicated that LncRNA Could Regulate eIF2D to Enhance Protein Translation Under Heat Stress in <i>Populus simonii</i> . <i>Plant Molecular Biology Reporter</i> , 2021, 39, 240-250.	1.0	4
20532	Identification and validation of a new gene signature predicting prognosis of hepatocellular carcinoma patients by network analysis of stemness indices. <i>Expert Review of Gastroenterology and Hepatology</i> , 2021, 15, 699-709.	1.4	9
20533	Physiological Characteristic Changes and Full-Length Transcriptome of Rose (<i>Rosa chinensis</i>) Roots and Leaves in Response to Drought Stress. <i>Plant and Cell Physiology</i> , 2021, 61, 2153-2166.	1.5	25
20534	PAR-TERRA is the main contributor to telomeric repeat-containing RNA transcripts in normal and cancer mouse cells. <i>Rna</i> , 2021, 27, 106-121.	1.6	16
20536	Use Chou's 5-steps rule with different word embedding types to boost performance of electron transport protein prediction model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	9
20538	m6A-Atlas: a comprehensive knowledgebase for unraveling the N ⁶ -methyladenosine (m6A) epitranscriptome. <i>Nucleic Acids Research</i> , 2021, 49, D134-D143.	6.5	185
20539	Isolating structural errors in reaction networks in systems biology. <i>Bioinformatics</i> , 2021, 37, 388-395.	1.8	1

#	ARTICLE	IF	CITATIONS
20540	Environmental stability impacts the differential sensitivity of marine microbiomes to increases in temperature and acidity. <i>ISME Journal</i> , 2021, 15, 19-28.	4.4	35
20541	An immune-related gene signature for determining Ewing sarcoma prognosis based on machine learning. <i>Journal of Cancer Research and Clinical Oncology</i> , 2021, 147, 153-165.	1.2	22
20542	TREND-DB—a transcriptome-wide atlas of the dynamic landscape of alternative polyadenylation. <i>Nucleic Acids Research</i> , 2021, 49, D243-D253.	6.5	23
20543	RNF40 exerts stage-dependent functions in differentiating osteoblasts and is essential for bone cell crosstalk. <i>Cell Death and Differentiation</i> , 2021, 28, 700-714.	5.0	13
20544	Incorporating prior knowledge into regularized regression. <i>Bioinformatics</i> , 2021, 37, 514-521.	1.8	15
20545	EMODMI: A Multi-Objective Optimization Based Method to Identify Disease Modules. <i>IEEE Transactions on Emerging Topics in Computational Intelligence</i> , 2021, 5, 570-582.	3.4	38
20546	Gene expression in rat placenta after exposure to di(2-ethylhexyl) phthalate. <i>Human and Experimental Toxicology</i> , 2021, 40, 504-514.	1.1	8
20547	Oncoprotein-specific molecular interaction maps (SigMaps) for cancer network analyses. <i>Nature Biotechnology</i> , 2021, 39, 215-224.	9.4	21
20548	Quantitative proteomic profiling of shake flask versus bioreactor growth reveals distinct responses of <i>Agrobacterium tumefaciens</i> for preparation in molecular pharming. <i>Canadian Journal of Microbiology</i> , 2021, 67, 75-84.	0.8	8
20549	Signatures of selection in a recent invasion reveal adaptive divergence in a highly vagile invasive species. <i>Molecular Ecology</i> , 2021, 30, 1419-1434.	2.0	24
20550	Genome-wide Association Study and Meta-analysis on Alcohol-Associated Liver Cirrhosis Identifies Genetic Risk Factors. <i>Hepatology</i> , 2021, 73, 1920-1931.	3.6	54
20551	Single-cell RNA expression profiling of SARS-CoV-2-related ACE2 and TMPRSS2 in human trophoblast and placenta. <i>Ultrasound in Obstetrics and Gynecology</i> , 2021, 57, 248-256.	0.9	54
20552	A novel prognostic index of hepatocellular carcinoma based on immunogenomic landscape analysis. <i>Journal of Cellular Physiology</i> , 2021, 236, 2572-2591.	2.0	26
20553	Complete Genome Sequence of <i>Enterobacter roggenkampii</i> Strain KQ-01, Isolated from Bacterial Wilt-Resistant Mulberry Cultivar YS283. <i>Plant Disease</i> , 2021, 105, 688-690.	0.7	4
20554	A Gene Rank Based Approach for Single Cell Similarity Assessment and Clustering. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 431-442.	1.9	12
20555	Relation Prediction of Co-Morbid Diseases Using Knowledge Graph Completion. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 708-717.	1.9	17
20556	Arbuscular mycorrhizal fungus alleviates alfalfa leaf spots caused by <i>Phoma medicaginis</i> revealed by RNA-seq analysis. <i>Journal of Applied Microbiology</i> , 2021, 130, 547-560.	1.4	38
20557	Predicting drug-induced hepatotoxicity based on biological feature maps and diverse classification strategies. <i>Briefings in Bioinformatics</i> , 2021, 22, 428-437.	3.2	18

#	ARTICLE	IF	CITATIONS
20558	Sustained Postnatal Skin Regeneration Upon Prenatal Application of Functionalized Collagen Scaffolds. <i>Tissue Engineering - Part A</i> , 2021, 27, 10-25.	1.6	3
20559	Long-Term Waterlogging as Factor Contributing to Hypoxia Stress Tolerance Enhancement in Cucumber: Comparative Transcriptome Analysis of Waterlogging Sensitive and Tolerant Accessions. <i>Genes</i> , 2021, 12, 189.	1.0	27
20560	Deep Learning System for Biomedical Relation Extraction Combining External Sources of Knowledge. <i>Lecture Notes in Computer Science</i> , 2021, , 688-693.	1.0	0
20561	The iPPI-DB initiative: a community-centered database of protein-protein interaction modulators. <i>Bioinformatics</i> , 2021, 37, 89-96.	1.8	24
20562	Data-driven biological network alignment that uses topological, sequence, and functional information. <i>BMC Bioinformatics</i> , 2021, 22, 34.	1.2	3
20563	Sinbase 2.0: An Updated Database to Study Multi-Omics in <i>Sesamum indicum</i> . <i>Plants</i> , 2021, 10, 272.	1.6	6
20564	Linking gene regions jointly with environment and depression. , 2021, , 69-76.		0
20565	Comprehensive assessments of germline deletion structural variants reveal the association between prognostic MUC4 and CEP72 deletions and immune response gene expression in colorectal cancer patients. <i>Human Genomics</i> , 2021, 15, 3.	1.4	4
20566	Likelihood ratio statistics for gene set enrichment in Alzheimer's disease pathways. <i>Alzheimer's and Dementia</i> , 2021, 17, 561-573.	0.4	4
20568	Computational Methods for Protein-Protein Interaction Network Alignment. , 2021, , 45-63.		0
20569	Transcriptional response of <i>Asarum heterotropoides</i> Fr. Schmidt var. <i>mandshuricum</i> (Maxim.) Kitag. leaves grown under full and partial daylight conditions. <i>BMC Genomics</i> , 2021, 22, 16.	1.2	1
20570	HIF-1 α promotes cellular growth in lymphatic endothelial cells exposed to chronically elevated pulmonary lymph flow. <i>Scientific Reports</i> , 2021, 11, 1468.	1.6	5
20572	Transcriptome profiling analysis of two contrasting barley genotypes in general combining ability for yield traits. <i>Revista Brasileira De Botanica</i> , 2021, 44, 117-123.	0.5	0
20573	Identifying protein subcellular localisation in scientific literature using bidirectional deep recurrent neural network. <i>Scientific Reports</i> , 2021, 11, 1696.	1.6	3
20574	Genome Sequence and Adaptation Analysis of the Human and Rice Pathogenic Strain <i>Burkholderia glumae</i> AU6208. <i>Pathogens</i> , 2021, 10, 87.	1.2	5
20575	TraCurate: Efficiently curating cell tracks. <i>SoftwareX</i> , 2021, 13, 100656.	1.2	5
20576	PC2P: parameter-free network-based prediction of protein complexes. <i>Bioinformatics</i> , 2021, 37, 73-81.	1.8	19
20577	CellML Model Discovery with the Physiome Model Repository. , 2021, , 354-361.		0

#	ARTICLE	IF	CITATIONS
20578	The Hunt for Ancient Prions: Archaeal Prion-Like Domains Form Amyloid-Based Epigenetic Elements. <i>Molecular Biology and Evolution</i> , 2021, 38, 2088-2103.	3.5	15
20579	The BMP signaling gradient is interpreted through concentration thresholds in dorsal-ventral axial patterning. <i>PLoS Biology</i> , 2021, 19, e3001059.	2.6	32
20580	Chronic pain susceptibility is associated with anhedonic behavior and alterations in the accumbal ubiquitin-proteasome system. <i>Pain</i> , 2021, 162, 1722-1731.	2.0	4
20582	Latent Variable Modelling and Variational Inference for scRNA-seq Differential Expression Analysis. <i>Lecture Notes in Computer Science</i> , 2021, , 56-68.	1.0	0
20583	An Ensemble Tf-Idf Based Approach to Protein Function Prediction via Sequence Segmentation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 2685-2696.	1.9	7
20584	Screening and functional analysis of potential <i>S</i> genes in <i>Chrysanthemum morifolium</i> . <i>Ornamental Plant Research</i> , 2021, 1, 1-11.	0.2	1
20585	Bioinformatic Analysis of Differentially Expressed Genes (DEGs) Detected from RNA-Sequence Profiles of Mouse Striatum. , 2021, , 101-122.		0
20586	Genome Assembly and Analyses of the Macrofungus <i>Macrocybe gigantea</i> . <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	4
20587	An overview of machine learning methods for monotherapy drug response prediction. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	19
20589	Deciphering the architecture and interactome of hnRNP proteins and enigmRBPs. <i>Molecular Omics</i> , 2021, 17, 503-516.	1.4	1
20590	Transcriptome of Lingzhi. <i>Compendium of Plant Genomes</i> , 2021, , 89-116.	0.3	0
20592	Elucidation of the Genomic-Epigenomic Interaction Landscape of Aggressive Prostate Cancer. <i>BioMed Research International</i> , 2021, 2021, 1-15.	0.9	1
20593	Integrative Identification of Hub Genes Associated With Immune Cells in Atrial Fibrillation Using Weighted Gene Correlation Network Analysis. <i>Frontiers in Cardiovascular Medicine</i> , 2020, 7, 631775.	1.1	11
20594	Improving Biomedical Pretrained Language Models with Knowledge. , 2021, , .		22
20595	Multi-omic analysis unveils biological pathways in peripheral immune system associated to minimal hepatic encephalopathy appearance in cirrhotic patients. <i>Scientific Reports</i> , 2021, 11, 1907.	1.6	9
20596	The transcriptional repressor <i>Rev-erbβ</i> regulates circadian expression of the astrocyte <i>Fabp7</i> mRNA. <i>Current Research in Neurobiology</i> , 2021, 2, 100009.	1.1	7
20597	Hybrid Approach to Define Semantic Relationships. <i>Advances in Intelligent Systems and Computing</i> , 2021, , 1404-1413.	0.5	0
20598	Challenges and solutions for big data in personalized healthcare. , 2021, , 69-94.		7

#	ARTICLE	IF	CITATIONS
20599	CTD anatomy: Analyzing chemical-induced phenotypes and exposures from an anatomical perspective, with implications for environmental health studies. <i>Current Research in Toxicology</i> , 2021, 2, 128-139.	1.3	27
20600	Functionathon: a manual data mining workflow to generate functional hypotheses for uncharacterized human proteins and its application by undergraduate students. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	8
20601	Databases and Bioinformatics Tools for Data Mining. , 2021, , 103-128.		0
20602	Gene Ontology and Pathway Enrichment Analysis. , 2021, , 257-279.		1
20603	Auxin is involved in arbuscular mycorrhizal fungi-promoted tomato growth and NADP-malic enzymes expression in continuous cropping substrates. <i>BMC Plant Biology</i> , 2021, 21, 48.	1.6	22
20604	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
20606	TIDB: a comprehensive database of trained immunity. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	7
20607	Biclustering via Semiparametric Bayesian Inference. <i>Bayesian Analysis</i> , 2022, 17, .	1.6	1
20608	Identifying RBM47, HCK, CD53, TYROBP, and HAVCR2 as Hub Genes in Advanced Atherosclerotic Plaques by Network-Based Analysis and Validation. <i>Frontiers in Genetics</i> , 2020, 11, 602908.	1.1	19
20609	Identification of haploinsufficient genes from epigenomic data using deep forest. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	0
20610	Induced organoids derived from patients with ulcerative colitis recapitulate colitic reactivity. <i>Nature Communications</i> , 2021, 12, 262.	5.8	51
20611	Knowledge Network Embedding of Transcriptomic Data from Spaceflown Mice Uncovers Signs and Symptoms Associated with Terrestrial Diseases. <i>Life</i> , 2021, 11, 42.	1.1	10
20612	Genomic diversity and post-admixture adaptation in the Uyghurs. <i>National Science Review</i> , 2022, 9, nwab124.	4.6	20
20613	Unipept Desktop: A Faster, More Powerful Metaproteomics Results Analysis Tool. <i>Journal of Proteome Research</i> , 2021, 20, 2005-2009.	1.8	17
20614	De novo genome assembly of the potent medicinal plant <i>Rehmannia glutinosa</i> using nanopore technology. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3954-3963.	1.9	26
20615	Integration of gene expression data identifies key genes and pathways in colorectal cancer. <i>Medical Oncology</i> , 2021, 38, 7.	1.2	17
20616	Six mutator-derived lncRNA signature of genome instability for predicting the clinical outcome of colon cancer. <i>Journal of Gastrointestinal Oncology</i> , 2021, 12, 0-0.	0.6	4
20617	Non-canonical Wnt/PCP signalling regulates intestinal stem cell lineage priming towards enteroendocrine and Paneth cell fates. <i>Nature Cell Biology</i> , 2021, 23, 23-31.	4.6	46

#	ARTICLE	IF	CITATIONS
20620	Subtypes identification on heart failure with preserved ejection fraction via network enhancement fusion using multi-omics data. Computational and Structural Biotechnology Journal, 2021, 19, 1567-1578.	1.9	13
20621	iTRAQ-based proteomic analysis of the hippocampus of pentylenetetrazole-kindled epileptic rats. International Journal of Developmental Neuroscience, 2021, 81, 125-141.	0.7	5
20622	Graph and Heterogeneous Network Transformations. , 2021, , 107-142.		0
20623	Integrated analysis of the molecular mechanisms in idiopathic pulmonary fibrosis. International Journal of Medical Sciences, 2021, 18, 3412-3424.	1.1	8
20624	Bioinformatics analysis identified shared differentially expressed genes as potential biomarkers for Hashimoto's thyroiditis-related papillary thyroid cancer. International Journal of Medical Sciences, 2021, 18, 3478-3487.	1.1	10
20625	Identification of fibronectin 1 (FN1) and complement component 3 (C3) as immune infiltration-related biomarkers for diabetic nephropathy using integrated bioinformatic analysis. Bioengineered, 2021, 12, 5386-5401.	1.4	21
20626	Dynamic Module Detection in Temporal Attributed Networks of Cancers. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2219-2230.	1.9	31
20627	Ontological modeling and analysis of experimentally or clinically verified drugs against coronavirus infection. Scientific Data, 2021, 8, 16.	2.4	14
20630	Biomedical Ontologies: Coverage, Access and Use. , 2021, , 382-395.		4
20631	Transcriptomic analysis identifies organ-specific metastasis genes and pathways across different primary sites. Journal of Translational Medicine, 2021, 19, 31.	1.8	13
20632	Biocontrol Using Bacillus amyloliquefaciens PP19 Against Litchi Downy Blight Caused by Peronophythora litchii. Frontiers in Microbiology, 2020, 11, 619423.	1.5	4
20633	A Knowledge-Enhanced Multi-View Framework for Drug-Target Interaction Prediction. IEEE Transactions on Big Data, 2022, 8, 1387-1398.	4.4	2
20634	Screening and identification of hub genes in bladder cancer by bioinformatics analysis and KIF11 is a potential prognostic biomarker. Oncology Letters, 2021, 21, 205.	0.8	9
20635	Long read sequencing of <i>Toona sinensis</i> (A. Juss) Roem: A chromosome-level reference genome for the family Meliaceae. Molecular Ecology Resources, 2021, 21, 1243-1255.	2.2	20
20636	In Silico Inference of Synthetic Cytotoxic Interactions from Paclitaxel Responses. International Journal of Molecular Sciences, 2021, 22, 1097.	1.8	0
20637	Biotin Proximity Labeling for Protein-Protein Interaction Discovery: The BioID Method. Methods in Molecular Biology, 2021, 2261, 357-379.	0.4	3
20638	Computational Functional Genomics-Based AmpliSeq Panel for Next-Generation Sequencing of Key Genes of Pain. International Journal of Molecular Sciences, 2021, 22, 878.	1.8	1
20639	Serum proteome profiling provides a deep understanding of the 'gut-liver axis' in relation to liver injury and regeneration. Acta Biochimica Et Biophysica Sinica, 2021, 53, 372-380.	0.9	5

#	ARTICLE	IF	CITATIONS
20640	Transcriptome profiling of cells exposed to particular and intense electromagnetic radiation emitted by the "SG-III" prototype laser facility. <i>Scientific Reports</i> , 2021, 11, 2017.	1.6	4
20642	Microarray Data Mining and Preliminary Bioinformatics Analysis of Hepatitis D Virus-Associated Hepatocellular Carcinoma. <i>BioMed Research International</i> , 2021, 2021, 1-18.	0.9	5
20644	Overcoming Sparseness of Biomedical Networks to Identify Drug Repositioning Candidates. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 2377-2384.	1.9	3
20645	The Epstein-Barr virus deubiquitinase BPLF1 targets SQSTM1/p62 to inhibit selective autophagy. <i>Autophagy</i> , 2021, 17, 3461-3474.	4.3	22
20646	Genome-wide association analysis reveals regulation of at-risk loci by DNA methylation in prostate cancer. <i>Asian Journal of Andrology</i> , 2021, 23, 472.	0.8	1
20647	Transcriptome Analysis Reveals the Immune Response of Chicken Erythrocytes to Marek's Disease Virus Infection. <i>Pakistan Journal of Zoology</i> , 2021, 53, .	0.1	0
20648	Identifying the miRNA Signature Association with Aging-Related Senescence in Glioblastoma. <i>International Journal of Molecular Sciences</i> , 2021, 22, 517.	1.8	5
20649	Genome Annotation and Gene Families in Sesame. <i>Compendium of Plant Genomes</i> , 2021, , 255-266.	0.3	2
20650	Ascending dorsal column sensory neurons respond to spinal cord injury and downregulate genes related to lipid metabolism. <i>Scientific Reports</i> , 2021, 11, 374.	1.6	14
20651	Investigation of a new oxazolidinone derivative in human resistance acute leukemia cells: deciphering its mechanism of action by label-free proteomic. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , 2021, 394, 1153-1166.	1.4	0
20652	Severe acute respiratory syndrome coronavirus (SARS-CoV)-2 infection induces dysregulation of immunity: <i>in silico</i> gene expression analysis. <i>International Journal of Medical Sciences</i> , 2021, 18, 1143-1152.	1.1	13
20653	Cross-platform genomic identification and clinical validation of breast cancer diagnostic biomarkers. <i>Aging</i> , 2021, 13, 4258-4273.	1.4	21
20654	Gene co-expression in the interactome: moving from correlation toward causation via an integrated approach to disease module discovery. <i>Npj Systems Biology and Applications</i> , 2021, 7, 3.	1.4	64
20656	Systematic Analysis of Functionally Related Gene Clusters in the Opportunistic Pathogen, <i>Candida albicans</i> . <i>Microorganisms</i> , 2021, 9, 276.	1.6	5
20658	Network pharmacology-based analysis for unraveling potential cancer-related molecular targets of Egyptian propolis phytoconstituents accompanied with molecular docking and <i>in vitro</i> studies. <i>RSC Advances</i> , 2021, 11, 11610-11626.	1.7	22
20659	Multiplex gene and phenotype network to characterize shared genetic pathways of epilepsy and autism. <i>Scientific Reports</i> , 2021, 11, 952.	1.6	27
20660	Effect of Aging on Homeostasis in the Soft Tissue of the Periodontium: A Narrative Review. <i>Journal of Personalized Medicine</i> , 2021, 11, 58.	1.1	14
20661	High-throughput screening in postimplantation haploid epiblast stem cells reveals Hs3st3b1 as a modulator for reprogramming. <i>Stem Cells Translational Medicine</i> , 2021, 10, 743-755.	1.6	13

#	ARTICLE	IF	CITATIONS
20662	Causal network inference from gene transcriptional time-series response to glucocorticoids. <i>PLoS Computational Biology</i> , 2021, 17, e1008223.	1.5	20
20663	DM3Loc: multi-label mRNA subcellular localization prediction and analysis based on multi-head self-attention mechanism. <i>Nucleic Acids Research</i> , 2021, 49, e46-e46.	6.5	95
20664	Lipids, lysosomes and mitochondria: insights into Lewy body formation from rare monogenic disorders. <i>Acta Neuropathologica</i> , 2021, 141, 511-526.	3.9	31
20665	The fobitools framework: the first steps towards food enrichment analysis. <i>Bioinformatics</i> , 2021, 37, 3969-3971.	1.8	0
20666	Transcriptome Analysis of the Inhibitory Effect of Senoside A on the Metastasis of Hepatocellular Carcinoma Cells. <i>Frontiers in Pharmacology</i> , 2020, 11, 566099.	1.6	11
20667	Analysis method of Tissue-specific gene set weight. , 2021, , .		0
20668	Gene expression evaluation of antioxidant enzymes in patients with hepatocellular carcinoma: RT-qPCR and bioinformatic analyses. <i>Genetics and Molecular Biology</i> , 2021, 44, e20190373.	0.6	9
20669	biotoolsSchema: a formalized schema for bioinformatics software description. <i>GigaScience</i> , 2021, 10, .	3.3	7
20670	Novel circRNA discovery in sheep shows evidence of high backsplice junction conservation. <i>Scientific Reports</i> , 2021, 11, 427.	1.6	8
20671	Identified GNCT1 and NMU as Combined Diagnosis Biomarker of Non-Small-Cell Lung Cancer Utilizing Bioinformatics and Logistic Regression. <i>Disease Markers</i> , 2021, 2021, 1-14.	0.6	8
20672	Study on mechanism of matrine in treatment of COVID-19 combined with liver injury by network pharmacology and molecular docking technology. <i>Drug Delivery</i> , 2021, 28, 325-342.	2.5	28
20674	Genome-Wide Identification and Analysis of Chitinase GH18 Gene Family in <i>Mycogone perniciosa</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 596719.	1.5	9
20676	An Integrative Transcriptomic Analysis of Systemic Juvenile Idiopathic Arthritis for Identifying Potential Genetic Markers and Drug Candidates. <i>International Journal of Molecular Sciences</i> , 2021, 22, 712.	1.8	6
20677	Genome-Wide Association Study of Maize Aboveground Dry Matter Accumulation at Seedling Stage. <i>Frontiers in Genetics</i> , 2020, 11, 571236.	1.1	9
20678	BSR-Seq analysis provides insights into the cold stress response of <i>Actinidia arguta</i> F1 populations. <i>BMC Genomics</i> , 2021, 22, 72.	1.2	7
20679	Systems Pharmacology: Enabling Multidimensional Therapeutics. , 2022, , 725-769.		1
20680	PM4NGS, a project management framework for next-generation sequencing data analysis. <i>GigaScience</i> , 2021, 10, .	3.3	0
20682	Identification of biomarkers associated with cervical lymph node metastasis in papillary thyroid carcinoma: Evidence from an integrated bioinformatic analysis. <i>Clinical Hemorheology and Microcirculation</i> , 2021, 78, 117-126.	0.9	8

#	ARTICLE	IF	CITATIONS
20683	Identification of Key Modules and Hub Genes of Annulus Fibrosus in Intervertebral Disc Degeneration. <i>Frontiers in Genetics</i> , 2020, 11, 596174.	1.1	4
20684	Circulating plasma exosomal miRNA profiles serve as potential metastasis-related biomarkers for hepatocellular carcinoma. <i>Oncology Letters</i> , 2021, 21, 168.	0.8	13
20685	Late p65 nuclear translocation in glioblastoma cells indicates non-canonical TLR4 signaling and activation of DNA repair genes. <i>Scientific Reports</i> , 2021, 11, 1333.	1.6	10
20686	iTRAQ-based proteomic analysis reveals the molecule mechanism of reducing higher alcohols in Chinese rice wine by nitrogen compensation. <i>Annals of Microbiology</i> , 2021, 71, .	1.1	4
20687	Bioinformatics analysis identifies COL1A1, THBS2 and SPP1 as potential predictors of patient prognosis and immunotherapy response in gastric cancer. <i>Bioscience Reports</i> , 2021, 41, .	1.1	16
20688	Majority Vote Cascading: A Semi-Supervised Framework for Improving Protein Function Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 1933-1945.	1.9	2
20689	Knowledge Graph Embedding by Double Limit Scoring Loss. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2022, 34, 5825-5839.	4.0	10
20690	Integrating Gene Ontology Based Grouping and Ranking into the Machine Learning Algorithm for Gene Expression Data Analysis. <i>Communications in Computer and Information Science</i> , 2021, , 205-214.	0.4	8
20691	Host metabolic shift during systemic <i>Salmonella</i> infection revealed by comparative proteomics. <i>Emerging Microbes and Infections</i> , 2021, 10, 1849-1861.	3.0	4
20692	UV-B-induced molecular mechanisms of stress physiology responses in the major northern Chinese conifer <i>Pinus tabulaeformis</i> Carr.. <i>Tree Physiology</i> , 2021, 41, 1247-1263.	1.4	12
20693	A systems-level gene regulatory network model for <i>Plasmodium falciparum</i> . <i>Nucleic Acids Research</i> , 2021, 49, 4891-4906.	6.5	2
20695	An empirical meta-analysis of the life sciences linked open data on the web. <i>Scientific Data</i> , 2021, 8, 24.	2.4	10
20696	Reporting on the Role of miRNAs and Affected Pathways on the Molecular Backbone of Ovarian Insufficiency: A Systematic Review and Critical Analysis Mapping of Future Research. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 590106.	1.8	2
20697	Significant pathway and biomarker identification of pancreatic cancer associated lung cancer. <i>Informatics in Medicine Unlocked</i> , 2021, 25, 100637.	1.9	2
20698	Identification of mortality-risk-related missense variant for renal clear cell carcinoma using deep learning. <i>Therapeutic Advances in Chronic Disease</i> , 2021, 12, 204062232199262.	1.1	5
20699	Genome sequence and transcriptome profiles of pathogenic fungus <i>Paecilomyces penicillatus</i> reveal its interactions with edible fungus <i>Morchella importuna</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2607-2617.	1.9	11
20700	Simultaneous profiling of <i>Arabidopsis thaliana</i> and <i>Vibrio vulnificus</i> MO6-24/O transcriptomes by dual RNA-seq analysis. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2084-2096.	1.9	5
20701	Alcohol use disorder causes global changes in splicing in the human brain. <i>Translational Psychiatry</i> , 2021, 11, 2.	2.4	25

#	ARTICLE	IF	CITATIONS
20702	Co-expression for Genotype-Phenotype Function Annotation in Potato Research. <i>Methods in Molecular Biology</i> , 2021, 2354, 261-272.	0.4	0
20703	An Integrated Platform for Skin Cancer Heterogenous and Multilayered Data Management. <i>Journal of Medical Systems</i> , 2021, 45, 10.	2.2	4
20704	Integrating Network Pharmacology and Experimental Validation to Investigate the Effects and Mechanism of Astragalus Flavonoids Against Hepatic Fibrosis. <i>Frontiers in Pharmacology</i> , 2020, 11, 618262.	1.6	32
20705	A seven-gene prognostic model related to immune checkpoint PD-1 revealing overall survival in patients with lung adenocarcinoma. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 6136-6154.	1.0	3
20706	Knowledge Graphs. , 2021, , 409-435.		0
20707	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2021, , .	3.2	2
20708	Mitochondrial bioenergetic deficits in C9orf72 amyotrophic lateral sclerosis motor neurons cause dysfunctional axonal homeostasis. <i>Acta Neuropathologica</i> , 2021, 141, 257-279.	3.9	76
20709	Proteomic identification and validation of novel interactions of the putative tumor suppressor PRELP with membrane proteins including IGF1R and p75NTR. <i>Journal of Biological Chemistry</i> , 2021, 296, 100278.	1.6	9
20710	Identification of the Relationships between Tumor Mutation Burden with Immune Infiltrates in Liver Hepatocellular Carcinoma. <i>Advances in Clinical Medicine</i> , 2021, 11, 2880-2890.	0.0	0
20711	Integrative analysis of transcriptomic data for identification of T-cell activation-related mRNA signatures indicative of preterm birth. <i>Scientific Reports</i> , 2021, 11, 2392.	1.6	3
20712	Changes on proteomic and metabolomic profile in serum of mice induced by chronic exposure to tramadol. <i>Scientific Reports</i> , 2021, 11, 1454.	1.6	5
20713	Blood-derived mitochondrial DNA copy number is associated with gene expression across multiple tissues and is predictive for incident neurodegenerative disease. <i>Genome Research</i> , 2021, 31, 349-358.	2.4	52
20714	Comprehensive Analysis of ceRNA Regulation Network Involved in the Development of Coronary Artery Disease. <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	6
20715	Evolutionary Algorithms for Applications of Biological Networks: A Review. <i>Lecture Notes in Computer Science</i> , 2021, , 102-114.	1.0	1
20716	Identification and analysis of short open reading frames (sORFs) in the initially annotated noncoding RNA LINC00493 from human cells. <i>Journal of Biochemistry</i> , 2021, 169, 421-434.	0.9	7
20717	Genome-Wide Functional Screen for Calcium Transients in Escherichia coli Identifies Increased Membrane Potential Adaptation to Persistent DNA Damage. <i>Journal of Bacteriology</i> , 2021, 203, .	1.0	7
20718	Gene signature of children with severe respiratory syncytial virus infection. <i>Pediatric Research</i> , 2021, 89, 1664-1672.	1.1	13
20719	MULocDeep: A deep-learning framework for protein subcellular and suborganellar localization prediction with residue-level interpretation. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4825-4839.	1.9	43

#	ARTICLE	IF	CITATIONS
20720	Features and Limitations of Ontologies for Coronavirus Data Management in Libraries. <i>Advances in Library and Information Science</i> , 2021, , 18-40.	0.2	0
20721	Comparative transcriptomics and host-specific parasite gene expression profiles inform on drivers of proliferative kidney disease. <i>Scientific Reports</i> , 2021, 11, 2149.	1.6	15
20723	Application of learning to rank in bioinformatics tasks. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
20724	A Comprehensive Guide to Potato Transcriptome. <i>Methods in Molecular Biology</i> , 2021, 2354, 155-192.	0.4	0
20726	Local adaptation contributes to gene expression divergence in maize. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	7
20727	Clinical Proteomics of Metastatic Melanoma Reveals Profiles of Organ Specificity and Treatment Resistance. <i>Clinical Cancer Research</i> , 2021, 27, 2074-2086.	3.2	12
20728	RNA-sequencing indicates high hemocyanin expression as a key strategy for cold adaptation in the Antarctic amphipod <i>Eusirus cf. giganteus</i> clade g3. <i>Biocell</i> , 2021, 45, 1611-1619.	0.4	5
20729	Identification of unique long non-coding RNAs as putative biomarkers for chromophobe renal cell carcinoma. <i>Personalized Medicine</i> , 2021, 18, 9-19.	0.8	2
20730	Extensive Linkage and Genetic Coupling of Song and Preference Loci Underlying Rapid Speciation in <i>Laupala</i> Crickets. <i>Journal of Heredity</i> , 2021, 112, 204-213.	1.0	18
20731	Exposure of <i>Agrobacterium tumefaciens</i> to agroinfiltration medium demonstrates cellular remodelling and may promote enhanced adaptability for molecular pharming. <i>Canadian Journal of Microbiology</i> , 2021, 67, 85-97.	0.8	6
20732	Biomedical Knowledge Graph Refinement and Completion Using Graph Representation Learning and Top-K Similarity Measure. <i>Lecture Notes in Computer Science</i> , 2021, , 112-123.	1.0	3
20734	Screening of Key Genes Affecting the Diagnosis and Treatment of Glioblastoma Based on Bioinformatics. <i>Advances in Clinical Medicine</i> , 2021, 11, 1250-1260.	0.0	0
20735	Wormicloud: a new text summarization tool based on word clouds to explore the <i>C. elegans</i> literature. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	8
20736	UbiNet 2.0: a verified, classified, annotated and updated database of E3 ubiquitin ligase–substrate interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	27
20737	Target identification and validation. , 2021, , 61-80.		0
20738	Representation of behaviour change interventions and their evaluation: Development of the Upper Level of the Behaviour Change Intervention Ontology. <i>Wellcome Open Research</i> , 2020, 5, 123.	0.9	41
20740	HELQ and EGR3 expression correlate with IGHV mutation status and prognosis in chronic lymphocytic leukemia. <i>Journal of Translational Medicine</i> , 2021, 19, 42.	1.8	2
20741	Transcriptome annotation in the cloud: complexity, best practices, and cost. <i>GigaScience</i> , 2021, 10, .	3.3	9

#	ARTICLE	IF	CITATIONS
20742	SinEx DB 2.0 update 2020: database for eukaryotic single-exon coding sequences. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	3
20743	Bioinformatics analysis of common key genes and pathways of intracranial, abdominal, and thoracic aneurysms. BMC Cardiovascular Disorders, 2021, 21, 14.	0.7	4
20746	Host Transcriptomic Response Following Administration of Rotavirus Vaccine in Infantsâ€™ Mimics Wild Type Infection. Frontiers in Immunology, 2020, 11, 580219.	2.2	4
20747	<i>BIRC5</i>, <i>GAJ5</i> and lncRNA NPHP3-AS1 Are Correlated with the Development of Atrial Fibrillation-Valvular Heart Disease. International Heart Journal, 2021, 62, 153-161.	0.5	13
20749	Prior Biological Knowledge Improves Genomic Prediction of Growth-Related Traits in Arabidopsis thaliana. Frontiers in Genetics, 2020, 11, 609117.	1.1	4
20750	Bioinformatic analysis of key pathways and genes involved in pediatric atopic dermatitis. Bioscience Reports, 2021, 41, .	1.1	3
20751	Integration of full-length transcriptomics and targeted metabolomics to identify benzylisoquinoline alkaloid biosynthetic genes in Corydalis yanhusuo. Horticulture Research, 2021, 8, 16.	2.9	23
20752	Potential interactions between the TBX4-FCF10 and SHH-FOXF1 signaling during human lung development revealed using ChIP-seq. Respiratory Research, 2021, 22, 26.	1.4	11
20753	Re-purposing software for functional characterization of the microbiome. Microbiome, 2021, 9, 4.	4.9	7
20754	Attenuation of Antiviral Immune Response Caused by Perturbation of TRIM25-Mediated RIG-I Activation under Simulated Microgravity. Cell Reports, 2021, 34, 108600.	2.9	11
20755	A novel Foxp3-related immune prognostic signature for glioblastoma multiforme based on immunogenomic profiling. Aging, 2021, 13, 3501-3517.	1.4	11
20756	DYRK1A regulates B cell acute lymphoblastic leukemia through phosphorylation of FOXO1 and STAT3. Journal of Clinical Investigation, 2021, 131, .	3.9	47
20757	Positive Selection in Human Populations: Practical Aspects and Current Knowledge. Evolutionary Studies, 2021, , 29-65.	0.2	1
20758	A New Family of Similarity Measures for Scoring Confidence of Protein Interactions Using Gene Ontology. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 19-30.	1.9	3
20759	Meta-analysis of host transcriptional responses to SARS-CoV-2 infection reveals their manifestation in human tumors. Scientific Reports, 2021, 11, 2459.	1.6	17
20760	Semankey: A Semantics-Driven Approach for Querying RDF Repositories Using Keywords. IEEE Access, 2021, 9, 91282-91302.	2.6	4
20761	Tissue Specificity Based Isoform Function Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 3048-3059.	1.9	0
20762	Animals Models of Inherited Retinal Disease. International Ophthalmology Clinics, 2021, 61, 113-130.	0.3	8

#	ARTICLE	IF	CITATIONS
20763	Chromosome-level genome assembly of the Chinese longsnout catfish <i>Leiocassis longirostris</i> . <i>Zoological Research</i> , 2021, 42, 417-422.	0.9	14
20764	Protopanaxadiol improves endometriosis associated infertility and miscarriage in sex hormones receptors-dependent and independent manners. <i>International Journal of Biological Sciences</i> , 2021, 17, 1878-1894.	2.6	16
20765	Metagenomics survey unravels diversity of biogas microbiomes with potential to enhance productivity in Kenya. <i>PLoS ONE</i> , 2021, 16, e0244755.	1.1	8
20766	Summarizing RNA-Seq Data or Differentially Expressed Genes Using Gene Set, Network, or Pathway Analysis. <i>Methods in Molecular Biology</i> , 2021, 2284, 147-179.	0.4	4
20767	Bioinformatics Tools for Gene and Genome Annotation Analysis of Microbes for Synthetic Biology and Cancer Biology Applications. , 2021, , 317-332.		0
20768	Molecular Genetics in the Next Generation Sequencing Era. , 2021, , 215-230.		0
20769	Gene co-expression network analysis of <i>Trypanosoma brucei</i> in tsetse fly vector. <i>Parasites and Vectors</i> , 2021, 14, 74.	1.0	7
20770	Systems biology analysis identifies TNFRSF9 as a functional marker of tumor-infiltrating regulatory T-cell enabling clinical outcome prediction in lung cancer. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 860-868.	1.9	12
20771	Construction of an mRNA-miRNA-lncRNA network prognostic for triple-negative breast cancer. <i>Aging</i> , 2021, 13, 1153-1175.	1.4	22
20772	Transcriptomic profiling reveals gene expression in human peripheral blood after exposure to low-dose ionizing radiation. <i>Journal of Radiation Research</i> , 2022, 63, 8-18.	0.8	3
20773	A mixed community of skin microbiome representatives influences cutaneous processes more than individual members. <i>Microbiome</i> , 2021, 9, 22.	4.9	27
20774	Prognostic gene expression signatures of breast cancer are lacking a sensible biological meaning. <i>Scientific Reports</i> , 2021, 11, 156.	1.6	26
20775	Longitudinal saliva omics responses to immune perturbation: a case study. <i>Scientific Reports</i> , 2021, 11, 710.	1.6	19
20776	Employing Cross-Species Approaches to Construct Humanized Genetic Interaction Networks. <i>Methods in Molecular Biology</i> , 2021, 2381, 115-133.	0.4	0
20777	Protective Immune Trajectories in Early Viral Containment of Non-Pneumonic SARS-CoV-2 Infection. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3
20778	Mapping the SARS-CoV-2 "Host Protein" Protein Interactome by Affinity Purification Mass Spectrometry and Proximity-Dependent Biotin Labeling: A Rational and Straightforward Route to Discover Host-Directed Anti-SARS-CoV-2 Therapeutics. <i>International Journal of Molecular Sciences</i> , 2021, 22, 532.	1.8	38
20780	Transcript levels of keratin 1/5/6/14/15/16/17 as potential prognostic indicators in melanoma patients. <i>Scientific Reports</i> , 2021, 11, 1023.	1.6	35
20781	Integrated Genomic and Transcriptomic Analysis reveals key genes for predicting dual-phenotype Hepatocellular Carcinoma Prognosis. <i>Journal of Cancer</i> , 2021, 12, 2993-3010.	1.2	5

#	ARTICLE	IF	CITATIONS
20782	Potential therapeutic target genes for systemic lupus erythematosus: a bioinformatics analysis. <i>Bioengineered</i> , 2021, 12, 2810-2819.	1.4	8
20783	<i>Translational Bioinformatics.</i> , 2021, , 867-911.		0
20784	Establishment and application of information resource of mutant mice in RIKEN BioResource Research Center. <i>Laboratory Animal Research</i> , 2021, 37, 6.	1.1	6
20785	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
20786	A systems pharmacology approach to identify the autophagy-inducing effects of Traditional Persian medicinal plants. <i>Scientific Reports</i> , 2021, 11, 336.	1.6	7
20787	Inflammation and regulatory T cell genes are differentially expressed in peripheral blood mononuclear cells of Parkinson's disease patients. <i>Scientific Reports</i> , 2021, 11, 2316.	1.6	20
20788	Transcriptional signatures of human peripheral blood mononuclear cells can identify the risk of tuberculosis progression from latent infection among individuals with silicosis. <i>Emerging Microbes and Infections</i> , 2021, 10, 1536-1544.	3.0	4
20789	<i>Bioinformatic Platforms for Metagenomics.</i> , 2021, , 91-112.		0
20790	<i>Current In Silico Drug Repurposing Strategies.</i> , 2021, , 257-268.		0
20792	Novel signaling pathways regulate SARS-CoV and SARS-CoV-2 infectious disease. <i>Medicine (United Tj ETQq1 1 0.784314 rgBT /Overl</i>	0.4	16
20793	Knockdown of RIPK2 Inhibits Proliferation and Migration, and Induces Apoptosis via the NF- κ B Signaling Pathway in Gastric Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 627464.	1.1	32
20794	Sex-biased DNA methylation in papillary thyroid cancer. <i>Biomarkers in Medicine</i> , 2021, 15, 109-121.	0.6	9
20796	GMO Genetic Elements Thesaurus (GMO-GET): a controlled vocabulary for the consensus designation of introduced or modified genetic elements in genetically modified organisms. <i>BMC Bioinformatics</i> , 2021, 22, 48.	1.2	1
20797	Identification of potential Parkinson's disease biomarkers using computational biology approaches. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2021, 10, 1.	1.2	0
20798	5-Aza-2'-deoxycytidine induces a greater inflammatory change, at the molecular levels, in normoxic than hypoxic tumor microenvironment. <i>Molecular Biology Reports</i> , 2021, 48, 1161-1169.	1.0	2
20799	Comprehensive circRNA Expression Profile and Construction of circRNAs-Related ceRNA Network in a Mouse Model of Autism. <i>Frontiers in Genetics</i> , 2020, 11, 623584.	1.1	6
20804	DeCompress: tissue compartment deconvolution of targeted mRNA expression panels using compressed sensing. <i>Nucleic Acids Research</i> , 2021, 49, e48-e48.	6.5	4
20805	Inheritance of <i>Solanum</i> chloroplast genomic DNA in interspecific hybrids. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 351-357.	0.2	4

#	ARTICLE	IF	CITATIONS
20807	Development of a prognostic signature for esophageal cancer based on nine immune related genes. BMC Cancer, 2021, 21, 113.	1.1	17
20808	JMJD6 Is a Druggable Oxygenase That Regulates AR-V7 Expression in Prostate Cancer. Cancer Research, 2022, 81, 1087-1100.	0.4	23
20809	Protuberances are organized distinct regions of long-term callus: histological and transcriptomic analyses in kiwifruit. Plant Cell Reports, 2021, 40, 637-665.	2.8	6
20810	Quantitative proteomic analysis of pear (<i>Pyrus pyrifolia</i> cv. "Hosui") flesh provides novel insights about development and quality characteristics of fruit. Planta, 2021, 253, 69.	1.6	5
20811	An edge-based statistical analysis of long non-coding RNA expression profiles reveals a negative association between Parkinson's disease and colon cancer. BMC Medical Genomics, 2021, 14, 36.	0.7	1
20812	Systematic auditing is essential to debiasing machine learning in biology. Communications Biology, 2021, 4, 183.	2.0	14
20813	Toxicity Testing of Effluent-Dominated Stream Using Predictive Molecular-Level Toxicity Signatures Based on High-Resolution Mass Spectrometry: A Case Study of the Lubbock Canyon Lake System. Environmental Science & Technology, 2021, 55, 3070-3080.	4.6	6
20814	Identification of genes that correlate clear cell renal cell carcinoma and obesity and exhibit potential prognostic value. Translational Andrology and Urology, 2021, 10, 680-691.	0.6	7
20815	Large fragment insertion activates gene <i>GaFZ</i> (<i>Ga08G0121</i>) and is associated with the fuzz and trichome reduction in cotton (<i>Gossypium arboreum</i>). Plant Biotechnology Journal, 2021, 19, 1110-1124.	4.1	17
20816	Application and evaluation of knowledge graph embeddings in biomedical data. PeerJ Computer Science, 2021, 7, e341.	2.7	21
20817	Deleterious variants in X-linked CFAP47 induce asthenoteratozoospermia and primary male infertility. American Journal of Human Genetics, 2021, 108, 309-323.	2.6	74
20818	The histone demethylase KDM5 is required for synaptic structure and function at the Drosophila neuromuscular junction. Cell Reports, 2021, 34, 108753.	2.9	15
20819	Investigating the relevance of major signaling pathways in cancer survival using a biologically meaningful deep learning model. BMC Bioinformatics, 2021, 22, 47.	1.2	11
20820	Activity of bacteria isolated from bats against <i>Pseudogymnoascus destructans</i> in China. Microbial Biotechnology, 2022, 15, 469-481.	2.0	7
20821	Identification of miRNAs as diagnostic and prognostic markers in hepatocellular carcinoma. Aging, 2021, 13, 6115-6133.	1.4	6
20822	redPATH: Reconstructing the Pseudo Development Time of Cell Lineages in Single-cell RNA-seq Data and Applications in Cancer. Genomics, Proteomics and Bioinformatics, 2021, 19, 292-305.	3.0	2
20825	Identification of differentially expressed genes involved in amino acid and lipid accumulation of winter turnip rape (<i>Brassica rapa</i> L.) in response to cold stress. PLoS ONE, 2021, 16, e0245494.	1.1	9
20826	The CLAIRE COVID-19 initiative: approach, experiences and recommendations. Ethics and Information Technology, 2021, 23, 127-133.	2.3	0

#	ARTICLE	IF	CITATIONS
20827	Analyses of transcriptomes and the first complete genome of <i>Leucocalocybe mongolica</i> provide new insights into phylogenetic relationships and conservation. <i>Scientific Reports</i> , 2021, 11, 2930.	1.6	7
20828	Novel prognostic genes and subclasses of acute myeloid leukemia revealed by survival analysis of gene expression data. <i>BMC Medical Genomics</i> , 2021, 14, 39.	0.7	7
20829	QAUST: Protein Function Prediction Using Structure Similarity, Protein Interaction, and Functional Motifs. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 998-1011.	3.0	14
20830	Integrated analysis of viral miRNAs, mRNA and protein in the caudal fin cells of <i>C. auratus gibelio</i> with cyprinid herpesvirus 2 infection. <i>Journal of Fish Diseases</i> , 2021, 44, 441-460.	0.9	2
20831	Ontology-guided segmentation and object identification for developmental mouse lung immunofluorescent images. <i>BMC Bioinformatics</i> , 2021, 22, 82.	1.2	2
20832	Genetic characteristics of <i>Bursaphelenchus xylophilus</i> third-stage dispersal juveniles. <i>Scientific Reports</i> , 2021, 11, 3908.	1.6	4
20834	An Embryonic Diapause-like Adaptation with Suppressed Myc Activity Enables Tumor Treatment Persistence. <i>Cancer Cell</i> , 2021, 39, 240-256.e11.	7.7	143
20835	IgA transcytosis and antigen recognition govern ovarian cancer immunity. <i>Nature</i> , 2021, 591, 464-470.	13.7	99
20836	ETS-Domain Transcription Factor Elk-1 Regulates Stemness Genes in Brain Tumors and CD133+ BrainTumor-Initiating Cells. <i>Journal of Personalized Medicine</i> , 2021, 11, 125.	1.1	9
20837	<i>Kushneria phosphatilytica</i> sp. nov., a phosphate-solubilizing bacterium isolated from a solar saltern. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
20838	Comparative analysis using the draft genome sequence of California poppy (<i>Eschscholzia californica</i>) for exploring the candidate genes involved in benzyloquinoline alkaloid biosynthesis. <i>Bioscience, Biotechnology and Biochemistry</i> , 2021, 85, 851-859.	0.6	10
20839	A High-Throughput Method for Identifying Novel Genes That Influence Metabolic Pathways Reveals New Iron and Heme Regulation in <i>Pseudomonas aeruginosa</i> . <i>MSystems</i> , 2021, 6, .	1.7	11
20840	Mass-spectrometry-based proteomic correlates of grade and stage reveal pathways and kinases associated with aggressive human cancers. <i>Oncogene</i> , 2021, 40, 2081-2095.	2.6	22
20841	Ferroptosis-related gene signature as a prognostic marker for lower-grade gliomas. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 3080-3090.	1.6	29
20842	Discovery of molecular features underlying the morphological landscape by integrating spatial transcriptomic data with deep features of tissue images. <i>Nucleic Acids Research</i> , 2021, 49, e55-e55.	6.5	25
20843	IL-22 promotes the formation of a MUC17 glycocalyx barrier in the postnatal small intestine during weaning. <i>Cell Reports</i> , 2021, 34, 108757.	2.9	22
20844	Nongenetic Evolution Drives Lung Adenocarcinoma Spatial Heterogeneity and Progression. <i>Cancer Discovery</i> , 2021, 11, 1490-1507.	7.7	67
20845	The immune-related biomarker TEK inhibits the development of clear cell renal cell carcinoma (ccRCC) by regulating AKT phosphorylation. <i>Cancer Cell International</i> , 2021, 21, 119.	1.8	12

#	ARTICLE	IF	CITATIONS
20846	Computational resources for identifying and describing proteins driving liquidâ€“liquid phase separation. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	40
20847	Proteomic characterization of the human lens and Cataractogenesis. <i>Expert Review of Proteomics</i> , 2021, 18, 119-135.	1.3	8
20849	Integrative analysis of chloroplast DNA methylation in a marine algaâ€“ <i>Saccharina japonica</i> . <i>Plant Molecular Biology</i> , 2021, 105, 611-623.	2.0	5
20850	Possible roles for the hominoid-specific DSCR4 gene in human cells. <i>Genes and Genetic Systems</i> , 2021, 96, 1-11.	0.2	4
20852	The first complete mitochondrial genome of eggplant (<i>Solanum melongena</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 650-652.	0.2	0
20853	Linear Hypothesis Testing in Linear Models With High-Dimensional Responses. <i>Journal of the American Statistical Association</i> , 0, , 1-13.	1.8	3
20854	Human keratinocyte-derived extracellular vesicles activate the MAPKinase pathway and promote cell migration and proliferation in vitro. <i>Inflammation and Regeneration</i> , 2021, 41, 4.	1.5	22
20855	Ranking cancer drivers via betweenness-based outlier detection and random walks. <i>BMC Bioinformatics</i> , 2021, 22, 62.	1.2	6
20856	Aberrant proteins expressed in skin fibroblasts of Parkinson's disease patients carrying heterozygous variants of glucocerebrosidase and parkin genes. <i>Biomedical Reports</i> , 2021, 14, 36.	0.9	1
20857	Coronary artery disease: differential expression of ceRNAs and interaction analyses. <i>Annals of Translational Medicine</i> , 2021, 9, 229-229.	0.7	3
20861	Comparative transcriptomic analysis revealed novel potential therapeutic targets of traditional Chinese medicine (Pinggan-Qianyang decoction) on vascular remodeling in spontaneously hypertensive rats. <i>Chinese Medicine</i> , 2021, 16, 21.	1.6	2
20862	Analysis of MicroRNAs Associated With Carotid Atherosclerotic Plaque Rupture With Thrombosis. <i>Frontiers in Genetics</i> , 2021, 12, 599350.	1.1	4
20863	Whole-Genome Diversification Analysis of the Hornbeam Species Reveals Speciation and Adaptation Among Closely Related Species. <i>Frontiers in Plant Science</i> , 2021, 12, 581704.	1.7	2
20864	Peptidomics analysis revealed that a novel peptide VMPâ€“19 protects against AngIIâ€“induced injury in human umbilical vein endothelial cells. <i>Molecular Medicine Reports</i> , 2021, 23, .	1.1	2
20865	Conserved Epigenetic Programming and Enhanced Heme Metabolism Drive Memory B Cell Reactivation. <i>Journal of Immunology</i> , 2021, 206, 1493-1504.	0.4	15
20866	Comprehensive Proteomics Analysis of In Vitro Canine Oviductal Cell-Derived Extracellular Vesicles. <i>Animals</i> , 2021, 11, 573.	1.0	7
20867	Exploring existing drugs: proposing potential compounds in the treatment of COVID-19. <i>Heliyon</i> , 2021, 7, e06284.	1.4	5
20868	Patients with Proliferative Lupus Nephritis Have Autoantibodies That React to Moesin and Demonstrate Increased Glomerular Moesin Expression. <i>Journal of Clinical Medicine</i> , 2021, 10, 793.	1.0	3

#	ARTICLE	IF	CITATIONS
20869	GEOlimma: differential expression analysis and feature selection using pre-existing microarray data. <i>BMC Bioinformatics</i> , 2021, 22, 44.	1.2	6
20870	Transcriptome data for tissue-specific genes in four reproductive organs at three developmental stages of micro-tom tomato. <i>Data in Brief</i> , 2021, 34, 106715.	0.5	1
20871	The Changes of Leukocytes in Brain and Blood After Intracerebral Hemorrhage. <i>Frontiers in Immunology</i> , 2021, 12, 617163.	2.2	18
20872	A neuronal blood marker is associated with mortality in old age. <i>Nature Aging</i> , 2021, 1, 218-225.	5.3	30
20873	Four potential microRNAs affect the progression of pancreatic ductal adenocarcinoma by targeting MET via the PI3K/AKT signaling pathway. <i>Oncology Letters</i> , 2021, 21, 326.	0.8	4
20874	NetQuilt: deep multispecies network-based protein function prediction using homology-informed network similarity. <i>Bioinformatics</i> , 2021, 37, 2414-2422.	1.8	12
20875	Modular Reorganization of Signaling Networks during the Development of Colon Adenoma and Carcinoma. <i>Journal of Physical Chemistry B</i> , 2021, 125, 1716-1726.	1.2	1
20876	Phosphoproteomic Landscape of AML Cells Treated with the ATP-Competitive CK2 Inhibitor CX-4945. <i>Cells</i> , 2021, 10, 338.	1.8	7
20877	PFP-WGAN: Protein function prediction by discovering Gene Ontology term correlations with generative adversarial networks. <i>PLoS ONE</i> , 2021, 16, e0244430.	1.1	7
20878	Comparative rna-seq analysis of region-specific miRNA expression in the epididymis of cattleyak. <i>Reproduction in Domestic Animals</i> , 2021, 56, 555-576.	0.6	9
20879	Retroviral integrations contribute to elevated host cancer rates during germline invasion. <i>Nature Communications</i> , 2021, 12, 1316.	5.8	16
20880	Evolving Up-regulation of Biliary Fibrosis-Related Extracellular Matrix Molecules After Successful Portoenterostomy. <i>Hepatology Communications</i> , 2021, 5, 1036-1050.	2.0	7
20881	Genome-wide analysis suggests the importance of vascular processes and neuroinflammation in late-life antidepressant response. <i>Translational Psychiatry</i> , 2021, 11, 127.	2.4	22
20882	CogNet: classification of gene expression data based on ranked active-subnetwork-oriented KEGG pathway enrichment analysis. <i>PeerJ Computer Science</i> , 2021, 7, e336.	2.7	24
20886	RNA-binding protein syncrin regulates starvation-induced hyperactivity in adult <i>Drosophila</i> . <i>PLoS Genetics</i> , 2021, 17, e1009396.	1.5	4
20887	Integrative Analysis Identified Key Schizophrenia Risk Factors from an Abnormal Behavior Mouse Gene Set. <i>Life</i> , 2021, 11, 172.	1.1	2
20888	Enrichment analyses of diseases and pathways associated with precocious puberty using PrecocityDB. <i>Scientific Reports</i> , 2021, 11, 4203.	1.6	4
20889	A New Family of Bacteriolytic Proteins in <i>Dictyostelium discoideum</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 617310.	1.8	2

#	ARTICLE	IF	CITATIONS
20890	Genomic Expression Profiling and Bioinformatics Analysis of Chronic Recurrent Multifocal Osteomyelitis. <i>BioMed Research International</i> , 2021, 2021, 1-10.	0.9	3
20891	The microRNA let-7b-5p Is Negatively Associated with Inflammation and Disease Severity in Multiple Sclerosis. <i>Cells</i> , 2021, 10, 330.	1.8	24
20892	Insulin-like 3 affects zebrafish spermatogenic cells directly and via Sertoli cells. <i>Communications Biology</i> , 2021, 4, 204.	2.0	11
20893	RAMP2-AS1 Regulates Endothelial Homeostasis and Aging. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 635307.	1.8	10
20895	Transcriptome-Wide High-Throughput m6A Sequencing of Differential m6A Methylation Patterns in the Human Rheumatoid Arthritis Fibroblast-Like Synoviocytes Cell Line MH7A. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 575-586.	1.6	30
20896	A comprehensive evaluation of skin aging-related circular RNA expression profiles. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e23714.	0.9	8
20897	Limited effects of long-term daily cranberry consumption on the gut microbiome in a placebo-controlled study of women with recurrent urinary tract infections. <i>BMC Microbiology</i> , 2021, 21, 53.	1.3	21
20899	Restoration of type I interferon signaling in intrahepatically primed CD8+ T cells promotes functional differentiation. <i>JCI Insight</i> , 2021, 6, .	2.3	6
20900	Germline and Somatic Whole-Exome Sequencing Identifies New Candidate Genes Involved in Familial Predisposition to Serrated Polyposis Syndrome. <i>Cancers</i> , 2021, 13, 929.	1.7	12
20901	Gene expression and epigenetics reveal species-specific mechanisms acting upon common molecular pathways in the evolution of task division in bees. <i>Scientific Reports</i> , 2021, 11, 3654.	1.6	12
20902	Applications of Machine Learning in Human Microbiome Studies: A Review on Feature Selection, Biomarker Identification, Disease Prediction and Treatment. <i>Frontiers in Microbiology</i> , 2021, 12, 634511.	1.5	157
20903	A draft phased assembly of the diploid Cascade hop (<i>Humulus lupulus</i>) genome. <i>Plant Genome</i> , 2021, 14, e20072.	1.6	25
20904	ViralLink: An integrated workflow to investigate the effect of SARS-CoV-2 on intracellular signalling and regulatory pathways. <i>PLoS Computational Biology</i> , 2021, 17, e1008685.	1.5	11
20905	Single-cell transcriptomes of developing and adult olfactory receptor neurons in <i>Drosophila</i> . <i>ELife</i> , 2021, 10, .	2.8	71
20906	Recent Evolutionary History of Tigers Highlights Contrasting Roles of Genetic Drift and Selection. <i>Molecular Biology and Evolution</i> , 2021, 38, 2366-2379.	3.5	35
20907	Genome annotation of disease-causing microorganisms. <i>Briefings in Bioinformatics</i> , 2021, 22, 845-854.	3.2	13
20908	Comprehensive Quantitative Proteome Analysis of <i>Aedes aegypti</i> Identifies Proteins and Pathways Involved in <i>Wolbachia pipientis</i> and Zika Virus Interference Phenomenon. <i>Frontiers in Physiology</i> , 2021, 12, 642237.	1.3	17
20909	Integrative clustering methods for multi-omics data. <i>Wiley Interdisciplinary Reviews: Computational Statistics</i> , 2022, 14, e1553.	2.1	7

#	ARTICLE	IF	CITATIONS
20910	Transcriptome analysis of the role of autophagy in plant response to heat stress. PLoS ONE, 2021, 16, e0247783.	1.1	5
20911	Identification of Tumor Tissue of Origin with RNA-Seq Data and Using Gradient Boosting Strategy. BioMed Research International, 2021, 2021, 1-14.	0.9	8
20913	Whole-genome comparative analysis of Malaysian Burkholderia pseudomallei clinical isolates. Microbial Genomics, 2021, 7, .	1.0	7
20914	Genomic Resource Development for Hydrangea (Hydrangea macrophylla (Thunb.) Ser.)â€™A Transcriptome Assembly and a High-Density Genetic Linkage Map. Horticulturae, 2021, 7, 25.	1.2	6
20915	Guidelines for biomarker discovery in endometrium: correcting for menstrual cycle bias reveals new genes associated with uterine disorders. Molecular Human Reproduction, 2021, 27, .	1.3	14
20916	Classification of node-positive melanomas into prognostic subgroups using keratin, immune, and melanogenesis expression patterns. Oncogene, 2021, 40, 1792-1805.	2.6	12
20917	Genomic Comparison of Lactobacillus casei AP and Lactobacillus plantarum DR131 with Emphasis on the Butyric Acid Biosynthetic Pathways. Microorganisms, 2021, 9, 425.	1.6	5
20918	Screening and verification of hub genes involved in osteoarthritis using bioinformatics. Experimental and Therapeutic Medicine, 2021, 21, 330.	0.8	4
20919	<i>Trans</i> -acting genetic variation affects the expression of adjacent genes. Genetics, 2021, 217, .	1.2	4
20920	Genomic insight into diet adaptation in the biological control agent <i>Cryptolaemus montrouzieri</i> . BMC Genomics, 2021, 22, 135.	1.2	7
20922	Transcriptome analysis reveals major transcriptional changes during regrowth after mowing of red clover (<i>Trifolium pratense</i>). BMC Plant Biology, 2021, 21, 95.	1.6	10
20924	Maca Root (<i>Lepidium meyenii</i>) Extract Increases the Expression of MMP-1 and Stimulates Migration of Triple-Negative Breast Cancer Cells. Nutrition and Cancer, 2021, , 1-11.	0.9	0
20925	The Genetics of Sudden Infant Death Syndromeâ€™Towards a Gene Reference Resource. Genes, 2021, 12, 216.	1.0	5
20926	New validated Eucalyptus SSR markers located in candidate genes involved in growth and plant development. Forest Systems, 2021, 29, eSC08.	0.1	0
20927	Delivering Behaviour Change Interventions: Development of a Mode of Delivery Ontology. Wellcome Open Research, 2020, 5, 125.	0.9	38
20928	Genome sequencing and annotation and phylogenomic analysis of the medicinal mushroom <i>Amauroderma rugosum</i> , a traditional medicinal species in the family Ganodermataceae. Mycologia, 2021, 113, 268-277.	0.8	7
20929	Runs of homozygosity provide a genome landscape picture of inbreeding and genetic history of European autochthonous and commercial pig breeds. Animal Genetics, 2021, 52, 155-170.	0.6	26
20930	Screening of Hub Gene Targets for Lung Cancer via Microarray Data. Combinatorial Chemistry and High Throughput Screening, 2021, 24, 269-285.	0.6	8

#	ARTICLE	IF	CITATIONS
20933	Cross-species data integration to prioritize causal genes in lipid metabolism. <i>Current Opinion in Lipidology</i> , 2021, 32, 141-146.	1.2	6
20934	Sulfur Metabolites Play Key System-Level Roles in Modulating Denitrification. <i>MSystems</i> , 2021, 6, .	1.7	10
20935	Decreased p53 is associated with a decline in asymmetric stem cell self-renewal in aged human epidermis. <i>Aging Cell</i> , 2021, 20, e13310.	3.0	8
20936	RNA-Seq used to identify ipsdienone reductase (IDONER): A novel monoterpene carbon-carbon double bond reductase central to <i>Ips confusus</i> pheromone production. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 129, 103513.	1.2	5
20937	Identification of Primary and Metastatic Lung Cancer-Related lncRNAs and Potential Targeted Drugs Based on ceRNA Network. <i>Frontiers in Oncology</i> , 2020, 10, 628930.	1.3	6
20938	Tumor-specific cytolytic CD4 T cells mediate immunity against human cancer. <i>Science Advances</i> , 2021, 7, .	4.7	157
20939	20S proteasomes secreted by the malaria parasite promote its growth. <i>Nature Communications</i> , 2021, 12, 1172.	5.8	45
20940	Infection trains the host for microbiota-enhanced resistance to pathogens. <i>Cell</i> , 2021, 184, 615-627.e17.	13.5	148
20941	Regulatory genomic circuitry of human disease loci by integrative epigenomics. <i>Nature</i> , 2021, 590, 300-307.	13.7	232
20942	Spatiotemporal dissection of the cell cycle with single-cell proteogenomics. <i>Nature</i> , 2021, 590, 649-654.	13.7	104
20943	Discovering microbe-disease associations from the literature using a hierarchical long short-term memory network and an ensemble parser model. <i>Scientific Reports</i> , 2021, 11, 4490.	1.6	7
20944	Identification of an N-acetylneuraminic acid-presenting bacteria isolated from a human microbiome. <i>Scientific Reports</i> , 2021, 11, 4763.	1.6	16
20945	Identification of microRNA-16-5p and microRNA-21-5p in feces as potential noninvasive biomarkers for inflammatory bowel disease. <i>Aging</i> , 2021, 13, 4634-4646.	1.4	18
20946	Identifying Breast Cancer-induced Gene Perturbations and its Application in Guiding Drug Repurposing. <i>Current Bioinformatics</i> , 2021, 15, 1075-1089.	0.7	12
20947	Long non-coding RNA LINC00491 promotes proliferation and inhibits apoptosis in esophageal squamous cell carcinoma. <i>International Journal of Molecular Medicine</i> , 2021, 47, .	1.8	6
20948	Pharaoh Cuttlefish, <i>Sepia pharaonis</i> , Genome Reveals Unique Reflectin Camouflage Gene Set. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	10
20950	Transcriptomic Signatures and Functional Network Analysis of Chronic Rhinosinusitis With Nasal Polyps. <i>Frontiers in Genetics</i> , 2021, 12, 609754.	1.1	6
20952	BSGatlas: a unified <i>Bacillus subtilis</i> genome and transcriptome annotation atlas with enhanced information access. <i>Microbial Genomics</i> , 2021, 7, .	1.0	12

#	ARTICLE	IF	CITATIONS
20954	Macrophage M2 Co-expression Factors Correlate With the Immune Microenvironment and Predict Outcome of Renal Clear Cell Carcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 615655.	1.1	31
20955	Genome wide methylation analysis to uncover genes related to recurrent pregnancy loss. <i>Genes and Genomics</i> , 2021, 43, 361-369.	0.5	9
20959	Potential Molecular Mechanism of TNF Superfamily-Related Genes in Glioblastoma Multiforme Based on Transcriptome and Epigenome. <i>Frontiers in Neurology</i> , 2021, 12, 576382.	1.1	6
20960	Improving isobutanol tolerance and titers through EMS mutagenesis in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	5
20961	Multiple Regionalized Genes and Their Putative Networks in the Interpeduncular Nucleus Suggest Complex Mechanisms of Neuron Development and Axon Guidance. <i>Frontiers in Neuroanatomy</i> , 2021, 15, 643320.	0.9	4
20963	Methanol Skin Mucus Extract of Mrigal (<i>Cirrhinus mrigala</i>) Fish Peptide Targeting Viral Particles of Infectious Pancreatic Necrosis Virus (IPNV) and Infectious Salmon Anemia Virus (ISAV): an in silico Approach. <i>International Journal of Peptide Research and Therapeutics</i> , 2021, 27, 1429-1440.	0.9	3
20964	Insights into triterpene synthesis and unsaturated fatty-acid accumulation provided by chromosomal-level genome analysis of <i>Akebia trifoliata</i> subsp. <i>australis</i> . <i>Horticulture Research</i> , 2021, 8, 33.	2.9	23
20965	<i>Arabidopsis thaliana</i> and poly(ADP-ribose) polymerases regulate gene expression in the day but do not affect circadian rhythms. <i>Plant, Cell and Environment</i> , 2021, 44, 1451-1467.	2.8	1
20966	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299.	13.7	1,069
20967	Characterization of mice bearing humanized androgen receptor genes (h/mAr) varying in polymorphism length. <i>NeuroImage</i> , 2021, 226, 117594.	2.1	0
20968	<i>Salmonella enterica</i> Serovars Dublin and Enteritidis Comparative Proteomics Reveals Differential Expression of Proteins Involved in Stress Resistance, Virulence, and Anaerobic Metabolism. <i>Infection and Immunity</i> , 2021, 89, .	1.0	6
20969	Comprehensive Analysis of Gene Expression Changes and Validation in Hepatocellular Carcinoma. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 1021-1031.	1.0	20
20970	Inhibitory effect of sodium butyrate on colorectal cancer cells and construction of the related molecular network. <i>BMC Cancer</i> , 2021, 21, 127.	1.1	18
20971	Correlation between cortical gene expression and resting-state functional network centrality in healthy young adults. <i>Human Brain Mapping</i> , 2021, 42, 2236-2249.	1.9	27
20972	Regional Differences in S-Nitrosylation in the Cortex, Striatum, and Hippocampus of Juvenile Male Mice. <i>Journal of Molecular Neuroscience</i> , 2021, 71, 2383-2392.	1.1	8
20975	Withholding of M-CSF Supplement Reprograms Macrophages to M2-Like via Endogenous CSF-1 Activation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3532.	1.8	13
20976	The identification of neutrophils-mediated mechanisms and potential therapeutic targets for the management of sepsis-induced acute immunosuppression using bioinformatics. <i>Medicine (United Kingdom)</i> , 2021, 100, 31407.	0.0	0
20977	A Wnt-mediated phenotype switch along the epithelial-mesenchymal axis defines resistance and invasion downstream of ionising radiation in oral squamous cell carcinoma. <i>British Journal of Cancer</i> , 2021, 124, 1921-1933.	2.9	3

#	ARTICLE	IF	CITATIONS
20978	Pregnancy-induced changes in the transcriptome of the bovine corpus luteum during and after embryonic interferon-tau secretion. <i>Biology of Reproduction</i> , 2021, 105, 148-163.	1.2	6
20979	Mask blast with a new chemical logic of amino acids for improved protein function prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 922-924.	1.5	1
20980	CircRNA-Protein Interactions in Muscle Development and Diseases. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3262.	1.8	38
20981	Analysing the yeast complexome—the Complex Portal rising to the challenge. <i>Nucleic Acids Research</i> , 2021, 49, 3156-3167.	6.5	5
20982	Brain proteomic changes by histone deacetylase inhibition after traumatic brain injury. <i>Trauma Surgery and Acute Care Open</i> , 2021, 6, e000682.	0.8	2
20983	A novel DNA methylation-based model that effectively predicts prognosis in hepatocellular carcinoma. <i>Bioscience Reports</i> , 2021, 41, .	1.1	5
20984	Construction of the optimization prognostic model based on differentially expressed immune genes of lung adenocarcinoma. <i>BMC Cancer</i> , 2021, 21, 213.	1.1	9
20986	Prognostic Implication of the Expression Level of PECAM-1 in Non-small Cell Lung Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 587744.	1.3	3
20987	Transcriptomic Analysis of Mouse Brain After Traumatic Brain Injury Reveals That the Angiotensin Receptor Blocker Candesartan Acts Through Novel Pathways. <i>Frontiers in Neuroscience</i> , 2021, 15, 636259.	1.4	13
20989	Deciphering the transcriptomic regulation of heat stress responses in <i>Nothofagus pumilio</i> . <i>PLoS ONE</i> , 2021, 16, e0246615.	1.1	6
20990	Weighted Gene Coexpression Network Analysis Uncovers Critical Genes and Pathways for Multiple Brain Regions in Parkinson's Disease. <i>BioMed Research International</i> , 2021, 2021, 1-46.	0.9	5
20991	An Extracellular Matrix-Based Signature Associated With Immune Microenvironment Predicts the Prognosis and Therapeutic Responses of Patients With Oesophageal Squamous Cell Carcinoma. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 598427.	1.6	8
20992	Comparison of plasma and cerebrospinal fluid proteomes identifies gene products guiding adult neurogenesis and neural differentiation in birds. <i>Scientific Reports</i> , 2021, 11, 5312.	1.6	1
20993	Phosphoproteomics-Based Characterization of Prostaglandin E2 Signaling in T Cells. <i>Molecular Pharmacology</i> , 2021, 99, 370-382.	1.0	2
20994	Screening of osteoarthritis diagnostic markers based on immune-related genes and immune infiltration. <i>Scientific Reports</i> , 2021, 11, 7032.	1.6	16
20995	Characterization of a Deep Sea <i>Bacillus toyonensis</i> Isolate: Genomic and Pathogenic Features. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 629116.	1.8	12
20996	Regulation of Juvenile Hormone on Summer Diapause of <i>Geleruca daurica</i> and Its Pathway Analysis. <i>Insects</i> , 2021, 12, 237.	1.0	34
20997	Chromosome-level assembly of the mangrove plant <i>Aegiceras corniculatum</i> genome generated through Illumina, PacBio and Hi-C sequencing technologies. <i>Molecular Ecology Resources</i> , 2021, 21, 1593-1607.	2.2	16

#	ARTICLE	IF	CITATIONS
20998	Hepatic steatosis and steatohepatitis: a functional meta-analysis of sex-based differences in transcriptomic studies. <i>Biology of Sex Differences</i> , 2021, 12, 29.	1.8	18
21000	Ginsenoside F2 induces cellular toxicity to glioblastoma through the impairment of mitochondrial function. <i>Phytomedicine</i> , 2021, 83, 153483.	2.3	9
21001	OXPHOS deficiency activates global adaptation pathways to maintain mitochondrial membrane potential. <i>EMBO Reports</i> , 2021, 22, e51606.	2.0	34
21002	The "Matrisome" reveals the characterization of skin keloid microenvironment. <i>FASEB Journal</i> , 2021, 35, e21237.	0.2	3
21003	Complete Metamorphosis in <i>Manduca sexta</i> Involves Specific Changes in DNA Methylation Patterns. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	10
21004	PIWI-interacting RNA sequencing profiles in maternal plasma-derived exosomes reveal novel non-invasive prenatal biomarkers for the early diagnosis of nonsyndromic cleft lip and palate. <i>EBioMedicine</i> , 2021, 65, 103253.	2.7	24
21005	SBCN Bricks Ontology as a tool to describe recurring concepts in molecular networks. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
21006	Proteomics-Based Approach Reveals the Involvement of SERPINB9 in Recurrent and Relapsed Multiple Myeloma. <i>Journal of Proteome Research</i> , 2021, 20, 2673-2686.	1.8	9
21008	1, 2, 3, GO! Venture beyond gene ontologies in plant evolutionary research. <i>American Journal of Botany</i> , 2021, 108, 361-365.	0.8	5
21009	Integrated analysis of three newly sequenced fern chloroplast genomes: Genome structure and comparative analysis. <i>Ecology and Evolution</i> , 2021, 11, 4550-4563.	0.8	16
21010	Identification and Validation of a Tumor Microenvironment-Related Gene Signature for Prognostic Prediction in Advanced-Stage Non-Small-Cell Lung Cancer. <i>BioMed Research International</i> , 2021, 2021, 1-18.	0.9	9
21011	A developmental lineage-based gene co-expression network for mouse pancreatic β^2 -cells reveals a role for <i>Zfp800</i> in pancreas development. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	12
21012	Genetic-variant hotspots and hotspot clusters in the human genome facilitating adaptation while increasing instability. <i>Human Genomics</i> , 2021, 15, 19.	1.4	9
21013	Strategies to Modulate Specialized Metabolism in Mediterranean Crops: From Molecular Aspects to Field. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2887.	1.8	29
21014	FoxO1-GAB1 axis regulates homing capacity and tonic AKT activity in chronic lymphocytic leukemia. <i>Blood</i> , 2021, 138, 758-772.	0.6	19
21015	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. <i>Science Advances</i> , 2021, 7, .	4.7	36
21016	Seascape genomics reveals candidate molecular targets of heat stress adaptation in three coral species. <i>Molecular Ecology</i> , 2021, 30, 1892-1906.	2.0	14
21017	Identification of four key prognostic genes and three potential drugs in human papillomavirus negative head and neck squamous cell carcinoma. <i>Cancer Cell International</i> , 2021, 21, 167.	1.8	7

#	ARTICLE	IF	CITATIONS
21019	Genome assembly and annotation at the chromosomal level of first Pleuronectidae: <i>Verasper variegatus</i> provides a basis for phylogenetic study of Pleuronectiformes. <i>Genomics</i> , 2021, 113, 717-726.	1.3	8
21020	Identification of a Metabolism-Related Signature for the Prediction of Survival in Endometrial Cancer Patients. <i>Frontiers in Oncology</i> , 2021, 11, 630905.	1.3	14
21023	Transcriptome and metabolome profiling provide insights into molecular mechanism of pseudostem elongation in banana. <i>BMC Plant Biology</i> , 2021, 21, 125.	1.6	11
21024	Integrated microRNA and transcriptome profiling reveal key miRNA-mRNA interaction pairs associated with seed development in Tartary buckwheat (<i>Fagopyrum tataricum</i>). <i>BMC Plant Biology</i> , 2021, 21, 132.	1.6	11
21026	Identification of Candidate Genes Conferring Cold Tolerance to Rice (<i>Oryza sativa</i> L.) at the Bud-Bursting Stage Using Bulk Segregant Analysis Sequencing and Linkage Mapping. <i>Frontiers in Plant Science</i> , 2021, 12, 647239.	1.7	18
21027	Comprehensive In Silico Analysis of a Novel Serum Exosome-Derived Competitive Endogenous RNA Network for Constructing a Prognostic Model for Glioblastoma. <i>Frontiers in Oncology</i> , 2021, 11, 553594.	1.3	11
21028	Plasma Chemical Reactions. <i>Journal of the Institute of Electrical Engineers of Japan</i> , 2021, 141, 155-158.	0.0	0
21030	Identify potential miRNA-mRNA regulatory networks contributing to high-risk neuroblastoma. <i>Investigational New Drugs</i> , 2021, 39, 901-913.	1.2	4
21032	Complete genome sequencing of <i>Bacillus</i> sp. TK-2, analysis of its cold evolution adaptability. <i>Scientific Reports</i> , 2021, 11, 4836.	1.6	11
21033	Critical role of the BAF chromatin remodeling complex during murine neural crest development. <i>PLoS Genetics</i> , 2021, 17, e1009446.	1.5	17
21034	Primary Metabolism co-Opted for Defensive Chemical Production in the Carabid Beetle, <i>Harpalus pensylvanicus</i> . <i>Journal of Chemical Ecology</i> , 2021, 47, 334-349.	0.9	0
21035	Perspective: targeting VEGF-A and YKL-40 in glioblastoma “matter matters”. <i>Cell Cycle</i> , 2021, 20, 702-715.	1.3	6
21036	Changes in protein expression due to metformin treatment and hyperinsulinemia in a human endometrial cancer cell line. <i>PLoS ONE</i> , 2021, 16, e0248103.	1.1	9
21037	An expanding manifold in transmodal regions characterizes adolescent reconfiguration of structural connectome organization. <i>ELife</i> , 2021, 10, .	2.8	47
21038	Differential regulation of β -catenin-mediated transcription via N- and C-terminal co-factors governs identity of murine intestinal epithelial stem cells. <i>Nature Communications</i> , 2021, 12, 1368.	5.8	9
21041	Distinct miRNA Signatures and Networks Discern Fetal from Adult Erythroid Differentiation and Primary from Immortalized Erythroid Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3626.	1.8	12
21042	Candidate Genes for the High-Altitude Adaptations of Two Mountain Pine Taxa. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3477.	1.8	4
21043	Functional Annotation of a Full-Length Transcriptome and Identification of Genes Associated with Flower Development in <i>Rhododendron simsii</i> (Ericaceae). <i>Plants</i> , 2021, 10, 649.	1.6	10

#	ARTICLE	IF	CITATIONS
21044	Genome-wide transcriptome profiling uncovers differential miRNAs and lncRNAs in ovaries of Hu sheep at different developmental stages. <i>Scientific Reports</i> , 2021, 11, 5865.	1.6	16
21048	Validation of intraosseous delivery of valproic acid in a swine model of polytrauma. <i>Trauma Surgery and Acute Care Open</i> , 2021, 6, e000683.	0.8	0
21049	Differential microRNAs expression profiles in liver from three different lifestyle modification mice models. <i>BMC Genomics</i> , 2021, 22, 196.	1.2	2
21050	Identification of molecular biomarkers and pathways of NSCLC: insights from a systems biomedicine perspective. <i>Journal of Genetic Engineering and Biotechnology</i> , 2021, 19, 43.	1.5	8
21051	Identification ACTA2 and KDR as key proteins for prognosis of PD-1/PD-L1 blockade therapy in melanoma. <i>Animal Models and Experimental Medicine</i> , 2021, 4, 138-150.	1.3	4
21052	The Counteracting Effects of Demography on Functional Genomic Variation: The Roma Paradigm. <i>Molecular Biology and Evolution</i> , 2021, 38, 2804-2817.	3.5	14
21053	Dysregulation of circRNA expression in the peripheral blood of individuals with schizophrenia and bipolar disorder. <i>Journal of Molecular Medicine</i> , 2021, 99, 981-991.	1.7	18
21054	The relationship among Circin DNA methylation, its high expression, and immune infiltration in hepatocellular carcinoma: Clues from <i>in silico</i> analysis. <i>Bioscience Reports</i> , 2021, 41, .	1.1	4
21056	Pleiotropic Roles for the Plasmodium berghei RNA Binding Protein UIS12 in Transmission and Oocyst Maturation. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 624945.	1.8	11
21059	Use of data-independent acquisition mass spectrometry for comparative proteomics analyses of sera from pregnant women with intrahepatic cholestasis of pregnancy. <i>Journal of Proteomics</i> , 2021, 236, 104124.	1.2	7
21060	Biological mechanisms of growth performance and meat quality in porcine muscle tissue. <i>Animal Biotechnology</i> , 2022, 33, 1246-1254.	0.7	3
21061	Complete Genome Sequence Analysis of <i>Brevibacillus laterosporus</i> Bl-zj Reflects its Potential Algicidal Response. <i>Current Microbiology</i> , 2021, 78, 1409-1417.	1.0	8
21062	A Comparison of the Transcriptomes of Cowpeas in Response to Two Different Ionizing Radiations. <i>Plants</i> , 2021, 10, 567.	1.6	9
21063	Expression and clinical significance of circular RNAs related to immunity and inflammation in patients with rheumatoid arthritis. <i>International Immunopharmacology</i> , 2021, 92, 107366.	1.7	19
21064	Innate Resistance and Phosphite Treatment Affect Both the Pathogen's and Host's Transcriptomes in the Tanoak-Phytophthora ramorum Pathosystem. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 198.	1.5	11
21065	Genomically Complex Human Angiosarcoma and Canine Hemangiosarcoma Establish Convergent Angiogenic Transcriptional Programs Driven by Novel Gene Fusions. <i>Molecular Cancer Research</i> , 2021, 19, 847-861.	1.5	12
21066	Mitochondrial arginase-2 is essential for IL-10 metabolic reprogramming of inflammatory macrophages. <i>Nature Communications</i> , 2021, 12, 1460.	5.8	74
21067	Genomes of 12 fig wasps provide insights into the adaptation of pollinators to fig syconia. <i>Journal of Genetics and Genomics</i> , 2021, 48, 225-236.	1.7	6

#	ARTICLE	IF	CITATIONS
21068	Rice Transcriptome Analysis Reveals Nitrogen Starvation Modulates Differential Alternative Splicing and Transcript Usage in Various Metabolism-Related Genes. <i>Life</i> , 2021, 11, 285.	1.1	6
21069	Identification of Novel Sensitive and Reliable Serovar-Specific Targets for PCR Detection of <i>Salmonella</i> Serovars Hadar and Albany by Pan-Genome Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 605984.	1.5	8
21070	DeepViral: prediction of novel virus-host interactions from protein sequences and infectious disease phenotypes. <i>Bioinformatics</i> , 2021, 37, 2722-2729.	1.8	35
21071	Noise regularization removes correlation artifacts in single-cell RNA-seq data preprocessing. <i>Patterns</i> , 2021, 2, 100211.	3.1	9
21072	Comprehensive analysis of cancer breakpoints reveals signatures of genetic and epigenetic contribution to cancer genome rearrangements. <i>PLoS Computational Biology</i> , 2021, 17, e1008749.	1.5	12
21073	The Biological Meaning of Radiomic Features. <i>Radiology</i> , 2021, 298, 505-516.	3.6	242
21074	Oncolytic virotherapy-mediated anti-tumor response: a single-cell perspective. <i>Cancer Cell</i> , 2021, 39, 394-406.e4.	7.7	63
21075	Phosphorylation state of the histone variant H2A.X controls human stem and progenitor cell fate decisions. <i>Cell Reports</i> , 2021, 34, 108818.	2.9	10
21076	Maternal Iron Deficiency Modulates Placental Transcriptome and Proteome in Mid-Gestation of Mouse Pregnancy. <i>Journal of Nutrition</i> , 2021, 151, 1073-1083.	1.3	16
21077	Multi-influential genetic interactions alter behaviour and cognition through six main biological cascades in Down syndrome mouse models. <i>Human Molecular Genetics</i> , 2021, 30, 771-788.	1.4	24
21078	Transcriptome differences between <i>Cupriavidus necator</i> NH9 grown with 3-chlorobenzoate and that grown with benzoate. <i>Bioscience, Biotechnology and Biochemistry</i> , 2021, 85, 1546-1561.	0.6	4
21079	Metabolome and Transcriptome Analyses Reveal the Regulatory Mechanisms of Photosynthesis in Developing <i>Ginkgo biloba</i> Leaves. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2601.	1.8	7
21080	Single-Molecule Long-Read Sequencing of Purslane (<i>Portulaca oleracea</i>) and Differential Gene Expression Related with Biosynthesis of Unsaturated Fatty Acids. <i>Plants</i> , 2021, 10, 655.	1.6	5
21081	Cu(II)-Binding N-terminal Sequences of Human Proteins. <i>Chemistry and Biodiversity</i> , 2021, 18, e2100043.	1.0	18
21082	Joint analysis of expression levels and histological images identifies genes associated with tissue morphology. <i>Nature Communications</i> , 2021, 12, 1609.	5.8	45
21083	Biodegradation of lignin monomers and bioconversion of ferulic acid to vanillic acid by <i>Paraburkholderia aromaticivorans</i> AR20-38 isolated from Alpine forest soil. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 2967-2977.	1.7	19
21084	Regulatory Function of Sympathetic Innervation on the Endo/Lysosomal Trafficking of Acetylcholine Receptor. <i>Frontiers in Physiology</i> , 2021, 12, 626707.	1.3	6
21085	The deubiquitinase Usp9x regulates PRC2-mediated chromatin reprogramming during mouse development. <i>Nature Communications</i> , 2021, 12, 1865.	5.8	11

#	ARTICLE	IF	CITATIONS
21087	Genome-wide identification of MIKC-type genes related to stamen and gynoecium development in <i>Liriodendron</i> . <i>Scientific Reports</i> , 2021, 11, 6585.	1.6	3
21088	Transcriptome Analysis Reveals Genes Involved in Thermogenesis in Two Cold-Exposed Sheep Breeds. <i>Genes</i> , 2021, 12, 375.	1.0	4
21089	Integration of multi-omics approaches for functional characterization of muscle related selective sweep genes in <i>Nanchukmacdon</i> . <i>Scientific Reports</i> , 2021, 11, 7219.	1.6	8
21091	Comparative analysis of chloroplast genomes of kenaf cytoplasmic male sterile line and its maintainer line. <i>Scientific Reports</i> , 2021, 11, 5301.	1.6	1
21092	Comparative transcriptome and metabolome analysis of <i>Ostrinia furnacalis</i> female adults under UV-A exposure. <i>Scientific Reports</i> , 2021, 11, 6797.	1.6	8
21093	MegaGO: A Fast Yet Powerful Approach to Assess Functional Gene Ontology Similarity across Meta-Omics Data Sets. <i>Journal of Proteome Research</i> , 2021, 20, 2083-2088.	1.8	8
21094	Editor's introduction to this issue (<i>G&A</i> ; 19:1, 2021). <i>Genomics and Informatics</i> , 2021, 19, e1.	0.4	2
21095	Antennal transcriptome analysis and candidate olfactory genes in <i>Crematogaster rogenhoferi</i> . <i>Bulletin of Entomological Research</i> , 2021, 111, 464-475.	0.5	8
21097	Identification and validation of three core genes in p53 signaling pathway in hepatitis B virus-related hepatocellular carcinoma. <i>World Journal of Surgical Oncology</i> , 2021, 19, 66.	0.8	11
21098	MACMIC Reveals A Dual Role of CTCF in Epigenetic Regulation of Cell Identity Genes. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 140-153.	3.0	4
21099	Gene expression profiles of diabetic kidney disease and neuropathy in eNOS knockout mice: Predictors of pathology and RAS blockade effects. <i>FASEB Journal</i> , 2021, 35, e21467.	0.2	10
21101	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
21102	Mutations of Intrinsically Disordered Protein Regions Can Drive Cancer but Lack Therapeutic Strategies. <i>Biomolecules</i> , 2021, 11, 381.	1.8	26
21103	A perfusable, multifunctional epicardial device improves cardiac function and tissue repair. <i>Nature Medicine</i> , 2021, 27, 480-490.	15.2	61
21104	Computationally predicted SARS-COV-2 encoded microRNAs target NFKB, JAK/STAT and TGFB signaling pathways. <i>Gene Reports</i> , 2021, 22, 101012.	0.4	58
21105	Functional repertoire of EV-associated miRNA profiles after lipoprotein depletion via ultracentrifugation and size exclusion chromatography from autologous blood products. <i>Scientific Reports</i> , 2021, 11, 5823.	1.6	19
21106	Single Nucleotide Polymorphism (SNP) Discovery and Association Study of Flowering Times, Crude Fat and Fatty Acid Composition in Rapeseed (<i>Brassica napus</i> L.) Mutant Lines Using Genotyping-by-Sequencing (GBS). <i>Agronomy</i> , 2021, 11, 508.	1.3	10
21107	CD8+ T Lymphocyte Coexpression Genes Correlate with Immune Microenvironment and Overall Survival in Breast Cancer. <i>Journal of Oncology</i> , 2021, 2021, 1-13.	0.6	0

#	ARTICLE	IF	CITATIONS
21108	Intestinal microbiota and functional characteristics of black soldier fly larvae (<i>Hermetia illucens</i>). <i>Annals of Microbiology</i> , 2021, 71, .	1.1	19
21109	Construction of a Prognostic Gene Signature Associated with Immune Infiltration in Glioma: A Comprehensive Analysis Based on the CGGA. <i>Journal of Oncology</i> , 2021, 2021, 1-19.	0.6	9
21110	Unraveling Heterogeneity of Tumor Cells and Microenvironment and Its Clinical Implications for Triple Negative Breast Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 557477.	1.3	15
21112	Weighted Gene Coexpression Network Analysis Reveals Essential Genes and Pathways in Bipolar Disorder. <i>Frontiers in Psychiatry</i> , 2021, 12, 553305.	1.3	10
21113	The Molecular Basis of Kale Domestication: Transcriptional Profiling of Developing Leaves Provides New Insights Into the Evolution of a Brassica oleracea Vegetative Morphotype. <i>Frontiers in Plant Science</i> , 2021, 12, 637115.	1.7	12
21114	M2 Macrophage Co-Expression Factors Correlate With Immune Phenotype and Predict Prognosis of Bladder Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 609334.	1.3	19
21115	Identification of permissive amber suppression sites for efficient non-canonical amino acid incorporation in mammalian cells. <i>Nucleic Acids Research</i> , 2021, 49, e62-e62.	6.5	30
21116	Transcriptomic Diversity in the Livers of South African Sardines Participating in the Annual Sardine Run. <i>Genes</i> , 2021, 12, 368.	1.0	2
21117	Targeted molecular profiling of rare olfactory sensory neurons identifies fate, wiring, and functional determinants. <i>ELife</i> , 2021, 10, .	2.8	6
21119	Genomic Loci Affecting Milk Production in German Black Pied Cattle (DSN). <i>Frontiers in Genetics</i> , 2021, 12, 640039.	1.1	14
21120	Selective Activation of CNS and Reference PPARGC1A Promoters Is Associated with Distinct Gene Programs Relevant for Neurodegenerative Diseases. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3296.	1.8	5
21121	Overexpression of CCNE1 confers a poorer prognosis in triple-negative breast cancer identified by bioinformatic analysis. <i>World Journal of Surgical Oncology</i> , 2021, 19, 86.	0.8	13
21123	Long non-coding RNAs ENST00000429730.1 and MSTRG.93125.4 are associated with metabolic activity in tuberculosis lesions of sputum-negative tuberculosis patients. <i>Aging</i> , 2021, 13, 8228-8247.	1.4	5
21124	Measuring diversity in heterogeneous information networks. <i>Theoretical Computer Science</i> , 2021, 859, 80-115.	0.5	8
21125	Tumor Microenvironment Proteomics: Lessons From Multiple Myeloma. <i>Frontiers in Oncology</i> , 2021, 11, 563384.	1.3	2
21129	Prediction of LncRNA-encoded small peptides in glioma and oligomer channel functional analysis using in silico approaches. <i>PLoS ONE</i> , 2021, 16, e0248634.	1.1	6
21130	Modular genome-wide gene expression architecture shared by early traits of osteoporosis and atherosclerosis in the Young Finns Study. <i>Scientific Reports</i> , 2021, 11, 7111.	1.6	7
21131	The identification of circular RNAs from peripheral blood mononuclear cells in systemic lupus erythematosus. <i>BMC Medical Genomics</i> , 2021, 14, 70.	0.7	5

#	ARTICLE	IF	CITATIONS
21132	Copper Availability Influences the Transcriptomic Response of <i>Candida albicans</i> to Fluconazole Stress. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
21133	KRAS, YWHAE, SP1 and MSRA as biomarkers in endometrial cancer. <i>Translational Cancer Research</i> , 2021, 10, 1295-1312.	0.4	7
21134	Metabolic and immunological effects of gut microbiota in leaf beetles at the local and systemic levels. <i>Integrative Zoology</i> , 2021, 16, 313-323.	1.3	41
21135	Identification of Biomarkers Related to Atrial Fibrillation With Mitral Regurgitation. <i>American Journal of the Medical Sciences</i> , 2021, 361, 319-326.	0.4	4
21136	G-quadruplexes originating from evolutionary conserved L1 elements interfere with neuronal gene expression in Alzheimer's disease. <i>Nature Communications</i> , 2021, 12, 1828.	5.8	21
21137	Identification of Pivotal MicroRNAs and Target Genes Associated with Persistent Atrial Fibrillation Based on Bioinformatics Analysis. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-13.	0.7	5
21138	PTEN μ suppresses tumor metastasis through regulation of filopodia formation. <i>EMBO Journal</i> , 2021, 40, e105806.	3.5	16
21139	Transcriptome Analysis of <i>Acer truncatum</i> Seeds Reveals Candidate Genes Related to Oil Biosynthesis and Fatty Acid Metabolism. <i>Journal of the American Society for Horticultural Science</i> , 2021, 146, 99-108.	0.5	1
21140	Integration of summary data from GWAS and eQTL studies identified novel risk genes for coronary artery disease. <i>Medicine (United States)</i> , 2021, 100, e24769.	0.4	9
21141	High BLM Expression Predicts Poor Clinical Outcome and Contributes to Malignant Progression in Human Cholangiocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 633899.	1.3	8
21142	Comparative transcriptome analysis of gene expression patterns on B16F10 melanoma cells under Photobiomodulation of different light modes. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2021, 216, 112127.	1.7	10
21143	Ultrafast functional profiling of RNA-seq data for nonmodel organisms. <i>Genome Research</i> , 2021, 31, 713-720.	2.4	15
21144	Mouse models for hereditary spastic paraplegia uncover a role of PI4K2A in autophagic lysosome reformation. <i>Autophagy</i> , 2021, 17, 3690-3706.	4.3	18
21145	Human Chorionic Gonadotropin Modulates the Transcriptome of the Myometrium and Cervix in Late Gestation. <i>Reproductive Sciences</i> , 2021, 28, 2246-2260.	1.1	1
21147	Unique Human and Mouse β^2 -Cell Senescence-Associated Secretory Phenotype (SASP) Reveal Conserved Signaling Pathways and Heterogeneous Factors. <i>Diabetes</i> , 2021, 70, 1098-1116.	0.3	27
21148	Transcriptome Expression of Biomineralization Genes in <i>Littoraria flava</i> Gastropod in Brazilian Rocky Shore Reveals Evidence of Local Adaptation. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	5
21149	Going with the flow: How corals in high-flow environments can beat the heat. <i>Molecular Ecology</i> , 2021, 30, 2009-2024.	2.0	16
21150	A KDM5 α Prospero transcriptional axis functions during early neurodevelopment to regulate mushroom body formation. <i>ELife</i> , 2021, 10, .	2.8	17

#	ARTICLE	IF	CITATIONS
21151	Identification of Meat Quality Determining Marker Genes in Fibroblasts of Bovine Muscle Using Transcriptomic Profiling. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 3776-3786.	2.4	10
21152	TALE: Transformer-based protein function Annotation with joint sequence Label Embedding. <i>Bioinformatics</i> , 2021, 37, 2825-2833.	1.8	52
21154	Identification of the potential function of circRNA in hypertrophic cardiomyopathy based on mutual RNA-RNA and RNA-RBP relationships shown by microarray data. <i>Journal of Electronic Science and Technology</i> , 2021, 19, 100097.	2.0	0
21156	Challenges in the Computational Modeling of the Protein Structure-Activity Relationship. <i>Computation</i> , 2021, 9, 39.	1.0	0
21157	The protein phosphatase with EF-hand domain 1 is a calmodulin-binding protein that interacts with proteins involved in sperm capacitation, binding to the zona pellucida, and motility. <i>Molecular Reproduction and Development</i> , 2021, 88, 302-317.	1.0	1
21158	Bioinformatic Analysis of Exosomal MicroRNAs of Cerebrospinal Fluid in Ischemic Stroke Rats After Physical Exercise. <i>Neurochemical Research</i> , 2021, 46, 1540-1553.	1.6	5
21160	Identification of Genomic Regions Associated with Concentrations of Milk Fat, Protein, Urea and Efficiency of Crude Protein Utilization in Grazing Dairy Cows. <i>Genes</i> , 2021, 12, 456.	1.0	12
21162	IL-8, MSPa, MIF, FGF-9, ANG-2 and AgRP collection were identified for the diagnosis of colorectal cancer based on the support vector machine model. <i>Cell Cycle</i> , 2021, 20, 781-791.	1.3	8
21163	AP-1 subunits converge promiscuously at enhancers to potentiate transcription. <i>Genome Research</i> , 2021, 31, 538-550.	2.4	14
21164	A Comparative Transcriptome Analysis of Human and Porcine Choroid Plexus Cells in Response to <i>Streptococcus suis</i> Serotype 2 Infection Points to a Role of Hypoxia. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 639620.	1.8	5
21165	Dual-process brain mitochondria isolation preserves function and clarifies protein composition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	7
21166	Usefulness of candidate mRNAs and miRNAs as biomarkers for mild cognitive impairment and Alzheimer's disease. <i>International Journal of Neuroscience</i> , 2023, 133, 89-102.	0.8	9
21167	Natural variation in the regulation of neurodevelopmental genes modifies flight performance in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2021, 17, e1008887.	1.5	10
21168	Genome-wide ancestry and introgression in a Zambian baboon hybrid zone. <i>Molecular Ecology</i> , 2021, 30, 1907-1920.	2.0	9
21169	Immunogenomic Profiling Demonstrate AC003092.1 as an Immune-Related eRNA in Glioblastoma Multiforme. <i>Frontiers in Genetics</i> , 2021, 12, 633812.	1.1	12
21170	Cooperation of LIM domain-binding 2 (LDB2) with EGR in the pathogenesis of schizophrenia. <i>EMBO Molecular Medicine</i> , 2021, 13, e12574.	3.3	2
21172	Transcriptome and Comparative Chloroplast Genome Analysis of <i>Vincetoxicum versicolor</i> : Insights Into Molecular Evolution and Phylogenetic Implication. <i>Frontiers in Genetics</i> , 2021, 12, 602528.	1.1	10
21173	Combined proteomics and transcriptomics analysis of <i>Lactococcus lactis</i> under different culture conditions. <i>Journal of Dairy Science</i> , 2021, 104, 2564-2580.	1.4	12

#	ARTICLE	IF	CITATIONS
21174	The very early evolution of protein translocation across membranes. <i>PLoS Computational Biology</i> , 2021, 17, e1008623.	1.5	13
21175	Zbtb10 transcription factor is crucial for murine cDC1 activation and cytokine secretion. <i>European Journal of Immunology</i> , 2021, 51, 1126-1142.	1.6	7
21176	Coexpressed Genes That Promote the Infiltration of M2 Macrophages in Melanoma Can Evaluate the Prognosis and Immunotherapy Outcome. <i>Journal of Immunology Research</i> , 2021, 2021, 1-15.	0.9	15
21177	Piggybacking on Niche Adaptation Improves the Maintenance of Multidrug-Resistance Plasmids. <i>Molecular Biology and Evolution</i> , 2021, 38, 3188-3201.	3.5	23
21178	Identification of disease treatment mechanisms through the multiscale interactome. <i>Nature Communications</i> , 2021, 12, 1796.	5.8	72
21179	Comparative Analysis of <i>Adelphocoris suturalis</i> Jakovlev (Hemiptera: Miridae) Immune Responses to Fungal and Bacterial Pathogens. <i>Frontiers in Physiology</i> , 2021, 12, 646721.	1.3	5
21180	Identification of the hub genes in gastric cancer through weighted gene co-expression network analysis. <i>PeerJ</i> , 2021, 9, e10682.	0.9	9
21181	How to Get Started with Single Cell RNA Sequencing Data Analysis. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 1279-1292.	3.0	19
21182	The evolution of ancestral and species-specific adaptations in snowfinches at the Qinghai-Tibet Plateau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	22
21183	Disparate Interferon Signaling and Shared Aberrant Basaloid Cells in Single-Cell Profiling of Idiopathic Pulmonary Fibrosis and Systemic Sclerosis-Associated Interstitial Lung Disease. <i>Frontiers in Immunology</i> , 2021, 12, 595811.	2.2	54
21185	Transcriptome Analysis of Ovarian Follicles Reveals Potential Pivotal Genes Associated With Increased and Decreased Rates of Chicken Egg Production. <i>Frontiers in Genetics</i> , 2021, 12, 622751.	1.1	19
21186	Stromal NRG1 in luminal breast cancer defines pro-fibrotic and migratory cancer-associated fibroblasts. <i>Oncogene</i> , 2021, 40, 2651-2666.	2.6	13
21187	Transcriptomic alterations in malignant pleural mesothelioma cells in response to long-term treatment with bullfrog sialic acid-binding lectin. <i>Molecular Medicine Reports</i> , 2021, 23, .	1.1	5
21188	Transcriptomic Analysis of Seasonal Gene Expression and Regulation during Xylem Development in Shanxin-Hybrid Poplar (<i>Populus davidiana</i> × <i>Populus bolleana</i>). <i>Forests</i> , 2021, 12, 451.	0.9	5
21189	Common genetic associations between age-related diseases. <i>Nature Aging</i> , 2021, 1, 400-412.	5.3	55
21191	Building blocks and blueprints for bacterial autolysins. <i>PLoS Computational Biology</i> , 2021, 17, e1008889.	1.5	11
21193	An ensemble of the iCluster method to analyze longitudinal lncRNA expression data for psoriasis patients. <i>Human Genomics</i> , 2021, 15, 23.	1.4	2
21194	Comprehensive RNA-Seq Analysis of Potential Therapeutic Targets of Gan-Dou-Fu-Mu Decoction for Treatment of Wilson Disease Using a Toxic Milk Mouse Model. <i>Frontiers in Pharmacology</i> , 2021, 12, 622268.	1.6	5

#	ARTICLE	IF	CITATIONS
21195	27-Hydroxycholesterol is a specific factor in the neoplastic microenvironment of HCC that causes MDR via GRP75 regulation of the redox balance and metabolic reprogramming. <i>Cell Biology and Toxicology</i> , 2022, 38, 311-324.	2.4	7
21196	Isolation and Characterization of Strain <i>Exiguobacterium</i> sp. KRL4, a Producer of Bioactive Secondary Metabolites from a Tibetan Glacier. <i>Microorganisms</i> , 2021, 9, 890.	1.6	5
21197	Network Pharmacology-Based Prediction of Mechanism of Shenzhuo Formula for Application to DKD. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-13.	0.5	2
21198	Identification of a five-gene signature in association with overall survival for hepatocellular carcinoma. <i>PeerJ</i> , 2021, 9, e11273.	0.9	2
21199	The chromosome-level <i>Hemerocallis citrina</i> Borani genome provides new insights into the rutin biosynthesis and the lack of colchicine. <i>Horticulture Research</i> , 2021, 8, 89.	2.9	25
21200	Improved characterisation of clinical text through ontology-based vocabulary expansion. <i>Journal of Biomedical Semantics</i> , 2021, 12, 7.	0.9	8
21201	Genomic insights into population history and biological adaptation in Oceania. <i>Nature</i> , 2021, 592, 583-589.	13.7	100
21202	Preliminary investigations on the pathogenesis-related protein expression profile of the medicinal herb <i>Macleaya cordata</i> and anti-bacterial properties of recombinant proteins. <i>Phytochemistry</i> , 2021, 184, 112667.	1.4	2
21203	Identification of pivotal genes associated with the prognosis of gastric carcinoma through integrated analysis. <i>Bioscience Reports</i> , 2021, 41, .	1.1	7
21204	Insights into salvianolic acid B biosynthesis from chromosome-scale assembly of the <i>Salvia bowleyana</i> genome. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1309-1323.	4.1	18
21205	Sharing biological data: why, when, and how. <i>FEBS Letters</i> , 2021, 595, 847-863.	1.3	26
21206	RUNX2 as a Potential Prognosis Biomarker and New Target for Human Lung Cancer. <i>Exploratory Research and Hypothesis in Medicine</i> , 2021, 000, 000-000.	0.1	1
21207	The Links of Ghrelin to Incretins, Insulin, Glucagon, and Leptin After Bariatric Surgery. <i>Frontiers in Genetics</i> , 2021, 12, 612501.	1.1	11
21208	Bioinformatic analysis identifies potential biomarkers and therapeutic targets of septic-shock-associated acute kidney injury. <i>Hereditas</i> , 2021, 158, 13.	0.5	30
21209	Decomposition Profile Data Analysis for Deep Understanding of Multiple Effects of Natural Products. <i>Journal of Natural Products</i> , 2021, 84, 1283-1293.	1.5	14
21210	The construction and analysis of a ferroptosis-related gene prognostic signature for pancreatic cancer. <i>Aging</i> , 2021, 13, 10396-10414.	1.4	28
21211	Improved de novo chromosome-level genome assembly of the vulnerable walnut tree <i>Juglans mandshurica</i> reveals gene family evolution and possible genome basis of resistance to lesion nematode. <i>Molecular Ecology Resources</i> , 2021, 21, 2063-2076.	2.2	20
21212	Soluble ACE2-mediated cell entry of SARS-CoV-2 via interaction with proteins related to the renin-angiotensin system. <i>Cell</i> , 2021, 184, 2212-2228.e12.	13.5	216

#	ARTICLE	IF	CITATIONS
21213	Multi-Omics Approaches to Define Calcific Aortic Valve Disease Pathogenesis. <i>Circulation Research</i> , 2021, 128, 1371-1397.	2.0	39
21214	FAD-BERT: Improved prediction of FAD binding sites using pre-training of deep bidirectional transformers. <i>Computers in Biology and Medicine</i> , 2021, 131, 104258.	3.9	26
21215	Bioinformatics analysis of laryngeal squamous cell carcinoma: seeking key candidate genes and pathways. <i>PeerJ</i> , 2021, 9, e11259.	0.9	5
21216	Protein Secondary Structure Prediction Using Character Bi-gram Embedding and Bi-LSTM. <i>Current Bioinformatics</i> , 2021, 16, 333-338.	0.7	19
21217	Boosting Detection of Low-Abundance Proteins in Thermal Proteome Profiling Experiments by Addition of an Isobaric Trigger Channel to TMT Multiplexes. <i>Analytical Chemistry</i> , 2021, 93, 7000-7010.	3.2	15
21218	Transcriptomic and microRNA Expression Profiles Identify Biomarkers for Predicting Neo-Chemoradiotherapy Response in Esophageal Squamous Cell Carcinomas (ESCC). <i>Frontiers in Pharmacology</i> , 2021, 12, 626972.	1.6	9
21219	Use of Network Pharmacology to Explore the Mechanism of Gegen (<i>Puerariae lobatae Radix</i>) in the Treatment of Type 2 Diabetes Mellitus Associated with Hyperlipidemia. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-14.	0.5	18
21220	IrGO: Iranian traditional medicine General Ontology and knowledge base. <i>Journal of Biomedical Semantics</i> , 2021, 12, 9.	0.9	4
21221	Genome and Pangenome Analysis of <i>Lactobacillus hilgardii</i> FLUBâ€™A New Strain Isolated from Mead. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3780.	1.8	2
21222	Specifying who delivers behaviour change interventions: development of an Intervention Source Ontology. <i>Wellcome Open Research</i> , 2021, 6, 77.	0.9	14
21223	Reproductive Proteins Evolve Faster Than Non-reproductive Proteins Among Solanum Species. <i>Frontiers in Plant Science</i> , 2021, 12, 635990.	1.7	12
21225	Nanopore long-read RNA-seq and absolute quantification delineate transcription dynamics in early embryo development of an insect pest. <i>Scientific Reports</i> , 2021, 11, 7878.	1.6	12
21226	Network analysis in aged <i>C. elegans</i> reveals candidate regulatory genes of ageing. <i>Biogerontology</i> , 2021, 22, 345-367.	2.0	0
21227	Genome-wide gene expression changes of <i>Pseudomonas veronii</i> 1YdBTEX2 during bioaugmentation in polluted soils. <i>Environmental Microbiomes</i> , 2021, 16, 8.	2.2	7
21228	The prognostic value of an autophagy-related lncRNA signature in hepatocellular carcinoma. <i>BMC Bioinformatics</i> , 2021, 22, 217.	1.2	21
21229	An EPIC predictor of gestational age and its application to newborns conceived by assisted reproductive technologies. <i>Clinical Epigenetics</i> , 2021, 13, 82.	1.8	24
21231	Transcriptomic analysis of Î±-linolenic acid content and biosynthesis in <i>Paeonia ostii</i> fruits and seeds. <i>BMC Genomics</i> , 2021, 22, 297.	1.2	9
21232	Common low complexity regions for SARS-CoV-2 and human proteomes as potential multidirectional risk factor in vaccine development. <i>BMC Bioinformatics</i> , 2021, 22, 182.	1.2	7

#	ARTICLE	IF	CITATIONS
21233	In silico annotation of unreviewed acetylcholinesterase (AChE) in some lepidopteran insect pest species reveals the causes of insecticide resistance. Saudi Journal of Biological Sciences, 2021, 28, 2197-2209.	1.8	5
21234	GAPGOM an R package for gene annotation prediction using GO metrics. BMC Research Notes, 2021, 14, 162.	0.6	1
21235	Multi-label Learning for the Diagnosis of Cancer and Identification of Novel Biomarkers with High-throughput Omics. Current Bioinformatics, 2021, 16, 261-273.	0.7	5
21237	PCprophet: a framework for protein complex prediction and differential analysis using proteomic data. Nature Methods, 2021, 18, 520-527.	9.0	32
21238	Single-Cell Transcriptomics: Current Methods and Challenges in Data Acquisition and Analysis. Frontiers in Neuroscience, 2021, 15, 591122.	1.4	53
21239	miRSM: an R package to infer and analyse miRNA sponge modules in heterogeneous data. RNA Biology, 2021, 18, 2308-2320.	1.5	5
21240	Comparative transcriptomic analysis reveals the regulatory mechanism of the gibberellic acid pathway of Tartary buckwheat (<i>Fagopyrum tataricum</i> (L.) Gaertn.) dwarf mutants. BMC Plant Biology, 2021, 21, 206.	1.6	5
21243	Complex-dependent histone acetyltransferase activity of KAT8 determines its role in transcription and cellular homeostasis. Molecular Cell, 2021, 81, 1749-1765.e8.	4.5	42
21244	High expression of COL5A2, a member of COL5 family, indicates the poor survival and facilitates cell migration in gastric cancer. Bioscience Reports, 2021, 41, .	1.1	25
21245	System-Level Analysis of Alzheimer's Disease Prioritizes Candidate Genes for Neurodegeneration. Frontiers in Genetics, 2021, 12, 625246.	1.1	9
21246	ARTEMIS: A Novel Mass-Spec Platform for HLA-Restricted Self and Disease-Associated Peptide Discovery. Frontiers in Immunology, 2021, 12, 658372.	2.2	7
21247	Genomic and transcriptomic insights into the habitat adaptation of the diazotrophic paddy field cyanobacterium <i>Nostoc sphaeroides</i> . Environmental Microbiology, 2021, 23, 5802-5822.	1.8	5
21248	A First Insight into the Gonad Transcriptome of Hong Kong Catfish (<i>Clarias fuscus</i>). Animals, 2021, 11, 1131.	1.0	14
21249	The mechanism of TiaoGanYiPi formula for treating chronic hepatitis B by network pharmacology and molecular docking verification. Scientific Reports, 2021, 11, 8402.	1.6	10
21250	GraphMS: Drug Target Prediction Using Graph Representation Learning with Substructures. Applied Sciences (Switzerland), 2021, 11, 3239.	1.3	6
21251	Identification of Metastasis-Associated MicroRNAs in Metastatic Melanoma by miRNA Expression Profile and Experimental Validation. Frontiers in Genetics, 2021, 12, 663110.	1.1	9
21252	Molecular mechanisms detected in yak lung tissue via transcriptome-wide analysis provide insights into adaptation to high altitudes. Scientific Reports, 2021, 11, 7786.	1.6	9
21254	MicroCellClust: mining rare and highly specific subpopulations from single-cell expression data. Bioinformatics, 2021, 37, 3220-3227.	1.8	7

#	ARTICLE	IF	CITATIONS
21256	Role of DNA Repair Variants and Diagnostic Radiology Exams in Differentiated Thyroid Cancer Risk: A Pooled Analysis of Two Caseâ€“Control Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1208-1217.	1.1	2
21257	Identification of Critical Functional Modules and Signaling Pathways in Osteoporosis. <i>Current Bioinformatics</i> , 2021, 16, 90-97.	0.7	1
21258	Complementary transcriptomic and proteomic analysis of <i>Bombyx mori</i> middle silk glands reveals a predominant ribosome-biogenesis regulating network during silkworm yellow-cocoon color formation. <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 260-270.	0.4	2
21259	Identification of the specific long-noncoding RNAs involved in night-break mediated flowering retardation in <i>Chenopodium quinoa</i> . <i>BMC Genomics</i> , 2021, 22, 284.	1.2	8
21260	Identification of transcriptomic signatures and crucial pathways involved in non-alcoholic steatohepatitis. <i>Endocrine</i> , 2021, 73, 52-64.	1.1	17
21261	Proteomic reveals the influences of smokeâ€“water and karrikinolide on the biosynthesis of salvianolic acids and lignins in <i>Salvia miltiorrhiza</i> hairy roots. <i>Planta</i> , 2021, 253, 87.	1.6	1
21262	Social organization and the evolution of life-history traits in two queen morphs of the ant <i>Temnothorax rugatulus</i> . <i>Journal of Experimental Biology</i> , 2021, 224, .	0.8	4
21263	Identification of key genes and pathways in discoid lupus skin via bioinformatics analysis. <i>Medicine (United States)</i> , 2021, 100, e25433.	0.4	10
21264	Evaluating the Consistency of Gene Methylation in Liver Cancer Using Bisulfite Sequencing Data. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 671302.	1.8	11
21265	MAPLE: A Microbiome Analysis Pipeline Enabling Optimal Peptide Search and Comparative Taxonomic and Functional Analysis. <i>Journal of Proteome Research</i> , 2021, 20, 2882-2894.	1.8	4
21266	Targeting Adenosine with Adenosine Deaminase 2 to Inhibit Growth of Solid Tumors. <i>Cancer Research</i> , 2021, 81, 3319-3332.	0.4	18
21267	Microbial community characterization of shrimp survivors to AHPND challenge test treated with an effective shrimp probiotic (<i>Vibrio diabolicus</i>). <i>Microbiome</i> , 2021, 9, 88.	4.9	36
21268	Machine learning revealed stemness features and a novel stemness-based classification with appealing implications in discriminating the prognosis, immunotherapy and temozolomide responses of 906 glioblastoma patients. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	74
21269	Large-Scale Phenomic and Genomic Analysis of Brain Asymmetrical Skew. <i>Cerebral Cortex</i> , 2021, 31, 4151-4168.	1.6	26
21270	Transcriptomic analysis of diapauseâ€“associated genes in <i>Exorista civilis</i> Rondani (Diptera:Tachinidae). <i>Archives of Insect Biochemistry and Physiology</i> , 2021, 107, e21789.	0.6	1
21271	Bioinformatic analysis of differentially expressed genes as prognostic markers in pheochromocytoma and paraganglioma tumors. <i>Genes and Genetic Systems</i> , 2021, 96, 55-69.	0.2	5
21272	Altered microRNA Transcriptome in Cultured Human Liver Cells upon Infection with Ebola Virus. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3792.	1.8	12
21273	Utilizing network pharmacology and molecular docking to explore the underlying mechanism of Guizhi Fuling Wan in treating endometriosis. <i>PeerJ</i> , 2021, 9, e11087.	0.9	7

#	ARTICLE	IF	CITATIONS
21274	Single-Cell Atlas Reveals Fatty Acid Metabolites Regulate the Functional Heterogeneity of Mesenchymal Stem Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 653308.	1.8	7
21275	lncRNA C2dat2 facilitates autophagy and apoptosis via the miR-30d-5p/DDIT4/mTOR axis in cerebral ischemia-reperfusion injury. <i>Aging</i> , 2021, 13, 11315-11335.	1.4	27
21276	Connectivity Map Analysis of a Single-Cell RNA-Sequencing -Derived Transcriptional Signature of mTOR Signaling. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4371.	1.8	8
21279	Identification of Key Genes and Underlying Mechanisms in Acute Kawasaki Disease Based on Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2021, 27, e930547.	0.5	6
21280	Harvestman: a framework for hierarchical feature learning and selection from whole genome sequencing data. <i>BMC Bioinformatics</i> , 2021, 22, 174.	1.2	1
21281	Integrated bioinformatics analysis to identify key genes related to the prognosis of esophageal squamous cell carcinoma. <i>Translational Cancer Research</i> , 2021, 10, 1679-1691.	0.4	1
21282	Comparative Analysis of piRNA Profiles Helps to Elucidate Cryoinjury Between Giant Panda and Boar Sperm During Cryopreservation. <i>Frontiers in Veterinary Science</i> , 2021, 8, 635013.	0.9	5
21283	Chronic villitis of unknown etiology: Investigations into viral pathogenesis. <i>Placenta</i> , 2021, 107, 24-30.	0.7	11
21284	lncRNA HHIP-AS1 Promotes the Osteogenic Differentiation Potential and Inhibits the Migration Ability of Periodontal Ligament Stem Cells. <i>Stem Cells International</i> , 2021, 2021, 1-12.	1.2	7
21285	5-hydroxymethylcytosine is dynamically regulated during forebrain organoid development and aberrantly altered in Alzheimer's disease. <i>Cell Reports</i> , 2021, 35, 109042.	2.9	24
21286	Hypericum perforatum L. Regulates Glutathione Redox Stress and Normalizes Ggt1/Anpep Signaling to Alleviate OVX-Induced Kidney Dysfunction. <i>Frontiers in Pharmacology</i> , 2021, 12, 628651.	1.6	3
21287	Properties and gene expression profiling of acquired radioresistance in mouse breast cancer cells. <i>Annals of Translational Medicine</i> , 2021, 9, 628-628.	0.7	4
21288	Mutant PRPF8 Causes Widespread Splicing Changes in Spliceosome Components in Retinitis Pigmentosa Patient iPSC-Derived RPE Cells. <i>Frontiers in Neuroscience</i> , 2021, 15, 636969.	1.4	9
21290	Ontology-based Precision Vaccinology for Deep Mechanism Understanding and Precision Vaccine Development. <i>Current Pharmaceutical Design</i> , 2021, 27, 900-910.	0.9	5
21291	Construction and analysis of protein-protein interaction network of non-alcoholic fatty liver disease. <i>Computers in Biology and Medicine</i> , 2021, 131, 104243.	3.9	10
21292	Comparative transcriptome profiling identifies maize line specificity of fungal effectors in the maize-Ustilago maydis interaction. <i>Plant Journal</i> , 2021, 106, 733-752.	2.8	12
21293	Transcriptome-based metabolic profiling of flavonoids in Agave lechuguilla waste biomass. <i>Plant Science</i> , 2021, 305, 110748.	1.7	12
21294	The KbvR Regulator Contributes to Capsule Production, Outer Membrane Protein Biosynthesis, Antiphagocytosis, and Virulence in <i>Klebsiella pneumoniae</i> . <i>Infection and Immunity</i> , 2021, 89, .	1.0	5

#	ARTICLE	IF	CITATIONS
21295	Interacting impact of maternal inflammatory response and stress on the amygdala transcriptome of pigs. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	13
21296	Extracellular Vesicles from Human Adipose-Derived Mesenchymal Stem Cells: A Review of Common Cargos. <i>Stem Cell Reviews and Reports</i> , 2022, 18, 854-901.	1.7	24
21297	Summary Visualizations of Gene Ontology Terms With GO-Figure!. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	51
21298	Performance Comparison of Deep Learning Autoencoders for Cancer Subtype Detection Using Multi-Omics Data. <i>Cancers</i> , 2021, 13, 2013.	1.7	31
21300	Genome-Wide Mapping of Histone H3 Lysine 4 Trimethylation (H3K4me3) and Its Involvement in Fatty Acid Biosynthesis in Sunflower Developing Seeds. <i>Plants</i> , 2021, 10, 706.	1.6	10
21301	The transcriptomic responses of Atlantic salmon (<i>Salmo salar</i>) to high temperature stress alone, and in combination with moderate hypoxia. <i>BMC Genomics</i> , 2021, 22, 261.	1.2	39
21302	Multi-omic profiling of pituitary thyrotropic cells and progenitors. <i>BMC Biology</i> , 2021, 19, 76.	1.7	5
21304	Isolation and genomic characterization of five novel strains of <i>Erysipelotrichaceae</i> from commercial pigs. <i>BMC Microbiology</i> , 2021, 21, 125.	1.3	29
21307	Identification of a novel autophagy signature for predicting survival in patients with lung adenocarcinoma. <i>PeerJ</i> , 2021, 9, e11074.	0.9	5
21308	Investigation of the Initial Host Response of Na ⁺ -ve Atlantic Salmon (<i>Salmo salar</i>) Inoculated with <i>Paramoeba perurans</i> . <i>Microorganisms</i> , 2021, 9, 746.	1.6	2
21309	Comprehensive RNA-Seq Profiling Reveals Temporal and Tissue-Specific Changes in Gene Expression in Sprague-Dawley Rats as Response to Heat Stress Challenges. <i>Frontiers in Genetics</i> , 2021, 12, 651979.	1.1	11
21310	The VRNetzer platform enables interactive network analysis in Virtual Reality. <i>Nature Communications</i> , 2021, 12, 2432.	5.8	33
21311	Genome variation in colorectal cancer patient with liver metastasis measured by whole-exome sequencing. <i>Journal of Gastrointestinal Oncology</i> , 2021, 12, 507-515.	0.6	10
21312	Systematic Analysis of the Transcriptome Profiles and Co-Expression Networks of Tumour Endothelial Cells Identifies Several Tumour-Associated Modules and Potential Therapeutic Targets in Hepatocellular Carcinoma. <i>Cancers</i> , 2021, 13, 1768.	1.7	10
21313	Complete genome sequence analysis of the peanut pathogen <i>Ralstonia solanacearum</i> strain Rs-P.362200. <i>BMC Microbiology</i> , 2021, 21, 118.	1.3	5
21314	The Chinese mitten crab genome provides insights into adaptive plasticity and developmental regulation. <i>Nature Communications</i> , 2021, 12, 2395.	5.8	38
21315	Predicting Anticancer Drug Response With Deep Learning Constrained by Signaling Pathways. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	19
21316	Integrative Systems Biology Approaches to Identify Potential Biomarkers and Pathways of Cervical Cancer. <i>Journal of Personalized Medicine</i> , 2021, 11, 363.	1.1	9

#	ARTICLE	IF	CITATIONS
21318	Predictive Models of Genetic Redundancy in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 3397-3414.	3.5	16
21319	Metaproteomic analysis of enzymatic composition in Baobaoqu fermentation starter for Wuliangye baijiu. <i>International Journal of Food Science and Technology</i> , 2021, 56, 4170-4181.	1.3	8
21320	Volume-constrained microcontainers enable myoepithelial functional differentiation in highly parallel mammary organoid culture. <i>IScience</i> , 2021, 24, 102253.	1.9	3
21321	Mapping of Genetic Locus for Leaf Trichome Formation in Chinese Cabbage Based on Bulk Segregant Analysis. <i>Plants</i> , 2021, 10, 771.	1.6	6
21322	Transcriptomic Analysis of <i>Pseudomonas aeruginosa</i> Response to Pine Honey via RNA Sequencing Indicates Multiple Mechanisms of Antibacterial Activity. <i>Foods</i> , 2021, 10, 936.	1.9	18
21323	The fourth scientific discovery paradigm for precision medicine and healthcare: Challenges ahead. <i>Precision Clinical Medicine</i> , 2021, 4, 80-84.	1.3	21
21324	Genome-wide characterization of human minisatellite VNTRs: population-specific alleles and gene expression differences. <i>Nucleic Acids Research</i> , 2021, 49, 4308-4324.	6.5	15
21326	Complete chloroplast genome sequencing of Job's tears (<i>Coix</i> L.): genome structure, comparative analysis, and phylogenetic relationships. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1399-1405.	0.2	3
21327	Cell-Type-Specific Gene Modules Related to the Regional Homogeneity of Spontaneous Brain Activity and Their Associations With Common Brain Disorders. <i>Frontiers in Neuroscience</i> , 2021, 15, 639527.	1.4	6
21328	Lipoprotein DolP supports proper folding of BamA in the bacterial outer membrane promoting fitness upon envelope stress. <i>ELife</i> , 2021, 10, .	2.8	15
21329	Silencing SHMT2 inhibits the progression of tongue squamous cell carcinoma through cell cycle regulation. <i>Cancer Cell International</i> , 2021, 21, 220.	1.8	13
21332	Measuring and Modelling the Epithelial- Mesenchymal Hybrid State in Cancer: Clinical Implications. <i>Cells Tissues Organs</i> , 2022, 211, 110-133.	1.3	28
21333	Insight into the denitrification mechanism of <i>Bacillus subtilis</i> JD-014 and its application potential in bioremediation of nitrogen wastewater. <i>Process Biochemistry</i> , 2021, 103, 78-86.	1.8	23
21334	Controlling for cellular heterogeneity using single-cell deconvolution of gene expression reveals novel markers of colorectal tumors exhibiting microsatellite instability. <i>Oncotarget</i> , 2021, 12, 767-782.	0.8	5
21335	A genome-wide atlas of co-essential modules assigns function to uncharacterized genes. <i>Nature Genetics</i> , 2021, 53, 638-649.	9.4	86
21336	Sphingosine Promotes Embryo Biomass in Upland Cotton: A Biochemical and Transcriptomic Analysis. <i>Biomolecules</i> , 2021, 11, 525.	1.8	3
21337	Categorization of Orthologous Gene Clusters in 92 Ascomycota Genomes Reveals Functions Important for Phytopathogenicity. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 337.	1.5	3
21338	Cycad-Weevil Pollination Symbiosis Is Characterized by Rapidly Evolving and Highly Specific Plant-Insect Chemical Communication. <i>Frontiers in Plant Science</i> , 2021, 12, 639368.	1.7	8

#	ARTICLE	IF	CITATIONS
21341	Transcriptome-Wide Gene Expression in a Murine Model of Ventilator-Induced Lung Injury. <i>Disease Markers</i> , 2021, 2021, 1-23.	0.6	1
21342	RIP1 Perturbation Induces Chondrocyte Necroptosis and Promotes Osteoarthritis Pathogenesis via Targeting BMP7. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 638382.	1.8	22
21343	Molecular evidence of the avocado defense response to <i>Fusarium kuroshium</i> infection: a deep transcriptome analysis using RNA-Seq. <i>PeerJ</i> , 2021, 9, e11215.	0.9	10
21344	Best practices on the differential expression analysis of multi-species RNA-seq. <i>Genome Biology</i> , 2021, 22, 121.	3.8	51
21345	Bioinformatics analysis of the expression and role of microRNA-221-3p in head and neck squamous cell carcinoma. <i>BMC Cancer</i> , 2021, 21, 395.	1.1	3
21346	Genome-Wide Gene Expression Analysis of Mtb-Infected DC Highlights the Rapamycin-Driven Modulation of Regulatory Cytokines via the mTOR/GSK-3 ^β Axis. <i>Frontiers in Immunology</i> , 2021, 12, 649475.	2.2	4
21347	Subcellular proteomics. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	159
21348	Transcriptome analysis reveals gene responses to herbicide, tribenuron methyl, in <i>Brassica napus</i> L. during seed germination. <i>BMC Genomics</i> , 2021, 22, 299.	1.2	6
21349	Differential Expression of Insulin-Like Growth Factor 1 and Wnt Family Member 4 Correlates With Functional Heterogeneity of Human Dermal Fibroblasts. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 628039.	1.8	3
21350	CCR7 Has Potential to Be a Prognosis Marker for Cervical Squamous Cell Carcinoma and an Index for Tumor Microenvironment Change. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 583028.	1.6	4
21351	Prediction of <i>Streptococcus uberis</i> clinical mastitis treatment success in dairy herds by means of mass spectrometry and machine-learning. <i>Scientific Reports</i> , 2021, 11, 7736.	1.6	3
21352	Comparison and Functional Analysis of Chemosensory Protein Genes From <i>Eucryptorrhynchus scrobiculatus</i> Motschulsky and <i>Eucryptorrhynchus brandti</i> Harold. <i>Frontiers in Physiology</i> , 2021, 12, 661310.	1.3	1
21353	Characterization of the Survival Influential Genes in Carcinogenesis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4384.	1.8	1
21354	A newly-isolated Cd-loving <i>Purpureocillium</i> sp. strain YZ1 substantially alleviates Cd toxicity to wheat. <i>Plant and Soil</i> , 2021, 464, 289.	1.8	12
21357	Establishing a consensus for the hallmarks of cancer based on gene ontology and pathway annotations. <i>BMC Bioinformatics</i> , 2021, 22, 178.	1.2	15
21359	Discovery of Post-Translational Modifications in <i>Emiliana huxleyi</i> . <i>Molecules</i> , 2021, 26, 2027.	1.7	2
21360	De-novo Assembly of <i>Limnospira fusiformis</i> Using Ultra-Long Reads. <i>Frontiers in Microbiology</i> , 2021, 12, 657995.	1.5	3
21361	Diversity in genetic and peptidase activity of <i>Lactobacillus helveticus</i> strains biodiversity of <i>Lactobacillus helveticus</i> . <i>Food Bioscience</i> , 2021, 40, 100915.	2.0	7

#	ARTICLE	IF	CITATIONS
21362	Expression and prognosis analyses of BUB1, BUB1B and BUB3 in human sarcoma. <i>Aging</i> , 2021, 13, 12395-12409.	1.4	16
21363	EV11 activates tumor-promoting transcriptional enhancers in pancreatic cancer. <i>NAR Cancer</i> , 2021, 3, zcab023.	1.6	10
21364	FINER: enhancing the prediction of tissue-specific functions of isoforms by refining isoform interaction networks. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab057.	1.5	3
21366	A homozygous variant in <i>TBPL2</i> was identified in women with oocyte maturation defects and infertility. <i>Human Reproduction</i> , 2021, 36, 2011-2019.	0.4	14
21367	BRAF paradox breakers PLX8394, PLX7904 are more effective against BRAFV600E CRC cells compared with the BRAF inhibitor PLX4720 and shown by detailed pathway analysis. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 166061.	1.8	14
21368	An atlas of the tissue and blood metagenome in cancer reveals novel links between bacteria, viruses and cancer. <i>Microbiome</i> , 2021, 9, 94.	4.9	10
21369	Conserved long-range base pairings are associated with pre-mRNA processing of human genes. <i>Nature Communications</i> , 2021, 12, 2300.	5.8	27
21371	Identification of Expression Patterns and Potential Prognostic Significance of m5C-Related Regulators in Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 592107.	1.3	12
21372	Assessing Various Control Samples for Microarray Gene Expression Profiling of Laryngeal Squamous Cell Carcinoma. <i>Biomolecules</i> , 2021, 11, 588.	1.8	2
21375	Simple biochemical features underlie transcriptional activation domain diversity and dynamic, fuzzy binding to Mediator. <i>ELife</i> , 2021, 10, .	2.8	87
21376	Resilience, plasticity and robustness in gene expression during aging in the brain of outbred deer mice. <i>BMC Genomics</i> , 2021, 22, 291.	1.2	2
21377	Hippocampal transcriptome deconvolution reveals differences in cell architecture of not demented elderly subjects underwent late-life physical activity. <i>Journal of Chemical Neuroanatomy</i> , 2021, 113, 101934.	1.0	7
21378	Modular, efficient and constant-memory single-cell RNA-seq preprocessing. <i>Nature Biotechnology</i> , 2021, 39, 813-818.	9.4	252
21380	Chromosome-level genome assembly of the hard-shelled mussel <i>Mytilus coruscus</i> , a widely distributed species from the temperate areas of East Asia. <i>GigaScience</i> , 2021, 10, .	3.3	45
21381	Gene network analysis using SWIM reveals interplay between the transcription factor-encoding genes HMGA1, FOXM1, and MYBL2 in triple-negative breast cancer. <i>FEBS Letters</i> , 2021, 595, 1569-1586.	1.3	12
21382	Characterization of Extracellular Vesicles Secreted in Lentiviral Producing HEK293SF Cell Cultures. <i>Viruses</i> , 2021, 13, 797.	1.5	9
21383	Light cycle phase advance as a model for jet lag reprograms the circadian rhythms of murine extraorbital lacrimal glands. <i>Ocular Surface</i> , 2021, 20, 95-114.	2.2	14
21384	Basic leucine zipper (bZIP) transcription factor genes and their responses to drought stress in ginseng, <i>Panax ginseng</i> C.A. Meyer. <i>BMC Genomics</i> , 2021, 22, 316.	1.2	10

#	ARTICLE	IF	CITATIONS
21386	In-Frame and Frameshift Mutations in Zebrafish Presenilin 2 Affect Different Cellular Functions in Young Adult Brains. <i>Journal of Alzheimer's Disease Reports</i> , 2021, 5, 395-404.	1.2	8
21387	Cholesterol-Induced M4-Like Macrophages Recruit Neutrophils and Induce NETosis. <i>Frontiers in Immunology</i> , 2021, 12, 671073.	2.2	11
21388	Protein structure-based gene expression signatures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	5
21389	Role of cytoplasmic localization of maspin in promoting cell invasion in breast cancer with aggressive phenotype. <i>Scientific Reports</i> , 2021, 11, 11321.	1.6	9
21391	Retinoic acid induces NELFA-mediated 2Ca-like state of mouse embryonic stem cells associates with epigenetic modifications and metabolic processes in chemically defined media. <i>Cell Proliferation</i> , 2021, 54, e13049.	2.4	13
21392	Comparative Transcriptome Analysis of Two Contrasting Maize Inbred Lines Provides Insights on Molecular Mechanisms of Stalk Rot Resistance. <i>PhytoFrontiers</i> , 2021, 1, 314-329.	0.8	3
21393	A novel diagnostic signature based on three circulating exosomal mircoRNAs for chronic obstructive pulmonary disease. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 717.	0.8	12
21394	Construction of mRNA Regulatory Networks Reveals the Key Genes in Atrial Fibrillation. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-10.	0.7	0
21396	Multimodality assessment of heart failure with preserved ejection fraction skeletal muscle reveals differences in the machinery of energy fuel metabolism. <i>ESC Heart Failure</i> , 2021, 8, 2698-2712.	1.4	16
21397	The nuclear receptor HNF4 drives a brush border gene program conserved across murine intestine, kidney, and embryonic yolk sac. <i>Nature Communications</i> , 2021, 12, 2886.	5.8	24
21398	Molecular Characterization of Secreted Proteins from Salivary Gland Immunogenic Protein of <i>Anopheles vagus</i> . <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 747, 012055.	0.2	0
21399	Platelets orchestrate the resolution of pulmonary inflammation in mice by T reg cell repositioning and macrophage education. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	30
21400	Chromatin-associated MRN complex protects highly transcribing genes from genomic instability. <i>Science Advances</i> , 2021, 7, .	4.7	18
21401	Transcriptional signatures of synaptic vesicle genes define myotonic dystrophy type I neurodegeneration. <i>Neuropathology and Applied Neurobiology</i> , 2021, 47, 1092-1108.	1.8	14
21402	A miR-375/YAP axis regulates neuroendocrine differentiation and tumorigenesis in lung carcinoid cells. <i>Scientific Reports</i> , 2021, 11, 10455.	1.6	7
21403	Integrative Analysis of lncRNA and mRNA and Profiles in Postoperative Delirium Patients. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 665935.	1.7	5
21404	Overlap of vitamin A and vitamin D target genes with CAKUT-related processes. <i>F1000Research</i> , 2021, 10, 395.	0.8	5
21405	Transcriptome analysis reveals hub genes in the hepatopancreas of <i>Exopalaemon carinicauda</i> in response to hypoxia and reoxygenation. <i>Aquaculture International</i> , 2021, 29, 1785-1811.	1.1	2

#	ARTICLE	IF	CITATIONS
21406	The genomic basis of evolutionary differentiation among honey bees. <i>Genome Research</i> , 2021, 31, 1203-1215.	2.4	17
21407	snpXplorer: a web application to explore human SNP-associations and annotate SNP-sets. <i>Nucleic Acids Research</i> , 2021, 49, W603-W612.	6.5	14
21408	Drug-Drug Interaction between Metformin and Sorafenib Alters Antitumor Effect in Hepatocellular Carcinoma Cells. <i>Molecular Pharmacology</i> , 2021, 100, 32-45.	1.0	9
21410	Enhancing the production of amphotericin B by <i>Streptomyces nodosus</i> in a 50-ton bioreactor based on comparative genomic analysis. <i>3 Biotech</i> , 2021, 11, 299.	1.1	2
21411	Integrated analysis of virus and host transcriptomes in cervical cancer in Asian and Western populations. <i>Genomics</i> , 2021, 113, 1554-1564.	1.3	9
21412	GWENA: gene co-expression networks analysis and extended modules characterization in a single Bioconductor package. <i>BMC Bioinformatics</i> , 2021, 22, 267.	1.2	20
21413	Synergistic Effects of Thermal Stress and Estuarine Discharge on Transcriptomic Variation of <i>Montastraea cavernosa</i> Corals in Southeast Florida. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	4
21414	Centromere protein N may be a novel malignant prognostic biomarker for hepatocellular carcinoma. <i>PeerJ</i> , 2021, 9, e11342.	0.9	7
21415	Functional dynamic genetic effects on gene regulation are specific to particular cell types and environmental conditions. <i>ELife</i> , 2021, 10, .	2.8	41
21417	Transcriptomic analysis of atopic dermatitis in African Americans is characterized by Th2/Th17-centered cutaneous immune activation. <i>Scientific Reports</i> , 2021, 11, 11175.	1.6	28
21418	Genome-wide histone acetylation analysis reveals altered transcriptional regulation in the Parkinson's disease brain. <i>Molecular Neurodegeneration</i> , 2021, 16, 31.	4.4	51
21419	In <i>Arabidopsis thaliana</i> Cd differentially impacts on hormone genetic pathways in the methylation defective <i>ddc</i> mutant compared to wild type. <i>Scientific Reports</i> , 2021, 11, 10965.	1.6	16
21420	The liver-clock coordinates rhythmicity of peripheral tissues in response to feeding. <i>Nature Metabolism</i> , 2021, 3, 829-842.	5.1	70
21423	Transcriptional Analysis of Liver Tissue Identifies Distinct Phenotypes of Indeterminate Pediatric Acute Liver Failure. <i>Hepatology Communications</i> , 2021, 5, 1373-1384.	2.0	15
21424	Epigenetic effects of parasites and pesticides on captive and wild nestling birds. <i>Ecology and Evolution</i> , 2021, 11, 7713-7729.	0.8	8
21425	Intestinal mucosa-derived DNA methylation signatures in the penetrating intestinal mucosal lesions of Crohn's disease. <i>Scientific Reports</i> , 2021, 11, 9771.	1.6	8
21426	Genoppi is an open-source software for robust and standardized integration of proteomic and genetic data. <i>Nature Communications</i> , 2021, 12, 2580.	5.8	15
21428	CPA: a web-based platform for consensus pathway analysis and interactive visualization. <i>Nucleic Acids Research</i> , 2021, 49, W114-W124.	6.5	20

#	ARTICLE	IF	CITATIONS
21429	DeepGOWeb: fast and accurate protein function prediction on the (Semantic) Web. <i>Nucleic Acids Research</i> , 2021, 49, W140-W146.	6.5	15
21430	Network-based identification of key master regulators associated with an immune-silent cancer phenotype. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	11
21431	Updates to HCOP: the HGNC comparison of orthology predictions tool. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	20
21432	Comprehensive Phosphoproteomic Analysis of <i>Nostoc flagelliforme</i> in Response to Dehydration Provides Insights into Plant ROS Signaling Transduction. <i>ACS Omega</i> , 2021, 6, 13554-13566.	1.6	7
21433	Cabazitaxel-loaded poly(alkyl cyanoacrylate) nanoparticles: Toxicity and changes in the proteome of breast, colon and prostate cancer cells. <i>Nanotoxicology</i> , 2021, 15, 1-20.	1.6	5
21434	Transcriptome Profiling Analysis of the Testis After Eystalk Ablation for Selection of the Candidate Genes Involved in the Male Sexual Development in <i>Macrobrachium nipponense</i> . <i>Frontiers in Genetics</i> , 2021, 12, 675928.	1.1	12
21435	ANOX: A robust computational model for predicting the antioxidant proteins based on multiple features. <i>Analytical Biochemistry</i> , 2021, 631, 114257.	1.1	2
21436	Host Response of Atlantic Salmon (<i>Salmo salar</i>) Re-Inoculated with <i>Paramoeba perurans</i> . <i>Microorganisms</i> , 2021, 9, 993.	1.6	1
21437	Gene and protein expression in human megakaryocytes derived from induced pluripotent stem cells. <i>Journal of Thrombosis and Haemostasis</i> , 2021, 19, 1783-1799.	1.9	6
21438	Pluripotent stem cell-derived endometrial stromal fibroblasts in a cyclic, hormone-responsive, coculture model of human decidua. <i>Cell Reports</i> , 2021, 35, 109138.	2.9	30
21439	Regulation of Oxalate Metabolism in Spinach Revealed by RNA-Seq-Based Transcriptomic Analysis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5294.	1.8	7
21440	Multi-Dimensional Transcriptome Analysis Reveals Modulation of Cholesterol Metabolism as Highly Integrated Response to Brain Injury. <i>Frontiers in Neuroscience</i> , 2021, 15, 671249.	1.4	8
21441	Comparative genomics and analysis of the mechanism of PQQ overproduction in <i>Methylobacterium</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 100.	1.7	6
21442	Haplotype-resolved genome assembly enables gene discovery in the red palm weevil <i>Rhynchophorus ferrugineus</i> . <i>Scientific Reports</i> , 2021, 11, 9987.	1.6	20
21443	Defining the role of the polyasparagine repeat domain of the <i>S. cerevisiae</i> transcription factor Azf1p. <i>PLoS ONE</i> , 2021, 16, e0247285.	1.1	3
21444	Comparing Statistical Tests for Differential Network Analysis of Gene Modules. <i>Frontiers in Genetics</i> , 2021, 12, 630215.	1.1	4
21446	Exploring the genetic features and signatures of selection in South China indigenous pigs. <i>Journal of Integrative Agriculture</i> , 2021, 20, 1359-1371.	1.7	9
21447	Common pathways and functional profiles reveal underlying patterns in Breast, Kidney and Lung cancers. <i>Biology Direct</i> , 2021, 16, 9.	1.9	7

#	ARTICLE	IF	CITATIONS
21448	Rapid evolution of mammalian APLP1 as a synaptic adhesion molecule. <i>Scientific Reports</i> , 2021, 11, 11305.	1.6	6
21450	AMOTL2 knockdown promotes the proliferation, migration and invasion of glioma by regulating β -catenin nuclear localization. <i>Oncology Reports</i> , 2021, 46, .	1.2	5
21451	Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. <i>Nature</i> , 2021, 595, 309-314.	13.7	181
21452	Integrating protein networks and machine learning for disease stratification in the Hereditary Spastic Paraplegias. <i>IScience</i> , 2021, 24, 102484.	1.9	8
21453	An evolutionary genomic approach reveals both conserved and species-specific genetic elements related to human disease in closely related <i>Aspergillus</i> fungi. <i>Genetics</i> , 2021, 218, .	1.2	18
21454	Temporal Transcriptome Analysis Reveals Dynamic Gene Expression Patterns Driving β -Cell Maturation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 648791.	1.8	9
21455	Overcoming false-positive gene-category enrichment in the analysis of spatially resolved transcriptomic brain atlas data. <i>Nature Communications</i> , 2021, 12, 2669.	5.8	74
21456	Inferring Genome-Wide Correlations of Mutation Fitness Effects between Populations. <i>Molecular Biology and Evolution</i> , 2021, 38, 4588-4602.	3.5	23
21457	Skeletal Muscle Gene Expression Profile in Response to Caloric Restriction and Aging: A Role for SirT1. <i>Genes</i> , 2021, 12, 691.	1.0	6
21458	Strategies for detecting and identifying biological signals amidst the variation commonly found in RNA sequencing data. <i>BMC Genomics</i> , 2021, 22, 322.	1.2	6
21460	Simultaneous learning of individual microRNA-gene interactions and regulatory comodules. <i>BMC Bioinformatics</i> , 2021, 22, 237.	1.2	1
21461	G2PDeep: a web-based deep-learning framework for quantitative phenotype prediction and discovery of genomic markers. <i>Nucleic Acids Research</i> , 2021, 49, W228-W236.	6.5	12
21462	ITGAX: A Potential Biomarker of Acute Myeloid Leukemia (AML) through Bioinformatic Analysis. , 2021, , .		0
21464	Vesicle transporter GOLT1B mediates the cell membrane localization of DVL2 and PD-L2 and promotes colorectal cancer metastasis. <i>Cancer Cell International</i> , 2021, 21, 287.	1.8	8
21465	Construction of a prognostic risk model of colorectal adenocarcinoma through integrated analysis of RNA-binding proteins. <i>Translational Cancer Research</i> , 2021, 10, 1962-1974.	0.4	0
21466	Evolution of the 'world's only alpine parrot': Genomic adaptation or phenotypic plasticity, behaviour and ecology?. <i>Molecular Ecology</i> , 2021, 30, 6370-6386.	2.0	11
21470	Characterization of the small RNA transcriptomes of cell protrusions and cell bodies of highly metastatic hepatocellular carcinoma cells via RNA sequencing. <i>Oncology Letters</i> , 2021, 22, 568.	0.8	4
21471	Transcription factor overexpression drives reliable differentiation of retinal pigment epithelium from human induced pluripotent stem cells. <i>Stem Cell Research</i> , 2021, 53, 102368.	0.3	7

#	ARTICLE	IF	CITATIONS
21472	Learning from Embryogenesis—A Comparative Expression Analysis in Melanoblast Differentiation and Tumorigenesis Reveals miRNAs Driving Melanoma Development. <i>Journal of Clinical Medicine</i> , 2021, 10, 2259.	1.0	5
21473	Proteomic Analyses of Vitreous in Proliferative Diabetic Retinopathy: Prior Studies and Future Outlook. <i>Journal of Clinical Medicine</i> , 2021, 10, 2309.	1.0	6
21474	Gene Instability-Related lncRNA Prognostic Model of Melanoma Patients via Machine Learning Strategy. <i>Journal of Oncology</i> , 2021, 2021, 1-22.	0.6	8
21476	Comprehensive Transcriptome and Metabolome Analysis of <i>Lithocarpus polystachyus</i> Leaf Revealed Key Genes in Flavonoid Biosynthesis Pathways. <i>Journal of the American Society for Horticultural Science</i> , 2021, 146, 147-157.	0.5	1
21477	Gene Cascade Shift and Pathway Enrichment in Rat Kidney Induced by Acarbose Through Comparative Analysis. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 659700.	2.0	2
21478	Screening and identification of LMNB1 and DLGAP5, two key biomarkers in gliomas. <i>Bioscience Reports</i> , 2021, 41, .	1.1	7
21480	Identification of rye B chromosome-associated peptides by mass spectrometry. <i>New Phytologist</i> , 2021, 230, 2179-2185.	3.5	6
21482	Chromosomal instability by mutations in the novel minor spliceosome component <i>CENATAC</i> . <i>EMBO Journal</i> , 2021, 40, e106536.	3.5	26
21483	Chromosome-scale assembly of the <i>Sparassis latifolia</i> genome obtained using long-read and Hi-C sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	4
21484	Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease. <i>Nature Communications</i> , 2021, 12, 2444.	5.8	58
21485	Identification of viral-mediated pathogenic mechanisms in neurodegenerative diseases using network-based approaches. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
21486	The IDIP framework for assessing protein function and its application to the prion protein. <i>Biological Reviews</i> , 2021, 96, 1907-1932.	4.7	5
21487	Transcriptome analysis reveals potential function of long non-coding RNAs in 20-hydroxyecdysone regulated autophagy in <i>Bombyx mori</i> . <i>BMC Genomics</i> , 2021, 22, 374.	1.2	12
21488	Subtelomeric assembly of a multi-gene pathway for antimicrobial defense compounds in cereals. <i>Nature Communications</i> , 2021, 12, 2563.	5.8	51
21489	Identification of the EMT-Related Genes Signature for Predicting Occurrence and Progression in Thyroid Cancer. <i>OncoTargets and Therapy</i> , 2021, Volume 14, 3119-3131.	1.0	5
21490	Transcriptomic meta-analysis of disuse muscle atrophy vs. resistance exercise-induced hypertrophy in young and older humans. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2021, 12, 629-645.	2.9	15
21491	Exogenous phytohormone application and transcriptome analysis of <i>Mikania micrantha</i> provides insights for a potential control strategy. <i>Genomics</i> , 2021, 113, 964-975.	1.3	6
21492	Novel ultra-rare exonic variants identified in a founder population implicate cadherins in schizophrenia. <i>Neuron</i> , 2021, 109, 1465-1478.e4.	3.8	21

#	ARTICLE	IF	CITATIONS
21494	Functional and genetic determinants of mutation rate variability in regulatory elements of cancer genomes. <i>Genome Biology</i> , 2021, 22, 133.	3.8	12
21496	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
21497	Genome-wide bioinformatic analyses predict key host and viral factors in SARS-CoV-2 pathogenesis. <i>Communications Biology</i> , 2021, 4, 590.	2.0	38
21498	Microarray and qPCR Analysis of Mitochondrial Metabolism Activation during Prenatal and Early Postnatal Development in Rats and Humans with Emphasis on CoQ10 Biosynthesis. <i>Biology</i> , 2021, 10, 418.	1.3	1
21499	Comparative transcriptomics between <i>Drosophila mojavensis</i> and <i>D. arizonae</i> reveals transgressive gene expression and underexpression of spermatogenesis-related genes in hybrid testes. <i>Scientific Reports</i> , 2021, 11, 9844.	1.6	12
21500	Whole-genome resequencing of <i>Osmanthus fragrans</i> provides insights into flower color evolution. <i>Horticulture Research</i> , 2021, 8, 98.	2.9	35
21501	A termination-independent role of Rat1 in cotranscriptional splicing. <i>Nucleic Acids Research</i> , 2021, 49, 5520-5536.	6.5	3
21502	Rcl1 depletion impairs 18S pre-rRNA processing at the A1-site and up-regulates a cohort of ribosome biogenesis genes in zebrafish. <i>Nucleic Acids Research</i> , 2021, 49, 5743-5759.	6.5	7
21503	Reactome and the Gene Ontology: digital convergence of data resources. <i>Bioinformatics</i> , 2021, 37, 3343-3348.	1.8	19
21504	Integrated genomic analysis reveals key features of long undecoded transcript isoform-based gene repression. <i>Molecular Cell</i> , 2021, 81, 2231-2245.e11.	4.5	20
21509	Development of a multiplex assay to determine the expression of mitochondrial genes in human skeletal muscle. <i>Experimental Physiology</i> , 2021, 106, 1659-1670.	0.9	2
21510	Network Pharmacology-Based Validation of the Efficacy of Huiyangjiuji Decoction in the Treatment of Experimental Colitis. <i>Frontiers in Pharmacology</i> , 2021, 12, 666432.	1.6	7
21511	Glycoproteomic analysis of the changes in protein N-glycosylation during neuronal differentiation in human-induced pluripotent stem cells and derived neuronal cells. <i>Scientific Reports</i> , 2021, 11, 11169.	1.6	8
21513	Genome-wide analysis identifies a novel LINC-PINT splice variant associated with vascular amyloid pathology in Alzheimer's disease. <i>Acta Neuropathologica Communications</i> , 2021, 9, 93.	2.4	9
21514	Unification of functional annotation descriptions using text mining. <i>Biological Chemistry</i> , 2021, 402, 983-990.	1.2	6
21515	Activated mast cells in skeletal muscle can be a potential mediator for cancer-associated cachexia. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2021, 12, 1079-1097.	2.9	15
21516	MSCFS: inferring circRNA functional similarity based on multiple data sources. <i>BMC Bioinformatics</i> , 2021, 22, 371.	1.2	2
21517	Gene Ontology Meta Annotator for Plants (GOMAP). <i>Plant Methods</i> , 2021, 17, 54.	1.9	21

#	ARTICLE	IF	CITATIONS
21519	hu.MAP 2.0: integration of over 15,000 proteomic experiments builds a global compendium of human multiprotein assemblies. <i>Molecular Systems Biology</i> , 2021, 17, e10016.	3.2	82
21520	A multifactorial proteomics approach to sex-specific effects of diet composition and social environment in an omnivorous insect. <i>Ecology and Evolution</i> , 2021, 11, 8623-8639.	0.8	2
21521	TIGIT and PD-1 Immune Checkpoint Pathways Are Associated With Patient Outcome and Anti-Tumor Immunity in Glioblastoma. <i>Frontiers in Immunology</i> , 2021, 12, 637146.	2.2	32
21522	Transcriptome analysis of immune-related genes in <i>Sesamops sinensis</i> hepatopancreas in reaction to peptidoglycan challenge. <i>Genomics</i> , 2021, 113, 946-954.	1.3	6
21523	Integrated Gene Co-expression Analysis and Metabolites Profiling Highlight the Important Role of ZmHIR3 in Maize Resistance to <i>Gibberella Stalk Rot</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 664733.	1.7	10
21524	Identification and characterization of novel microRNAs in disease-resistant and disease-susceptible <i>Penaeus monodon</i> . <i>Fish and Shellfish Immunology</i> , 2021, 119, 347-372.	1.6	1
21526	Bibliometric Analysis on Bibliometric-based Ontology Research. <i>Science and Technology Libraries</i> , 0, , 1-19.	0.8	3
21527	The genome of a wild <i>Medicago</i> species provides insights into the tolerant mechanisms of legume forage to environmental stress. <i>BMC Biology</i> , 2021, 19, 96.	1.7	39
21528	Dynamic expression of miRNAs and functional analysis of target genes involved in the response to male sterility of the wheat line YS3038. <i>Plant Physiology and Biochemistry</i> , 2021, 162, 363-377.	2.8	4
21529	Enhanced production of nonanedioic acid from nonanoic acid by engineered <i>Escherichia coli</i> . <i>Biotechnology Journal</i> , 2022, 17, e2000416.	1.8	5
21530	Use of waggle dance information in honey bees is linked to gene expression in the antennae, but not in the brain. <i>Molecular Ecology</i> , 2021, 30, 2676-2688.	2.0	11
21531	Transcriptome Analysis Reveals Differentially Expressed Genes and Long Non-coding RNAs Associated With Fecundity in Sheep Hypothalamus With Different FecB Genotypes. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 633747.	1.8	15
21532	Context-Dependent miR-21 Regulation of TLR7-Mediated Autoimmune and Foreign Antigen-Driven Antibody-Forming Cell and Germinal Center Responses. <i>Journal of Immunology</i> , 2021, 206, 2803-2818.	0.4	5
21533	Adaptation to mitochondrial stress requires CHOP-directed tuning of ISR. <i>Science Advances</i> , 2021, 7, .	4.7	68
21534	Transcriptomic Signature Differences Between SARS-CoV-2 and Influenza Virus Infected Patients. <i>Frontiers in Immunology</i> , 2021, 12, 666163.	2.2	27
21536	The Value of Immune-Related Genes Signature in Osteosarcoma Based on Weighted Gene Co-expression Network Analysis. <i>Journal of Immunology Research</i> , 2021, 2021, 1-17.	0.9	26
21537	RNA-seq derived identification of coronatine-regulated genes putatively involved in terpenoid biosynthetic pathway in the rubber tree <i>Hevea brasiliensis</i> . <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 749, 012033.	0.2	1
21538	A Computational Framework to Identify Cross Association Between Complex Disorders by Protein-protein Interaction Network Analysis. <i>Current Bioinformatics</i> , 2021, 16, 433-445.	0.7	6

#	ARTICLE	IF	CITATIONS
21539	Identification of Critical Genes and Signaling Pathways in Human Monocytes Following High-Intensity Exercise. <i>Healthcare (Switzerland)</i> , 2021, 9, 618.	1.0	2
21540	Synthesis, Characterization, and Specific Localization of Mitochondrial-Targeted Antioxidant Peptide SS31 Probe. <i>BioMed Research International</i> , 2021, 2021, 1-12.	0.9	2
21541	Interferon regulatory factor 7 impairs cellular metabolism with age in adipose-derived stromal cells. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	5
21543	Accelerating Biological Insight for Understudied Genes. <i>Integrative and Comparative Biology</i> , 2021, , .	0.9	2
21545	Multi-Omics Approach in the Identification of Potential Therapeutic Biomolecule for COVID-19. <i>Frontiers in Pharmacology</i> , 2021, 12, 652335.	1.6	17
21546	Integrating Transcriptome and Coexpression Network Analyses to Characterize Salicylic Acid- and Jasmonic Acid-Related Genes in Tolerant Poplars Infected with Rust. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5001.	1.8	12
21547	Functionally distinct POMC-expressing neuron subpopulations in hypothalamus revealed by intersectional targeting. <i>Nature Neuroscience</i> , 2021, 24, 913-929.	7.1	64
21548	Integration of machine learning and genome-scale metabolic modeling identifies multi-omics biomarkers for radiation resistance. <i>Nature Communications</i> , 2021, 12, 2700.	5.8	95
21549	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	2.8	808
21550	Pneumolysin Is Responsible for Differential Gene Expression and Modifications in the Epigenetic Landscape of Primary Monocyte Derived Macrophages. <i>Frontiers in Immunology</i> , 2021, 12, 573266.	2.2	6
21551	Collagen fiber regulation in human pediatric aortic valve development and disease. <i>Scientific Reports</i> , 2021, 11, 9751.	1.6	15
21552	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , 2021, 184, 2633-2648.e19.	13.5	94
21554	Identification of Potential Bisphenol A (BPA) Exposure Biomarkers in Ovarian Cancer. <i>Journal of Clinical Medicine</i> , 2021, 10, 1979.	1.0	11
21555	Comprehensive analysis of the long non-coding RNA expression profile and functional roles in a contrast-induced acute kidney injury rat model. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 739.	0.8	2
21556	Schistosomiasis Drug Discovery in the Era of Automation and Artificial Intelligence. <i>Frontiers in Immunology</i> , 2021, 12, 642383.	2.2	10
21558	Incorporating domain ontology information into clustering in heterogeneous networks. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2021, 11, e1413.	4.6	1
21559	PhenCards: a data resource linking human phenotype information to biomedical knowledge. <i>Genome Medicine</i> , 2021, 13, 91.	3.6	6
21560	Functional genomics meta-analysis to identify gene set enrichment networks in cardiac hypertrophy. <i>Biological Chemistry</i> , 2021, 402, 953-972.	1.2	3

#	ARTICLE	IF	CITATIONS
21561	Learning adaptive representations for entity recognition in the biomedical domain. <i>Journal of Biomedical Semantics</i> , 2021, 12, 10.	0.9	1
21562	circRNA landscape of non-pregnant endometrium during the estrus cycle in dairy goats. <i>Journal of Integrative Agriculture</i> , 2021, 20, 1346-1358.	1.7	1
21563	Effects of Three-Month Administration of High-Saturated Fat Diet and High-Polyunsaturated Fat Diets with Different Linoleic Acid (LA, C18:2nâ€“6) to \pm -Linolenic Acid (ALA, C18:3nâ€“3) Ratio on the Mouse Liver Proteome. <i>Nutrients</i> , 2021, 13, 1678.	1.7	6
21564	Sharp Downregulation of Hub Genes Associated With the Pathogenesis of Breast Cancer From Ductal Carcinoma In Situ to Invasive Ductal Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 634569.	1.3	2
21565	NetGO 2.0: improving large-scale protein function prediction with massive sequence, text, domain, family and network information. <i>Nucleic Acids Research</i> , 2021, 49, W469-W475.	6.5	53
21566	Complete genome sequence of <i>Metabacillus</i> sp. cB07, a bacterium inducing settlement and metamorphosis of coral larvae. <i>Marine Genomics</i> , 2021, 60, 100877.	0.4	3
21568	Estimates of gene ensemble noise highlight critical pathways and predict disease severity in H1N1, COVID-19 and mortality in sepsis patients. <i>Scientific Reports</i> , 2021, 11, 10793.	1.6	8
21569	Measuring pathway database coverage of the phosphoproteome. <i>PeerJ</i> , 2021, 9, e11298.	0.9	1
21570	De novo transcriptome sequencing and anthocyanin metabolite analysis reveals leaf color of <i>Acer pseudosieboldianum</i> in autumn. <i>BMC Genomics</i> , 2021, 22, 383.	1.2	17
21571	Identification of docetaxelâ€“related biomarkers for prostate cancer. <i>Andrologia</i> , 2021, 53, e14079.	1.0	7
21572	Up-regulated RFC2 predicts unfavorable progression in hepatocellular carcinoma. <i>Hereditas</i> , 2021, 158, 17.	0.5	9
21574	A method for benchmarking genetic screens reveals a predominant mitochondrial bias. <i>Molecular Systems Biology</i> , 2021, 17, e10013.	3.2	8
21575	Interaction Between the Intestinal Microbial Community and Transcriptome Profile in Common Carp (<i>Cyprinus carpio</i> L.). <i>Frontiers in Microbiology</i> , 2021, 12, 659602.	1.5	11
21576	Pan-Genome Analysis of <i>Vibrio cholerae</i> and <i>Vibrio metschnikovii</i> Strains Isolated From Migratory Birds at Dali Nouer Lake in Chifeng, China. <i>Frontiers in Veterinary Science</i> , 2021, 8, 638820.	0.9	10
21578	Stretchable and Soft Organicâ€“Ionic Devices for Bodyâ€“Integrated Electronic Systems. <i>Advanced Materials Technologies</i> , 2022, 7, 2001273.	3.0	16
21579	Exploring ecological specialization in pipefish using genomic, morphometric and ecological evidence. <i>Diversity and Distributions</i> , 2021, 27, 1393-1406.	1.9	7
21580	Sherlock: an open-source data platform to store, analyze and integrate Big Data for biology. <i>F1000Research</i> , 0, 10, 409.	0.8	1
21581	Evaluating disease similarity based on gene network reconstruction and representation. <i>Bioinformatics</i> , 2021, 37, 3579-3587.	1.8	15

#	ARTICLE	IF	CITATIONS
21582	Large-scale plasma proteomic analysis identifies proteins and pathways associated with dementia risk. <i>Nature Aging</i> , 2021, 1, 473-489.	5.3	69
21583	Identification of significant genes as prognostic markers and potential tumor suppressors in lung adenocarcinoma via bioinformatical analysis. <i>BMC Cancer</i> , 2021, 21, 616.	1.1	17
21584	Screening and Identification of Differentially Expressed Genes Between Diabetic Nephropathy Glomerular and Normal Glomerular via Bioinformatics Technology. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, 645-655.	0.6	1
21585	SynLeGG: analysis and visualization of multiomics data for discovery of cancer "Achilles Heels" and gene function relationships. <i>Nucleic Acids Research</i> , 2021, 49, W613-W618.	6.5	6
21586	Structure-based protein function prediction using graph convolutional networks. <i>Nature Communications</i> , 2021, 12, 3168.	5.8	300
21587	Coordination of microbe-host homeostasis by crosstalk with plant innate immunity. <i>Nature Plants</i> , 2021, 7, 814-825.	4.7	95
21588	Complete Genome Sequence Data of Rare Actinomycetes Strain <i>Saccharothrix texasensis</i> 6-C, a Biological Control Agent for Potato Late Blight. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 571-574.	1.4	7
21589	Detection of Prognostic Biomarkers for Hepatocellular Carcinoma through CircRNA-associated CeRNA Analysis. <i>Journal of Clinical and Translational Hepatology</i> , 2022, 10, 80-89.	0.7	5
21590	Dual proteome-scale networks reveal cell-specific remodeling of the human interactome. <i>Cell</i> , 2021, 184, 3022-3040.e28.	13.5	455
21591	Germinating seed can sense low temperature for the floral transition and vernalization of winter rapeseed (<i>Brassica rapa</i>). <i>Plant Science</i> , 2021, 307, 110900.	1.7	3
21592	Gut Microbiome Changes with Acute Diarrheal Disease in Urban Versus Rural Settings in Northern Ecuador. <i>American Journal of Tropical Medicine and Hygiene</i> , 2021, 104, 2275-2285.	0.6	7
21593	Effect of the Expression of ELOVL5 and IGFBP6 Genes on the Metastatic Potential of Breast Cancer Cells. <i>Frontiers in Genetics</i> , 2021, 12, 662843.	1.1	6
21594	A Universal and High-Throughput Proteomics Sample Preparation Platform. <i>Analytical Chemistry</i> , 2021, 93, 8423-8431.	3.2	24
21595	Expression levels of specific microRNAs are increased after exercise and are associated with cognitive improvement in Parkinson's disease. <i>Molecular Medicine Reports</i> , 2021, 24, .	1.1	9
21596	Conservation of Zebrafish MicroRNA-145 and Its Role during Neural Crest Cell Development. <i>Genes</i> , 2021, 12, 1023.	1.0	5
21597	Immune-Related Genes: Potential Prognostic Factors and Regulatory Targets for Cervical Carcinoma. <i>Journal of Nanomaterials</i> , 2021, 2021, 1-15.	1.5	0
21598	Relationship of the Pine Growth Promoting <i>Pantoea eucalypti</i> FBS135 with Type Strains <i>P. eucalypti</i> LMG 24197T and <i>P. vagans</i> 24199T. <i>Life</i> , 2021, 11, 608.	1.1	3
21599	Genome instability-related long non-coding RNA in clear renal cell carcinoma determined using computational biology. <i>BMC Cancer</i> , 2021, 21, 727.	1.1	12

#	ARTICLE	IF	CITATIONS
21600	Upregulated CD58 is associated with clinicopathological characteristics and poor prognosis of patients with pancreatic ductal adenocarcinoma. <i>Cancer Cell International</i> , 2021, 21, 327.	1.8	6
21601	The brain transcriptome of the wolf spider, <i>Schizocosa ocreata</i> . <i>BMC Research Notes</i> , 2021, 14, 236.	0.6	0
21602	Secretory microRNA Profiles of Third- and Fourth-Stage <i>Dirofilaria immitis</i> Larvae with Different Macrocyclic Lactone Susceptibility: In Search of Biomarkers for Early Detection of Infection. <i>Pathogens</i> , 2021, 10, 786.	1.2	4
21603	Genome wide identification and characterization of light-harvesting Chloro a/b binding (LHC) genes reveals their potential role in enhancing drought tolerance in <i>Gossypium hirsutum</i> . <i>Journal of Cotton Research</i> , 2021, 4, .	1.0	8
21604	Peptides Released from Extruded Adzuki Bean Protein through Simulated Gastrointestinal Digestion Exhibit Anti-inflammatory Activity. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 7028-7036.	2.4	18
21610	Low Expression of ADCY4 Predicts Worse Survival of Lung Squamous Cell Carcinoma Based on Integrated Analysis and Immunohistochemical Verification. <i>Frontiers in Oncology</i> , 2021, 11, 637733.	1.3	3
21611	Rapid Body-Wide Transcriptomic Turnover During Rhesus Macaque Perinatal Development. <i>Frontiers in Physiology</i> , 2021, 12, 690540.	1.3	1
21612	PIGNON: a protein-protein interaction-guided functional enrichment analysis for quantitative proteomics. <i>BMC Bioinformatics</i> , 2021, 22, 302.	1.2	4
21613	Highly connected, non-redundant microRNA functional control in breast cancer molecular subtypes. <i>Interface Focus</i> , 2021, 11, 20200073.	1.5	6
21614	Role of opiorphin genes in prostate cancer growth and progression. <i>Future Oncology</i> , 2021, 17, 2209-2223.	1.1	3
21615	An in vitro model of tumor heterogeneity resolves genetic, epigenetic, and stochastic sources of cell state variability. <i>PLoS Biology</i> , 2021, 19, e3000797.	2.6	21
21616	Microglia RAGE exacerbates the progression of neurodegeneration within the SOD1G93A murine model of amyotrophic lateral sclerosis in a sex-dependent manner. <i>Journal of Neuroinflammation</i> , 2021, 18, 139.	3.1	16
21617	Genome-Wide Transcriptomic Analysis of Non-Tumorigenic Tissues Reveals Aging-Related Prognostic Markers and Drug Targets in Renal Cell Carcinoma. <i>Cancers</i> , 2021, 13, 3045.	1.7	10
21618	Disentangling transcriptional responses in plant defense against arthropod herbivores. <i>Scientific Reports</i> , 2021, 11, 12996.	1.6	9
21619	Single-Cell Transcriptional Heterogeneity of Lymphatic Endothelial Cells in Normal and Inflamed Murine Lymph Nodes. <i>Cells</i> , 2021, 10, 1371.	1.8	19
21620	Bioinformatic Analysis of Hepatocellular Carcinoma Cell Lines to the Efficacy of Nimotuzumab. <i>International Journal of General Medicine</i> , 2021, Volume 14, 2611-2621.	0.8	1
21621	Reconstruction of the full-length transcriptome of cigar tobacco without a reference genome and characterization of anion channel/transporter transcripts. <i>BMC Plant Biology</i> , 2021, 21, 299.	1.6	3
21622	The roles of long non-coding RNAs in ocular diseases. <i>Experimental Eye Research</i> , 2021, 207, 108561.	1.2	5

#	ARTICLE	IF	CITATIONS
21624	MetamORF: a repository of unique short open reading frames identified by both experimental and computational approaches for gene and metagene analyses. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	19
21625	Postmating gene expression of <i>Scp</i> Mexican fruit fly females: disentangling the effects of the male accessory glands. <i>Insect Molecular Biology</i> , 2021, 30, 480-496.	1.0	10
21626	Slow Transcription of the 99a/let-7c/125b-2 Cluster Results in Differential MiRNA Expression and Promotes Melanoma Phenotypic Plasticity. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2944-2956.e6.	0.3	3
21627	Revealing the Characteristics of the Antarctic Snow Alga <i>Chlorominima collina</i> gen. et sp. nov. Through Taxonomy, Physiology, and Transcriptomics. <i>Frontiers in Plant Science</i> , 2021, 12, 662298.	1.7	9
21628	Transcriptomic analyses of gastrulation-stage mouse embryos with differential susceptibility to alcohol. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	1.2	19
21629	MCDB: A comprehensive curated mitotic catastrophe database for retrieval, protein sequence alignment, and target prediction. <i>Acta Pharmaceutica Sinica B</i> , 2021, 11, 3092-3104.	5.7	28
21630	Multiple responses contribute to the enhanced drought tolerance of the autotetraploid <i>Ziziphus jujuba</i> Mill. var. <i>spinosa</i> . <i>Cell and Bioscience</i> , 2021, 11, 119.	2.1	20
21631	Single-Cell RNA-seq Identification of the Cellular Molecular Characteristics of Sporadic Bilateral Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 659251.	1.3	12
21632	The subtype-specific molecular function of <i>SPDEF</i> in breast cancer and insights into prognostic significance. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 7307-7320.	1.6	6
21635	ACSNI: An unsupervised machine-learning tool for prediction of tissue-specific pathway components using gene expression profiles. <i>Patterns</i> , 2021, 2, 100270.	3.1	1
21636	Identical sequences found in distant genomes reveal frequent horizontal transfer across the bacterial domain. <i>ELife</i> , 2021, 10, .	2.8	23
21637	Genomic Analysis of the Mycoparasite <i>Pestalotiopsis</i> sp. PG52. <i>Polish Journal of Microbiology</i> , 2021, 70, 189-199.	0.6	5
21638	Full-Length Transcriptome Analysis Reveals Candidate Genes Involved in Terpenoid Biosynthesis in <i>Artemisia argyi</i> . <i>Frontiers in Genetics</i> , 2021, 12, 659962.	1.1	11
21639	Protein Prenylation and Hsp40 in Thermotolerance of <i>Plasmodium falciparum</i> Malaria Parasites. <i>MBio</i> , 2021, 12, e0076021.	1.8	15
21640	Crowdsourcing assessment of maternal blood multi-omics for predicting gestational age and preterm birth. <i>Cell Reports Medicine</i> , 2021, 2, 100323.	3.3	47
21641	Comparative transcriptome analysis of different developmental stage of <i>Bactrocera minax</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Over Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 38, 100818.	0.4	3
21642	Morphometric and population genomic evidence for species divergence in the <i>Chimarrichthys</i> fish complex of the Tibetan Plateau. <i>Molecular Phylogenetics and Evolution</i> , 2021, 159, 107117.	1.2	5
21643	Genetic Divergence and Population Structure in Weedy and Cultivated Broomcorn Millets (<i>Panicum</i>) Tj ETQq1 1 0.784314 rgBT /Over Science, 2021, 12, 688444.	1.7	13

#	ARTICLE	IF	CITATIONS
21645	Bioinformatics Analysis Reveals Crosstalk Among Platelets, Immune Cells, and the Glomerulus That May Play an Important Role in the Development of Diabetic Nephropathy. <i>Frontiers in Medicine</i> , 2021, 8, 657918.	1.2	6
21646	Transcriptomic and Metabolic Profiling of High-Temperature Treated Storage Roots Reveals the Mechanism of Saccharification in Sweetpotato (<i>Ipomoea batatas</i> (L.) Lam.). <i>International Journal of Molecular Sciences</i> , 2021, 22, 6641.	1.8	6
21648	Cell landscape atlas for patients with chronic thromboembolic pulmonary hypertension after pulmonary endarterectomy constructed using single-cell RNA sequencing. <i>Aging</i> , 2021, 13, 16485-16499.	1.4	10
21649	Variable Length Character N-Gram Embedding of Protein Sequences for Secondary Structure Prediction. <i>Protein and Peptide Letters</i> , 2021, 28, 501-507.	0.4	4
21650	De novo genome assembly of a foxtail millet cultivar Huagu11 uncovered the genetic difference to the cultivar Yugu1, and the genetic mechanism of imazethapyr tolerance. <i>BMC Plant Biology</i> , 2021, 21, 271.	1.6	9
21652	Bacterioplankton respond with similar transcriptional activity to allochthonous dissolved organic matter in coastal and offshore Lake Michigan. <i>Limnology and Oceanography</i> , 2021, 66, 3162-3175.	1.6	2
21654	A combination of Class-I fumarases and metabolites (\pm -ketoglutarate and fumarate) signal the DNA damage response in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	7
21655	The REASON score: an epigenetic and clinicopathologic score to predict risk of poor survival in patients with early stage oral squamous cell carcinoma. <i>Biomarker Research</i> , 2021, 9, 42.	2.8	16
21656	Precision omics data integration and analysis with interoperable ontologies and their application for COVID-19 research. <i>Briefings in Functional Genomics</i> , 2021, 20, 235-248.	1.3	8
21659	Large-scale genome sampling reveals unique immunity and metabolic adaptations in bats. <i>Molecular Ecology</i> , 2021, 30, 6449-6467.	2.0	40
21660	An <i>Axin2</i> mutation and perinatal risk factors contribute to sagittal craniosynostosis: evidence from a Chinese female monozygotic diamniotic twin family. <i>Hereditas</i> , 2021, 158, 20.	0.5	1
21661	Combining QTL-seq and linkage mapping to fine map a candidate gene in qCTS6 for cold tolerance at the seedling stage in rice. <i>BMC Plant Biology</i> , 2021, 21, 278.	1.6	18
21662	The synergistic actions of hydrolytic genes reveal the mechanism of <i>Trichoderma harzianum</i> for cellulose degradation. <i>Journal of Biotechnology</i> , 2021, 334, 1-10.	1.9	14
21663	Complete genomic data of <i>Enterobacter asburiae</i> strain SD4L associated with bacterial palea browning of rice in China. <i>Plant Disease</i> , 2021, , PDIS03210642A.	0.7	0
21664	A report of two cases of bulbospinal form Alexander disease and preliminary exploration of the disease. <i>Molecular Medicine Reports</i> , 2021, 24, .	1.1	2
21665	Gene Expression Profiling in the Skin Reveals Strong Similarities between Subacute and Chronic Cutaneous Lupus that Are Distinct from Lupus Nephritis. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2808-2819.	0.3	14
21666	Patterns of recent natural selection on genetic loci associated with sexually differentiated human body size and shape phenotypes. <i>PLoS Genetics</i> , 2021, 17, e1009562.	1.5	3
21667	Biological Mechanisms Induced by Soybean Agglutinin Using an Intestinal Cell Model of Monogastric Animals. <i>Frontiers in Veterinary Science</i> , 2021, 8, 639792.	0.9	3

#	ARTICLE	IF	CITATIONS
21668	Transcriptome Analysis Reveals Putative Target Genes of APETALA3-3 During Early Floral Development in <i>Nigella damascena</i> L. <i>Frontiers in Plant Science</i> , 2021, 12, 660803.	1.7	4
21669	Analysis of single-cell RNA sequencing data based on autoencoders. <i>BMC Bioinformatics</i> , 2021, 22, 309.	1.2	15
21670	Shared genetic architecture between neuroticism, coronary artery disease and cardiovascular risk factors. <i>Translational Psychiatry</i> , 2021, 11, 368.	2.4	10
21671	Dissecting regulatory pathways for transcription recovery following DNA damage reveals a non-canonical function of the histone chaperone HIRA. <i>Nature Communications</i> , 2021, 12, 3835.	5.8	14
21672	Promoting a More Integrated Approach to Structure and Function. <i>Integrative and Comparative Biology</i> , 2021, , .	0.9	1
21673	Survival prediction based on the gene expression associated with cancer morphology and microenvironment in primary central nervous system lymphoma. <i>PLoS ONE</i> , 2021, 16, e0251272.	1.1	7
21674	Identifying a Serum Exosomal-Associated lncRNA/circRNA-miRNA-mRNA Network in Coronary Heart Disease. <i>Cardiology Research and Practice</i> , 2021, 2021, 1-10.	0.5	11
21676	Screening of cervical cancer-related hub genes based on comprehensive bioinformatics analysis. <i>Cancer Biomarkers</i> , 2021, 32, 1-13.	0.8	6
21677	Heat-killed endophytic bacterium induces robust plant defense responses against important pathogens. <i>Scientific Reports</i> , 2021, 11, 12182.	1.6	14
21678	Characterization of nucleic acids from extracellular vesicle-enriched human sweat. <i>BMC Genomics</i> , 2021, 22, 425.	1.2	21
21679	RNA sequencing of long-term label-retaining colon cancer stem cells identifies novel regulators of quiescence. <i>IScience</i> , 2021, 24, 102618.	1.9	6
21680	Somatic mutation subtypes of lung adenocarcinoma in East Asian reveal divergent biological characteristics and therapeutic vulnerabilities. <i>IScience</i> , 2021, 24, 102522.	1.9	4
21681	Inter-individual body mass variations relate to fractionated functional brain hierarchies. <i>Communications Biology</i> , 2021, 4, 735.	2.0	25
21682	Tumor Purity Coexpressed Genes Related to Immune Microenvironment and Clinical Outcomes of Lung Adenocarcinoma. <i>Journal of Oncology</i> , 2021, 2021, 1-13.	0.6	9
21684	miR-1224 contributes to ischemic stroke-mediated natural killer cell dysfunction by targeting Sp1 signaling. <i>Journal of Neuroinflammation</i> , 2021, 18, 133.	3.1	14
21685	High-throughput sequencing reveals differential expression of miRNAs in yak and cattleyak epididymis. <i>Reproduction in Domestic Animals</i> , 2021, , .	0.6	2
21686	Transcriptome response of maize (<i>Zea mays</i> L.) seedlings to heat stress. <i>Protoplasma</i> , 2022, 259, 357-369.	1.0	10
21687	Competing Endogenous RNA in Colorectal Cancer: An Analysis for Colon, Rectum, and Rectosigmoid Junction. <i>Frontiers in Oncology</i> , 2021, 11, 681579.	1.3	8

#	ARTICLE	IF	CITATIONS
21688	Acute Effects on the Human Peripheral Blood Transcriptome of Decompression Sickness Secondary to Scuba Diving. <i>Frontiers in Physiology</i> , 2021, 12, 660402.	1.3	10
21689	Annotating the Insect Regulatory Genome. <i>Insects</i> , 2021, 12, 591.	1.0	4
21690	The amniotic fluid cell-free transcriptome in spontaneous preterm labor. <i>Scientific Reports</i> , 2021, 11, 13481.	1.6	11
21691	Identification and Expression Analysis of miR160 and Their Target Genes in Cucumber. <i>Biochemical Genetics</i> , 2022, 60, 127-152.	0.8	6
21692	Surface-Shaving Proteomics of <i>Mycobacterium marinum</i> Identifies Biofilm Subtype-Specific Changes Affecting Virulence, Tolerance, and Persistence. <i>MSystems</i> , 2021, 6, e0050021.	1.7	7
21693	Mapping chromatin accessibility and active regulatory elements reveals pathological mechanisms in human gliomas. <i>Nature Communications</i> , 2021, 12, 3621.	5.8	22
21694	Evolutionary Local Search Algorithm for the biclustering of gene expression data based on biological knowledge. <i>Applied Soft Computing Journal</i> , 2021, 104, 107177.	4.1	12
21695	ivTerm—An R package for interactive visualization of functional analysis results of meta-omics data. <i>Journal of Cellular Biochemistry</i> , 2021, 122, 1428-1434.	1.2	0
21696	Inhibiting an RBM39/MLL1 epigenomic regulatory complex with dominant-negative peptides disrupts cancer cell transcription and proliferation. <i>Cell Reports</i> , 2021, 35, 109156.	2.9	14
21697	DGLinker: flexible knowledge-graph prediction of disease-gene associations. <i>Nucleic Acids Research</i> , 2021, 49, W153-W161.	6.5	19
21698	WheatGene: A genomics database for common wheat and its related species. <i>Crop Journal</i> , 2021, 9, 1486-1491.	2.3	5
21699	Applying Never-Ending Learning (NEL) Principles to Build a Gene Ontology (GO) Biocurator. , 2021, , .		0
21700	Mapping the multiscale structure of biological systems. <i>Cell Systems</i> , 2021, 12, 622-635.	2.9	19
21701	Droplet microarrays for cell culture: effect of surface properties and nanoliter culture volume on global transcriptomic landscape. <i>Materials Today Bio</i> , 2021, 11, 100112.	2.6	7
21702	A small RNA regulates pprM, a modulator of pleiotropic proteins promoting DNA repair, in <i>Deinococcus radiodurans</i> under ionizing radiation. <i>Scientific Reports</i> , 2021, 11, 12949.	1.6	13
21704	S-Palmitoylation of Synaptic Proteins as a Novel Mechanism Underlying Sex-Dependent Differences in Neuronal Plasticity. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6253.	1.8	7
21705	Transcription in fungal conidia before dormancy produces phenotypically variable conidia that maximize survival in different environments. <i>Nature Microbiology</i> , 2021, 6, 1066-1081.	5.9	48
21706	Insights into mesophilic virulence, antibiotic resistant and human pathogenicity: A genomics study on the <i>Aeromonas salmonicida</i> SRW-OG1 newly isolated from the Asian fish <i>Epinephelus coioides</i> . <i>Aquaculture</i> , 2021, 539, 736630.	1.7	13

#	ARTICLE	IF	CITATIONS
21707	9-Gene Signature Correlated With CD8+ T Cell Infiltration Activated by IFN- γ : A Biomarker of Immune Checkpoint Therapy Response in Melanoma. <i>Frontiers in Immunology</i> , 2021, 12, 622563.	2.2	26
21708	Transcriptomic analysis reveals the parallel transcriptional regulation of UV-B-induced artemisinin and flavonoid accumulation in <i>Artemisia annua</i> L. <i>Plant Physiology and Biochemistry</i> , 2021, 163, 189-200.	2.8	23
21709	Transcriptomics of type 2 diabetic and healthy human neutrophils. <i>BMC Immunology</i> , 2021, 22, 37.	0.9	11
21711	Differential Glycosite Profiling—A Versatile Method to Compare Membrane Glycoproteomes. <i>Molecules</i> , 2021, 26, 3564.	1.7	0
21712	A network-based approach to identify key genes between follicular thyroid cancer and follicular thyroid adenoma. <i>Gene Reports</i> , 2021, 23, 101075.	0.4	1
21713	A comparison expression analysis of CXCR4, CXCL9 and Caspase-9 in dermal vascular endothelial cells between keloids and normal skin on chemotaxis and apoptosis. <i>Journal of Plastic Surgery and Hand Surgery</i> , 2022, 56, 93-102.	0.4	2
21714	Comprehensive Analysis of Regulatory Network for LINC00472 in Clear Cell Renal Cell Carcinoma. <i>Journal of Healthcare Engineering</i> , 2021, 2021, 1-20.	1.1	8
21715	Mapping Proximity Associations of Core Spindle Assembly Checkpoint Proteins. <i>Journal of Proteome Research</i> , 2021, 20, 3414-3427.	1.8	10
21716	Comparative transcriptomic analysis of the I-4i silkworm (<i>Lepidoptera: Bombyx mori</i>) mutants and its wild-type strain P33 by RNA-Seq. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 38, 100800.	0.4	1
21717	TIGA: target illumination GWAS analytics. <i>Bioinformatics</i> , 2021, 37, 3865-3873.	1.8	9
21718	TNF blockade uncouples toxicity from antitumor efficacy induced with CD40 chemoimmunotherapy. <i>JCI Insight</i> , 2021, 6, .	2.3	6
21719	Identification and Validation of a Novel Prognosis Prediction Model in Adrenocortical Carcinoma by Integrative Bioinformatics Analysis, Statistics, and Machine Learning. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 671359.	1.8	4
21720	The chromosome-level <i>Stevia</i> genome provides insights into steviol glycoside biosynthesis. <i>Horticulture Research</i> , 2021, 8, 129.	2.9	35
21721	Comparative transcriptome analysis of <i>Salix cupularis</i> under drought stress. <i>Global Ecology and Conservation</i> , 2021, 27, e01532.	1.0	3
21722	Genetic diversity and relationships among populations of <i>Camellia japonica</i> , an endangered species in China. <i>Canadian Journal of Plant Science</i> , 2022, 102, 136-146.	0.3	1
21723	Molecular omics resources should require sex annotation: a call for action. <i>Nature Methods</i> , 2021, 18, 585-588.	9.0	17
21724	Evolution of fibroblasts in the lung metastatic microenvironment is driven by stage-specific transcriptional plasticity. <i>ELife</i> , 2021, 10, .	2.8	23
21725	Phytohormonal and Transcriptomic Response of Hulless Barley Leaf in Response to Powdery Mildew Infection. <i>Agronomy</i> , 2021, 11, 1248.	1.3	3

#	ARTICLE	IF	CITATIONS
21726	Short Time-Series Expression Transcriptome Data Reveal the Gene Expression Patterns of Dairy Cow Mammary Gland as Milk Yield Decreased Process. <i>Genes</i> , 2021, 12, 942.	1.0	8
21727	Genomic sequence resource of <i>Kabatiella zeae</i> , the causative pathogen of corn eyespot disease. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1223-1226.	1.4	1
21728	Transcriptome Reveals Roles of Lignin-Modifying Enzymes and Abscisic Acid in the Symbiosis of <i>Mycena</i> and <i>Gastrodia elata</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 6557.	1.8	6
21733	Sensory-based quantification of male colour patterns in Trinidadian guppies reveals no support for parallel phenotypic evolution in multivariate trait space. <i>Molecular Ecology</i> , 2022, 31, 1337-1357.	2.0	10
21735	Study of the Active Components and Molecular Mechanism of <i>Tripterygium wilfordii</i> in the Treatment of Diabetic Nephropathy. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 664416.	1.6	9
21736	Protein functional module identification method combining topological features and gene expression data. <i>BMC Genomics</i> , 2021, 22, 423.	1.2	2
21738	Transmembrane adaptor protein PAG is a mediator of PD-1 inhibitory signaling in human T cells. <i>Communications Biology</i> , 2021, 4, 672.	2.0	7
21739	A genetic interaction of <i>NRXN2</i> with <i>GABRE</i> , <i>SYT1</i> and <i>CASK</i> in migraine patients: a case-control study. <i>Journal of Headache and Pain</i> , 2021, 22, 57.	2.5	6
21740	Transcriptomic Profiling of Femoral Veins in Deep Vein Thrombosis in a Porcine Model. <i>Cells</i> , 2021, 10, 1576.	1.8	8
21741	Global Proteomic Profiling of Pediatric AML: A Pilot Study. <i>Cancers</i> , 2021, 13, 3161.	1.7	6
21742	Transcriptomic Signature of Human Embryonic Thyroid Reveals Transition From Differentiation to Functional Maturation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 669354.	1.8	7
21743	Improving the understanding of cancer in a descriptive way: An emerging pattern mining-based approach. <i>International Journal of Intelligent Systems</i> , 2022, 37, 2822-2848.	3.3	5
21745	Systems genetics in diversity outbred mice inform BMD GWAS and identify determinants of bone strength. <i>Nature Communications</i> , 2021, 12, 3408.	5.8	31
21746	Signalling pathways and key genes involved in regulation of ovarian development of <i>Sepia esculenta</i> . <i>Aquaculture Research</i> , 2021, 52, 4874-4888.	0.9	1
21747	Machine learning for perturbational single-cell omics. <i>Cell Systems</i> , 2021, 12, 522-537.	2.9	52
21748	Expression Status and Prognostic Value of m6A RNA Methylation Regulators in Lung Adenocarcinoma. <i>Life</i> , 2021, 11, 619.	1.1	3
21749	Comparative Transcriptome Analysis Reveals Regulatory Networks during the Maize Ear Shank Elongation Process. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7029.	1.8	3
21750	GenOrigin: A comprehensive protein-coding gene origination database on the evolutionary timescale of life. <i>Journal of Genetics and Genomics</i> , 2021, 48, 1122-1129.	1.7	11

#	ARTICLE	IF	CITATIONS
21751	Cross-tolerance and transcriptional shifts underlying abiotic stress in the seabird tick, <i>Ixodes uriae</i> . <i>Polar Biology</i> , 2021, 44, 1379-1389.	0.5	3
21753	Hsa-miR-372-5p regulates the NIMA related kinase 7 and IL-1 β release in NK/T-cell lymphoma. <i>Leukemia and Lymphoma</i> , 2021, 62, 2648-2656.	0.6	4
21754	Revealing the Modular Similarities and Differences Among Alzheimer's Disease, Vascular Dementia, and Parkinson's Disease in Genomic Networks. <i>NeuroMolecular Medicine</i> , 2022, 24, 125-138.	1.8	7
21756	Differential Transcript Profiles in Cumulus-Oocyte Complexes Originating from Pre-Ovulatory Follicles of Varied Physiological Maturity in Beef Cows. <i>Genes</i> , 2021, 12, 893.	1.0	10
21757	Evolutionary and phylogenetic insights from a nuclear genome sequence of the extinct, giant, <i>Megaladapis edwardsi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12
21758	Chamber-enriched gene expression profiles in failing human hearts with reduced ejection fraction. <i>Scientific Reports</i> , 2021, 11, 11839.	1.6	14
21759	Transcriptomic coordination at hepatic steatosis indicates robust immune cell engagement prior to inflammation. <i>BMC Genomics</i> , 2021, 22, 454.	1.2	3
21760	A Comprehensive Bioinformatics Analysis of Notch Pathways in Bladder Cancer. <i>Cancers</i> , 2021, 13, 3089.	1.7	13
21761	MYC-Mediated Ribosomal Gene Expression Sensitizes Enzalutamide-resistant Prostate Cancer Cells to EP300/CREBBP Inhibitors. <i>American Journal of Pathology</i> , 2021, 191, 1094-1107.	1.9	14
21762	Characterization of Human Genes Modulated by <i>Porphyromonas gingivalis</i> Highlights the Ribosome, Hypothalamus, and Cholinergic Neurons. <i>Frontiers in Immunology</i> , 2021, 12, 646259.	2.2	12
21763	Critical COVID-19 is associated with distinct leukocyte phenotypes and transcriptome patterns. <i>Journal of Internal Medicine</i> , 2021, 290, 677-692.	2.7	20
21764	Association of medically assisted reproduction with offspring cord blood DNA methylation across cohorts. <i>Human Reproduction</i> , 2021, 36, 2403-2413.	0.4	17
21765	Neuronal Cytoskeleton in Intellectual Disability: From Systems Biology and Modeling to Therapeutic Opportunities. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6167.	1.8	13
21767	Evaluation of Indigenous Olive Biocontrol Rhizobacteria as Protectants against Drought and Salt Stress. <i>Microorganisms</i> , 2021, 9, 1209.	1.6	8
21770	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
21771	FGGA-Inc: automatic gene ontology annotation of lncRNA sequences based on secondary structures. <i>Interface Focus</i> , 2021, 11, 20200064.	1.5	1
21772	CCDC114, DNAI2 and TOP2A involves in the effects of tibolone treatment on postmenopausal endometrium. <i>BMC Women's Health</i> , 2021, 21, 240.	0.8	0
21773	The cervicovaginal microbiome and its resistome in a random selection of Afro-Caribbean women. <i>Human Microbiome Journal</i> , 2021, 20, 100079.	3.8	8

#	ARTICLE	IF	CITATIONS
21775	Extracellular matrix remodeling associated with bleomycin-induced lung injury supports pericyte-to-myofibroblast transition. <i>Matrix Biology Plus</i> , 2021, 10, 100056.	1.9	12
21776	DNA methylation profile of liver of mice conceived by <i>in vitro</i> fertilization. <i>Journal of Developmental Origins of Health and Disease</i> , 2022, 13, 358-366.	0.7	3
21777	The extremely large chloroplast genome of the green alga <i>Haematococcus pluvialis</i> : Genome structure, and comparative analysis. <i>Algal Research</i> , 2021, 56, 102308.	2.4	9
21779	Tankyrase regulates epithelial lumen formation via suppression of Rab11 GEFs. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	6
21780	Exosomes Derived From Heat Stroke Cases Carry miRNAs Associated With Inflammation and Coagulation Cascade. <i>Frontiers in Immunology</i> , 2021, 12, 624753.	2.2	11
21781	Analysing Complex Oral Protein Samples: Complete Workflow and Case Analysis of Salivary Pellicles. <i>Journal of Clinical Medicine</i> , 2021, 10, 2801.	1.0	1
21783	â€œDialogueâ€ between Caco-2 and DCs regulated by <i>Ganoderma atrum</i> polysaccharide in intestinal-like Caco-2/DCs co-culture model. <i>Food Research International</i> , 2021, 144, 110310.	2.9	12
21784	Individuality in the Immune Repertoire and Induced Response of the Sponge <i>Halichondria panicea</i> . <i>Frontiers in Immunology</i> , 2021, 12, 689051.	2.2	14
21785	The highly conserved FOXJ1 target CFAP161 is dispensable for motile ciliary function in mouse and <i>Xenopus</i> . <i>Scientific Reports</i> , 2021, 11, 13333.	1.6	3
21786	Chromosome-scale genome assembly of areca palm (<i>Areca catechu</i>). <i>Molecular Ecology Resources</i> , 2021, 21, 2504-2519.	2.2	20
21787	A large-scale assessment of exact lumping of quantitative models in the BioModels repository. <i>Theoretical Computer Science</i> , 2021, 893, 41-59.	0.5	3
21788	Purification and quantitative proteomic analysis of cell bodies and protrusions. <i>STAR Protocols</i> , 2021, 2, 100462.	0.5	0
21789	Filtering the Rejection Set While Preserving False Discovery Rate Control. <i>Journal of the American Statistical Association</i> , 2023, 118, 165-176.	1.8	6
21790	A proximity-dependent biotinylation map of a human cell. <i>Nature</i> , 2021, 595, 120-124.	13.7	263
21791	Gene Expression and Survival of Acute Lymphoblastic Leukemia Cells After Allogeneic Transplant. <i>Anticancer Research</i> , 2021, 41, 2781-2793.	0.5	1
21792	<i>Agrobacterium</i> VirE2 Protein Modulates Plant Gene Expression and Mediates Transformation From Its Location Outside the Nucleus. <i>Frontiers in Plant Science</i> , 2021, 12, 684192.	1.7	8
21793	Clotting in COVID-19: Is It All in the Genes?. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2021, 64, 647-649.	1.4	3
21794	Identification of CD8+ T Cell-Related Genes: Correlations with Immune Phenotypes and Outcomes of Liver Cancer. <i>Journal of Immunology Research</i> , 2021, 2021, 1-17.	0.9	8

#	ARTICLE	IF	CITATIONS
21795	Methodology to identify candidate genes from beef carcass traits at weaning: A pilot study. <i>Animal Gene</i> , 2021, 20, 200113.	0.2	1
21796	Gene expression changes and DNA damage after ex vivo exposure of peripheral blood cells to various CT photon spectra. <i>Scientific Reports</i> , 2021, 11, 12060.	1.6	7
21797	Identification of Dysregulated Complement Activation Pathways Driven by N-Glycosylation Alterations in T2D Patients. <i>Frontiers in Chemistry</i> , 2021, 9, 677621.	1.8	7
21798	Semantic standards of external exposome data. <i>Environmental Research</i> , 2021, 197, 111185.	3.7	12
21799	The effect of methanol fixation on single-cell RNA sequencing data. <i>BMC Genomics</i> , 2021, 22, 420.	1.2	25
21800	A network-biology approach for identification of key genes and pathways involved in malignant peritoneal mesothelioma. <i>Genomics and Informatics</i> , 2021, 19, e16.	0.4	4
21801	A protein interactions map of multiple organ systems associated with COVID-19 disease. <i>Genomics and Informatics</i> , 2021, 19, e14.	0.4	2
21802	IGFBP2 Is a Potential Master Regulator Driving the Dysregulated Gene Network Responsible for Short Survival in Glioblastoma Multiforme. <i>Frontiers in Genetics</i> , 2021, 12, 670240.	1.1	8
21803	Beach sand oil spills select for generalist microbial populations. <i>ISME Journal</i> , 2021, 15, 3418-3422.	4.4	3
21804	Overlapping Structures Detection in Protein-Protein Interaction Networks Using Community Detection Algorithm Based on Neighbor Clustering Coefficient. <i>Frontiers in Genetics</i> , 2021, 12, 689515.	1.1	1
21805	Trajectories of Homoeolog-Specific Expression in Allotetraploid <i>Tragopogon castellanus</i> Populations of Independent Origins. <i>Frontiers in Plant Science</i> , 2021, 12, 679047.	1.7	3
21806	Multiple allelic associations from genes involved in energy metabolism were identified in celiac disease. <i>Journal of Biosciences</i> , 2021, 46, 1.	0.5	1
21807	Identification of sex-specific biomarkers predicting new-onset heart failure. <i>ESC Heart Failure</i> , 2021, 8, 3512-3520.	1.4	11
21808	RXRA DT448/9PP generates a dominant active variant capable of inducing maturation in acute myeloid leukemia cells. <i>Haematologica</i> , 2022, 107, 417-426.	1.7	3
21809	A prognostic nomogram based on competing endogenous RNA network for clear-cell renal cell carcinoma. <i>Cancer Medicine</i> , 2021, 10, 5499-5512.	1.3	2
21810	Genotoxicity and Gene Expression in the Rat Lung Tissue following Instillation and Inhalation of Different Variants of Amorphous Silica Nanomaterials (aSiO ₂ NM). <i>Nanomaterials</i> , 2021, 11, 1502.	1.9	11
21811	Construction of a mammalian embryo model from stem cells organized by a morphogen signalling centre. <i>Nature Communications</i> , 2021, 12, 3277.	5.8	60
21812	The relationship between LncRNAs and lung adenocarcinoma as well as their ceRNA network. <i>Cancer Biomarkers</i> , 2021, 31, 165-176.	0.8	6

#	ARTICLE	IF	CITATIONS
21813	Proteomic and Transcriptomic Analyses Provide Novel Insights into the Crucial Roles of Host-Induced Carbohydrate Metabolism Enzymes in <i>Xanthomonas oryzae pv. oryzae</i> Virulence and Rice-Xoo Interaction. <i>Rice</i> , 2021, 14, 57.	1.7	10
21814	Predicting Lifestyle from Positive Selection Data and Genome Properties in Oomycetes. <i>Pathogens</i> , 2021, 10, 807.	1.2	7
21815	CLARINET: Efficient learning of dynamic network models from literature. <i>Bioinformatics Advances</i> , 0, , .	0.9	5
21816	Dysregulation of core circadian genes, BMAL1 and CLOCK, in colorectal cancer. <i>Biological Rhythm Research</i> , 0, , 1-14.	0.4	1
21817	Single-cell RNA-seq reveals fibroblast heterogeneity and increased mesenchymal fibroblasts in human fibrotic skin diseases. <i>Nature Communications</i> , 2021, 12, 3709.	5.8	171
21818	Biomedical Entity Explorer: A Web Server for Biomedical Entity Exploration. <i>Journal of Computational Biology</i> , 2021, 28, 619-628.	0.8	0
21820	Integrating longitudinal clinical laboratory tests with targeted proteomic and transcriptomic analyses reveal the landscape of host responses in COVID-19. <i>Cell Discovery</i> , 2021, 7, 42.	3.1	23
21821	Altered hypothalamic DNA methylation and stress-induced hyperactivity following early life stress. <i>Epigenetics and Chromatin</i> , 2021, 14, 31.	1.8	9
21822	Altered transcriptome and disease-related phenotype emerge only after fibroblasts harvested from patients with age-related macular degeneration are differentiated into retinal pigment epithelium. <i>Experimental Eye Research</i> , 2021, 207, 108576.	1.2	2
21823	A methyl esterase 1 (PvMES1) promotes the salicylic acid pathway and enhances <i>Fusarium</i> wilt resistance in common beans. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2379-2398.	1.8	6
21824	A comprehensive review of integrative pharmacology-based investigation: A paradigm shift in traditional Chinese medicine. <i>Acta Pharmaceutica Sinica B</i> , 2021, 11, 1379-1399.	5.7	61
21825	Identifying Genomic Regions Targeted During Eggplant Domestication Using Transcriptome Data. <i>Journal of Heredity</i> , 2021, 112, 519-525.	1.0	3
21826	Identification of genes predicting unfavorable prognosis in hepatitis B virus-associated hepatocellular carcinoma. <i>Annals of Translational Medicine</i> , 2021, 9, 975-975.	0.7	5
21827	A chromosome-level genome assembly of rugged rose (<i>Rosa rugosa</i>) provides insights into its evolution, ecology, and floral characteristics. <i>Horticulture Research</i> , 2021, 8, 141.	2.9	29
21828	Inhibitors of bacterial H ₂ S biogenesis targeting antibiotic resistance and tolerance. <i>Science</i> , 2021, 372, 1169-1175.	6.0	112
21829	De Novo SNP Discovery and Genotyping of Iranian <i>Pimpinella</i> Species Using ddRAD Sequencing. <i>Agronomy</i> , 2021, 11, 1342.	1.3	6
21830	Vascular Endothelial Growth Factor and/or Nerve Growth Factor Treatment Induces Expression of Dentinogenic, Neuronal, and Healing Markers in Stem Cells of the Apical Papilla. <i>Journal of Endodontics</i> , 2021, 47, 924-931.	1.4	10
21831	Full-length transcriptome analysis and identification of genes involved in asarinin and aristolochic acid biosynthesis in medicinal plant <i>Asarum sieboldii</i> . <i>Genome</i> , 2021, 64, 639-653.	0.9	8

#	ARTICLE	IF	CITATIONS
21832	Mortalin/glucose-regulated protein 75 promotes the cisplatin-resistance of gastric cancer via regulating anti-oxidation/apoptosis and metabolic reprogramming. <i>Cell Death Discovery</i> , 2021, 7, 140.	2.0	8
21833	Differential Expression and Functional Analysis of CircRNA in the Ovaries of Low and High Fecundity Hanper Sheep. <i>Animals</i> , 2021, 11, 1863.	1.0	11
21834	Transcriptomic Analysis Exploring the Molecular Mechanisms of Hanchuan Zupa Granules in Alleviating Asthma in Rat. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-15.	0.5	2
21835	Accurate transcriptome assembly by Nanopore RNA sequencing reveals novel functional transcripts in hepatocellular carcinoma. <i>Cancer Science</i> , 2021, 112, 3555-3568.	1.7	6
21836	In silico analysis of HOX-associated transcription factors as potential regulators of oral cancer. <i>Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology</i> , 2021, 132, 72-79.	0.2	3
21837	Bioinformatics study on genes related to a high-risk postoperative recurrence of lung adenocarcinoma. <i>Science Progress</i> , 2021, 104, 003685042110180.	1.0	5
21838	RNA-seq bulked segregant analysis combined with KASP genotyping rapidly identified <i>PmCH7087</i> as responsible for powdery mildew resistance in wheat. <i>Plant Genome</i> , 2021, 14, e20120.	1.6	8
21839	Analysis of long intergenic non-coding RNAs transcriptomic profiling in skeletal muscle growth during porcine embryonic development. <i>Scientific Reports</i> , 2021, 11, 15240.	1.6	2
21840	Genes and Pathways Affecting Sheep Productivity Traits: Genetic Parameters, Genome-Wide Association Mapping, and Pathway Enrichment Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 710613.	1.1	8
21841	DTI-Voodoo: machine learning over interaction networks and ontology-based background knowledge predicts drug-target interactions. <i>Bioinformatics</i> , 2021, 37, 4835-4843.	1.8	10
21842	Identification of differential key biomarkers in the synovial tissue between rheumatoid arthritis and osteoarthritis using bioinformatics analysis. <i>Clinical Rheumatology</i> , 2021, 40, 5103-5110.	1.0	7
21843	Transcriptomic analysis of the black tiger shrimp (<i>Penaeus monodon</i>) reveals insights into immune development in their early life stages. <i>Scientific Reports</i> , 2021, 11, 13881.	1.6	5
21844	The Role of INAPERTURATE POLLEN1 as a Pollen Aperture Factor Is Conserved in the Basal Eudicot <i>Eschscholzia californica</i> (Papaveraceae). <i>Frontiers in Plant Science</i> , 2021, 12, 701286.	1.7	4
21845	Endophytic <i>Bacillus subtilis</i> TR21 Improves Banana Plant Resistance to <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> and Promotes Root Growth by Upregulating the Jasmonate and Brassinosteroid Biosynthesis Pathways. <i>Phytopathology</i> , 2022, 112, 219-231.	1.1	14
21846	Circulating long non-coding RNA signature in knee osteoarthritis patients with postoperative pain one-year after total knee replacement. <i>Scandinavian Journal of Pain</i> , 2021, 21, 823-830.	0.5	9
21848	In silico-driven analysis of the <i>Glossina morsitans morsitans</i> antennae transcriptome in response to repellent or attractant compounds. <i>PeerJ</i> , 2021, 9, e11691.	0.9	2
21849	Comparative Transcriptome and Weighted Gene Co-expression Network Analysis Identify Key Transcription Factors of <i>Rosa chinensis</i> "Old Blush" After Exposure to a Gradual Drought Stress Followed by Recovery. <i>Frontiers in Genetics</i> , 2021, 12, 690264.	1.1	7
21851	Identification and Confirmation of the miR-30 Family as a Potential Central Player in Tobacco-Related Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 616372.	1.3	5

#	ARTICLE	IF	CITATIONS
21852	Genome Size Estimation and Full-Length Transcriptome of <i>Sphingonotus tsinlingensis</i> : Genetic Background of a Drought-Adapted Grasshopper. <i>Frontiers in Genetics</i> , 2021, 12, 678625.	1.1	3
21854	Genome Sequence Resource of <i>Fusarium brachygibbosum</i> Padwick Strain HN-1, a Causal Agent of Maize Stalk Rot Disease. <i>Plant Disease</i> , 2021, . .	0.7	1
21855	Transcriptional Profiling of Exosomes Derived from <i>Staphylococcus aureus</i> -Infected Bovine Mammary Epithelial Cell Line MAC-T by RNA-Seq Analysis. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-18.	1.9	21
21856	Analysis of the Taxonomy and Pathogenic Factors of <i>Pectobacterium aroidearum</i> L6 Using Whole-Genome Sequencing and Comparative Genomics. <i>Frontiers in Microbiology</i> , 2021, 12, 679102.	1.5	11
21857	Comparative Label-Free Quantitative Proteomics Analysis Reveals the Essential Roles of N-Glycans in Salt Tolerance by Modulating Protein Abundance in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 646425.	1.7	9
21858	Quantitative Peptidomics of Mouse Brain After Infection With Cyst-Forming <i>Toxoplasma gondii</i> . <i>Frontiers in Immunology</i> , 2021, 12, 681242.	2.2	5
21859	Transcriptome sequencing and multi-plex imaging of prostate cancer microenvironment reveals a dominant role for monocytic cells in progression. <i>BMC Cancer</i> , 2021, 21, 846.	1.1	3
21860	VarSAn: associating pathways with a set of genomic variants using network analysis. <i>Nucleic Acids Research</i> , 2021, 49, 8471-8487.	6.5	1
21861	Host preference and invasiveness of commensal bacteria in the Lotus and <i>Arabidopsis</i> root microbiota. <i>Nature Microbiology</i> , 2021, 6, 1150-1162.	5.9	89
21862	<i>Microbacterium chengjingii</i> sp. nov. and <i>Microbacterium fandaimingii</i> sp. nov., isolated from bat faeces of <i>Hipposideros</i> and <i>Rousettus</i> species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	14
21863	Correlation between targeted RNAseq signature of breast cancer CTCs and onset of bone-only metastases. <i>British Journal of Cancer</i> , 2022, 126, 419-429.	2.9	10
21864	Identification of Somatic Gene Signatures in Circulating <scp>Cell-Free DNA</scp> Associated with Disease Progression in Metastatic Prostate Cancer by a Novel Machine Learning Platform. <i>Oncologist</i> , 2021, 26, 751-760.	1.9	9
21865	ReporterSeq reveals genome-wide dynamic modulators of the heat shock response across diverse stressors. <i>ELife</i> , 2021, 10, .	2.8	9
21867	Analysis of the Genome Sequence of Strain GiC-126 of <i>Gloeostereum incarnatum</i> with Genetic Linkage Map. <i>Mycobiology</i> , 2021, 49, 406-420.	0.6	2
21868	Network Pharmacology Combined with Bioinformatics to Investigate the Mechanisms and Molecular Targets of <i>Astragalus Radix</i> - <i>Panax notoginseng</i> Herb Pair on Treating Diabetic Nephropathy. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-19.	0.5	6
21869	Multimarker profiling identifies protective and harmful immune processes in heart failure: findings from BIOSAT-CHF. <i>Cardiovascular Research</i> , 2022, 118, 1964-1977.	1.8	10
21870	Genomic Analysis of <i>Sarcomyxa edulis</i> Reveals the Basis of Its Medicinal Properties and Evolutionary Relationships. <i>Frontiers in Microbiology</i> , 2021, 12, 652324.	1.5	6
21872	JDSNMF: Joint Deep Semi-Non-Negative Matrix Factorization for Learning Integrative Representation of Molecular Signals in Alzheimer's Disease. <i>Journal of Personalized Medicine</i> , 2021, 11, 686.	1.1	5

#	ARTICLE	IF	CITATIONS
21874	Comparative transcriptome analysis reveals regulatory network and regulators associated with proanthocyanidin accumulation in persimmon. <i>BMC Plant Biology</i> , 2021, 21, 356.	1.6	13
21875	Two Reference-Quality Sea Snake Genomes Reveal Their Divergent Evolution of Adaptive Traits and Venom Systems. <i>Molecular Biology and Evolution</i> , 2021, 38, 4867-4883.	3.5	20
21876	RNfuzzyApp: an R shiny RNA-seq data analysis app for visualisation, differential expression analysis, time-series clustering and enrichment analysis. <i>F1000Research</i> , 2021, 10, 654.	0.8	11
21877	RCA2: a scalable supervised clustering algorithm that reduces batch effects in scRNA-seq data. <i>Nucleic Acids Research</i> , 2021, 49, 8505-8519.	6.5	7
21878	Computationally scalable regression modeling for ultrahigh-dimensional omics data with ParProx. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	2
21879	Comparing Host Module Activation Patterns and Temporal Dynamics in Infection by Influenza H1N1 Viruses. <i>Frontiers in Immunology</i> , 2021, 12, 691758.	2.2	0
21881	Resident Kupffer cells and neutrophils drive liver toxicity in cancer immunotherapy. <i>Science Immunology</i> , 2021, 6, .	5.6	47
21882	Osmoregulation of the transcriptome of the hypothalamic supraoptic nucleus: A resource for the community. <i>Journal of Neuroendocrinology</i> , 2021, 33, e13007.	1.2	12
21883	Differential Packaging Into Outer Membrane Vesicles Upon Oxidative Stress Reveals a General Mechanism for Cargo Selectivity. <i>Frontiers in Microbiology</i> , 2021, 12, 561863.	1.5	21
21884	Transcriptome changes in resistant and susceptible rose in response to powdery mildew. <i>Journal of Phytopathology</i> , 2021, 169, 556-569.	0.5	5
21885	Ontoclick: a web browser extension to facilitate biomedical knowledge curation. <i>Bioinformatics</i> , 2021, 38, 301-302.	1.8	0
21886	Gene expression profile of the murine ischemic retina and its response to Aflibercept (VEGF-Trap). <i>Scientific Reports</i> , 2021, 11, 15313.	1.6	6
21888	Transcriptome and Small RNA Combined Sequencing Analysis of Cold Tolerance in Non-heading Chinese Cabbage. <i>Frontiers in Genetics</i> , 2021, 12, 605292.	1.1	0
21889	Prognostic value and immunological characteristics of a novel autophagy-related signature in pancreatic cancer. <i>Journal of Biosciences</i> , 2021, 46, 1.	0.5	0
21890	Dissecting the shared genetic basis of migraine and mental disorders using novel statistical tools. <i>Brain</i> , 2022, 145, 142-153.	3.7	27
21893	Intra- ϵ heterogeneity in transcription and chemoresistant property of leukemia-initiating cells in murine $\text{Setd2}^{\text{KO}}/\text{acute}$ myeloid leukemia. <i>Cancer Communications</i> , 2021, 41, 867-888.	3.7	4
21894	The effect of season of birth on brain epigenome-wide DNA methylation of older adults. <i>Journal of Developmental Origins of Health and Disease</i> , 2022, 13, 367-377.	0.7	2
21895	Spectrum of Protein Location in Proteomes Captures Evolutionary Relationship Between Species. <i>Journal of Molecular Evolution</i> , 2021, 89, 544-553.	0.8	4

#	ARTICLE	IF	CITATIONS
21896	Coordinated changes in gene expression kinetics underlie both mouse and human erythroid maturation. <i>Genome Biology</i> , 2021, 22, 197.	3.8	40
21897	Transcriptome analysis of differentially expressed genes in chrysanthemum MET1 RNA interference lines. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1455-1468.	1.4	3
21898	MicroRNA-378a-3p is overexpressed in psoriasis and modulates cell cycle arrest in keratinocytes via targeting BMP2 gene. <i>Scientific Reports</i> , 2021, 11, 14186.	1.6	8
21899	Drugs and Epigenetic Molecular Functions. A Pharmacological Data Scientometric Analysis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7250.	1.8	10
21900	Profiling NSD3-dependent neural crest gene expression reveals known and novel candidate regulatory factors. <i>Developmental Biology</i> , 2021, 475, 118-130.	0.9	7
21901	Chromosomal-scale genome assembly of <i>Eleutherococcus senticosus</i> provides insights into chromosome evolution in Araliaceae. <i>Molecular Ecology Resources</i> , 2021, 21, 2204-2220.	2.2	10
21902	A novel risk score predicts prognosis in melanoma: The combination of three tumor-infiltrating immune cells and four immune-related genes. <i>Clinical Immunology</i> , 2021, 228, 108751.	1.4	4
21903	Metatranscriptomics for the Human Microbiome and Microbial Community Functional Profiling. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 279-311.	2.8	36
21904	SPTAN1 Expression Predicts Treatment and Survival Outcomes in Colorectal Cancer. <i>Cancers</i> , 2021, 13, 3638.	1.7	2
21905	Identification of pathological transcription in autosomal dominant polycystic kidney disease epithelia. <i>Scientific Reports</i> , 2021, 11, 15139.	1.6	1
21906	DNA Methylation Alterations in Blood Cells of Toddlers with Down Syndrome. <i>Genes</i> , 2021, 12, 1115.	1.0	6
21908	Genome sequence of <i>Apostasia ramifera</i> provides insights into the adaptive evolution in orchids. <i>BMC Genomics</i> , 2021, 22, 536.	1.2	9
21909	Key Candidate Genes " VSIG2 of Colon Cancer Identified by Weighted Gene Co-Expression Network Analysis. <i>Cancer Management and Research</i> , 2021, Volume 13, 5739-5750.	0.9	2
21910	ACE2-lentiviral transduction enables mouse SARS-CoV-2 infection and mapping of receptor interactions. <i>PLoS Pathogens</i> , 2021, 17, e1009723.	2.1	28
21911	Transcriptomic analyses of cacao flavonoids produced in photobioreactors. <i>BMC Genomics</i> , 2021, 22, 551.	1.2	3
21915	Analyzing the gonadal transcriptome of the frog <i>Hoplobatrachus rugulosus</i> to identify genes involved in sex development. <i>BMC Genomics</i> , 2021, 22, 552.	1.2	7
21916	DNA methylation analysis reveals epimutation hotspots in patients with dilated cardiomyopathy-associated laminopathies. <i>Clinical Epigenetics</i> , 2021, 13, 139.	1.8	5
21917	Mitochondrial-encoded MOTS-c prevents pancreatic islet destruction in autoimmune diabetes. <i>Cell Reports</i> , 2021, 36, 109447.	2.9	21

#	ARTICLE	IF	CITATIONS
21918	Study on potential differentially expressed genes in stroke by bioinformatics analysis. <i>Neurological Sciences</i> , 2022, 43, 1155-1166.	0.9	8
21920	Evaluating, Filtering and Clustering Genetic Disease Cohorts Based on Human Phenotype Ontology Data with Cohort Analyzer. <i>Journal of Personalized Medicine</i> , 2021, 11, 730.	1.1	2
21922	High Expression Levels of CDK1 and CDC20 in Patients With Lung Squamous Cell Carcinoma are Associated With Worse Prognosis. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 653805.	1.6	4
21923	A circular RNAs dataset landscape reveals potential signatures for the detection and prognosis of early-stage lung adenocarcinoma. <i>BMC Cancer</i> , 2021, 21, 781.	1.1	6
21924	Consensus clustering applied to multi-omics disease subtyping. <i>BMC Bioinformatics</i> , 2021, 22, 361.	1.2	36
21925	Biomarker Categorization in Transcriptomic Meta-Analysis by Concordant Patterns With Application to Pan-Cancer Studies. <i>Frontiers in Genetics</i> , 2021, 12, 651546.	1.1	5
21926	The Wild Sugarcane and Sorghum Kinomes: Insights Into Expansion, Diversification, and Expression Patterns. <i>Frontiers in Plant Science</i> , 2021, 12, 668623.	1.7	18
21927	Identification of endometriosis-associated genes and pathways based on bioinformatic analysis. <i>Medicine (United States)</i> , 2021, 100, e26530.	0.4	7
21928	Limitations of Explainability for Established Prognostic Biomarkers of Prostate Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 649429.	1.1	5
21929	An Ontology-Based Framework for Psychological Monitoring in Education During the COVID-19 Pandemic. <i>Frontiers in Psychology</i> , 2021, 12, 673586.	1.1	5
21930	Identification of Hub Genes Associated with Diabetes Mellitus and Tuberculosis Using Bioinformatic Analysis. <i>International Journal of General Medicine</i> , 2021, Volume 14, 4061-4072.	0.8	7
21931	Clinal and seasonal changes are correlated in <i>Drosophila melanogaster</i> natural populations. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 2042-2054.	1.1	8
21932	Prediction of Protein-Protein Interactions using Deep Multi-Modal Representations. , 2021, , .		2
21933	Epigenetic Analysis of the Chromatin Landscape Identifies a Repertoire of Murine Eosinophil-Specific PU.1-Bound Enhancers. <i>Journal of Immunology</i> , 2021, 207, 1044-1054.	0.4	4
21934	ULK overexpression mitigates motor deficits and neuropathology in mouse models of Machado-Joseph disease. <i>Molecular Therapy</i> , 2022, 30, 370-387.	3.7	10
21935	Enhancing the interoperability of glycan data flow between ChEBI, PubChem, and GlyGen. <i>Glycobiology</i> , 2021, , .	1.3	2
21936	Global patterns of enhancer activity during sea urchin embryogenesis assessed by eRNA profiling. <i>Genome Research</i> , 2021, 31, 1680-1692.	2.4	9
21937	Abnormalities of mitochondrial dynamics and bioenergetics in neuronal cells from CDKL5 deficiency disorder. <i>Neurobiology of Disease</i> , 2021, 155, 105370.	2.1	6

#	ARTICLE	IF	CITATIONS
21938	InpherNet accelerates monogenic disease diagnosis using patients' candidate genes' neighbors. <i>Genetics in Medicine</i> , 2021, 23, 1984-1992.	1.1	1
21939	Axl inhibitor bemcentinib alleviates mitochondrial dysfunction in the unilateral ureter obstruction murine model. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 7407-7417.	1.6	11
21940	Single-cell analysis of mouse and human prostate reveals novel fibroblasts with specialized distribution and microenvironment interactions. <i>Journal of Pathology</i> , 2021, 255, 141-154.	2.1	39
21941	<i>Gossypium tomentosum</i> genome and interspecific ultra-dense genetic maps reveal genomic structures, recombination landscape and flowering depression in cotton. <i>Genomics</i> , 2021, 113, 1999-2009.	1.3	8
21942	Integrated transcriptome and metabolome analyses of biochar-induced pathways in response to <i>Fusarium</i> wilt infestation in pepper. <i>Genomics</i> , 2021, 113, 2085-2095.	1.3	12
21943	Transcription factor MaMADS36 plays a central role in regulating banana fruit ripening. <i>Journal of Experimental Botany</i> , 2021, 72, 7078-7091.	2.4	21
21944	Two-Pore Channels Regulate Expression of Various Receptors and Their Pathway-Related Proteins in Multiple Ways. <i>Cells</i> , 2021, 10, 1807.	1.8	2
21945	Comparative transcriptomic analysis brings new insights into the response to acute temperature acclimation in burbot (<i>Lota lota lota</i>). <i>Aquaculture Reports</i> , 2021, 20, 100657.	0.7	8
21946	Financiando al rey: negociaci3n e inicios del «encabezamiento por alcabalas» en Burgos (1495-1513). <i>Hispania - Revista Espanola De Historia</i> , 2021, 81, 425-454.	0.2	0
21947	Differential gene expression profile by RNA sequencing study of elderly osteoporotic hip fracture patients with sarcopenia. <i>Journal of Orthopaedic Translation</i> , 2021, 29, 10-18.	1.9	17
21949	Transcriptomic and metabolomic profiles of <i>Zea mays</i> fed with urea and ammonium. <i>Physiologia Plantarum</i> , 2021, 173, 935-953.	2.6	4
21950	Exosomal miR-218-5p/miR-363-3p from Endothelial Progenitor Cells Ameliorate Myocardial Infarction by Targeting the p53/JMY Signaling Pathway. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-23.	1.9	34
21951	Predicting Panel of Metabolism and Immune-Related Genes for the Prognosis of Human Ovarian Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 690542.	1.8	8
21952	Metatranscriptomic Analysis of Bacterial Communities on Laundered Textiles: A Pilot Case Study. <i>Microorganisms</i> , 2021, 9, 1591.	1.6	5
21953	Context-dependent effects of whole-genome duplication during mammary tumor recurrence. <i>Scientific Reports</i> , 2021, 11, 14932.	1.6	7
21954	Grand Challenges for Artificial Intelligence in Molecular Medicine. <i>Frontiers in Molecular Medicine</i> , 2021, 1, .	0.6	1
21959	Single-subject studies-derived analyses unveil altered biomechanisms between very small cohorts: implications for rare diseases. <i>Bioinformatics</i> , 2021, 37, i67-i75.	1.8	2
21960	Male Differentiation in the Marine Copepod <i>Oithona nana</i> Reveals the Development of a New Nervous Ganglion and Lin12-Notch-Repeat Protein-Associated Proteolysis. <i>Biology</i> , 2021, 10, 657.	1.3	1

#	ARTICLE	IF	CITATIONS
21961	Transcriptome Profiling of <i>Micromelalopha troglodyta</i> (Lepidoptera: Notodontidae) Larvae under Tannin Stress Using Solexa Sequencing Technology. <i>Journal of Entomological Science</i> , 2021, 56, 321-342.	0.2	1
21962	Transcriptome analysis of resistant and susceptible mulberry responses to <i>Meloidogyne enterolobii</i> infection. <i>BMC Plant Biology</i> , 2021, 21, 338.	1.6	5
21963	Comparative transcriptome analysis of mixed tissues of black porgy (<i>Acanthopagrus schlegelii</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.9	9
21964	CAD Genes: Genome-Wide Identification, Evolution, and Their Contribution to Lignin Biosynthesis in Pear (<i>Pyrus bretschneideri</i>). <i>Plants</i> , 2021, 10, 1444.	1.6	6
21965	<i>ASPM</i> is a Novel Candidate Gene Associated with Colorectal Cancer Cell Growth. <i>DNA and Cell Biology</i> , 2021, 40, 921-935.	0.9	7
21966	Regulatory Network Analysis in Estradiol-Treated Human Endothelial Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8193.	1.8	0
21967	Patient-derived iPSC-cerebral organoid modeling of the 17q11.2 microdeletion syndrome establishes <i>CRLF3</i> as a critical regulator of neurogenesis. <i>Cell Reports</i> , 2021, 36, 109315.	2.9	28
21968	Proteomics as a tool to disclose the cellular and molecular mechanisms of selected anticancer gold compounds. <i>Coordination Chemistry Reviews</i> , 2021, 438, 213905.	9.5	23
21969	An ancestral recombination graph of human, Neanderthal, and Denisovan genomes. <i>Science Advances</i> , 2021, 7, .	4.7	47
21970	Transcriptome and metabolome profiling in naturally infested <i>Casuarina equisetifolia</i> clones by <i>Ralstonia solanacearum</i> . <i>Genomics</i> , 2021, 113, 1906-1918.	1.3	12
21971	Highly accurate protein structure prediction for the human proteome. <i>Nature</i> , 2021, 596, 590-596.	13.7	1,773
21972	Improved SÃ©zary cell detection and novel insights into immunophenotypic and molecular heterogeneity in SÃ©zary syndrome. <i>Blood</i> , 2021, 138, 2539-2554.	0.6	28
21974	Integrated Analysis of Long Non-Coding RNA and mRNA Expression Profiles in Testes of Calves and Sexually Mature Wandong Bulls (<i>Bos taurus</i>). <i>Animals</i> , 2021, 11, 2006.	1.0	6
21976	The Compressed Vocabulary of Microbial Life. <i>Frontiers in Microbiology</i> , 2021, 12, 655990.	1.5	8
21977	Plasma proteomic profiling reveals biomarkers associated with aortic dilation in patients with bicuspid aortic valve. <i>Annals of Translational Medicine</i> , 2021, 9, 1182-1182.	0.7	2
21978	Transcriptome-based analysis reveals that the biosynthesis of anthocyanins is more active than that of flavonols and proanthocyanins in the colorful flowers of <i>Lagerstroemia indica</i> . <i>Biologia Futura</i> , 2021, 72, 473-488.	0.6	5
21979	Genome-wide profiles of UV lesion susceptibility, repair, and mutagenic potential in melanoma. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2021, 823, 111758.	0.4	4
21980	Identification of m6A-Related Biomarkers Associated with Prognosis of Colorectal Cancer. <i>Medical Science Monitor</i> , 2021, 27, e932370.	0.5	9

#	ARTICLE	IF	CITATIONS
21981	Aurora kinase A (AURKA) promotes the progression and imatinib resistance of advanced gastrointestinal stromal tumors. <i>Cancer Cell International</i> , 2021, 21, 407.	1.8	2
21982	DeepGraphGO: graph neural network for large-scale, multispecies protein function prediction. <i>Bioinformatics</i> , 2021, 37, i262-i271.	1.8	50
21983	The critical role of B4GALT4 in promoting microtubule spindle assembly in HCC through the regulation of PLK1 and RHAMM expression. <i>Journal of Cellular Physiology</i> , 2022, 237, 617-636.	2.0	6
21984	Single-cell transcriptome of bronchoalveolar lavage fluid reveals sequential change of macrophages during SARS-CoV-2 infection in ferrets. <i>Nature Communications</i> , 2021, 12, 4567.	5.8	43
21985	Transcriptome analysis of the spleen provides insight into the immunoregulation of <i>Cyprinus carpio koi</i> under <i>Aeromonas veronii</i> infection. <i>Aquaculture</i> , 2021, 540, 736650.	1.7	7
21986	LncRNA AC007255.1, an immune-related prognostic enhancer RNA in esophageal cancer. <i>PeerJ</i> , 2021, 9, e11698.	0.9	6
21987	Dissecting immune cell stat regulation network reveals biomarkers to predict ICB therapy responders in melanoma. <i>Journal of Translational Medicine</i> , 2021, 19, 296.	1.8	4
21988	Transcriptome Characterization and Identification of Molecular Markers (SNP, SSR, and Indels) in the Medicinal Plant <i>Sarcandra glabra</i> spp.. <i>BioMed Research International</i> , 2021, 2021, 1-11.	0.9	6
21989	Focal white matter lesions induce long-lasting axonal degeneration, neuroinflammation and behavioral deficits. <i>Neurobiology of Disease</i> , 2021, 155, 105371.	2.1	4
21990	Application across species of a one health approach to liquid sample handling for respiratory based -omics analysis. <i>Scientific Reports</i> , 2021, 11, 14292.	1.6	3
21991	Eukaryotic initiation factor EIF-3.G augments mRNA translation efficiency to regulate neuronal activity. <i>ELife</i> , 2021, 10, .	2.8	8
21992	Preterm labor is a distinct process from term labor following computational analysis of human myometrium. <i>American Journal of Obstetrics and Gynecology</i> , 2022, 226, 106.e1-106.e16.	0.7	9
21993	Hippocampus chronic deep brain stimulation induces reversible transcript changes in a macaque model of mesial temporal lobe epilepsy. <i>Chinese Medical Journal</i> , 2021, 134, 1845-1854.	0.9	2
21994	Comparative analysis of fatty acid metabolism based on transcriptome sequencing of wild and cultivated <i>Ophiocordyceps sinensis</i> . <i>PeerJ</i> , 2021, 9, e11681.	0.9	5
21995	IRF7-Associated Immunophenotypes Have Dichotomous Responses to Virus/Allergen Coexposure and OM-85-Induced Reprogramming. <i>Frontiers in Immunology</i> , 2021, 12, 699633.	2.2	4
21997	CFTR Lifecycle Map—A Systems Medicine Model of CFTR Maturation to Predict Possible Active Compound Combinations. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7590.	1.8	6
21998	<i>ARHGDI1</i> Confers Selective Advantage to Dissociated Human Pluripotent Stem Cells. <i>Stem Cells and Development</i> , 2021, 30, 705-713.	1.1	3
21999	Computational Probing the Methylation Sites Related to EGFR Inhibitor-Responsive Genes. <i>Biomolecules</i> , 2021, 11, 1042.	1.8	2

#	ARTICLE	IF	CITATIONS
22000	A graph centrality-based approach for candidate gene prediction for type 1 diabetes. <i>Immunologic Research</i> , 2021, 69, 422-428.	1.3	0
22001	Pre-conditioning modifies the TME to enhance solid tumor CAR T cell efficacy and endogenous protective immunity. <i>Molecular Therapy</i> , 2021, 29, 2335-2349.	3.7	51
22002	Screening of intestinal probiotics and the effects of feeding probiotics on the digestive enzyme activity, immune, intestinal flora and WSSV resistance of <i>Procambarus clarkii</i> . <i>Aquaculture</i> , 2021, 540, 736748.	1.7	18
22003	SCISSOR _{sc} : a single-cell inferred site-specific omics resource for tumor microenvironment association study. <i>NAR Cancer</i> , 2021, 3, zcab037.	1.6	1
22004	Histone H2A.X phosphorylation and Caspase-Initiated Chromatin Condensation in late-stage erythropoiesis. <i>Epigenetics and Chromatin</i> , 2021, 14, 37.	1.8	6
22005	Comparative transcriptome analysis reveals the candidate genes involved in SDR unreduced female gamete formation in the diploid rubber tree (<i>Hevea brasiliensis</i> (Willd. ex A. Juss.) Mill. Arg.). <i>Journal of Rubber Research (Kuala Lumpur, Malaysia)</i> , 2021, 24, 355-368.	0.4	0
22006	Approximate search for known gene clusters in new genomes using PQ-trees. <i>Algorithms for Molecular Biology</i> , 2021, 16, 16.	0.3	2
22007	Genetic mapping of novel modifiers for ApcMin induced intestinal polyps development using the genetic architecture power of the collaborative cross mice. <i>BMC Genomics</i> , 2021, 22, 566.	1.2	8
22008	Transcriptome analysis of chloride intracellular channel knockdown in <i>Drosophila</i> identifies oxidation-reduction function as possible mechanism of altered sensitivity to ethanol sedation. <i>PLoS ONE</i> , 2021, 16, e0246224.	1.1	2
22009	Autophagy-Related Genes in Atherosclerosis. <i>Journal of Healthcare Engineering</i> , 2021, 2021, 1-11.	1.1	6
22011	<i>Hanseniaspora smithiae</i> sp. nov., a Novel Apiculate Yeast Species From Patagonian Forests That Lacks the Typical Genomic Domestication Signatures for Fermentative Environments. <i>Frontiers in Microbiology</i> , 2021, 12, 679894.	1.5	10
22012	Identification of potential core genes in esophageal carcinoma using bioinformatics analysis. <i>Medicine (United States)</i> , 2021, 100, e26428.	0.4	7
22013	Bioinformatics analysis of PAE family in <i>Populus trichocarpa</i> and responsiveness to carbon and nitrogen treatment. <i>3 Biotech</i> , 2021, 11, 370.	1.1	2
22014	Gentamicin-induced hearing loss: A retrospective study using the Food and Drug Administration Adverse Event Reporting System and a toxicological study using drug-gene network analysis. <i>Heliyon</i> , 2021, 7, e07429.	1.4	2
22015	A Reassessment of Copy Number Variations in Congenital Heart Defects: Picturing the Whole Genome. <i>Genes</i> , 2021, 12, 1048.	1.0	6
22017	In-Cell Labeling and Mass Spectrometry for Systems-Level Structural Biology. <i>Chemical Reviews</i> , 2022, 122, 7647-7689.	23.0	17
22018	Genome assembly of <i>Scorias spongiosa</i> and comparative genomics provide insights into ecological adaptation of honeydew-dependent sooty mould fungi. <i>Genomics</i> , 2021, 113, 2189-2198.	1.3	2
22019	Integrative transcriptome analysis identifies new oxidosqualene cyclase genes involved in ginsenoside biosynthesis in Jilin ginseng. <i>Genomics</i> , 2021, 113, 2304-2316.	1.3	7

#	ARTICLE	IF	CITATIONS
22020	stPlus: a reference-based method for the accurate enhancement of spatial transcriptomics. <i>Bioinformatics</i> , 2021, 37, i299-i307.	1.8	42
22021	Identification of Rhythmically Expressed LncRNAs in the Zebrafish Pineal Gland and Testis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7810.	1.8	7
22022	Capturing the transcription factor interactome in response to sub-lethal insecticide exposure. <i>Current Research in Insect Science</i> , 2021, 1, 100018.	0.8	4
22023	Protein-Protein Interface Topology as a Predictor of Secondary Structure and Molecular Function Using Convolutional Deep Learning. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 3292-3303.	2.5	4
22024	Effects of low lead exposure on sperm quality and sperm DNA methylation in adult men. <i>Cell and Bioscience</i> , 2021, 11, 150.	2.1	7
22025	A novel computational drug repurposing approach for Systemic Lupus Erythematosus (SLE) treatment using Semantic Web technologies. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 3886-3892.	1.8	6
22026	Global analysis of protein lysine 2-hydroxyisobutyrylation (Khib) profiles in Chinese herb rhubarb (Dahuang). <i>BMC Genomics</i> , 2021, 22, 542.	1.2	7
22027	Chronic Kidney Disease Cohort Studies: A Guide to Metabolome Analyses. <i>Metabolites</i> , 2021, 11, 460.	1.3	4
22028	Control of tissue development and cell diversity by cell cycle-dependent transcriptional filtering. <i>ELife</i> , 2021, 10, .	2.8	7
22029	Linear functional organization of the omic embedding space. <i>Bioinformatics</i> , 2021, 37, 3839-3847.	1.8	2
22032	The USDA-ARS Ag100Pest Initiative: High-Quality Genome Assemblies for Agricultural Pest Arthropod Research. <i>Insects</i> , 2021, 12, 626.	1.0	31
22034	FOXC2 controls adult lymphatic endothelial specialization, function, and gut lymphatic barrier preventing multiorgan failure. <i>Science Advances</i> , 2021, 7, .	4.7	43
22035	Prognostic impact of a lymphocyte activation-associated gene signature in GBM based on transcriptome analysis. <i>PeerJ</i> , 2021, 9, e12070.	0.9	1
22036	Discovery of Cellular RhoA Functions by the Integrated Application of Gene Set Enrichment Analysis. <i>Biomolecules and Therapeutics</i> , 2021, , .	1.1	3
22037	Interpretable, Scalable, and Transferrable Functional Projection of Large-Scale Transcriptome Data Using Constrained Matrix Decomposition. <i>Frontiers in Genetics</i> , 2021, 12, 719099.	1.1	2
22038	Inflammatory gene expression profiling in peripheral blood from patients with Alzheimer's disease reveals key pathways and hub genes with potential diagnostic utility: a preliminary study. <i>PeerJ</i> , 2021, 9, e12016.	0.9	1
22041	Inferring Functional Epigenetic Modules by Integrative Analysis of Multiple Heterogeneous Networks. <i>Frontiers in Genetics</i> , 2021, 12, 706952.	1.1	0
22042	Comprehensive Strain-Level Analysis of the Gut Microbe <i>Faecalibacterium prausnitzii</i> in Patients with Liver Cirrhosis. <i>MSystems</i> , 2021, 6, e0077521.	1.7	6

#	ARTICLE	IF	CITATIONS
22043	Proteomic Analysis of Copper Toxicity in Human Fungal Pathogen <i>Cryptococcus neoformans</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 662404.	1.8	5
22045	Use of Network Pharmacology to Investigate the Mechanism of the Compound Xuanju Capsule in the Treatment of Rheumatoid Arthritis. <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	1
22046	CANVS: an easy-to-use application for the analysis and visualization of mass spectrometry-based protein-protein interaction/association data. <i>Molecular Biology of the Cell</i> , 2021, 32, br9.	0.9	0
22047	Establishment of a ferroptosis-related gene signature for prognosis in lung adenocarcinoma patients. <i>PeerJ</i> , 2021, 9, e11931.	0.9	4
22048	Deciphering the Therapeutic Mechanisms of Wuzi Ershen Decoction in Treating Oligoasthenozoospermia through the Network Pharmacology Approach. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-17.	0.5	2
22050	Bacterial surface properties influence the activity of the TAT-RasGAP317-326 antimicrobial peptide. <i>IScience</i> , 2021, 24, 102923.	1.9	5
22051	Predictability of polygenic risk score for progression to dementia and its interaction with APOE ϵ 4 in mild cognitive impairment. <i>Translational Neurodegeneration</i> , 2021, 10, 32.	3.6	11
22052	Differential expression of striatal proteins in a mouse model of DOPA-responsive dystonia reveals shared mechanisms among dystonic disorders. <i>Molecular Genetics and Metabolism</i> , 2021, 133, 352-361.	0.5	4
22053	A Birds-Eye (Re)View of Acid-Suppression Drugs, COVID-19, and the Highly Variable Literature. <i>Frontiers in Pharmacology</i> , 2021, 12, 700703.	1.6	5
22054	CD86 Molecule Might Be a Novel Immune-Related Prognostic Biomarker for Patients With Bladder Cancer by Bioinformatics and Experimental Assays. <i>Frontiers in Oncology</i> , 2021, 11, 679851.	1.3	4
22056	Integrative Analyses of Genes Associated with Hashimoto's Thyroiditis. <i>Journal of Immunology Research</i> , 2021, 2021, 1-9.	0.9	10
22058	From a genome assembly to full regulatory network prediction: the case study of <i>Rhodotorula toruloides</i> putative Haa1-regulon. <i>BMC Bioinformatics</i> , 2021, 22, 399.	1.2	4
22059	Evaluation of the molecular response of corpora lutea to manganese amino acid complex supplementation in gilts. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	0
22060	Genome-wide DNA polymorphisms of <i>Citrus unshiu</i> Marc. cv. Miyagawa-wase cultivated in different regions based on whole-genome re-sequencing. <i>Plant Biotechnology Reports</i> , 2021, 15, 551-559.	0.9	3
22061	Gene expression profile analysis of gallic acid-induced cell death process. <i>Scientific Reports</i> , 2021, 11, 16743.	1.6	4
22062	Cadherin and Wnt signaling pathways as key regulators in diabetic nephropathy. <i>PLoS ONE</i> , 2021, 16, e0255728.	1.1	2
22065	Marine-Derived Xyloketal Compound Ameliorates MPP ⁺ -Induced Neuronal Injury through Regulating of the IRE1/XBP1 Signaling Pathway. <i>ACS Chemical Neuroscience</i> , 2021, 12, 3101-3111.	1.7	4
22066	Identification of Long Non-Coding RNAs Involved in Porcine Fat Deposition Using Two High-Throughput Sequencing Methods. <i>Genes</i> , 2021, 12, 1374.	1.0	6

#	ARTICLE	IF	CITATIONS
22067	Motherhood-induced gene expression in the mouse medial amygdala: Changes induced by pregnancy and lactation but not by pup stimuli. <i>FASEB Journal</i> , 2021, 35, e21806.	0.2	3
22068	Decellularization Enables Characterization and Functional Analysis of Extracellular Matrix in Planarian Regeneration. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100137.	2.5	11
22069	Microfluidic device with brain extracellular matrix promotes structural and functional maturation of human brain organoids. <i>Nature Communications</i> , 2021, 12, 4730.	5.8	164
22070	Identification of significant alteration genes, pathways and TFs induced by LPS in ARDS via bioinformatical analysis. <i>BMC Infectious Diseases</i> , 2021, 21, 852.	1.3	3
22071	Deep learning from HE slides predicts the clinical benefit from adjuvant chemotherapy in hormone receptor-positive breast cancer patients. <i>Scientific Reports</i> , 2021, 11, 17363.	1.6	7
22074	A Genome-Wide Association Study on Liver Stiffness Changes during Hepatitis C Virus Infection Cure. <i>Diagnostics</i> , 2021, 11, 1501.	1.3	2
22075	Integrative analysis of metabolome and transcriptome profiles provides insight into the fruit pericarp pigmentation disorder caused by <i>Candidatus Liberibacter asiaticus</i> ™ infection. <i>BMC Plant Biology</i> , 2021, 21, 397.	1.6	8
22077	Perturbed transcriptional profiles after chronic low dose rate radiation in mice. <i>PLoS ONE</i> , 2021, 16, e0256667.	1.1	5
22078	Classification and Treatment of Diseases in the Age of Genome Medicine Based on Pathway Pathology. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9418.	1.8	3
22079	Employing bioinformatics analysis to identify hub genes and microRNAs involved in colorectal cancer. <i>Medical Oncology</i> , 2021, 38, 114.	1.2	11
22080	Clinical Genetic Risk Variants Inform a Functional Protein Interaction Network for Tetralogy of Fallot. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003410.	1.6	15
22081	Icariin, an Up-and-Coming Bioactive Compound Against Neurological Diseases: Network Pharmacology-Based Study and Literature Review. <i>Drug Design, Development and Therapy</i> , 2021, Volume 15, 3619-3641.	2.0	24
22082	Assembling stable syntrophic <i>Escherichia coli</i> communities by comprehensively identifying beneficiaries of secreted goods. <i>Cell Systems</i> , 2021, 12, 1064-1078.e7.	2.9	24
22084	Utilization of Transcriptome, Small RNA, and Degradome Sequencing to Provide Insights Into Drought Stress and Rewatering Treatment in <i>Medicago ruthenica</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 675903.	1.7	9
22085	Pan-cancer analysis of longitudinal metastatic tumors reveals genomic alterations and immune landscape dynamics associated with pembrolizumab sensitivity. <i>Nature Communications</i> , 2021, 12, 5137.	5.8	63
22086	Human reference gut microbiome catalog including newly assembled genomes from under-represented Asian metagenomes. <i>Genome Medicine</i> , 2021, 13, 134.	3.6	47
22087	Genetic diversity of tomato response to heat stress at the QTL and transcriptome levels. <i>Plant Journal</i> , 2021, 107, 1213-1227.	2.8	28
22088	The chromosome-scale assembly of the Canary Islands endemic spider <i>Dysdera silvatica</i> (Arachnida, Araneae) sheds light on the origin and genome structure of chemoreceptor gene families in chelicerates. <i>Molecular Ecology Resources</i> , 2022, 22, 375-390.	2.2	12

#	ARTICLE	IF	CITATIONS
22089	Personalized single-cell networks: a framework to predict the response of any gene to any drug for any patient. <i>BioData Mining</i> , 2021, 14, 37.	2.2	2
22090	Depletion of TAX1BP1 Amplifies Innate Immune Responses during Respiratory Syncytial Virus Infection. <i>Journal of Virology</i> , 2021, 95, e0091221.	1.5	6
22091	The aging mouse lens transcriptome. <i>Experimental Eye Research</i> , 2021, 209, 108663.	1.2	11
22093	The molecular basis, genetic control and pleiotropic effects of local gene co-expression. <i>Nature Communications</i> , 2021, 12, 4842.	5.8	18
22095	Driver and novel genes correlated with metastasis of non-small cell lung cancer: A comprehensive analysis. <i>Pathology Research and Practice</i> , 2021, 224, 153551.	1.0	7
22096	Developmental lineage of human pluripotent stem cell-derived cardiac fibroblasts affects their functional phenotype. <i>FASEB Journal</i> , 2021, 35, e21799.	0.2	6
22097	Heparanase is a novel biomarker for immune infiltration and prognosis in breast cancer. <i>Aging</i> , 2021, 13, 20836-20852.	1.4	9
22098	A high-resolution temporal atlas of the SARS-CoV-2 translome and transcriptome. <i>Nature Communications</i> , 2021, 12, 5120.	5.8	57
22099	A multi-objective genetic algorithm to find active modules in multiplex biological networks. <i>PLoS Computational Biology</i> , 2021, 17, e1009263.	1.5	8
22100	Open chromatin in grapevine marks candidate CREs and with other chromatin features correlates with gene expression. <i>Plant Journal</i> , 2021, 107, 1631-1647.	2.8	17
22101	An integrated systematic approach for investigating microcurrent electrical nerve stimulation (MENS) efficacy in STZ-induced diabetes mellitus. <i>Life Sciences</i> , 2021, 279, 119650.	2.0	4
22103	Circulating microRNAs in Early Breast Cancer Patients and Its Association With Lymph Node Metastases. <i>Frontiers in Oncology</i> , 2021, 11, 627811.	1.3	14
22104	Complete Genomic Characterization and Identification of <i>Saccharomycopsis phalluae</i> sp. nov., a Novel Pathogen Causes Yellow Rot Disease on <i>Phallus rubrovolvatus</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 707.	1.5	8
22105	Quantitative proteomic analysis of human peripheral nerves from subjects with type 2 diabetes. <i>Diabetic Medicine</i> , 2021, 38, e14658.	1.2	8
22106	The canonical smooth muscle cell marker TAGLN is present in endothelial cells and is involved in angiogenesis. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	20
22107	Role of competitive endogenous RNA networks in the pathogenesis of coronary artery disease. <i>Annals of Translational Medicine</i> , 2021, 9, 1234-1234.	0.7	3
22108	Identification of EP300 as a Key Gene Involved in Antipsychotic-Induced Metabolic Dysregulation Based on Integrative Bioinformatics Analysis of Multi-Tissue Gene Expression Data. <i>Frontiers in Pharmacology</i> , 2021, 12, 729474.	1.6	3
22109	Analysis of transcripts and splice isoforms in red claw crayfish (<i>Cherax quadricarinatus</i>) using single-molecule long-read sequencing. <i>Aquaculture</i> , 2021, 541, 736828.	1.7	5

#	ARTICLE	IF	CITATIONS
22110	Corticosterone pattern-dependent glucocorticoid receptor binding and transcriptional regulation within the liver. <i>PLoS Genetics</i> , 2021, 17, e1009737.	1.5	10
22111	Transgenic modeling of Ndr2 gene amplification reveals disturbance of hippocampus circuitry and function. <i>IScience</i> , 2021, 24, 102868.	1.9	3
22112	Data on the first functionally-annotated de novo transcriptome assembly for North American flying squirrels (genus <i>Glaucomys</i>). <i>Data in Brief</i> , 2021, 37, 107267.	0.5	1
22113	Pan-cancer analysis of pathway-based gene expression pattern at the individual level reveals biomarkers of clinical prognosis. <i>Cell Reports Methods</i> , 2021, 1, 100050.	1.4	10
22114	Modeling the effects of EMT-immune dynamics on carcinoma disease progression. <i>Communications Biology</i> , 2021, 4, 983.	2.0	3
22115	A Novel miRNA-mRNA Axis Involves in Regulating Transcriptional Disorders in Pancreatic Adenocarcinoma. <i>Cancer Management and Research</i> , 2021, Volume 13, 5989-6004.	0.9	3
22116	Systematic Analysis Identifies a Specific RNA-Binding Protein-Related Gene Model for Prognostication and Risk-Adjustment in HBV-Related Hepatocellular Carcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 707305.	1.1	9
22117	Integrated analysis of transcriptomics to identify hub genes in primary Sjögren's syndrome. <i>Oral Diseases</i> , 2022, 28, 1831-1845.	1.5	5
22118	Comparative Transcriptome and Hormone Analysis of Mature Leaves and New Shoots in Tea Cuttings (<i>Camellia sinensis</i>) among Three Cultivars with Different Rooting Abilities. <i>Journal of Plant Growth Regulation</i> , 2022, 41, 2833-2845.	2.8	7
22120	Comparative transcriptomic analyses of glucosinolate metabolic genes during the formation of Chinese kale seeds. <i>BMC Plant Biology</i> , 2021, 21, 394.	1.6	9
22121	Catalyzing Knowledge-Driven Discovery in Environmental Health Sciences through a Community-Driven Harmonized Language. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 8985.	1.2	6
22122	Proteomic Analysis of Hypoxia-Induced Senescence of Human Bone Marrow Mesenchymal Stem Cells. <i>Stem Cells International</i> , 2021, 2021, 1-20.	1.2	8
22123	Molecular and functional characterization of detrusor PDGFR α positive cells in spinal cord injury-induced detrusor overactivity. <i>Scientific Reports</i> , 2021, 11, 16268.	1.6	2
22124	Differential Retinal Protein Expression in Primary and Secondary Retinal Ganglion Cell Degeneration Identified by Integrated SWATH and Target-Based Proteomics. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8592.	1.8	5
22125	Transcriptional Profiles of Diploid Mutant <i>Apis mellifera</i> Embryos after Knockout of <i>csd</i> by CRISPR/Cas9. <i>Insects</i> , 2021, 12, 704.	1.0	6
22126	Dynamic Patterns of N6-Methyladenosine Profiles of Messenger RNA Correlated with the Cardiomyocyte Regenerability during the Early Heart Development in Mice. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-15.	1.9	10
22127	Efficient Dicer processing of virus-derived double-stranded RNAs and its modulation by RIG-I-like receptor LGP2. <i>PLoS Pathogens</i> , 2021, 17, e1009790.	2.1	17
22128	Complete Genome Sequencing and Comparative Analysis of <i>Citrobacter koseri</i> , CKNJ, a Strain Isolated from a Patient with Endogenous Endophthalmitis. <i>Japanese Journal of Infectious Diseases</i> , 2022, 75, 148-155.	0.5	0

#	ARTICLE	IF	CITATIONS
22130	Identification of Novel Gene Signatures using Next-Generation Sequencing Data from COVID-19 Infection Models: Focus on Neuro-COVID and Potential Therapeutics. <i>Frontiers in Pharmacology</i> , 2021, 12, 688227.	1.6	9
22131	Human oocyte meiotic maturation is associated with a specific profile of alternatively spliced transcript isoforms. <i>Molecular Reproduction and Development</i> , 2021, 88, 605-617.	1.0	4
22132	Identification of cytokeratin24 as a tumor suppressor for the management of head and neck cancer. <i>Biological Chemistry</i> , 2022, 403, 869-890.	1.2	9
22133	Identification of key proteins in the signaling crossroads between wound healing and cancer hallmark phenotypes. <i>Scientific Reports</i> , 2021, 11, 17245.	1.6	7
22134	From DNA human sequence to the chromatin higher order organisation and its biological meaning: Using biomolecular interaction networks to understand the influence of structural variation on spatial genome organisation and its functional effect. <i>Seminars in Cell and Developmental Biology</i> , 2022, 121, 171-185.	2.3	17
22135	The first human induced pluripotent stem cell line of Kashinâ€œBeck disease reveals involvement of heparan sulfate proteoglycan biosynthesis and PPAR pathway. <i>FEBS Journal</i> , 2022, 289, 279-293.	2.2	3
22136	Haloalkaliphilic denitrifiers-dependent sulfate-reducing bacteria thrive in nitrate-enriched environments. <i>Water Research</i> , 2021, 201, 117354.	5.3	11
22137	Comprehensive analysis of DNA damage repair in squamous cell carcinoma subtypes. <i>Life Sciences</i> , 2021, 278, 119559.	2.0	1
22138	Will Plant Genome Editing Play a Decisive Role in â€œQuantum-Leapâ€œImprovements in Crop Yield to Feed an Increasing Global Human Population?. <i>Plants</i> , 2021, 10, 1667.	1.6	10
22139	Integrative Analysis of Minichromosome Maintenance Proteins and Their Prognostic Significance in Melanoma. <i>Frontiers in Oncology</i> , 2021, 11, 715173.	1.3	6
22140	Homozygous mutations in <i>CCDC34</i> cause male infertility with oligoasthenoteratozoospermia in humans and mice. <i>Journal of Medical Genetics</i> , 2022, 59, 710-718.	1.5	20
22141	PhenoDB, GeneMatcher and VariantMatcher, tools for analysis and sharing of sequence data. <i>Orphanet Journal of Rare Diseases</i> , 2021, 16, 365.	1.2	24
22142	The Salivary Secretome. , 0, , .		0
22143	Sequenceâ€œbased features that are determinant for tailâ€œanchored membrane protein sorting in eukaryotes. <i>Traffic</i> , 2021, 22, 306-318.	1.3	13
22145	Genomic divergence and differential gene expression between crustacean ecotypes across a marine thermal gradient. <i>Marine Genomics</i> , 2021, 58, 100847.	0.4	1
22146	Myeloid-resident neuropilin-1 influences brown adipose tissue in obesity. <i>Scientific Reports</i> , 2021, 11, 15767.	1.6	1
22147	Long Non-coding RNA RP11-395G23.3 Acts as a Competing Endogenous RNA of miR-124-3p to Regulate ROR1 in Anaplastic Thyroid Carcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 673242.	1.1	1
22150	Leaf Proteome Response to Drought Stress and Antioxidant Potential in Tomato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5	1.0	18

#	ARTICLE	IF	CITATIONS
22151	A marine bacterial community capable of degrading poly(ethylene terephthalate) and polyethylene. <i>Journal of Hazardous Materials</i> , 2021, 416, 125928.	6.5	120
22152	The chromosome-scale reference genome of <i>Rubus chingii</i> Hu provides insight into the biosynthetic pathway of hydrolyzable tannins. <i>Plant Journal</i> , 2021, 107, 1466-1477.	2.8	26
22154	A STUDY ON ACTIVATION OF THE CARBON CONCENTRATING MECHANISM BY CARBON DI-OXIDE DEPRIVATION OVERLAPS WITH MASSIVE TRANSCRIPTIONAL REARRANGEMENT IN <i>CHLAMYDOMONAS REINHARDTII</i> . , 2021, , 61-63.		0
22155	Protein function prediction with gene ontology: from traditional to deep learning models. <i>PeerJ</i> , 2021, 9, e12019.	0.9	8
22156	Identifying causal models between genetically regulated methylation patterns and gene expression in healthy colon tissue. <i>Clinical Epigenetics</i> , 2021, 13, 162.	1.8	6
22157	Identification of new target proteins of a Urotensin-II receptor antagonist using transcriptome-based drug repositioning approach. <i>Scientific Reports</i> , 2021, 11, 17138.	1.6	4
22158	Defining Color Change in Pitaya: A Close Look at Betacyanin Synthesis Genes in <i>Stenocereus queretaroensis</i> . <i>Frontiers in Sustainable Food Systems</i> , 2021, 5, .	1.8	1
22159	The Cancer Epitope Database and Analysis Resource: A Blueprint for the Establishment of a New Bioinformatics Resource for Use by the Cancer Immunology Community. <i>Frontiers in Immunology</i> , 2021, 12, 735609.	2.2	10
22161	Exploring Chemical Information in PubChem. <i>Current Protocols</i> , 2021, 1, e217.	1.3	42
22162	Conditional stomatal closure in a fern shares molecular features with flowering plant active stomatal responses. <i>Current Biology</i> , 2021, 31, 4560-4570.e5.	1.8	12
22163	Genomic introgression from a distant congener in the Levant fritillary butterfly, <i>Melitaea acentria</i> . <i>Molecular Ecology</i> , 2021, 30, 4819-4832.	2.0	7
22165	Full-length transcriptome assembly of <i>Andrias davidianus</i> (amphibia: caudata) skin via hybrid sequencing. <i>Bioscience Reports</i> , 2021, 41, .	1.1	3
22166	MAIT cells regulate NK cell-mediated tumor immunity. <i>Nature Communications</i> , 2021, 12, 4746.	5.8	45
22167	Association of CASC18/miR-20a-3p/TGFB2 ceRNA axis with occult lymph node metastasis in tongue squamous cell carcinoma. <i>Molecular Medicine</i> , 2021, 27, 85.	1.9	8
22168	One Health concepts and challenges for surveillance, forecasting, and mitigation of plant disease beyond the traditional scope of crop production. <i>Plant Pathology</i> , 2022, 71, 86-97.	1.2	18
22170	Computational Methods for Prediction of Human Protein-Phenotype Associations: A Review. <i>Phenomics</i> , 2021, 1, 171-185.	0.9	10
22172	Sustained expression of inflammatory monocytes and activated T cells in COVID-19 patients and recovered convalescent plasma donors. <i>Immunity, Inflammation and Disease</i> , 2021, 9, 1279-1290.	1.3	14
22173	Investigating the Molecular Processes behind the Cell-Specific Toxicity Response to Titanium Dioxide Nanobelts. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9432.	1.8	1

#	ARTICLE	IF	CITATIONS
22174	RNA-Seq, physiological, and biochemical analysis of burley tobacco response to nitrogen deficiency. <i>Scientific Reports</i> , 2021, 11, 16802.	1.6	6
22176	Searchlight: automated bulk RNA-seq exploration and visualisation using dynamically generated R scripts. <i>BMC Bioinformatics</i> , 2021, 22, 411.	1.2	10
22177	Bi-allelic mutations of DNAH10 cause primary male infertility with asthenoteratozoospermia in humans and mice. <i>American Journal of Human Genetics</i> , 2021, 108, 1466-1477.	2.6	50
22179	An Overview of Cell-Based Assay Platforms for the Solute Carrier Family of Transporters. <i>Frontiers in Pharmacology</i> , 2021, 12, 722889.	1.6	31
22180	Visual comprehension and orientation into the COVID-19 CIDO ontology. <i>Journal of Biomedical Informatics</i> , 2021, 120, 103861.	2.5	4
22181	Comprior: facilitating the implementation and automated benchmarking of prior knowledge-based feature selection approaches on gene expression data sets. <i>BMC Bioinformatics</i> , 2021, 22, 401.	1.2	1
22182	Proteome plasticity in response to persistent environmental change. <i>Molecular Cell</i> , 2021, 81, 3294-3309.e12.	4.5	12
22183	Low-Level Erbium-Doped Yttrium Aluminum Garnet Laser Irradiation Induced Alteration of Gene Expression in Osteogenic Cells from Rat Calvariae. <i>Photobiomodulation, Photomedicine, and Laser Surgery</i> , 2021, 39, 566-577.	0.7	4
22185	Planarian Anatomy Ontology: a resource to connect data within and across experimental platforms. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	11
22186	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. <i>Nature Communications</i> , 2021, 12, 4854.	5.8	42
22187	Systematic review of human post-mortem immunohistochemical studies and bioinformatics analyses unveil the complexity of astrocyte reaction in Alzheimer's disease. <i>Neuropathology and Applied Neurobiology</i> , 2022, 48, .	1.8	40
22188	Phenotyping stomatal closure by thermal imaging for GWAS and TWAS of water use efficiency-related genes. <i>Plant Physiology</i> , 2021, 187, 2544-2562.	2.3	23
22189	Comparison of gene expression in the red imported fire ant (<i>Solenopsis invicta</i>) under different temperature conditions. <i>Scientific Reports</i> , 2021, 11, 16476.	1.6	8
22190	Collagen fiber orientation disorder from H&E images is prognostic for early stage breast cancer: clinical trial validation. <i>Npj Breast Cancer</i> , 2021, 7, 104.	2.3	26
22191	TCF3 Regulates the Proliferation and Apoptosis of Human Spermatogonial Stem Cells by Targeting PODXL. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 695545.	1.8	8
22192	Activation of FcRn Mediates a Primary Resistance Response to Sorafenib in Hepatocellular Carcinoma by Single-Cell RNA Sequencing. <i>Frontiers in Pharmacology</i> , 2021, 12, 709343.	1.6	6
22194	Differential Protein Interactome in Esophageal Squamous Cell Carcinoma Offers Novel Systems Biomarker Candidates with High Diagnostic and Prognostic Performance. <i>OMICS A Journal of Integrative Biology</i> , 2021, 25, 495-512.	1.0	2
22195	Identifying potential association on gene-disease network via dual hypergraph regularized least squares. <i>BMC Genomics</i> , 2021, 22, 605.	1.2	3

#	ARTICLE	IF	CITATIONS
22196	Hepatic Proteomic Analysis of Selenoprotein T Knockout Mice by TMT: Implications for the Role of Selenoprotein T in Glucose and Lipid Metabolism. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8515.	1.8	6
22197	Evaluating whole-genome expression differences in idiopathic and diabetic adhesive capsulitis. <i>Journal of Shoulder and Elbow Surgery</i> , 2022, 31, e1-e13.	1.2	4
22198	Application of miRNA-seq in neuropsychiatry: A methodological perspective. <i>Computers in Biology and Medicine</i> , 2021, 135, 104603.	3.9	7
22199	High-Quality Genome Sequence Resource for <i>Fusarium andiyazi</i> Causing Pokkah Boeng Disease of Sugarcane in China. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, MPMI-11-20-0331.	1.4	2
22200	Ultrastructure observation and transcriptome analysis of Chinese chestnut (<i>Castanea mollissima</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.0	1
22201	TACR2 is associated with the immune microenvironment and inhibits migration and proliferation via the Wnt/ β -catenin signaling pathway in prostate cancer. <i>Cancer Cell International</i> , 2021, 21, 415.	1.8	5
22202	Chondrocytes from Osteoarthritis Patients Adopt Distinct Phenotypes in Response to Central TH1/TH2/TH17 Cytokines. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9463.	1.8	8
22203	Effect of Tension on Human Periodontal Ligament Cells: Systematic Review and Network Analysis. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 695053.	2.0	16
22205	Hypoxia-Inducible Factor 2-Alpha Mediated Gene Sets Differentiate Pulmonary Arterial Hypertension. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 701247.	1.8	5
22206	Improve isobutanol tolerance and production by engineering of TATA-binding protein Spt15 in <i>Saccharomyces cerevisiae</i> . <i>Letters in Applied Microbiology</i> , 2021, 73, 694-707.	1.0	0
22207	The blood transcriptome prior to ovarian cancer diagnosis: A case-control study in the NOWAC postgenome cohort. <i>PLoS ONE</i> , 2021, 16, e0256442.	1.1	2
22209	Time-series transcriptomics reveals a <i>BBX32</i> -directed control of acclimation to high light in mature <i>Arabidopsis</i> leaves. <i>Plant Journal</i> , 2021, 107, 1363-1386.	2.8	11
22210	Ubiquitination-Related miRNA-mRNA Interaction Is a Potential Mechanism in the Progression of Retinoblastoma. , 2021, 62, 3.		8
22211	Fimepinostat (CUDC-907) in patients with relapsed/refractory diffuse large B cell and high-grade B-cell lymphoma: report of a phase 2 trial and exploratory biomarker analyses. <i>British Journal of Haematology</i> , 2021, 195, 201-209.	1.2	17
22212	Exploring the longitudinal glioma microenvironment landscape uncovers reprogrammed pro-tumorigenic neutrophils in the bone marrow. <i>Cell Reports</i> , 2021, 36, 109480.	2.9	30
22213	A single amino acid residue substitution in BraA04g017190.3C, a histone methyltransferase, results in premature bolting in Chinese cabbage (<i>Brassica rapa</i> L. ssp. <i>Pekinensis</i>). <i>BMC Plant Biology</i> , 2021, 21, 373.	1.6	3
22214	Mapping gene and gene pathways associated with coronary artery disease: a CARDIoGRAM exome and multi-ancestry UK biobank analysis. <i>Scientific Reports</i> , 2021, 11, 16461.	1.6	4
22215	Transcriptome Profiles of the Liver in Two Cold-Exposed Sheep Breeds Revealed Different Mechanisms and Candidate Genes for Thermogenesis. <i>Genetical Research</i> , 2021, 2021, 1-11.	0.3	1

#	ARTICLE	IF	CITATIONS
22217	A systematic comparison of data- and knowledge-driven approaches to disease subtype discovery. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
22218	GraphDTI: A robust deep learning predictor of drug-target interactions from multiple heterogeneous data. <i>Journal of Cheminformatics</i> , 2021, 13, 58.	2.8	12
22219	Application of Weighted Gene Coexpression Network Analysis to Identify Key Modules and Hub Genes in Systemic Juvenile Idiopathic Arthritis. <i>BioMed Research International</i> , 2021, 2021, 1-13.	0.9	4
22220	Human iPS-derived pre-epicardial cells direct cardiomyocyte aggregation expansion and organization in vitro. <i>Nature Communications</i> , 2021, 12, 4997.	5.8	21
22222	Comparative Transcriptomic Analysis Reveals the Effects of Drought on the Biosynthesis of Methyleugenol in <i>Asarum sieboldii</i> Miq.. <i>Biomolecules</i> , 2021, 11, 1233.	1.8	8
22223	d-Serine Mediates Cellular Proliferation for Kidney Remodeling. <i>Kidney360</i> , 2021, 2, 1611-1624.	0.9	11
22224	Improved datasets and evaluation methods for the automatic prediction of DNA-binding proteins. <i>Bioinformatics</i> , 2021, 38, 44-51.	1.8	3
22225	Pathogenic variations in Germ Cell Nuclear Acidic Peptidase (GCNA) are associated with human male infertility. <i>European Journal of Human Genetics</i> , 2021, 29, 1781-1788.	1.4	10
22226	Sex- and Developmental Stage-Related Differences in the Hepatic Transcriptome of Japanese Quail (<i>Coturnix japonica</i>) Exposed to 17 β -trenbolone. <i>Environmental Toxicology and Chemistry</i> , 2021, 40, 2559-2570.	2.2	4
22227	A systems-level study reveals host-targeted repurposable drugs against SARS-CoV-2 infection. <i>Molecular Systems Biology</i> , 2021, 17, e10239.	3.2	22
22228	<i>Streptomyces luteolifulvus</i> sp. nov., a novel actinomycete isolated from soil in Nanjing, China. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1829-1839.	0.7	1
22230	The CCAAT/Enhancer Binding Protein Beta (cebpb) is essential for the development of enveloping layer (EVL) in zebrafish. <i>Aquaculture and Fisheries</i> , 2021, , .	1.2	0
22231	Basal and Luminal Molecular Subtypes in Naturally-Occurring Canine Urothelial Carcinoma are Associated with Tumor Immune Signatures and Dog Breed. <i>Bladder Cancer</i> , 2021, 7, 317-333.	0.2	3
22232	Nanopore-based full-length transcriptome sequencing of Muscovy duck (<i>Cairina moschata</i>) ovary. <i>Poultry Science</i> , 2021, 100, 101246.	1.5	16
22233	Investigation of RNA metabolism through large-scale genetic interaction profiling in yeast. <i>Nucleic Acids Research</i> , 2021, 49, 8535-8555.	6.5	4
22234	iBRET Screen of the ABCD1 Peroxisomal Network and Mutation-Induced Network Perturbations. <i>Journal of Proteome Research</i> , 2021, 20, 4366-4380.	1.8	3
22235	Complete Genome of Marine Microalgae Associated Algicidal Bacterium <i>Sulfitobacter pseudonitzschiae</i> H46 with Quorum Sensing System. <i>Current Microbiology</i> , 2021, 78, 3741-3750.	1.0	8
22236	20th International Workshop on Data Mining in Bioinformatics (BIOKDD 2021). , 2021, , .		0

#	ARTICLE	IF	CITATIONS
22237	Ferroptosis-Related Genes in Lung Adenocarcinoma: Prognostic Signature and Immune, Drug Resistance, Mutation Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 672904.	1.1	34
22238	Revealing protein-protein interactions at the transcriptome scale by sequencing. <i>Molecular Cell</i> , 2021, 81, 4091-4103.e9.	4.5	28
22239	Exploring tissue architecture using spatial transcriptomics. <i>Nature</i> , 2021, 596, 211-220.	13.7	593
22240	Identification of intracellular glycosaminoglycan-interacting proteins by affinity purification mass spectrometry. <i>Biological Chemistry</i> , 2021, 402, 1427-1440.	1.2	5
22241	Retos y oportunidades en el estudio de vesículas extracelulares: contexto institucional a nivel mundial y situación actual en Colombia. <i>Biomedica</i> , 2021, 41, 555-589.	0.3	0
22242	Integrative genomics analysis of nasal intestinal-type adenocarcinomas demonstrates the major role of CACNA1C and paves the way for a simple diagnostic tool in male woodworkers. <i>Clinical Epigenetics</i> , 2021, 13, 179.	1.8	4
22243	Generation of hypothalamic arcuate organoids from human induced pluripotent stem cells. <i>Cell Stem Cell</i> , 2021, 28, 1657-1670.e10.	5.2	72
22244	Application of active learning in DNA microarray data for cancerous gene identification. <i>Expert Systems With Applications</i> , 2021, 177, 114914.	4.4	10
22245	Clinico-genomic profiling and clonal dynamic modeling of TP53-aberrant myelodysplastic syndrome and acute myeloid leukemia. <i>Leukemia and Lymphoma</i> , 2021, 62, 3348-3360.	0.6	11
22246	Genome sequencing data analysis for rare disease gene discovery. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	6
22248	Expression and prognosis of CDC45 in cervical cancer based on the GEO database. <i>PeerJ</i> , 2021, 9, e12114.	0.9	10
22249	Large-Scale Protein Interactions Prediction by Multiple Evidence Analysis Associated With an In-Silico Curation Strategy. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	2
22250	Integrative Analysis of the Roles of lncRNAs and mRNAs in Itaconate-Mediated Protection Against Liver Ischemia-Reperfusion Injury in Mice. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 4519-4536.	1.6	5
22252	Transcriptomic profile of leg muscle during early growth and development in Haiyang yellow chicken. <i>Archives Animal Breeding</i> , 2021, 64, 405-416.	0.5	6
22253	Comprehensive molecular characterization of pediatric radiation-induced high-grade glioma. <i>Nature Communications</i> , 2021, 12, 5531.	5.8	31
22254	A Taxon-Wise Insight Into Rock Weathering and Nitrogen Fixation Functional Profiles of Proglacial Systems. <i>Frontiers in Microbiology</i> , 2021, 12, 627437.	1.5	7
22255	Comparative analysis of the complete mitochondrial genome sequences and anther development cytology between maintainer and Ogura-type cytoplasm male-sterile cabbage (<i>B. oleracea</i> Var. capitata). <i>BMC Genomics</i> , 2021, 22, 646.	1.2	5
22256	Transcriptome and Oxylipin Profiling Joint Analysis Reveals Opposite Roles of 9-Oxylipins and Jasmonic Acid in Maize Resistance to <i>Gibberella</i> Stalk Rot. <i>Frontiers in Plant Science</i> , 2021, 12, 699146.	1.7	10

#	ARTICLE	IF	CITATIONS
22257	Identification of direct transcriptional targets of NFATC2 that promote \hat{I}^2 cell proliferation. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	15
22258	Chromosome-scale assembly of the <i>Dendrobium chrysotoxum</i> genome enhances the understanding of orchid evolution. <i>Horticulture Research</i> , 2021, 8, 183.	2.9	41
22261	The Biocontrol and Plant Growth-Promoting Properties of <i>Streptomyces alfalfae</i> XN-04 Revealed by Functional and Genomic Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 745766.	1.5	13
22263	Identification of genes modulated by interferon gamma in breast cancer cells. <i>Biochemistry and Biophysics Reports</i> , 2021, 27, 101053.	0.7	6
22264	Genome-Wide Transcriptional Changes of <i>Rhodosporidium kratochvilovae</i> at Low Temperature. <i>Frontiers in Microbiology</i> , 2021, 12, 727105.	1.5	5
22265	Transcriptomic changes during stage progression of <i>mycosis fungoides</i> . <i>British Journal of Dermatology</i> , 2022, 186, 520-531.	1.4	4
22266	Intercrypt sentinel macrophages tune antibacterial NF- \hat{I}^B responses in gut epithelial cells via TNF. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	14
22267	Transcriptomic Analysis Reveals a Sex-Dimorphic Influence of GAT-2 on Murine Liver Function. <i>Frontiers in Nutrition</i> , 2021, 8, 751388.	1.6	1
22268	Morphological, physiological, and transcriptional responses to low nitrogen stress in <i>Populus deltoides</i> Marsh. clones with contrasting nitrogen use efficiency. <i>BMC Genomics</i> , 2021, 22, 697.	1.2	3
22269	H3K4 di-methylation governs smooth muscle lineage identity and promotes vascular homeostasis by restraining plasticity. <i>Developmental Cell</i> , 2021, 56, 2765-2782.e10.	3.1	21
22270	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	5.8	26
22271	Identification of Oil Palm's Consistently Upregulated Genes during Early Infections of <i>Ganoderma boninense</i> via RNA-Seq Technology and Real-Time Quantitative PCR. <i>Plants</i> , 2021, 10, 2026.	1.6	2
22272	Cilostazol Induces eNOS and TM Expression via Activation with Sirtuin 1/Krüppel-like Factor 2 Pathway in Endothelial Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10287.	1.8	5
22273	Alternative developmental and transcriptomic responses to host plant water limitation in a butterfly metapopulation. <i>Molecular Ecology</i> , 2022, 31, 5666-5683.	2.0	5
22274	Genetic dissection of complex traits using hierarchical biological knowledge. <i>PLoS Computational Biology</i> , 2021, 17, e1009373.	1.5	1
22275	Divergent patterns of selection on metabolite levels and gene expression. <i>Bmc Ecology and Evolution</i> , 2021, 21, 185.	0.7	4
22276	In vitro CSC-derived cardiomyocytes exhibit the typical microRNA-mRNA blueprint of endogenous cardiomyocytes. <i>Communications Biology</i> , 2021, 4, 1146.	2.0	15
22277	High-Quality Genome of the Medicinal Plant <i>Strobilanthes cusia</i> Provides Insights Into the Biosynthesis of Indole Alkaloids. <i>Frontiers in Plant Science</i> , 2021, 12, 742420.	1.7	10

#	ARTICLE	IF	CITATIONS
22278	A Chinese host genetic study discovered IFNs and causality of laboratory traits on COVID-19 severity. <i>IScience</i> , 2021, 24, 103186.	1.9	10
22280	LitCovid-AGAC: cellular and molecular level annotation data set based on COVID-19. <i>Genomics and Informatics</i> , 2021, 19, e23.	0.4	4
22281	Analyzing host-viral interactome of SARS-CoV-2 for identifying vulnerable host proteins during COVID-19 pathogenesis. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104921.	1.0	21
22282	A general role for TANGO1, encoded by <i>MIA3</i> , in secretory pathway organization and function. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	15
22284	Understanding Competitive Endogenous RNA Network Mechanism in Type 1 Diabetes Mellitus Using Computational and Bioinformatics Approaches. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2021, Volume 14, 3865-3945.	1.1	6
22285	The expression pattern, polymorphisms and association analyses of the porcine <i>NREP</i> gene. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 62-70.	0.8	2
22286	Computational identification of repurposed drugs against viruses causing epidemics and pandemics via drug-target network analysis. <i>Computers in Biology and Medicine</i> , 2021, 136, 104677.	3.9	8
22287	Overexpression of argonate dehydratase reveals an upstream point of metabolic control in phenylalanine biosynthesis. <i>Plant Journal</i> , 2021, 108, 737-751.	2.8	12
22288	Activity of the mouse Notch ligand DLL1 is sensitive to C-terminal tagging in vivo. <i>BMC Research Notes</i> , 2021, 14, 383.	0.6	1
22289	Early IFN- γ signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. <i>Immunity</i> , 2021, 54, 2650-2669.e14.	6.6	145
22290	Whole-genome assembly of <i>Ganoderma leucocontextum</i> (Ganodermataceae, Fungi) discovered from the Tibetan Plateau of China. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	11
22291	Tanshinone IIA affects the malignant growth of Cholangiocarcinoma cells by inhibiting the PI3K-Akt-mTOR pathway. <i>Scientific Reports</i> , 2021, 11, 19268.	1.6	7
22292	A network embedding framework based on integrating multiplex network for drug combination prediction. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	36
22293	Functional characterization of HIC, a P2Y1 agonist, as a p53 stabilizer for prostate cancer cell death induction. <i>Future Medicinal Chemistry</i> , 2021, 13, 1845-1864.	1.1	4
22294	Journal of Zhejiang University: Science B, 2021, 22(12), 1845-1864.		
22295	Characterization of m6A-Related Genes Landscape in Skin Cutaneous Melanoma to Aid Immunotherapy and Assess Prognosis. <i>International Journal of General Medicine</i> , 2021, Volume 14, 5345-5361.	0.8	7
22296	Genetic Analysis of Heterosis for Yield Influencing Traits in Brassica juncea Using a Doubled Haploid Population and Its Backcross Progenies. <i>Frontiers in Plant Science</i> , 2021, 12, 721631.	1.7	14
22297	Identification of FadT as a Novel Quorum Quenching Enzyme for the Degradation of Diffusible Signal Factor in <i>Cupriavidus pinatubonensis</i> Strain HN-2. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9862.	1.8	7

#	ARTICLE	IF	CITATIONS
22298	Nesterenkonia ebinurensis sp. nov., a Novel Actinobacterium Isolated From Populus euphratica. Current Microbiology, 2021, 78, 3804-3810.	1.0	3
22299	Human melanocyte development and melanoma dedifferentiation at single-cell resolution. Nature Cell Biology, 2021, 23, 1035-1047.	4.6	59
22300	Quantitative Proteomics and Phosphoproteomics Reveal TNF- α -Mediated Protein Functions in Hepatocytes. Molecules, 2021, 26, 5472.	1.7	4
22301	Release of Notch activity coordinated by IL-1 β signalling confers differentiation plasticity of airway progenitors via Fosl2 during alveolar regeneration. Nature Cell Biology, 2021, 23, 953-966.	4.6	37
22302	Differential transcript usage analysis of bulk and single-cell RNA-seq data with DTUrtle. Bioinformatics, 2021, 37, 3781-3787.	1.8	10
22303	Observation of Unique Circulating miRNA Signatures in Non-Human Primates Exposed to Total-Body vs. Whole Thorax Lung Irradiation. Radiation Research, 2021, 196, 547-559.	0.7	7
22304	Evolutionary history of two rare endemic conifer species from the eastern Qinghai-Tibet Plateau. Annals of Botany, 2021, 128, 903-918.	1.4	5
22307	A novel lncRNA Discn fine-tunes replication protein A (RPA) availability to promote genomic stability. Nature Communications, 2021, 12, 5572.	5.8	11
22309	Transcriptional profiles underlying the effects of salicylic acid on fruit ripening and senescence in pear (Pyrus pyrifolia Nakai). Journal of Integrative Agriculture, 2021, 20, 2424-2437.	1.7	13
22310	Syn Wiki : Functional annotation of the first artificial organism Mycoplasma mycoides JCVI-syn3A. Protein Science, 2021, , .	3.1	8
22311	Glycolysis-related gene expression profiling serves as a novel prognosis risk predictor for human hepatocellular carcinoma. Scientific Reports, 2021, 11, 18875.	1.6	13
22312	A prelude to the proximity interaction mapping of CXXC5. Scientific Reports, 2021, 11, 17587.	1.6	4
22313	Trends in the Application of Omics to Ecotoxicology and Stress Ecology. Genes, 2021, 12, 1481.	1.0	22
22316	Wnt pathway-related three-mRNA clinical outcome signature in bladder urothelial carcinoma: computational biology and experimental analyses. Journal of Translational Medicine, 2021, 19, 409.	1.8	5
22317	Human genetic analyses of organelles highlight the nucleus in age-related trait heritability. ELife, 2021, 10, .	2.8	20
22318	Integrative proteome analysis implicates aberrant RNA splicing in impaired developmental potential of aged mouse oocytes. Aging Cell, 2021, 20, e13482.	3.0	12
22320	Dramatic transcriptomic differences in Macaca mulatta and Macaca fascicularis with Plasmodium knowlesi infections. Scientific Reports, 2021, 11, 19519.	1.6	5
22322	The <i>Euscaphis japonica</i> genome and the evolution of malvids. Plant Journal, 2021, 108, 1382-1399.	2.8	6

#	ARTICLE	IF	CITATIONS
22324	Novel insights into the immune regulatory effects of <i>Megalobrama amblycephala</i> intelectin on the phagocytosis and killing activity of macrophages. <i>Molecular Immunology</i> , 2021, 137, 145-154.	1.0	9
22325	Recombinant Antigen of Type 2 Porcine Reproductive and Respiratory Syndrome Virus (PRRSV-2) Promotes M1 Repolarization of Porcine Alveolar Macrophages and Th1 Type Response. <i>Vaccines</i> , 2021, 9, 1009.	2.1	5
22326	Microarray analysis of hub genes and pathways in damaged cartilage tissues of knee. <i>Medicine (United Tj ETQq0 0.0 rgBT /Oyerlock 10</i>	0.4	1
22327	Analysis of differentially expressed genes responsible for the suppressive effect of anisomycin on cell proliferation of DLD-1 cells. <i>Biochemistry and Biophysics Reports</i> , 2021, 27, 101038.	0.7	4
22328	Profiling of MicroRNAs in Midguts of <i>Plutella xylostella</i> Provides Novel Insights Into the <i>Bacillus thuringiensis</i> Resistance. <i>Frontiers in Genetics</i> , 2021, 12, 739849.	1.1	3
22329	SNP Development in <i>Penaeus vannamei</i> via Next-Generation Sequencing and DNA Pool Sequencing. <i>Fishes</i> , 2021, 6, 36.	0.7	3
22330	Antioxidant and Antiproliferative Activity of Finasteride against Glioblastoma Cells. <i>Pharmaceutics</i> , 2021, 13, 1410.	2.0	4
22331	SNORA42 promotes oesophageal squamous cell carcinoma development through triggering the DHX9/p65 axis. <i>Genomics</i> , 2021, 113, 3015-3029.	1.3	6
22332	The temperature-regulated DEAD-box RNA helicase CrhR interactome: autoregulation and photosynthesis-related transcripts. <i>Journal of Experimental Botany</i> , 2021, , .	2.4	7
22333	Genome mining reveals the genes of carboxypeptidase for OTA-detoxification in <i>Bacillus subtilis</i> CW14. <i>International Journal of Biological Macromolecules</i> , 2021, 186, 800-810.	3.6	22
22335	Multi-omics network-based functional annotation of unknown <i>Arabidopsis</i> genes. <i>Plant Journal</i> , 2021, 108, 1193-1212.	2.8	39
22336	Characterization of Mesenchymal Stem Cells Derived from Bisphosphonate-Related Osteonecrosis of the Jaw Patients's™ Gingiva. <i>Stem Cell Reviews and Reports</i> , 2022, 18, 378-394.	1.7	4
22337	An efficient approach towards the generation and analysis of interoperable clinical data in a knowledge graph. , 0, , .		0
22338	Silver: Forging almost Gold Standard Datasets. <i>Genes</i> , 2021, 12, 1523.	1.0	1
22340	Transcriptome analysis of differentially expressed genes in the red swamp crayfish <i>Procambarus clarkii</i> challenged with <i>Aeromonas hydrophila</i> . <i>Fish and Shellfish Immunology</i> , 2021, 119, 280-288.	1.6	12
22341	Podocyte-specific KLF4 is required to maintain parietal epithelial cell quiescence in the kidney. <i>Science Advances</i> , 2021, 7, eabg6600.	4.7	12
22342	Transcriptome repository of North-Western Himalayan endangered medicinal herbs: a paramount approach illuminating molecular perspective of phytoactive molecules and secondary metabolism. <i>Molecular Genetics and Genomics</i> , 2021, 296, 1177-1202.	1.0	6
22343	Comprehensive Survey of Recent Drug Discovery Using Deep Learning. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9983.	1.8	55

#	ARTICLE	IF	CITATIONS
22344	Multipotent progenitors and hematopoietic stem cells arise independently from hemogenic endothelium in the mouse embryo. <i>Cell Reports</i> , 2021, 36, 109675.	2.9	50
22345	<i>Massilia rhizosphaerae</i> sp. nov., a rice-associated rhizobacterium with antibacterial activity against <i>Ralstonia solanacearum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	22
22346	A high-quality chromosome-level genome of wild <i>Rosa rugosa</i> . <i>DNA Research</i> , 2021, 28, .	1.5	10
22347	scMethBank: a database for single-cell whole genome DNA methylation maps. <i>Nucleic Acids Research</i> , 2022, 50, D380-D386.	6.5	20
22348	Quantitative Temporal Viromics. <i>Annual Review of Virology</i> , 2021, 8, 159-181.	3.0	5
22349	Isolation, characterization, and genome assembly of <i>Barnettozyma botsteinii</i> sp. nov. and novel strains of <i>Kurtzmaniella quercitrusa</i> isolated from the intestinal tract of the termite <i>Macrotermes bellicosus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	7
22350	Effects of Bacille Calmette Guerin (BCG) vaccination during COVID-19 infection. <i>Computers in Biology and Medicine</i> , 2021, 138, 104891.	3.9	3
22351	Repopulation of decellularized retinas with hiPSC-derived retinal pigment epithelial and ocular progenitor cells shows cell engraftment, organization and differentiation. <i>Biomaterials</i> , 2021, 276, 121049.	5.7	13
22353	Platelet-Released Growth Factors Induce Genes Involved in Extracellular Matrix Formation in Human Fibroblasts. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10536.	1.8	6
22355	Complete genome sequence of <i>Crassaminicella</i> sp. 143-2114E isolated from a deep-sea hydrothermal vent. <i>Marine Genomics</i> , 2021, 62, 100899.	0.4	2
22358	Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. <i>Nature Biotechnology</i> , 2022, 40, 74-85.	9.4	152
22359	Polychlorinated biphenyls induce oxidative stress and metabolic responses in astrocytes. <i>NeuroToxicology</i> , 2021, 86, 59-68.	1.4	19
22361	Marine natural products targeting the eukaryotic cell membrane. <i>Journal of Antibiotics</i> , 2021, 74, 769-785.	1.0	1
22362	Induction of dopaminergic neurons for neuronal subtype-specific modeling of psychiatric disease risk. <i>Molecular Psychiatry</i> , 2023, 28, 1970-1982.	4.1	13
22366	Viral Strain-Specific Activation of Pathogen-Associated Molecular Pattern-Triggered Immunity Enhances Symptom Severity in Broad Bean Wilt Virus 2 Infection. <i>Frontiers in Plant Science</i> , 2021, 12, 746543.	1.7	3
22367	Transcriptomics analysis of the infected tissue of gibel carp (<i>Carassius auratus gibelio</i>) with liver myxobolosis infers the underlying defense mechanisms from the perspective of immune-metabolic interactions. <i>Aquaculture</i> , 2021, 542, 736867.	1.7	8
22368	Comparative Transcriptome Analysis of Stage-Specific Changes in Gene Expression during Larval Development in <i>Monochamus alternatus</i> Hope. <i>Forests</i> , 2021, 12, 1312.	0.9	1
22369	Dynamics of TCR repertoire and T cell function in COVID-19 convalescent individuals. <i>Cell Discovery</i> , 2021, 7, 89.	3.1	27

#	ARTICLE	IF	CITATIONS
22370	Lymphocyte activation gene-3 is associated with programmed death-ligand 1 and programmed cell death protein 1 in small cell lung cancer. <i>Annals of Translational Medicine</i> , 2021, 9, 1468-1468.	0.7	10
22371	Genome-wide association study and transcriptome of olecranon-type traits in peach (<i>Prunus persica</i>) Tj ETQq1 1 0.784314 rgBT /Over	1.2	3
22372	Rapid Macrosatellite Evolution Promotes X-Linked Hybrid Male Sterility in a Feline Interspecies Cross. <i>Molecular Biology and Evolution</i> , 2021, 38, 5588-5609.	3.5	8
22373	Modelling the impact of decidual senescence on embryo implantation in human endometrial assembloids. <i>ELife</i> , 2021, 10, .	2.8	100
22375	Impact of pmrA on <i>Cronobacter sakazakii</i> planktonic and biofilm cells: A comprehensive transcriptomic study. <i>Food Microbiology</i> , 2021, 98, 103785.	2.1	10
22376	Egg incubation and plasma proteome alterations in response to brood care in maternal crayfish (<i>Procambarus clarkii</i>). <i>Aquaculture</i> , 2021, 542, 736888.	1.7	6
22377	Bioinformatic and experimental analyses of key biomarkers in pancreatic cancer. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 1359.	0.8	3
22378	Rare variants in the endocytic pathway are associated with Alzheimer's disease, its related phenotypes, and functional consequences. <i>PLoS Genetics</i> , 2021, 17, e1009772.	1.5	1
22380	Cell-specific gene association network construction from single-cell RNA sequence. <i>Cell Cycle</i> , 2021, 20, 1-16.	1.3	3
22382	Multiple Lesions Contribute to Infertility in Males Lacking Autoimmune Regulator. <i>American Journal of Pathology</i> , 2021, 191, 1592-1609.	1.9	7
22384	Fundamental limits on the rate of bacterial growth and their influence on proteomic composition. <i>Cell Systems</i> , 2021, 12, 924-944.e2.	2.9	45
22385	Network neighbors of viral targets and differentially expressed genes in COVID-19 are drug target candidates. <i>Scientific Reports</i> , 2021, 11, 18985.	1.6	5
22386	Identification of a miRNA-mRNA Regulatory Networks in Placental Tissue Associated With Tibetan High Altitude Adaptation. <i>Frontiers in Genetics</i> , 2021, 12, 671119.	1.1	3
22388	Quantifying adaptive divergence of the snowfinches in a common landscape. <i>Diversity and Distributions</i> , 2022, 28, 2579-2592.	1.9	3
22389	Transcriptional Landscapes of Long Non-coding RNAs and Alternative Splicing in <i>Pyricularia oryzae</i> Revealed by RNA-Seq. <i>Frontiers in Plant Science</i> , 2021, 12, 723636.	1.7	3
22390	Construction of competing endogenous RNA interaction network as prognostic markers in metastatic melanoma. <i>PeerJ</i> , 2021, 9, e12143.	0.9	1
22391	Automated conceptual model clustering: a relator-centric approach. <i>Software and Systems Modeling</i> , 2022, 21, 1363-1387.	2.2	7
22392	Viral suppressor of RNA silencing in vascular plants also interferes with the development of the bryophyte <i>Physcomitrella patens</i> . <i>Plant, Cell and Environment</i> , 2022, 45, 220-235.	2.8	3

#	ARTICLE	IF	CITATIONS
22393	<sc>PANNZER</sc>â€”A practical tool for protein function prediction. <i>Protein Science</i> , 2022, 31, 118-128.	3.1	55
22394	Antigen Presenting Cells Link the Female Genital Tract Microbiome to Mucosal Inflammation, With Hormonal Contraception as an Additional Modulator of Inflammatory Signatures. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 733619.	1.8	8
22395	Extracellular Matrix Proteome Remodeling in Human Glioblastoma and Medulloblastoma. <i>Journal of Proteome Research</i> , 2021, 20, 4693-4707.	1.8	12
22396	Microarray Analysis of Paramylon, Isolated from <i>Euglena Gracilis</i> EOD-1, and Its Effects on Lipid Metabolism in the Ileum and Liver in Diet-Induced Obese Mice. <i>Nutrients</i> , 2021, 13, 3406.	1.7	6
22397	Protein Aggregation Is an Early Manifestation of Phospholamban p.(Arg14del)-Related Cardiomyopathy: Development of PLN-R14del-Related Cardiomyopathy. <i>Circulation: Heart Failure</i> , 2021, 14, e008532.	1.6	17
22398	Whole-Genome Sequencing and Genome-Wide Studies of Spiny Head Croaker (<i>Collichthys lucidus</i>) Reveals Potential Insights for Well-Developed Otoliths in the Family Sciaenidae. <i>Frontiers in Genetics</i> , 2021, 12, 730255.	1.1	0
22399	Inositol polyphosphates and target of rapamycin kinase signalling govern photosystem II protein phosphorylation and photosynthetic function under light stress in <i>Chlamydomonas</i> . <i>New Phytologist</i> , 2021, 232, 2011-2025.	3.5	10
22400	The genome sequence provides insights into salt tolerance of <i>Achnatherum splendens</i> (Gramineae), a constructive species of alkaline grassland. <i>Plant Biotechnology Journal</i> , 2022, 20, 116-128.	4.1	18
22401	Network topology analysis of essential genes interactome of <i>Helicobacter pylori</i> to explore novel therapeutic targets. <i>Microbial Pathogenesis</i> , 2021, 158, 105059.	1.3	14
22402	An iteration model for identifying essential proteins by combining comprehensive PPI network with biological information. <i>BMC Bioinformatics</i> , 2021, 22, 430.	1.2	6
22403	Single-cell heterogeneity analysis and CRISPR screens in MIN6 cell line reveal transcriptional regulators of insulin. <i>Cell Cycle</i> , 2021, 20, 2053-2065.	1.3	5
22404	Hypergraph-based logistic matrix factorization for metabolite-disease interaction prediction. <i>Bioinformatics</i> , 2022, 38, 435-443.	1.8	10
22406	Construction and analysis of a novel ferroptosis-related gene signature predicting prognosis in lung adenocarcinoma. <i>FEBS Open Bio</i> , 2021, 11, 3005-3018.	1.0	2
22407	FORUM: building a Knowledge Graph from public databases and scientific literature to extract associations between chemicals and diseases. <i>Bioinformatics</i> , 2021, 37, 3896-3904.	1.8	8
22408	Distinct gene expression dynamics in germ line and somatic tissue during ovariole morphogenesis in <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
22409	Identifying GPSM Family Members as Potential Biomarkers in Breast Cancer: A Comprehensive Bioinformatics Analysis. <i>Biomedicines</i> , 2021, 9, 1144.	1.4	18
22410	Damage-Net: A program for DNA repair meta-analysis identifies a network of novel repair genes that facilitate cancer evolution. <i>DNA Repair</i> , 2021, 105, 103158.	1.3	3
22414	GRASP55 restricts early-stage autophagy and regulates spatial organization of the early secretory network. <i>Biology Open</i> , 2021, 10, .	0.6	2

#	ARTICLE	IF	CITATIONS
22415	LncRNA SNHG17 Contributes to Proliferation, Migration, and Poor Prognosis of Hepatocellular Carcinoma. <i>Canadian Journal of Gastroenterology and Hepatology</i> , 2021, 2021, 1-11.	0.8	11
22416	Differential Interactome Based Drug Repositioning Unraveled Abacavir, Exemestane, Nortriptyline Hydrochloride, and Tolcapone as Potential Therapeutics for Colorectal Cancers. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	2
22417	X-Ray Causes mRNA Transcripts Change to Enhance Orai2-Mediated Ca ²⁺ Influx in Rat Brain Microvascular Endothelial Cells. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 646730.	1.6	4
22418	Deregulation of microRNAs in oral squamous cell carcinoma, a bioinformatics analysis. <i>Gene Reports</i> , 2021, 24, 101241.	0.4	3
22419	Gene and prognostic value of N6-methyladenosine (m6A) modification regulatory factors in lung adenocarcinoma. <i>European Journal of Cancer Prevention</i> , 2022, 31, 354-362.	0.6	5
22420	The Interactions of Small Proline-Rich Proteins with Late Cornified Envelope Proteins are Involved in the Pathogenesis of Psoriasis. <i>Clinical, Cosmetic and Investigational Dermatology</i> , 2021, Volume 14, 1355-1365.	0.8	6
22422	The genome of the naturally evolved obesity-prone Ossabaw miniature pig. <i>IScience</i> , 2021, 24, 103081.	1.9	9
22423	Regulation of Long Non-coding RNA KCNQ1OT1 Network in Colorectal Cancer Immunity. <i>Frontiers in Genetics</i> , 2021, 12, 684002.	1.1	8
22424	Selective HIF stabilization alleviates hepatocellular steatosis and ballooning in a rodent model of 70% liver resection. <i>Clinical Science</i> , 2021, 135, 2285-2305.	1.8	5
22425	Learning interpretable cellular and gene signature embeddings from single-cell transcriptomic data. <i>Nature Communications</i> , 2021, 12, 5261.	5.8	38
22426	Comparative genome characterization of <i>Leptospira interrogans</i> from mild and severe leptospirosis patients. <i>Genomics and Informatics</i> , 2021, 19, e31.	0.4	0
22427	Proteomics Reveals an Increase in the Abundance of Glycolytic and Ethanolic Fermentation Enzymes in Developing Sugarcane Culms During Sucrose Accumulation. <i>Frontiers in Plant Science</i> , 2021, 12, 716964.	1.7	4
22430	Identification of anti-horn fly vaccine antigen candidates using a reverse vaccinology approach. <i>Parasites and Vectors</i> , 2021, 14, 442.	1.0	4
22431	Oxidation of Hemoglobin Drives a Proatherogenic Polarization of Macrophages in Human Atherosclerosis. <i>Antioxidants and Redox Signaling</i> , 2021, 35, 917-950.	2.5	16
22432	Bioinformatics analyses of gene expression profile identify key genes and functional pathways involved in cutaneous lupus erythematosus. <i>Clinical Rheumatology</i> , 2022, 41, 437-452.	1.0	4
22433	Chromosomal neighbourhoods allow identification of organ specific changes in gene expression. <i>PLoS Computational Biology</i> , 2021, 17, e1008947.	1.5	2
22434	MUNDO: protein function prediction embedded in a multispecies world. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	2
22435	Screening of anti-chronic nonbacterial prostatitis activity of different extractions of the aerial part of <i>Glycyrrhiza uralensis</i> , and network pharmacology research. <i>Biomedical Reports</i> , 2021, 15, 99.	0.9	5

#	ARTICLE	IF	CITATIONS
22436	Subtypes of schizophrenia identified by multi-omic measures associated with dysregulated immune function. <i>Molecular Psychiatry</i> , 2021, 26, 6926-6936.	4.1	21
22437	Whole Genome Sequence of <i>Alternaria alternata</i> , the Causal Agent of Black Spot of Kiwifruit. <i>Frontiers in Microbiology</i> , 2021, 12, 713462.	1.5	7
22438	Gene expression of intracortical bone demonstrates loading-induced increases in Wnt1 and Ngf and inhibition of bone remodeling processes. <i>Bone</i> , 2021, 150, 116019.	1.4	9
22439	mRNA Network: Solution for Tracking Chemotherapy Insensitivity in Small-Cell Lung Cancer. <i>Journal of Healthcare Engineering</i> , 2021, 2021, 1-11.	1.1	2
22440	Leveraging Experimental Strategies to Capture Different Dimensions of Microbial Interactions. <i>Frontiers in Microbiology</i> , 2021, 12, 700752.	1.5	8
22441	Genome Sequence Resource for <i>Colletotrichum viniferum</i> , the Cause of Grapevine Ripe Rot in China. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 90-93.	1.4	4
22443	Identifying molecular insight of synergistic complexities for SARS-CoV-2 infection with pre-existing type 2 diabetes. <i>Computers in Biology and Medicine</i> , 2021, 136, 104668.	3.9	12
22444	Graph representation learning in bioinformatics: trends, methods and applications. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	64
22445	Synaptic proteins associated with cognitive performance and neuropathology in older humans revealed by multiplexed fractionated proteomics. <i>Neurobiology of Aging</i> , 2021, 105, 99-114.	1.5	32
22446	Integrated analysis of lncRNA and mRNA in liver of <i>Megalobrama amblycephala</i> post <i>Aeromonas hydrophila</i> infection. <i>BMC Genomics</i> , 2021, 22, 653.	1.2	11
22448	Single-cell RNA sequencing reveals adverse effects of paraquat on the fate commitment of murine neural stem cells. <i>Science of the Total Environment</i> , 2021, 785, 147386.	3.9	6
22450	Integrated mRNA and miRNA Expression Analyses of <i>Pinus massoniana</i> Roots and Shoots in Long-Term Response to Phosphate Deficiency. <i>Journal of Plant Growth Regulation</i> , 0, , 1.	2.8	5
22452	Pharmacopuncture of <i>Taraxacum platycarpum</i> extract reduces localized fat by regulating the lipolytic pathway. <i>Biomedicine and Pharmacotherapy</i> , 2021, 141, 111905.	2.5	6
22453	Comparative transcriptomic analysis of <i>Macrobrachium nipponense</i> in response to <i>Aeromonas veronii</i> or <i>Staphylococcus aureus</i> infection. <i>Journal of Oceanology and Limnology</i> , 0, , 1.	0.6	0
22454	Basement membrane proteins in various arterial beds from individuals with and without type 2 diabetes mellitus: a proteome study. <i>Cardiovascular Diabetology</i> , 2021, 20, 182.	2.7	2
22455	Changes in the Gut Microbiome Contribute to the Development of Behçet's Disease via Adjuvant Effects. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 716760.	1.8	9
22456	The role of metadata in reproducible computational research. <i>Patterns</i> , 2021, 2, 100322.	3.1	45
22458	Transcriptomic Analysis of Short/Branched-Chain Acyl-Coenzyme a Dehydrogenase Knocked Out bMECs Revealed Its Regulatory Effect on Lipid Metabolism. <i>Frontiers in Veterinary Science</i> , 2021, 8, 744287.	0.9	7

#	ARTICLE	IF	CITATIONS
22460	Important chromosomal regions for genetic control of powdery mildew resistance under control, drought, and saline conditions in barley (<i>Hordeum vulgare</i> L.). <i>Tropical Plant Pathology</i> , 2021, 46, 622.	0.8	2
22461	Construction of a 5 immune-related lncRNA-based prognostic model of NSCLC via bioinformatics. <i>Medicine (United States)</i> , 2021, 100, e27222.	0.4	3
22462	KinOrtho: a method for mapping human kinase orthologs across the tree of life and illuminating understudied kinases. <i>BMC Bioinformatics</i> , 2021, 22, 446.	1.2	13
22463	A Candidate RNAi Screen Reveals Diverse RNA-Binding Protein Phenotypes in <i>Drosophila</i> Flight Muscle. <i>Cells</i> , 2021, 10, 2505.	1.8	5
22464	Examination of Gene Loss in the DNA Mismatch Repair Pathway and Its Mutational Consequences in a Fungal Phylum. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	10
22466	Deep impact of the inactivation of the SecA2-only protein export pathway on the proteosurfaceome of <i>Listeria monocytogenes</i> . <i>Journal of Proteomics</i> , 2021, 250, 104388.	1.2	3
22467	From many to (n)one: Meditation and the plasticity of the predictive mind. <i>Neuroscience and Biobehavioral Reviews</i> , 2021, 128, 199-217.	2.9	58
22468	Joint nonnegative matrix factorization and network embedding for graph co-clustering. <i>Neurocomputing</i> , 2021, 462, 453-465.	3.5	7
22469	Blood lead levels in Peruvian adults are associated with proximity to mining and DNA methylation. <i>Environment International</i> , 2021, 155, 106587.	4.8	13
22470	Spatiotemporal proteomic profiling of the pro-inflammatory response to lipopolysaccharide in the THP-1 human leukaemia cell line. <i>Nature Communications</i> , 2021, 12, 5773.	5.8	29
22471	Quantitative phosphoproteomics reveals GSK3A substrate network is involved in the cryodamage of sperm motility. <i>Bioscience Reports</i> , 2021, 41, .	1.1	4
22473	Integration of transcription coregulator complexes with sequence-specific DNA-binding factor interactomes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194749.	0.9	6
22474	Modulation of virulence factors of <i>Staphylococcus aureus</i> by nanostructured surfaces. <i>Materials and Design</i> , 2021, 208, 109879.	3.3	8
22475	Complete genome of <i>Pelagovum pacificum</i> SM1903T isolated from the marine surface oligotrophic environment. <i>Marine Genomics</i> , 2021, 59, 100874.	0.4	0
22476	Endogenous S-nitrosocysteine proteomic inventories identify a core of proteins in heart metabolic pathways. <i>Redox Biology</i> , 2021, 47, 102153.	3.9	8
22477	Proteomics changes after negative pressure wound therapy in diabetic foot ulcers. <i>Molecular Medicine Reports</i> , 2021, 24, .	1.1	7
22478	Identification of inflammation related lncRNAs and Gm33647 as a potential regulator in septic acute lung injury. <i>Life Sciences</i> , 2021, 282, 119814.	2.0	3
22479	Valproic Acid Protects Against Acute Kidney Injury in Hemorrhage and Trauma. <i>Journal of Surgical Research</i> , 2021, 266, 222-229.	0.8	8

#	ARTICLE	IF	CITATIONS
22480	The role of alcohol dehydrogenase 1C in regulating inflammatory responses in ulcerative colitis. <i>Biochemical Pharmacology</i> , 2021, 192, 114691.	2.0	8
22481	Quantitative trait mapping in Diversity Outbred mice identifies novel genomic regions associated with the hepatic glutathione redox system. <i>Redox Biology</i> , 2021, 46, 102093.	3.9	5
22482	Distinct gene-set burden patterns underlie common generalized and focal epilepsies. <i>EBioMedicine</i> , 2021, 72, 103588.	2.7	7
22484	Temporal transcriptome profiling reveals candidate genes involved in cold acclimation of <i>Camellia japonica</i> (Naidong). <i>Plant Physiology and Biochemistry</i> , 2021, 167, 795-805.	2.8	8
22485	Transcriptome analysis of postharvest pear (<i>Pyrus pyrifolia</i> Nakai) in response to <i>Penicillium expansum</i> infection. <i>Scientia Horticulturae</i> , 2021, 288, 110361.	1.7	7
22486	Convolutional neural network in proteomics and metabolomics for determination of comorbidity between cancer and schizophrenia. <i>Journal of Biomedical Informatics</i> , 2021, 122, 103890.	2.5	10
22487	Microvesicles transfer mitochondria and increase mitochondrial function in brain endothelial cells. <i>Journal of Controlled Release</i> , 2021, 338, 505-526.	4.8	65
22488	Genetic mapping of renal glutathione suggests a novel regulatory locus on the murine X chromosome and overlap with hepatic glutathione regulation. <i>Free Radical Biology and Medicine</i> , 2021, 174, 28-39.	1.3	1
22489	Evaluation of postmortem microarray data in bipolar disorder using traditional data comparison and artificial intelligence reveals novel gene targets. <i>Journal of Psychiatric Research</i> , 2021, 142, 328-336.	1.5	8
22490	Interpretation of cancer mutations using a multiscale map of protein systems. <i>Science</i> , 2021, 374, eabf3067.	6.0	29
22491	Primordial super-enhancers: heat shock-induced chromatin organization in yeast. <i>Trends in Cell Biology</i> , 2021, 31, 801-813.	3.6	20
22492	Ameliorative effects of miR-423-5p against polarization of microglial cells of the M1 phenotype by targeting a NLRP3 inflammasome signaling pathway. <i>International Immunopharmacology</i> , 2021, 99, 108006.	1.7	15
22493	An integrated transcriptomic and proteomic approach to dynamically study the mechanism of pollen-pistil interactions during jasmine crossing. <i>Journal of Proteomics</i> , 2021, 249, 104380.	1.2	4
22494	Subtype heterogeneity and epigenetic convergence in neuroendocrine prostate cancer. <i>Nature Communications</i> , 2021, 12, 5775.	5.8	59
22495	Mapping the Phospho-dependent ALK Interactome to Identify Novel Components in ALK Signaling. <i>Journal of Molecular Biology</i> , 2021, 433, 167283.	2.0	9
22496	Evaluating adaptive stress response gene signatures using transcriptomics. <i>Computational Toxicology</i> , 2021, 20, 100179.	1.8	5
22497	Transcriptome and anatomical comparisons reveal the specific characteristics and genes involved in distinct types of growing culms. <i>Industrial Crops and Products</i> , 2021, 171, 113865.	2.5	3
22498	Gene Ontology representation for transcription factor functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194752.	0.9	17

#	ARTICLE	IF	CITATIONS
22499	Longitudinal change of genetic variations in cetuximab-treated metastatic colorectal cancer. <i>Cancer Genetics</i> , 2021, 258-259, 27-36.	0.2	2
22500	Protein deep profile and model predictions for identifying the causal genes of male infertility based on deep learning. <i>Information Fusion</i> , 2021, 75, 70-89.	11.7	6
22501	Correlation guided Network Integration (CoNI) reveals novel genes affecting hepatic metabolism. <i>Molecular Metabolism</i> , 2021, 53, 101295.	3.0	4
22502	Anti-oxidant mechanisms of <i>Chlorella pyrenoidosa</i> under acute GenX exposure. <i>Science of the Total Environment</i> , 2021, 797, 149005.	3.9	24
22503	A NAC transcription factor BrNAC087 is involved in gibberellin-delayed leaf senescence in Chinese flowering cabbage. <i>Postharvest Biology and Technology</i> , 2021, 181, 111673.	2.9	14
22504	MiDSytem: A comprehensive online system for de novo assembly and analysis of microbial genomes. <i>New Biotechnology</i> , 2021, 65, 42-52.	2.4	2
22505	Adapting to one- and two-way classified structures of hypotheses while controlling the false discovery rate. <i>Journal of Statistical Planning and Inference</i> , 2021, 215, 95-108.	0.4	4
22506	Integrative analysis reveals clinically relevant molecular fingerprints in pancreatic cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 26, 11-21.	2.3	3
22507	Identification and analysis of novel microRNAs provide insights to reproductive capacity of the cultured Asian yellow pond turtle <i>Mauremys mutica</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 40, 100890.	0.4	1
22508	Transcriptome analysis reveals that high temperatures alter modes of lipid metabolism in juvenile turbot (<i>Scophthalmus maximus</i>) liver. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 40, 100887.	0.4	21
22509	Transcriptome analysis of growth variation in early juvenile stage sandfish <i>Holothuria scabra</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 40, 100904.	0.4	2
22510	Where the genome meets the connectome: Understanding how genes shape human brain connectivity. <i>NeuroImage</i> , 2021, 244, 118570.	2.1	34
22511	Deep_CNN_LSTM_GO: Protein function prediction from amino-acid sequences. <i>Computational Biology and Chemistry</i> , 2021, 95, 107584.	1.1	6
22512	A triple combination strategy of UHPLC-MSn, hypolipidemic activity and transcriptome sequencing to unveil the hypolipidemic mechanism of <i>Nelumbo nucifera</i> alkaloids. <i>Journal of Ethnopharmacology</i> , 2022, 282, 114608.	2.0	7
22513	Prologue to bioinformatics. , 2022, , 1-7.		1
22514	Gene and protein expression profiles of olfactory ensheathing cells from olfactory bulb versus olfactory mucosa. <i>Neural Regeneration Research</i> , 2022, 17, 440.	1.6	7
22515	Estimation of Simultaneous Signals Using Absolute Inner Product with Applications to Integrative Genomics. <i>Statistica Sinica</i> , 2022, , .	0.2	0
22516	Systems biology in diagnosis and treatment of kidney disease. , 2022, , 465-479.		0

#	ARTICLE	IF	CITATIONS
22517	Overexpression of miR-99a in hippocampus leads to impairment of reversal learning in mice. Behavioural Brain Research, 2022, 416, 113542.	1.2	1
22518	Dietary omega-3 fatty acid intake impacts peripheral blood DNA methylation -anti-inflammatory effects and individual variability in a pilot study. Journal of Nutritional Biochemistry, 2022, 99, 108839.	1.9	5
22519	Machine learning-based biomarkers identification from toxicogenomics “ Bridging to regulatory relevant phenotypic endpoints. Journal of Hazardous Materials, 2022, 423, 127141.	6.5	9
22520	OntoRepliCov: an Ontology-Based Approach for Modeling the SARS-CoV-2 Replication Process. Procedia Computer Science, 2021, 192, 487-496.	1.2	4
22521	OUP accepted manuscript. Human Molecular Genetics, 2021, , .	1.4	1
22522	Identification of potential and novel target genes in pituitary prolactinoma by bioinformatics analysis. AIMS Neuroscience, 2021, 8, 254-283.	1.0	7
22524	Proteins as Enzymes. , 2021, , 299-318.		0
22525	The functional analysis of ABCG transporters in the adaptation of pigeon pea (<i>Cajanus cajan</i>) to abiotic stresses. PeerJ, 2021, 9, e10688.	0.9	9
22528	MicroRNA Profiling of HL-1 Cardiac Cells-Derived Extracellular Vesicles. Cells, 2021, 10, 273.	1.8	3
22529	Bioinformatic analysis of potential hub genes in gastric adenocarcinoma. Science Progress, 2021, 104, 003685042110042.	1.0	9
22530	Deciphering the animal genomics using bioinformatics approaches. , 2021, , 281-297.		1
22531	Genome sequencing and functional annotation of Bacillus sp. strain BS-Z15 isolated from cotton rhizosphere soil having antagonistic activity against Verticillium dahliae. Archives of Microbiology, 2021, 203, 1565-1575.	1.0	8
22532	Computational analysis to repurpose drugs for COVID-19 based on transcriptional response of host cells to SARS-CoV-2. BMC Medical Informatics and Decision Making, 2021, 21, 15.	1.5	18
22533	Multimodal Transportation Overview and Optimization Ontology for a Greener Future. Lecture Notes in Networks and Systems, 2021, , 158-172.	0.5	1
22534	IFI27 may predict and evaluate the severity of respiratory syncytial virus infection in preterm infants. Hereditas, 2021, 158, 3.	0.5	13
22535	Context-aware query design combines knowledge and data for efficient reading and reasoning. , 2021, , .		0
22536	Candidate regulators and target genes of drought stress in needles and roots of Norway spruce. Tree Physiology, 2021, 41, 1230-1246.	1.4	20
22537	Clustering of Cancer Attributed Networks by Dynamically and Jointly Factorizing Multi-Layer Graphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2737-2748.	1.9	14

#	ARTICLE	IF	CITATIONS
22538	Integrative analysis of differential circular RNA and long non-coding RNA profiles and associated competing endogenous RNA networks in esophageal squamous cell carcinoma. <i>Functional and Integrative Genomics</i> , 2021, 21, 125-138.	1.4	5
22539	Identification of Seven Cell Cycle-Related Genes with Unfavorable Prognosis and Construction of their TF-miRNA-mRNA regulatory network in Breast Cancer. <i>Journal of Cancer</i> , 2021, 12, 740-753.	1.2	15
22540	<i>Amyntas corticis</i> genome reveals molecular mechanisms behind global distribution. <i>Communications Biology</i> , 2021, 4, 135.	2.0	6
22541	Prediction and analysis of hub genes between glioblastoma and low-grade glioma using bioinformatics analysis. <i>Medicine (United States)</i> , 2021, 100, e23513.	0.4	8
22542	Translational biomarkers in the era of precision medicine. <i>Advances in Clinical Chemistry</i> , 2021, 102, 191-232.	1.8	13
22543	Identifying daily changes in circRNAs and circRNA-associated-ceRNA networks in the rat pineal gland. <i>International Journal of Medical Sciences</i> , 2021, 18, 1225-1239.	1.1	6
22544	SARS-CoV-2 Proteins Exploit Host's Genetic and Epigenetic Mediators for the Annexation of Key Host Signaling Pathways. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 598583.	1.6	29
22545	Functional Signatures in Non-Small-Cell Lung Cancer: A Systematic Review and Meta-Analysis of Sex-Based Differences in Transcriptomic Studies. <i>Cancers</i> , 2021, 13, 143.	1.7	19
22546	Câ€“Xâ€“C motif chemokine ligand 12: a potential therapeutic target in Duchenne muscular dystrophy. <i>Bioengineered</i> , 2021, 12, 5428-5439.	1.4	2
22547	Gene Expression Microarray: Technical Fundamentals and Data Analysis. , 2021, , 291-312.		3
22548	Giant ankyrin-G regulates cardiac function. <i>Journal of Biological Chemistry</i> , 2021, 296, 100507.	1.6	4
22549	An Improved Methodology for Collaborative Construction of Reusable, Localized, and Shareable Ontology. <i>IEEE Access</i> , 2021, 9, 17463-17484.	2.6	7
22550	A Transcriptomic Approach Provides Insights on the Mycorrhizal Symbiosis of the Mediterranean Orchid <i>Limodorum abortivum</i> in Nature. <i>Plants</i> , 2021, 10, 251.	1.6	16
22551	A modular master regulator landscape controls cancer transcriptional identity. <i>Cell</i> , 2021, 184, 334-351.e20.	13.5	78
22552	RNA-Seq transcriptome analysis of ileum in Taiping chicken supplemented with the dietary probiotic. <i>Tropical Animal Health and Production</i> , 2021, 53, 131.	0.5	6
22553	Lignin Synthesis Related Genes with Potential Significance in the Response of Upland Cotton to Fusarium Wilt Identified by Transcriptome Profiling. <i>Tropical Plant Biology</i> , 2021, 14, 106-119.	1.0	5
22554	Insights from the cDNA and EST analysis of <i>Antrodia cinnamomea</i> . <i>Bioinformatics</i> , 2021, 17, 109-118.	0.2	0
22555	Identification and Analysis of <i>Aux/IAA</i> Family in <i>Acer rubrum</i>. <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432199412.	0.6	3

#	ARTICLE	IF	CITATIONS
22556	Expression Profiles Reveal Involvement of VEGF, IGF1, BIRC5, and MMP1 in Vulvar Carcinogenesis. Technology in Cancer Research and Treatment, 2021, 20, 153303382110049.	0.8	1
22557	Structural and Functional Genomic Resources and Database Development. Compendium of Plant Genomes, 2021, , 101-106.	0.3	0
22558	Metabolic Modeling of Fungi. , 2021, , 394-405.		0
22561	Machine Learning Background. , 2021, , 17-53.		0
22562	Label-free proteomic analysis of serum exosomes from paroxysmal atrial fibrillation patients. Clinical Proteomics, 2021, 18, 1.	1.1	17
22563	Genomics-guided isolation and identification of active secondary metabolites of <i>Bacillus velezensis</i> BA-26. Biotechnology and Biotechnological Equipment, 2021, 35, 895-904.	0.5	5
22564	Transcriptional Profiling During Neural Conversion. Methods in Molecular Biology, 2021, 2352, 171-181.	0.4	0
22565	DUSP7 regulates the activity of ERK2 to promote proper chromosome alignment during cell division. Journal of Biological Chemistry, 2021, 296, 100676.	1.6	6
22566	High-Throughput Analysis to Decipher Bacterial Diversity and their Functional Properties in Freshwater Bodies. , 2021, , 511-542.		0
22567	Identifying Protein Complexes From Protein-Protein Interaction Networks Based on Fuzzy Clustering and GO Semantic Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2882-2893.	1.9	18
22568	Evaluation of the potential of Pap test fluid and cervical swabs to serve as clinical diagnostic biospecimens for the detection of ovarian cancer by mass spectrometry-based proteomics. Clinical Proteomics, 2021, 18, 4.	1.1	11
22569	The role of gene to gene interaction in the breast's genomic signature of pregnancy. Scientific Reports, 2021, 11, 2643.	1.6	5
22570	Analysis of Serum miRNAs in Alzheimer's Disease. American Journal of Alzheimer's Disease and Other Dementias, 2021, 36, 153331752110217.	0.9	14
22571	From Whole Liver to Single Cell Transcriptomics in Sex-Dependent Liver Pathologies. , 2021, , 234-243.		0
22572	The Characteristics of Chemosensory and Opsin Genes in Newly Emerged and Sexually Mature Agrilus planipennis, an Important Quarantine Forest Beetle. Frontiers in Genetics, 2020, 11, 604757.	1.1	2
22573	Potential Drug Prediction of Glioblastoma Based on Drug Perturbation-Induced Gene Expression Signatures. BioMed Research International, 2021, 2021, 1-11.	0.9	3
22574	Food pathogens. , 2021, , 295-321.		1
22577	Integrative Analyses of Genes Associated With Osteoporosis in CD16+ Monocyte. Frontiers in Endocrinology, 2020, 11, 581878.	1.5	2

#	ARTICLE	IF	CITATIONS
22578	Analysing the mechanism of mitochondrial oxidation-induced cell death using a multifunctional iridium(III) photosensitiser. <i>Nature Communications</i> , 2021, 12, 26.	5.8	32
22579	How value-sensitive design can empower sustainable consumption. <i>Royal Society Open Science</i> , 2021, 8, 201418.	1.1	8
22580	HIV Protein Tat Induces Macrophage Dysfunction and Atherosclerosis Development in Low-Density Lipoprotein Receptor-Deficient Mice. <i>Cardiovascular Drugs and Therapy</i> , 2022, 36, 201-215.	1.3	7
22581	A Novel 10-Gene Signature Predicts Poor Prognosis in Low Grade Glioma. <i>Technology in Cancer Research and Treatment</i> , 2021, 20, 153303382199208.	0.8	9
22582	Transcriptome based high-throughput SSRs and SNPs discovery in the medicinal plant <i>Lagenaria siceraria</i> . <i>Biocell</i> , 2021, 45, 371-386.	0.4	3
22583	Genome-wide expression profiling of long non-coding RNAs and competing endogenous RNA networks in alopecia areata. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 696-711.	1.0	2
22584	Integrative multiomics analysis of <i>Premolis semirufa</i> caterpillar venom in the search for molecules leading to a joint disease. <i>Scientific Reports</i> , 2021, 11, 1995.	1.6	2
22585	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
22586	Hub biomarkers for the diagnosis and treatment of glioblastoma based on microarray technology. <i>Technology in Cancer Research and Treatment</i> , 2021, 20, 153303382199036.	0.8	3
22588	A genome-wide strategy to identify causes and consequences of retrotransposon expression finds activation by BRCA1 in ovarian cancer. <i>NAR Cancer</i> , 2021, 3, zcaa040.	1.6	2
22589	Evidence for phloem loading via the abaxial bundle sheath cells in maize leaves. <i>Plant Cell</i> , 2021, 33, 531-547.	3.1	85
22590	Tobacco smoking induces metabolic reprogramming of renal cell carcinoma. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	14
22591	The Rcs stress response inversely controls surface and CRISPR-Cas adaptive immunity to discriminate plasmids and phages. <i>Nature Microbiology</i> , 2021, 6, 162-172.	5.9	32
22592	Transcriptome of nasopharyngeal samples from COVID-19 patients and a comparative analysis with other SARS-CoV-2 infection models reveal disparate host responses against SARS-CoV-2. <i>Journal of Translational Medicine</i> , 2021, 19, 32.	1.8	44
22593	Transcriptome Based System Biology Exploration Reveals Homogeneous Tumorigenicity of Alimentary Tract Malignancy. <i>Frontiers in Oncology</i> , 2020, 10, 580276.	1.3	2
22594	Neural Multi-hop Reasoning with Logical Rules on Biomedical Knowledge Graphs. <i>Lecture Notes in Computer Science</i> , 2021, , 375-391.	1.0	17
22595	Homogentisic acid induces cytoskeleton and extracellular matrix alteration in alkaptonuric cartilage. <i>Journal of Cellular Physiology</i> , 2021, 236, 6011-6024.	2.0	3
22596	MiR-508-3p promotes proliferation and inhibits apoptosis of middle ear cholesteatoma cells by targeting PTEN/PI3K/AKT pathway. <i>International Journal of Medical Sciences</i> , 2021, 18, 3224-3235.	1.1	5

#	ARTICLE	IF	CITATIONS
22597	Identification of loci associated with susceptibility to bovine paratuberculosis and with the dysregulation of the MECOM, eEF1A2, and U1 spliceosomal RNA expression. <i>Scientific Reports</i> , 2021, 11, 313.	1.6	10
22598	Screening and identification of potential biomarkers and therapeutic drugs in melanoma via integrated bioinformatics analysis. <i>Investigational New Drugs</i> , 2021, 39, 928-948.	1.2	3
22599	Identification of Protein Subcellular Localization With Network and Functional Embeddings. <i>Frontiers in Genetics</i> , 2020, 11, 626500.	1.1	44
22600	The <i>Cymbidium goeringii</i> genome provides insight into organ development and adaptive evolution in orchids. <i>Ornamental Plant Research</i> , 2021, 1, 1-13.	0.2	7
22601	CyanoOmicsDB: an integrated omics database for functional genomic analysis of cyanobacteria. <i>Nucleic Acids Research</i> , 2022, 50, D758-D764.	6.5	9
22602	CNA2Subpathway: identification of dysregulated subpathway driven by copy number alterations in cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	16
22604	Viral miRNAs confer survival in host cells by targeting apoptosis related host genes. <i>Informatics in Medicine Unlocked</i> , 2021, 22, 100501.	1.9	5
22605	Centromere protein E as a novel biomarker and potential therapeutic target for retinoblastoma. <i>Bioengineered</i> , 2021, 12, 5950-5970.	1.4	10
22606	Identification of biomarkers, pathways and potential therapeutic target for docetaxel resistant prostate cancer. <i>Bioengineered</i> , 2021, 12, 2377-2388.	1.4	6
22607	An integrated approach in gene-expression landscape profiling to identify housekeeping and tissue-specific genes in cattle. <i>Animal Production Science</i> , 2021, , .	0.6	1
22608	TDP-43 aggregation induced by oxidative stress causes global mitochondrial imbalance in ALS. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 132-142.	3.6	92
22609	Diverse Taxonomies for Diverse Chemistries: Enhanced Representation of Natural Product Metabolism in UniProtKB. <i>Metabolites</i> , 2021, 11, 48.	1.3	3
22610	A cortical immune network map identifies distinct microglial transcriptional programs associated with β -amyloid and Tau pathologies. <i>Translational Psychiatry</i> , 2021, 11, 50.	2.4	19
22611	Post-transcriptional circadian regulation in macrophages organizes temporally distinct immunometabolic states. <i>Genome Research</i> , 2021, 31, 171-185.	2.4	55
22613	A roadmap for metagenomic enzyme discovery. <i>Natural Product Reports</i> , 2021, 38, 1994-2023.	5.2	76
22614	Mining plant endogenous target mimics from miRNA-lncRNA interactions based on dual-path parallel ensemble pruning method. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	10
22615	Curation of over 10 ⁶ transcriptomic studies to enable data reuse. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	21
22616	HiDeF: identifying persistent structures in multiscale omics data. <i>Genome Biology</i> , 2021, 22, 21.	3.8	29

#	ARTICLE	IF	CITATIONS
22617	Analyzing differentially expressed Genes and Pathways of Bex2-deficient mouse lung via RNA-seq. Turkish Journal of Biology, 2021, 45, 588-598.	2.1	1
22622	Systems Biology: Principles and Applications in Plant Research. , 0, , 1-40.		6
22626	Hesperidin modulates the rhythmic proteomic profiling in Drosophila melanogaster under oxidative stress. Archives of Insect Biochemistry and Physiology, 2020, 105, e21738.	0.6	2
22630	American lobster postlarvae alter gene regulation in response to ocean warming and acidification. Ecology and Evolution, 2021, 11, 806-819.	0.8	12
22631	Mesenchymal stromal cells reprogram monocytes and macrophages with processing bodies. Stem Cells, 2021, 39, 115-128.	1.4	22
22632	Scale-Free Evolution. , 2006, , 86-105.		2
22633	Literature and Genome Data Mining for Prioritizing Disease-Associated Genes. , 2006, , 74-81.		3
22634	Large Scale Gene Expression Profiles as Tools to Study Skeletal Muscle Adaptation. , 2006, , 29-54.		1
22635	Weighted Pseudo-distances for Categorization in Semantic Hierarchies. Lecture Notes in Computer Science, 2005, , 381-395.	1.0	4
22636	Multinomial Event Model Based Abstraction for Sequence and Text Classification. Lecture Notes in Computer Science, 2005, , 134-148.	1.0	15
22637	Information Integration and Knowledge Acquisition from Semantically Heterogeneous Biological Data Sources. Lecture Notes in Computer Science, 2005, , 175-190.	1.0	16
22638	A Framework for Aligning Ontologies. Lecture Notes in Computer Science, 2005, , 17-31.	1.0	8
22639	Learning Ontology-Aware Classifiers. Lecture Notes in Computer Science, 2005, , 308-321.	1.0	7
22640	The Ontological Lens: Zooming in and out from Genomic to Clinical Level. Lecture Notes in Computer Science, 2005, , 44-50.	1.0	1
22641	A Little Semantic Web Goes a Long Way in Biology. Lecture Notes in Computer Science, 2005, , 786-800.	1.0	28
22642	Supervised Learning in the Gene Ontology Part I: A Rough Set Framework. Lecture Notes in Computer Science, 2005, , 69-97.	1.0	6
22643	Supervised Learning in the Gene Ontology Part II: A Bottom-Up Algorithm. Lecture Notes in Computer Science, 2005, , 98-124.	1.0	7
22644	Faster Pattern Matching Algorithm for Arc-Annotated Sequences. Lecture Notes in Computer Science, 2006, , 25-39.	1.0	2

#	ARTICLE	IF	CITATIONS
22645	Sparse Nonnegative Matrix Factorization Applied to Microarray Data Sets. Lecture Notes in Computer Science, 2006, , 254-261.	1.0	4
22646	Alignment of Biomedical Ontologies Using Life Science Literature. Lecture Notes in Computer Science, 2006, , 1-17.	1.0	17
22647	Iterative Clustering Analysis for Grouping Missing Data in Gene Expression Profiles. Lecture Notes in Computer Science, 2006, , 129-138.	1.0	5
22648	Integrated Protein Interaction Networks for 11 Microbes. Lecture Notes in Computer Science, 2006, , 1-14.	1.0	24
22650	CEL – A Polynomial-Time Reasoner for Life Science Ontologies. Lecture Notes in Computer Science, 2006, , 287-291.	1.0	84
22651	Improving Term Extraction with Terminological Resources. Lecture Notes in Computer Science, 2006, , 380-387.	1.0	59
22652	A Scalable and Distributed NLP Architecture for Web Document Annotation. Lecture Notes in Computer Science, 2006, , 56-67.	1.0	5
22653	Ontological and Practical Issues in Using a Description Logic to Represent Medical Concept Systems: Experience from GALEN. Lecture Notes in Computer Science, 2006, , 197-231.	1.0	46
22654	Type Inference in Systems Biology. Lecture Notes in Computer Science, 2006, , 48-62.	1.0	3
22655	Learning Hierarchical Bayesian Networks for Large-Scale Data Analysis. Lecture Notes in Computer Science, 2006, , 670-679.	1.0	9
22657	A Proposal for a Gene Functions Wiki. Lecture Notes in Computer Science, 2006, , 669-678.	1.0	8
22658	Reactome – A Knowledgebase of Biological Pathways. Lecture Notes in Computer Science, 2006, , 710-719.	1.0	4
22659	The Semantics of Semantic Annotation. Lecture Notes in Computer Science, 2002, , 1152-1167.	1.0	27
22660	OilEd: A Reason-able Ontology Editor for the Semantic Web. Lecture Notes in Computer Science, 2001, , 396-408.	1.0	170
22661	Classification of Gene Expression Data in an Ontology. Lecture Notes in Computer Science, 2001, , 186-194.	1.0	12
22662	Coordinating Intelligent Agents. Lecture Notes in Computer Science, 2002, , 1-18.	1.0	2
22663	Functional Consequences in Metabolic Pathways from Phylogenetic Profiles. Lecture Notes in Computer Science, 2002, , 263-276.	1.0	1
22664	A Rough Set Framework for Learning in a Directed Acyclic Graph. Lecture Notes in Computer Science, 2002, , 144-155.	1.0	12

#	ARTICLE	IF	CITATIONS
22665	DAML+OIL: A Reason-able Web Ontology Language. Lecture Notes in Computer Science, 2002, , 2-13.	1.0	55
22666	Matrix and Tensor Decompositions. , 2010, , 291-318.		1
22667	Machine Learning in Computational Biology. , 2009, , 1663-1667.		4
22668	Knowledge Discovery for Biology with Taverna. , 2007, , 355-395.		12
22669	Biological Ontologies. , 2007, , 85-99.		28
22670	Gossypium Bioinformatics Resources. , 2009, , 227-254.		1
22671	Biomedical Literature Mining. , 2009, , 115-127.		1
22672	Gene Annotation Methods. , 2009, , 121-136.		2
22673	Metabolomic Data Exploration and Analysis with the Human Metabolome Database. Methods in Molecular Biology, 2020, 2104, 165-184.	0.4	6
22674	Using Neural Networks for Relation Extraction from Biomedical Literature. Methods in Molecular Biology, 2021, 2190, 289-305.	0.4	5
22675	RNA Crosslinking to Analyze the Mitochondrial RNA-Binding Proteome. Methods in Molecular Biology, 2021, 2192, 147-158.	0.4	4
22676	Functional Bioinformatics Analyses of the Matrisome and Integrin Adhesome. Methods in Molecular Biology, 2021, 2217, 285-300.	0.4	8
22677	Protein Clustering and Classification. , 2004, , 203-226.		1
22678	Getting familiar with familial colon cancer. , 0, , 27-60.		1
22680	Bioinformatics Approaches to the Structure and Function of Intrinsically Disordered Proteins. , 2009, , 113-140.		1
22681	Function Diversity Within Folds and Superfamilies. , 2009, , 143-166.		3
22682	3D Motifs. , 2009, , 187-216.		3
22684	Geometric Biclustering and Its Applications to Cancer Tissue Classification Based on DNA Microarray Gene Expression Data. , 2009, , 19-53.		2

#	ARTICLE	IF	CITATIONS
22685	Web Resources for Gene List Analysis in Biomedicine. <i>Annals of Information Systems</i> , 2010, , 117-141.	0.5	5
22686	Computational Grammars for Interrogation of Genomes. , 2010, , 263-278.		3
22687	Populus Resources and Bioinformatics. , 2010, , 135-152.		3
22688	The caBIGÂ® Life Sciences Distribution. , 2010, , 253-266.		3
22689	Interpreting and Comparing Clustering Experiments Through Graph Visualization and Ontology Statistical Enrichment with the ClutrFree Package. , 2010, , 315-333.		2
22690	Transcriptional Changes in Alzheimerâ€™s Disease. <i>Systems Biology</i> , 2010, , 611-643.	0.1	1
22691	Visual Presentation as a Welcome Alternative to Textual Presentation of Gene Annotation Information. <i>Advances in Experimental Medicine and Biology</i> , 2010, 680, 709-715.	0.8	5
22692	Finding High-Order Correlations in High-Dimensional Biological Data. , 2010, , 505-534.		6
22693	Discovering Geneâ€™Gene and Geneâ€™Environment Causal Interactions Using Bioinformatics Approaches. , 2010, , 115-138.		2
22694	Star Trek. <i>Advances in Experimental Medicine and Biology</i> , 2010, , 1-24.	0.8	18
22695	A Modular Approach to Scalable Ontology Development. , 2010, , 79-103.		2
22696	Experiment Databases. , 2010, , 335-361.		5
22697	Predicting Gene Function using Predictive Clustering Trees. , 2010, , 365-387.		6
22698	Analyzing Gene Expression Data with Predictive Clustering Trees. , 2010, , 389-406.		2
22699	Biomedical Named Entity Recognition, Whatizit. , 2013, , 132-134.		2
22700	The Potential of Family-Free Genome Comparison. <i>Computational Biology</i> , 2013, , 287-307.	0.1	12
22701	Serial Analysis of Gene Expression. , 2003, , 271-283.		1
22702	Bioinformatics Techniques for Understanding and Analyzing Tree Gene Expression Data. , 2012, , 17-38.		2

#	ARTICLE	IF	CITATIONS
22703	Informative Gene Discovery in DNA Microarray Data Using Statistical Approach. Lecture Notes in Electrical Engineering, 2012, , 377-394.	0.3	3
22704	Getting Past the Language Gap: Innovations in Machine Translation. , 2013, , 103-181.		2
22705	Characterization of Extracellular HSV-1 Virions by Proteomics. Methods in Molecular Biology, 2014, 1144, 181-190.	0.4	13
22706	Systematic Drug Repurposing Through Text Mining. Methods in Molecular Biology, 2014, 1159, 253-267.	0.4	42
22707	Accessing Biomedical Literature in the Current Information Landscape. Methods in Molecular Biology, 2014, 1159, 11-31.	0.4	32
22708	Mapping of Biomedical Text to Concepts of Lexicons, Terminologies, and Ontologies. Methods in Molecular Biology, 2014, 1159, 33-45.	0.4	11
22709	Roles for Text Mining in Protein Function Prediction. Methods in Molecular Biology, 2014, 1159, 95-108.	0.4	15
22710	Functional Molecular Units for Guiding Biomarker Panel Design. Methods in Molecular Biology, 2014, 1159, 109-133.	0.4	15
22711	Posttranscriptional Regulatory Networks: From Expression Profiling to Integrative Analysis of mRNA and MicroRNA Data. Methods in Molecular Biology, 2014, 1160, 165-188.	0.4	8
22712	Comprehensive Meta-analysis of MicroRNA Expression Using a Robust Rank Aggregation Approach. Methods in Molecular Biology, 2014, 1182, 361-373.	0.4	36
22713	Omics Approaches to Macrophage Biology. , 2014, , 587-615.		1
22714	Glycoprotein Enrichment Method Using a Selective Magnetic Nano-Probe Platform (MNP) Functionalized with Lectins. Methods in Molecular Biology, 2015, 1243, 83-100.	0.4	8
22715	Impact of Next-Generation Technologies on Exploring Socioeconomically Important Parasites and Developing New Interventions. Methods in Molecular Biology, 2015, 1247, 437-474.	0.4	9
22716	Computational Prediction of Short Linear Motifs from Protein Sequences. Methods in Molecular Biology, 2015, 1268, 89-141.	0.4	39
22717	In Silico Design of Antimicrobial Peptides. Methods in Molecular Biology, 2015, 1268, 195-219.	0.4	20
22718	Rfam: Annotating Families of Non-Coding RNA Sequences. Methods in Molecular Biology, 2015, 1269, 349-363.	0.4	35
22719	ASPicDB: A Database Web Tool for Alternative Splicing Analysis. Methods in Molecular Biology, 2015, 1269, 365-378.	0.4	5
22720	Gene Essentiality Analysis Based on DEG 10, an Updated Database of Essential Genes. Methods in Molecular Biology, 2015, 1279, 219-233.	0.4	40

#	ARTICLE	IF	CITATIONS
22721	Transcriptome Analysis of Feline Infectious Peritonitis Virus Infection. <i>Methods in Molecular Biology</i> , 2015, 1282, 241-250.	0.4	21
22722	Qualitative and Quantitative Proteomic Analysis of Formalin-Fixed Paraffin-Embedded (FFPE) Tissue. <i>Methods in Molecular Biology</i> , 2015, 1295, 109-115.	0.4	5
22723	Analysis of Proteomic Data for Toxicological Applications. <i>Methods in Pharmacology and Toxicology</i> , 2015, , 257-284.	0.1	1
22724	Systems Analysis for Interpretation of Phosphoproteomics Data. <i>Methods in Molecular Biology</i> , 2016, 1355, 341-360.	0.4	15
22725	How to Use the Candida Genome Database. <i>Methods in Molecular Biology</i> , 2016, 1356, 3-15.	0.4	5
22726	Set-Based Test Procedures for the Functional Analysis of Protein Lists from Differential Analysis. <i>Methods in Molecular Biology</i> , 2016, 1362, 143-156.	0.4	1
22727	From Systems Understanding to Personalized Medicine: Lessons and Recommendations Based on a Multidisciplinary and Translational Analysis of COPD. <i>Methods in Molecular Biology</i> , 2016, 1386, 283-303.	0.4	10
22728	Bioinformatics Methods to Deduce Biological Interpretation from Proteomics Data. <i>Methods in Molecular Biology</i> , 2017, 1549, 147-161.	0.4	2
22729	Functional Interaction Network Construction and Analysis for Disease Discovery. <i>Methods in Molecular Biology</i> , 2017, 1558, 235-253.	0.4	96
22730	Annotation of Alternatively Spliced Proteins and Transcripts with Protein-Folding Algorithms and Isoform-Level Functional Networks. <i>Methods in Molecular Biology</i> , 2017, 1558, 415-436.	0.4	2
22731	CATH-Gene3D: Generation of the Resource and Its Use in Obtaining Structural and Functional Annotations for Protein Sequences. <i>Methods in Molecular Biology</i> , 2017, 1558, 79-110.	0.4	24
22732	Bioinformatics Analysis of Protein Phosphorylation in Plant Systems Biology Using P3DB. <i>Methods in Molecular Biology</i> , 2017, 1558, 127-138.	0.4	12
22733	Databases, Repositories, and Other Data Resources in Structural Biology. <i>Methods in Molecular Biology</i> , 2017, 1607, 643-665.	0.4	6
22734	Data Warehousing with TargetMine for Omics Data Analysis. <i>Methods in Molecular Biology</i> , 2019, 1986, 35-64.	0.4	5
22735	Rat Genome Databases, Repositories, and Tools. <i>Methods in Molecular Biology</i> , 2019, 2018, 71-96.	0.4	14
22736	Bioinformatics Tools and Resources for Cancer Immunotherapy Study. <i>Methods in Molecular Biology</i> , 2020, 2055, 649-678.	0.4	7
22737	Characterization of Extracellular HSV-1 Virions by Proteomics. <i>Methods in Molecular Biology</i> , 2020, 2060, 279-288.	0.4	9
22738	Informed Use of Proteinâ€™Protein Interaction Data: A Focus on the Integrated Interactions Database (IID). <i>Methods in Molecular Biology</i> , 2020, 2074, 125-134.	0.4	12

#	ARTICLE	IF	CITATIONS
22739	Explore Protein-Protein Interactions for Cancer Target Discovery Using the OncoPPi Portal. <i>Methods in Molecular Biology</i> , 2020, 2074, 145-164.	0.4	7
22740	An Introductory Guide to Aligning Networks Using SANA, the Simulated Annealing Network Aligner. <i>Methods in Molecular Biology</i> , 2020, 2074, 263-284.	0.4	3
22741	Effects of Functional Bias on Supervised Learning of a Gene Network Model. <i>Methods in Molecular Biology</i> , 2009, 541, 463-475.	0.4	12
22742	Computational Representation of Biological Systems. <i>Methods in Molecular Biology</i> , 2009, 541, 535-549.	0.4	4
22743	Prediction of Protein-Protein Interactions: A Study of the Co-evolution Model. <i>Methods in Molecular Biology</i> , 2009, 541, 61-88.	0.4	6
22744	Integrated Analysis of Microarray Results. <i>Methods in Molecular Biology</i> , 2007, 382, 429-437.	0.4	1
22745	MitoP2, an Integrated Database for Mitochondrial Proteins. <i>Methods in Molecular Biology</i> , 2007, 372, 573-586.	0.4	11
22746	Interpreting Microarray Results With Gene Ontology and MeSH. <i>Methods in Molecular Biology</i> , 2007, 377, 223-241.	0.4	24
22747	Incorporation of Gene Ontology Annotations to Enhance Microarray Data Analysis. <i>Methods in Molecular Biology</i> , 2007, 377, 243-254.	0.4	17
22748	Protein Subcellular Localization Prediction Using Artificial Intelligence Technology. <i>Methods in Molecular Biology</i> , 2008, 484, 435-463.	0.4	25
22749	Computational Prediction of Subcellular Localization. , 2007, 390, 429-466.		41
22750	Microarray Analysis. <i>Methods in Molecular Biology</i> , 2007, 404, 409-430.	0.4	22
22751	Mining Expressed Sequence Tag (EST) Libraries for Cancer-Associated Genes. <i>Methods in Molecular Biology</i> , 2009, 576, 89-98.	0.4	2
22752	Association Analysis for Large-Scale Gene Set Data. <i>Methods in Molecular Biology</i> , 2007, 408, 19-33.	0.4	9
22753	Neural Networks Predict Protein Structure and Function. <i>Methods in Molecular Biology</i> , 2008, 458, 198-225.	0.4	8
22754	EST Processing: From Trace to Sequence. <i>Methods in Molecular Biology</i> , 2009, 533, 189-220.	0.4	3
22755	Developing an Ontology. <i>Methods in Molecular Biology</i> , 2008, 452, 111-124.	0.4	9
22756	Algorithms and Methods for Correlating Experimental Results with Annotation Databases. <i>Methods in Molecular Biology</i> , 2010, 593, 315-340.	0.4	2

#	ARTICLE	IF	CITATIONS
22757	Bioinformatics/Biostatistics: Microarray Analysis. <i>Methods in Molecular Biology</i> , 2012, 823, 347-358.	0.4	14
22758	Bioinformatic Tools for Identifying Disease Gene and SNP Candidates. <i>Methods in Molecular Biology</i> , 2010, 628, 307-319.	0.4	55
22759	Text Mining. <i>Methods in Molecular Biology</i> , 2008, 453, 471-491.	0.4	5
22760	Isolation Independent Methods of Characterizing Phage Communities 2: Characterizing a Metagenome. <i>Methods in Molecular Biology</i> , 2009, 502, 279-289.	0.4	11
22761	Semantic Data Integration and Knowledge Management to Represent Biological Network Associations. <i>Methods in Molecular Biology</i> , 2009, 563, 241-258.	0.4	29
22762	Human Protein Reference Database and Human Proteinpedia as Discovery Tools for Systems Biology. <i>Methods in Molecular Biology</i> , 2009, 577, 67-79.	0.4	245
22763	Microarray Data Analysis. <i>Methods in Molecular Biology</i> , 2011, 678, 27-43.	0.4	8
22764	Utilizing <i>Saccharomyces Cerevisiae</i> to Identify Aneuploidy and Cancer Susceptibility Genes. <i>Methods in Molecular Biology</i> , 2010, 653, 73-85.	0.4	1
22765	Computational Identification of Plant Transcription Factors and the Construction of the PlantTFDB Database. <i>Methods in Molecular Biology</i> , 2010, 674, 351-368.	0.4	16
22766	Practical Computational Methods for Regulatory Genomics: A cisGRN-Lexicon and cisGRN-Browser for Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2010, 674, 369-399.	0.4	4
22767	Protein-Centric Data Integration for Functional Analysis of Comparative Proteomics Data. <i>Methods in Molecular Biology</i> , 2011, 694, 323-339.	0.4	3
22768	Reactome Knowledgebase of Human Biological Pathways and Processes. <i>Methods in Molecular Biology</i> , 2011, 694, 49-61.	0.4	84
22769	A Tutorial on Protein Ontology Resources for Proteomic Studies. <i>Methods in Molecular Biology</i> , 2011, 694, 77-90.	0.4	4
22770	Text Mining for Systems Modeling. <i>Methods in Molecular Biology</i> , 2011, 696, 305-318.	0.4	5
22771	High-Throughput Analyses and Curation of Protein Interactions in Yeast. <i>Methods in Molecular Biology</i> , 2011, 759, 381-406.	0.4	5
22772	In Silico Protein Motif Discovery and Structural Analysis. <i>Methods in Molecular Biology</i> , 2011, 760, 341-353.	0.4	2
22773	Microarray-Based Genetic Footprinting Strategy to Identify Strain Improvement Genes after Competitive Selection of Transposon Libraries. <i>Methods in Molecular Biology</i> , 2011, 765, 83-97.	0.4	1
22774	Predicting Node Characteristics from Molecular Networks. <i>Methods in Molecular Biology</i> , 2011, 781, 399-414.	0.4	5

#	ARTICLE	IF	CITATIONS
22775	Network Analysis and Protein Function Prediction with the PRODISTIN Web Site. <i>Methods in Molecular Biology</i> , 2012, 804, 313-326.	0.4	2
22776	Directed Module Detection in a Large-Scale Expression Compendium. <i>Methods in Molecular Biology</i> , 2012, 804, 131-165.	0.4	3
22777	Using Phylogenetic Profiles to Predict Functional Relationships. <i>Methods in Molecular Biology</i> , 2012, 804, 167-177.	0.4	48
22778	A Database for Chemical Proteomics: ChEBI. <i>Methods in Molecular Biology</i> , 2012, 803, 273-296.	0.4	26
22779	Integrative Approaches for Microarray Data Analysis. <i>Methods in Molecular Biology</i> , 2012, 802, 157-182.	0.4	4
22780	Biclustering of Time Series Microarray Data. <i>Methods in Molecular Biology</i> , 2012, 802, 87-100.	0.4	2
22781	PhenomiR: MicroRNAs in Human Diseases and Biological Processes. <i>Methods in Molecular Biology</i> , 2012, 822, 249-260.	0.4	57
22782	The Integration and Annotation of the Human Interactome in the UniHI Database. <i>Methods in Molecular Biology</i> , 2012, 812, 175-188.	0.4	2
22783	Evolutionary Trace for Prediction and Redesign of Protein Functional Sites. <i>Methods in Molecular Biology</i> , 2012, 819, 29-42.	0.4	59
22784	Identifying Gene Interaction Networks. <i>Methods in Molecular Biology</i> , 2012, 850, 483-494.	0.4	14
22785	Developing a Practical Toxicogenomics Data Analysis System Utilizing Open-Source Software. <i>Methods in Molecular Biology</i> , 2013, 930, 357-374.	0.4	3
22786	Gene Expression Networks. <i>Methods in Molecular Biology</i> , 2013, 930, 165-178.	0.4	2
22787	Proteomics Data Exchange and Storage: The Need for Common Standards and Public Repositories. <i>Methods in Molecular Biology</i> , 2013, 1007, 317-333.	0.4	11
22788	BioModels Database: A Repository of Mathematical Models of Biological Processes. <i>Methods in Molecular Biology</i> , 2013, 1021, 189-199.	0.4	102
22789	Building Models Using Reactome Pathways as Templates. <i>Methods in Molecular Biology</i> , 2013, 1021, 273-283.	0.4	36
22790	Arabidopsis Database and Stock Resources. <i>Methods in Molecular Biology</i> , 2014, 1062, 65-96.	0.4	10
22791	Computational Analysis of Virus-Host Interactomes. <i>Methods in Molecular Biology</i> , 2013, 1064, 115-130.	0.4	3
22792	Functional Analysis of Legume Genome Arrays. <i>Methods in Molecular Biology</i> , 2013, 1069, 59-66.	0.4	1

#	ARTICLE	IF	CITATIONS
22793	Analysis of Rice Proteins Using SDS-PAGE Shotgun Proteomics. <i>Methods in Molecular Biology</i> , 2014, 1072, 289-302.	0.4	13
22794	Navigating the Global Protein-Protein Interaction Landscape Using iRefWeb. <i>Methods in Molecular Biology</i> , 2014, 1091, 315-331.	0.4	19
22795	Performing Integrative Functional Genomics Analysis in GeneWeaver.org. <i>Methods in Molecular Biology</i> , 2014, 1101, 13-29.	0.4	6
22796	Functional Annotation of Differentially Regulated Gene Set Using WebGestalt: A Gene Set Predictive of Response to Ipilimumab in Tumor Biopsies. <i>Methods in Molecular Biology</i> , 2014, 1101, 31-42.	0.4	17
22797	Pattern Identification in Time-Course Gene Expression Data with the CoGAPS Matrix Factorization. <i>Methods in Molecular Biology</i> , 2014, 1101, 87-112.	0.4	9
22798	Introduction to Bioinformatics. <i>Methods in Molecular Biology</i> , 2014, 1107, 51-71.	0.4	50
22799	Cross-Species Analysis of Protein-protein Interaction Networks. <i>Computational Biology</i> , 2008, , 163-185.	0.1	1
22800	Translational Bioinformatics and Clinical Research Informatics. <i>Computers in Health Care</i> , 2014, , 429-461.	0.2	2
22801	Automatic Ontology Development from Semi-structured Data in Web-Portal: Towards Ontology of Thai Rice Knowledge. <i>Lecture Notes in Computer Science</i> , 2018, , 262-276.	1.0	1
22802	Artificial Intelligence and Bioinformatics. , 2020, , 209-264.		6
22803	Biological Individuality - A Complex Pattern of Distributed Uniqueness. <i>Perspectives in Pragmatics, Philosophy and Psychology</i> , 2020, , 185-197.	0.2	2
22804	Tobacco Resources in the Sol Genomics Network and Nicotiana Metabolic Databases. <i>Compendium of Plant Genomes</i> , 2020, , 59-71.	0.3	3
22805	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
22806	A Large-Scale Assessment of Exact Model Reduction in the BioModels Repository. <i>Lecture Notes in Computer Science</i> , 2019, , 248-265.	1.0	5
22807	Designing and Evaluating Deep Learning Models for Cancer Detection on Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2020, , 249-261.	1.0	3
22808	Impact of the Continuous Evolution of Gene Ontology on Similarity Measures. <i>Lecture Notes in Computer Science</i> , 2019, , 122-129.	1.0	3
22809	Data Journeys Beyond Databases in Systems Biology: Cytoscape and NDEx. , 2020, , 121-143.		3
22810	BiOnt: Deep Learning Using Multiple Biomedical Ontologies for Relation Extraction. <i>Lecture Notes in Computer Science</i> , 2020, , 367-374.	1.0	6

#	ARTICLE	IF	CITATIONS
22811	Hyperbolic Knowledge Graph Embeddings for Knowledge Base Completion. Lecture Notes in Computer Science, 2020, , 199-214.	1.0	21
22812	GA-PPI-Net: A Genetic Algorithm for Community Detection in Protein-Protein Interaction Networks. Communications in Computer and Information Science, 2020, , 133-155.	0.4	2
22813	Global Alignment of PPI Networks. , 2021, , 3-25.		2
22814	Protein-protein interactions: analysis and prediction. , 2008, , 353-410.		1
22815	Evaluation of Machine Learning Algorithms on Protein-Protein Interactions. Advances in Intelligent Systems and Computing, 2014, , 211-218.	0.5	1
22816	Protein Function Prediction Using Adaptive Swarm Based Algorithm. Lecture Notes in Computer Science, 2013, , 55-68.	1.0	1
22817	Cells as Machines: Towards Deciphering Biochemical Programs in the Cell. Lecture Notes in Computer Science, 2014, , 50-67.	1.0	1
22818	Crisp Islands in Vague Seas: Cases of Determinate Parthood Relations in Biological Objects. , 2014, , 163-188.		2
22820	Methods of Gene Ontology Term Similarity Analysis in Graph Database Environment. Communications in Computer and Information Science, 2014, , 345-354.	0.4	1
22822	Network Analysis of Human Disease Comorbidity Patterns Based on Large-Scale Data Mining. Lecture Notes in Computer Science, 2014, , 243-254.	1.0	7
22824	Algorithm for Adapting Cases Represented in a Tractable Description Logic. Lecture Notes in Computer Science, 2014, , 63-78.	1.0	3
22825	Multi-label Classification for Tree and Directed Acyclic Graphs Hierarchies. Lecture Notes in Computer Science, 2014, , 409-425.	1.0	2
22826	Towards Annotating Potential Incoherences in BioPortal Mappings. Lecture Notes in Computer Science, 2014, , 17-32.	1.0	11
22827	Linked Biomedical Dataspace: Lessons Learned Integrating Data for Drug Discovery. Lecture Notes in Computer Science, 2014, , 114-130.	1.0	19
22828	What Is the Transcriptome and How it is Evaluated?. , 2014, , 3-48.		5
22830	Combating Infectious Diseases with Computational Immunology. Lecture Notes in Computer Science, 2015, , 398-407.	1.0	3
22831	Detecting Overlapping Protein Communities in Disease Networks. Lecture Notes in Computer Science, 2015, , 109-120.	1.0	2
22832	Efficient Axiom Pinpointing with EL2MCS. Lecture Notes in Computer Science, 2015, , 225-233.	1.0	9

#	ARTICLE	IF	CITATIONS
22833	Using Semantic Technologies for an Intelligent Medical Trainer. <i>Communications in Computer and Information Science</i> , 2016, , 74-82.	0.4	1
22835	On the Realism of Human and Machine Representational Constraints: A Functionalist Account on Cognitive Ontologies. <i>Studies in Applied Philosophy, Epistemology and Rational Ethics</i> , 2017, , 347-363.	0.2	1
22836	Malignant Pleural Mesothelioma: History, Controversy, and Future of a Man-Made Epidemic. <i>Current Cancer Research</i> , 2017, , 73-101.	0.2	2
22837	Can Existing Biomedical Ontologies Be More Useful for EHR and CDS?. <i>Lecture Notes in Computer Science</i> , 2017, , 3-20.	1.0	1
22838	Exploring Symmetric Substructures in Protein Interaction Networks for Pairwise Alignment. <i>Lecture Notes in Computer Science</i> , 2017, , 173-184.	1.0	3
22839	Gene Function Analysis. <i>Studies in Computational Intelligence</i> , 2017, , 163-193.	0.7	1
22840	Reproducibility of Finding Enriched Gene Sets in Biological Data Analysis. <i>Advances in Intelligent Systems and Computing</i> , 2017, , 146-154.	0.5	3
22841	Improved Knowledge Base Completion by the Path-Augmented TransR Model. <i>Lecture Notes in Computer Science</i> , 2017, , 149-159.	1.0	8
22842	BiOnIC: A Catalog of User Interactions with Biomedical Ontologies. <i>Lecture Notes in Computer Science</i> , 2017, 10588, 130-138.	1.0	3
22843	Computing Authoring Tests from Competency Questions: Experimental Validation. <i>Lecture Notes in Computer Science</i> , 2017, , 243-259.	1.0	7
22844	DeepBrain: Functional Representation of Neural In-Situ Hybridization Images for Gene Ontology Classification Using Deep Convolutional Autoencoders. <i>Lecture Notes in Computer Science</i> , 2017, , 287-296.	1.0	2
22845	Community-Based Semantic Subgroup Discovery. <i>Lecture Notes in Computer Science</i> , 2018, , 182-196.	1.0	7
22846	Enterprise Modelling. , 2003, , 515-541.		9
22847	PROVA: Rule-Based Java-Scripting for a Bioinformatics Semantic Web. <i>Lecture Notes in Computer Science</i> , 2004, , 17-30.	1.0	14
22848	On the Application of Formal Principles to Life Science Data: a Case Study in the Gene Ontology. <i>Lecture Notes in Computer Science</i> , 2004, , 79-94.	1.0	42
22849	Ontologies in Bioinformatics. , 2004, , 635-657.		26
22850	Proper Down-Coloring Simple Acyclic Digraphs. <i>Lecture Notes in Computer Science</i> , 2004, , 299-312.	1.0	1
22851	Poset Ontologies and Concept Lattices as Semantic Hierarchies. <i>Lecture Notes in Computer Science</i> , 2004, , 287-302.	1.0	12

#	ARTICLE	IF	CITATIONS
22852	Semantically Linking and Browsing Provenance Logs for E-science. Lecture Notes in Computer Science, 2004, , 158-176.	1.0	41
22854	Generation and Management of a Medical Ontology in a Semantic Web Retrieval System. Lecture Notes in Computer Science, 2004, , 637-653.	1.0	9
22855	Analyzing LBD Methods using a General Framework. Information Science and Knowledge Management, 2008, , 75-100.	0.1	2
22856	Bgee: Integrating and Comparing Heterogeneous Transcriptome Data Among Species. Lecture Notes in Computer Science, 2008, , 124-131.	1.0	137
22857	Predicting Types of Protein-Protein Interactions Using a Multiple-Instance Learning Model. Lecture Notes in Computer Science, 2007, , 42-53.	1.0	5
22858	XMAS: An Experiential Approach for Visualization, Analysis, and Exploration of Time Series Microarray Data. Communications in Computer and Information Science, 2008, , 16-31.	0.4	2
22859	A Tool for Evaluating Ontology Alignment Strategies. , 2007, , 182-202.		15
22860	Computational Intelligence in Clinical Oncology: Lessons Learned from an Analysis of a Clinical Study. Studies in Computational Intelligence, 2008, , 237-268.	0.7	3
22861	Integrating Local and Personalised Modelling with Global Ontology Knowledge Bases for Biomedical and Bioinformatics Decision Support. Studies in Computational Intelligence, 2008, , 93-116.	0.7	3
22862	Integrative Visual Data Mining of Biomedical Data: Investigating Cases in Chronic Fatigue Syndrome and Acute Lymphoblastic Leukaemia. Lecture Notes in Computer Science, 2008, , 367-388.	1.0	1
22863	Rough Sets in Bioinformatics. , 2007, , 225-243.		10
22864	QNet: A Tool for Querying Protein Interaction Networks. Lecture Notes in Computer Science, 2007, , 1-15.	1.0	28
22865	Network Legos: Building Blocks of Cellular Wiring Diagrams. , 2007, , 47-61.		2
22866	Interactive Visualization of Gene Regulatory Networks with Associated Gene Expression Time Series Data. Mathematics and Visualization, 2008, , 293-311.	0.4	5
22867	Understanding Large Volumes of Interconnected Individuals by Visual Exploration. Lecture Notes in Computer Science, 2007, , 799-808.	1.0	3
22868	Domains Mediate Protein-Protein Interactions and Nucleate Protein Assemblies. Handbook of Experimental Pharmacology, 2008, , 383-405.	0.9	6
22869	BIRD: Biomedical Information Integration and Discovery with Semantic Web Services. Lecture Notes in Computer Science, 2007, , 561-570.	1.0	3
22870	A Context-Specific Network of Protein-DNA and Protein-Protein Interactions Reveals New Regulatory Motifs in Human B Cells. Lecture Notes in Computer Science, 2006, , 42-56.	1.0	7

#	ARTICLE	IF	CITATIONS
22871	Grid and UTOPIA: An Integrated Approach to Enacting and Visualising in Silico Experiments in the Life Sciences. , 2007, , 59-70.		5
22872	Pinpointing in the Description Logic EL^+ . Lecture Notes in Computer Science, 2007, , 52-67.	1.0	58
22873	Integrating Gene Expression Data from Microarrays Using the Self-Organising Map and the Gene Ontology. Lecture Notes in Computer Science, 2007, , 206-217.	1.0	6
22874	Intelligent Approaches to Mining the Primary Research Literature: Techniques, Systems, and Examples. Studies in Computational Intelligence, 2008, , 17-50.	0.7	12
22875	OBO and OWL: Leveraging Semantic Web Technologies for the Life Sciences. Lecture Notes in Computer Science, 2007, , 169-182.	1.0	23
22876	End-to-End Information Management for Systems Biology. , 2007, , 77-91.		4
22877	Ontology Learning for Search Applications. , 2007, , 1050-1062.		18
22878	An Ontology-Based Mining System for Competitive Intelligence in Neuroscience. , 2006, , 291-304.		4
22879	A Framework to Analyze Biclustering Results on Microarray Experiments. , 2007, , 770-779.		3
22880	Methods to Bicluster Validation and Comparison in Microarray Data. , 2007, , 780-789.		19
22881	A Finite Basis for the Set of EL -Implications Holding in a Finite Model. Lecture Notes in Computer Science, 2008, , 46-61.	1.0	14
22882	Automatic Parameter Learning for Multiple Network Alignment. Lecture Notes in Computer Science, 2008, , 214-231.	1.0	58
22883	Bootstrapping the Interactome: Unsupervised Identification of Protein Complexes in Yeast. Lecture Notes in Computer Science, 2008, , 3-16.	1.0	48
22884	Pattern Matching in RNA Structures. , 2008, , 317-330.		6
22885	Integrative Neural Network Approach for Protein Interaction Prediction from Heterogeneous Data. Lecture Notes in Computer Science, 2008, , 532-539.	1.0	3
22886	Ontology Design and Reuse with Conceptual Roles. Lecture Notes in Computer Science, 2008, , 104-118.	1.0	4
22887	On the Concept of Cis-regulatory Information: From Sequence Motifs to Logic Functions. Natural Computing Series, 2009, , 731-742.	2.2	1
22888	Prediction of Protein Functions from Protein Interaction Networks: A Naïve Bayes Approach. Lecture Notes in Computer Science, 2008, , 788-798.	1.0	5

#	ARTICLE	IF	CITATIONS
22889	Exploiting Gene Ontology to Conceptualize Biomedical Document Collections. Lecture Notes in Computer Science, 2008, , 375-389.	1.0	3
22890	Description Logics. , 2009, , 21-43.		28
22891	Fuzzy Clustering and Gene Ontology Based Decision Rules for Identification and Description of Gene Groups. Advances in Intelligent and Soft Computing, 2009, , 141-149.	0.2	2
22892	Optimal Use of Expert Knowledge in Ant Colony Optimization for the Analysis of Epistasis in Human Disease. Lecture Notes in Computer Science, 2009, , 92-103.	1.0	21
22893	Integrating Multiple-Platform Expression Data through Gene Set Features. Lecture Notes in Computer Science, 2009, , 5-17.	1.0	7
22894	Exploring Finite Models in the Description Logic $\mathcal{EL}_{\text{m gfp}}$. Lecture Notes in Computer Science, 2009, , 146-161.	1.0	5
22895	An Overview of Modularity. Lecture Notes in Computer Science, 2009, , 5-23.	1.0	24
22896	Detection of Locally Over-Represented GO Terms in Protein-Protein Interaction Networks. Lecture Notes in Computer Science, 2009, , 302-320.	1.0	3
22897	Topology-Free Querying of Protein Interaction Networks. Lecture Notes in Computer Science, 2009, , 74-89.	1.0	15
22899	Bio-medical Ontologies Maintenance and Change Management. Studies in Computational Intelligence, 2009, , 143-168.	0.7	8
22900	True Path Rule Hierarchical Ensembles. Lecture Notes in Computer Science, 2009, , 232-241.	1.0	28
22901	Axiom Pinpointing in Lightweight Description Logics via Horn-SAT Encoding and Conflict Analysis. Lecture Notes in Computer Science, 2009, , 84-99.	1.0	23
22902	On Quality of Different Annotation Sources for Gene Expression Analysis. Lecture Notes in Computer Science, 2009, , 421-425.	1.0	3
22903	Bayesian Data Integration and Enrichment Analysis for Predicting Gene Function in Malaria. Lecture Notes in Computer Science, 2009, , 457-466.	1.0	1
22904	Prediction of Protein Subcellular Multi-localization by Using a Min-Max Modular Support Vector Machine. Advances in Intelligent and Soft Computing, 2009, , 133-143.	0.2	1
22905	A Prize-Collecting Steiner Tree Approach for Transduction Network Inference. Lecture Notes in Computer Science, 2009, , 83-95.	1.0	5
22906	MACs: Multi-Attribute Co-clusters with High Correlation Information. Lecture Notes in Computer Science, 2009, , 398-413.	1.0	4
22907	Exact Score Distribution Computation for Similarity Searches in Ontologies. Lecture Notes in Computer Science, 2009, , 298-309.	1.0	3

#	ARTICLE	IF	CITATIONS
22908	Aligning Biomolecular Networks Using Modular Graph Kernels. Lecture Notes in Computer Science, 2009, , 345-361.	1.0	18
22909	Information Integration in Bioinformatics with Ontologies and Standards. Lecture Notes in Computer Science, 2009, , 343-376.	1.0	17
22910	A Practical Approach for Scalable Conjunctive Query Answering on Acyclic EL^+ Knowledge Base. Lecture Notes in Computer Science, 2009, , 408-423.	1.0	4
22911	Protein Function Prediction Based on Neighborhood Profiles. , 2010, , 125-134.		1
22912	Semi-bipartite Graph Visualization for Gene Ontology Networks. Lecture Notes in Computer Science, 2010, , 244-255.	1.0	9
22913	An Experimental Comparison of Hierarchical Bayes and True Path Rule Ensembles for Protein Function Prediction. Lecture Notes in Computer Science, 2010, , 294-303.	1.0	5
22914	Dense Subgraphs with Restrictions and Applications to Gene Annotation Graphs. Lecture Notes in Computer Science, 2010, , 456-472.	1.0	64
22915	Hierarchical Generative Biclustering for MicroRNA Expression Analysis. Lecture Notes in Computer Science, 2010, , 65-79.	1.0	6
22916	Integrative Data Mining in Functional Genomics of Brassica napus and Arabidopsis thaliana. Lecture Notes in Computer Science, 2010, , 92-101.	1.0	2
22917	Modeling without Borders: Creating and Annotating VCell Models Using the Web. Lecture Notes in Computer Science, 2010, , 3-17.	1.0	1
22918	Improving Sequence Alignment Based Gene Functional Annotation with Natural Language Processing and Associative Clustering. Lecture Notes in Computer Science, 2010, , 312-321.	1.0	1
22919	PODD: An Ontology-Driven Data Repository for Collaborative Phenomics Research. Lecture Notes in Computer Science, 2010, , 179-188.	1.0	9
22920	Order Metrics for Semantic Knowledge Systems. Lecture Notes in Computer Science, 2010, , 399-409.	1.0	3
22921	Ideal Downward Refinement in the EL Description Logic. Lecture Notes in Computer Science, 2010, , 73-87.	1.0	25
22922	Tractable Extensions of the Description Logic EL with Numerical Datatypes. Lecture Notes in Computer Science, 2010, , 61-75.	1.0	3
22923	Epidemic Marketplace: An Information Management System for Epidemiological Data. Lecture Notes in Computer Science, 2010, , 31-44.	1.0	8
22924	Constructing and Mapping Fuzzy Thematic Clusters to Higher Ranks in a Taxonomy. Lecture Notes in Computer Science, 2010, , 329-340.	1.0	4
22925	Protein Interaction Networks: Protein Domain Interaction and Protein Function Prediction. , 2011, , 427-459.		3

#	ARTICLE	IF	CITATIONS
22926	Building Large Lexicalized Ontologies from Text: A Use Case in Automatic Indexing of Biotechnology Patents. Lecture Notes in Computer Science, 2010, , 514-523.	1.0	7
22927	Enriching the Gene Ontology via the Dissection of Labels Using the Ontology Pre-processor Language. Lecture Notes in Computer Science, 2010, , 59-73.	1.0	14
22928	Multi-view Text Mining for Disease Gene Prioritization and Clustering. Studies in Computational Intelligence, 2011, , 109-144.	0.7	2
22929	Enterprise Knowledge Structures. , 2011, , 29-59.		4
22930	A Practical Approach for Computing Generalization Inferences in \mathcal{EL} . Lecture Notes in Computer Science, 2011, , 410-423.	1.0	8
22931	A Reference Architecture for Building Semantic-Web Mediators. Lecture Notes in Business Information Processing, 2011, , 330-341.	0.8	5
22932	The Relevance of Measurement Data in Environmental Ontology Learning. IFIP Advances in Information and Communication Technology, 2011, , 445-453.	0.5	3
22934	Gene Function Prediction and Functional Network: The Role of Gene Ontology. Intelligent Systems Reference Library, 2012, , 123-162.	1.0	3
22935	Measuring Similarity in Description Logics Using Refinement Operators. Lecture Notes in Computer Science, 2011, , 289-303.	1.0	10
22936	Management of Genotyping-Related Documents by Integrated Use of Semantic Tagging. Lecture Notes in Computer Science, 2011, , 15-39.	1.0	2
22937	COSNet: A Cost Sensitive Neural Network for Semi-supervised Learning in Graphs. Lecture Notes in Computer Science, 2011, , 219-234.	1.0	21
22938	Lagrangian Relaxation Applied to Sparse Global Network Alignment. Lecture Notes in Computer Science, 2011, , 225-236.	1.0	29
22939	Using Semantic Web Technologies to Build a Community-Driven Knowledge Curation Platform for the Skeletal Dysplasia Domain. Lecture Notes in Computer Science, 2011, , 81-96.	1.0	6
22940	Conceptual Modeling of Human Genome: Integration Challenges. Lecture Notes in Computer Science, 2012, , 231-250.	1.0	7
22941	A Functional Model for Dataspace Management Systems. Intelligent Systems Reference Library, 2013, , 305-341.	1.0	4
22943	Complex Detection in Protein-Protein Interaction Networks: A Compact Overview for Researchers and Practitioners. Lecture Notes in Computer Science, 2012, , 211-223.	1.0	15
22944	Function-Function Correlated Multi-Label Protein Function Prediction over Interaction Networks. Lecture Notes in Computer Science, 2012, , 302-313.	1.0	7
22945	Predicting Protein-Protein Interactions from Multimodal Biological Data Sources via Nonnegative Matrix Tri-Factorization. Lecture Notes in Computer Science, 2012, , 314-325.	1.0	5

#	ARTICLE	IF	CITATIONS
22946	Exploiting Label Dependency for Hierarchical Multi-label Classification. Lecture Notes in Computer Science, 2012, , 294-305.	1.0	11
22947	Structural Pattern Discovery in Protein-Protein Interaction Networks. , 2014, , 375-398.		3
22948	A Machine Learning Pipeline for Identification of Discriminant Pathways. , 2014, , 951-968.		1
22949	Genome Structure, Functional Genomics, and Proteomics in Ascidians. , 2012, , 87-132.		2
22950	Towards Open Data for Linguistics: Linguistic Linked Data. Theory and Applications of Natural Language Processing, 2013, , 7-25.	0.3	31
22951	Biomine: A Network-Structured Resource of Biological Entities for Link Prediction. Lecture Notes in Computer Science, 2012, , 364-378.	1.0	5
22952	A Framework for Semantic-Based Similarity Measures for $\{ELH\}$ -Concepts. Lecture Notes in Computer Science, 2012, , 307-319.	1.0	31
22953	Detection of Multi-clustered Genes and Community Structure for the Plant Pathogenic Fungus <i>Fusarium graminearum</i> . Lecture Notes in Computer Science, 2012, , 69-86.	1.0	8
22954	Ontology-Based Genes Similarity Calculation with TF-IDF. Lecture Notes in Computer Science, 2012, , 600-607.	1.0	2
22955	Integration of Biomolecular Interaction Data in a Genomic and Proteomic Data Warehouse to Support Biomedical Knowledge Discovery. Lecture Notes in Computer Science, 2012, , 112-126.	1.0	10
22956	A Machine Learning Pipeline for Discriminant Pathways Identification. Lecture Notes in Computer Science, 2012, , 36-48.	1.0	3
22957	ACO-Based Bayesian Network Ensembles for the Hierarchical Classification of Ageing-Related Proteins. Lecture Notes in Computer Science, 2013, , 80-91.	1.0	4
22958	Temporal Classifiers for Predicting the Expansion of Medical Subject Headings. Lecture Notes in Computer Science, 2013, , 98-113.	1.0	4
22959	Enhancing Search: Events and Their Discourse Context. Lecture Notes in Computer Science, 2013, , 318-334.	1.0	32
22961	Measure the Semantic Similarity of GO Terms Using Aggregate Information Content. Lecture Notes in Computer Science, 2013, , 224-236.	1.0	26
22962	Graph-Based Ontology Classification in OWL 2 QL. Lecture Notes in Computer Science, 2013, , 320-334.	1.0	9
22963	Refinement-Based Similarity Measure over DL Conjunctive Queries. Lecture Notes in Computer Science, 2013, , 270-284.	1.0	8
22964	Introductions to Description Logics - A Guided Tour. Lecture Notes in Computer Science, 2013, , 150-161.	1.0	6

#	ARTICLE	IF	CITATIONS
22965	Path Knowledge Discovery: Multilevel Text Mining as a Methodology for Phenomics. <i>Studies in Big Data</i> , 2014, , 153-192.	0.8	2
22966	Learning Hierarchical Multi-label Classification Trees from Network Data. <i>Lecture Notes in Computer Science</i> , 2013, , 233-248.	1.0	2
22967	Protein Function Prediction Using Dependence Maximization. <i>Lecture Notes in Computer Science</i> , 2013, , 574-589.	1.0	21
22968	Probabilistic Clustering for Hierarchical Multi-Label Classification of Protein Functions. <i>Lecture Notes in Computer Science</i> , 2013, , 385-400.	1.0	9
22969	Information Retrieval in Life Sciences: A Programmatic Survey. , 2014, , 73-109.		6
22970	Simplifying Description Logic Ontologies. <i>Lecture Notes in Computer Science</i> , 2013, , 411-426.	1.0	6
22972	4 Genome Data Drives Change at Culture Collections. , 2014, , 81-96.		8
22973	Genomics for Fungi. , 2001, , 267-297.		15
22974	9 Subcellular Structure and Biochemical Characters in Fungal Phylogeny. , 2015, , 229-258.		5
22975	Crop Genome Annotation: A Case Study for the Brassica rapa Genome. <i>Compendium of Plant Genomes</i> , 2015, , 53-64.	0.3	1
22976	Orthology Relation and Gene Tree Correction: Complexity Results. <i>Lecture Notes in Computer Science</i> , 2015, , 66-79.	1.0	9
22977	Current challenges and approaches for the synergistic use of systems biology data in the scientific community. , 2007, 97, 277-307.		7
22978	Integrated data analysis for genome-wide research. , 2007, 97, 309-329.		24
22979	Indirect Comparison of Interaction Graphs. , 2010, , 249-265.		2
22980	Cryobionomics: Evaluating the Concept in Plant Cryopreservation. , 2015, , 655-682.		12
22981	Application of Bioinformatics in Cancer Research. , 2010, , 211-233.		7
22982	General Formal Ontology (GFO): A Foundational Ontology for Conceptual Modelling. , 2010, , 297-345.		114
22983	Transcriptomics Analysis Methods: Microarray Data Processing, Analysis and Visualization Using the Affymetrix Genechip [®] Vitis Vinifera Genome Array. , 2010, , 317-334.		4

#	ARTICLE	IF	CITATIONS
22984	Predicting Gene Function Using Omics Data: From Data Preparation to Data Integration. , 2011, , 215-242.		3
22985	The Urine Proteome as a Radiation Biodosimeter. <i>Advances in Experimental Medicine and Biology</i> , 2013, 990, 87-100.	0.8	23
22986	Reproducibility of Model-Based Results in Systems Biology. , 2013, , 301-320.		7
22987	A Survey of Current Integrative Network Algorithms for Systems Biology. , 2013, , 479-495.		4
22988	Identifying Biomarkers with Differential Analysis. <i>Translational Bioinformatics</i> , 2013, , 17-31.	0.0	4
22989	Surviving in a sea of data: a survey of plant genome data resources and issues in building data management systems. , 2002, , 59-74.		6
22990	Microarray data quality analysis: lessons from the AFGC project. , 2002, , 119-131.		2
22991	The GENIA Corpus: Annotation Levels and Applications. , 2017, , 1395-1432.		4
22992	3D Motifs. , 2017, , 361-392.		7
22993	Function Diversity Within Folds and Superfamilies. , 2017, , 295-325.		3
22994	A New Subcellular Localization Predictor for Human Proteins Considering the Correlation of Annotation Features and Protein Multi-localization. <i>Communications in Computer and Information Science</i> , 2016, , 499-512.	0.4	1
22995	Advancement in Sustainable Agriculture: Computational and Bioinformatics Tools. , 2019, , 465-547.		4
22996	Systems Biology and Integrated Computational Methods for Cancer-Associated Mutation Analysis. , 2020, , 335-362.		3
22997	Formal Ontological Analysis for Medical Protocols. , 2021, , 83-107.		2
22999	Identification of core biomarkers associated with pathogenesis and prognostic outcomes of laryngeal squamous-cell cancer using bioinformatics analysis. <i>European Archives of Oto-Rhino-Laryngology</i> , 2020, 277, 1397-1408.	0.8	9
23000	TRPM7 Mediates Neuronal Cell Death Upstream of Calcium/Calmodulin-Dependent Protein Kinase II and Calcineurin Mechanism in Neonatal Hypoxic-Ischemic Brain Injury. <i>Translational Stroke Research</i> , 2021, 12, 164-184.	2.3	31
23002	Learning Rule-Based Models - The Rough Set Approach. , 2014, , 19-39.		11
23003	A Practitioner's Guide to Data Management and Data Integration in Bioinformatics. , 2003, , 35-73.		12

#	ARTICLE	IF	CITATIONS
23004	Complex Query Formulation Over Diverse Information Sources in TAMBIS. , 2003, , 189-223.		15
23005	Integration Challenges in Gene Expression Data Management. , 2003, , 277-301.		2
23006	Medulloblastoma Arises from the Persistence of a Rare and Transient Sox2+ Granule Neuron Precursor. Cell Reports, 2020, 31, 107511.	2.9	35
23008	Transcriptomic changes in the nasal epithelium associated with diesel engine exhaust exposure. Environment International, 2020, 137, 105506.	4.8	18
23009	Comparative proteome analysis of matured dry and germinating Moringa oleifera seeds provides insights into protease activity during germination. Food Research International, 2020, 136, 109332.	2.9	10
23010	Proteomic profiling reveals mitochondrial alterations in Rett syndrome. Free Radical Biology and Medicine, 2020, 155, 37-48.	1.3	20
23011	The recognition of development-related genes in the testis and MAGs of time-series Harmonia axyridis adults using a time-series analysis by RNA-seq. Gene, 2019, 693, 52-60.	1.0	4
23012	Enhanced immortalization, HUWE1 mutations and other biological drivers of breast invasive carcinoma in Black/African American patients. Gene, 2020, 763, 100030.	1.0	3
23013	Methods for isolation and transcriptional profiling of individual cells from the human heart. Heliyon, 2020, 6, e05810.	1.4	10
23014	Enzyme-Constrained Models and Omics Analysis of Streptomyces coelicolor Reveal Metabolic Changes that Enhance Heterologous Production. IScience, 2020, 23, 101525.	1.9	30
23015	Absence of NLRP3 Inflammasome in Hematopoietic Cells Reduces Adverse Remodeling After Experimental Myocardial Infarction. JACC Basic To Translational Science, 2020, 5, 1210-1224.	1.9	19
23016	Profiling analysis reveals the potential contribution of long non-coding RNAs to preterm white matter injury. Life Sciences, 2020, 255, 117815.	2.0	5
23017	Identification of gene expression signatures for psoriasis classification using machine learning techniques. Medicine in Omics, 2021, 1, 100001.	0.6	14
23018	Complete genome sequence and bioinformatics analyses of Bacillus thuringiensis strain BM-BT15426. Microbial Pathogenesis, 2017, 108, 55-60.	1.3	23
23019	WheatGmap: a comprehensive platform for wheat gene mapping and genomic studies. Molecular Plant, 2021, 14, 187-190.	3.9	34
23020	ALS and Parkinson's disease genes CHCHD10 and CHCHD2 modify synaptic transcriptomes in human iPSC-derived motor neurons. Neurobiology of Disease, 2020, 141, 104940.	2.1	24
23021	Systems pharmacology unravels the synergic target space and therapeutic potential of Rhodiola rosea L. for non-small cell lung cancer. Phytomedicine, 2020, 79, 153326.	2.3	11
23022	Bioinformatics: harvesting information for plant and crop science. Seminars in Cell and Developmental Biology, 2004, 15, 721-31.	2.3	3

#	ARTICLE	IF	CITATIONS
23023	PlanTEenrichment: A tool for enrichment analysis of transposable elements in plants. <i>Genomics</i> , 2017, 109, 336-340.	1.3	12
23024	Gonadal transcriptomic analysis of the mud crab <i>Scylla olivacea</i> infected with rhizocephalan parasite <i>Sacculina beauforti</i> . <i>Genomics</i> , 2020, 112, 2959-2969.	1.3	13
23026	Generation of an Interactome for the Tetratricopeptide Repeat Domain of O-GlcNAc Transferase Indicates a Role for the Enzyme in Intellectual Disability. <i>Journal of Proteome Research</i> , 2021, 20, 1229-1242.	1.8	23
23027	Ontologies About Human Behavior. <i>European Psychologist</i> , 2017, 22, 180-197.	1.8	11
23028	Genetic variation in the exome: Associations with alcohol and tobacco co-use. <i>Psychology of Addictive Behaviors</i> , 2017, 31, 354-366.	1.4	10
23030	Constraint-Guided Workflow Composition Based on the EDAM Ontology. <i>Nature Precedings</i> , 0, , .	0.1	4
23031	Elevated T cell levels in peripheral blood predict poor clinical response following rituximab treatment in new-onset type 1 diabetes. <i>Genes and Immunity</i> , 2019, 20, 293-307.	2.2	41
23032	Arginine Î€-stacking drives binding to fibrils of the Alzheimer protein Tau. <i>Nature Communications</i> , 2020, 11, 571.	5.8	28
23033	Discrete populations of isotype-switched memory B lymphocytes are maintained in murine spleen and bone marrow. <i>Nature Communications</i> , 2020, 11, 2570.	5.8	54
23034	Clozapine-induced transcriptional changes in the zebrafish brain. <i>NPJ Schizophrenia</i> , 2020, 6, 3.	2.0	14
23035	Decoding myofibroblast origins in human kidney fibrosis. <i>Nature</i> , 2021, 589, 281-286.	13.7	380
23036	Single-cell transcriptomic atlas of the human endometrium during the menstrual cycle. <i>Nature Medicine</i> , 2020, 26, 1644-1653.	15.2	287
23037	An improved high-quality genome assembly and annotation of Tibetan hulless barley. <i>Scientific Data</i> , 2020, 7, 139.	2.4	27
23038	MicroRNA and mRNA interactions coordinate the immune response in non-lethal heat stressed <i>Litopenaeus vannamei</i> against AHPND-causing <i>Vibrio parahaemolyticus</i> . <i>Scientific Reports</i> , 2020, 10, 787.	1.6	19
23039	Biological and physical approaches on the role of piperlongumine (piperlongumine) in cancer. <i>Scientific Reports</i> , 2020, 10, 22283.	1.6	11
23040	Cerina: systematic circRNA functional annotation based on integrative analysis of ceRNA interactions. <i>Scientific Reports</i> , 2020, 10, 22165.	1.6	17
23041	Genome-wide correlation analysis to identify amplitude regulators of circadian transcriptome output. <i>Scientific Reports</i> , 2020, 10, 21839.	1.6	8
23042	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. <i>Scientific Data</i> , 2018, 5, 180185.	2.4	320

#	ARTICLE	IF	CITATIONS
23043	Building an octaploid genome and transcriptome of the medicinal plant <i>Pogostemon cablin</i> from Lamiales. <i>Scientific Data</i> , 2018, 5, 180274.	2.4	17
23044	Chemical diversity and mode of action of natural products targeting lipids in the eukaryotic cell membrane. <i>Natural Product Reports</i> , 2020, 37, 677-702.	5.2	21
23045	AK048794 maintains the mouse embryonic stem cell pluripotency by functioning as an miRNA sponge for miR-592. <i>Biochemical Journal</i> , 2016, 473, 3639-3654.	1.7	10
23046	Transcriptome profiling of digital flexor tendons after injury in a chicken model. <i>Bioscience Reports</i> , 2020, 40, .	1.1	1
23047	RNA-sequencing and bioinformatics analysis of long noncoding RNAs and mRNAs in the asthenozoospermia. <i>Bioscience Reports</i> , 2020, 40, .	1.1	18
23048	Epigenome-450K-wide methylation signatures of active cigarette smoking: The Young Finns Study. <i>Bioscience Reports</i> , 2020, 40, .	1.1	8
23049	Construction of a novel prognostic-predicting model correlated to ovarian cancer. <i>Bioscience Reports</i> , 2020, 40, .	1.1	4
23050	The "dark matter" of ubiquitin-mediated processes: opportunities and challenges in the identification of ubiquitin-binding domains. <i>Biochemical Society Transactions</i> , 2019, 47, 1949-1962.	1.6	15
23051	Understanding microcephaly through the study of centrosome regulation in <i>Drosophila</i> neural stem cells. <i>Biochemical Society Transactions</i> , 2020, 48, 2101-2115.	1.6	11
23053	Assembling Biomedical Big Data. , 2018, , 317-337.		3
23054	The mRNA and lncRNA landscape of the non-pregnant endometrium during the oestrus cycle in dairy goat. <i>Animal Production Science</i> , 2019, 59, 1803.	0.6	5
23055	The predicted subcellular localisation of the sugarcane proteome. <i>Functional Plant Biology</i> , 2009, 36, 242.	1.1	6
23056	Next-generation sequencing analysis reveals segmental patterns of microRNA expression in yak epididymis. <i>Reproduction, Fertility and Development</i> , 2020, 32, 1067.	0.1	9
23058	Standard genetic nomenclature.. , 2015, , 598-608.		1
23059	Molecular analyses of desiccation survival in Antarctic nematodes.. , 2011, , 205-232.		6
23060	CovMulNet19, Integrating Proteins, Diseases, Drugs, and Symptoms: A Network Medicine Approach to COVID-19. <i>Network and Systems Medicine</i> , 2020, 3, 130-141.	2.7	15
23061	Identification of Genes Periodically Expressed in the Human Cell Cycle and Their Expression in Tumors. <i>Molecular Biology of the Cell</i> , 2002, 13, 1977-2000.	0.9	928
23062	Probabilistic Graphical Models for Next-generation Genomics and Genetics. , 2014, , 3-29.		2

#	ARTICLE	IF	CITATIONS
23063	Bayesian Causal Phenotype Network Incorporating Genetic Variation and Biological Knowledge. , 2014, , 165-195.		3
23064	A review on viral data sources and search systems for perspective mitigation of COVID-19. Briefings in Bioinformatics, 2021, 22, 664-675.	3.2	22
23065	The status of causality in biological databases: data resources and data retrieval possibilities to support logical modeling. Briefings in Bioinformatics, 2021, 22, .	3.2	15
23066	A Siamese neural network model for the prioritization of metabolic disorders by integrating real and simulated data. Bioinformatics, 2020, 36, i787-i794.	1.8	4
23067	A Collection of Benchmark Data Sets for Knowledge Graph-based Similarity in the Biomedical Domain. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	9
23068	A hybrid approach toward biomedical relation extraction training corpora: combining distant supervision with crowdsourcing. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	5
23069	Large-scale inference of gene function through phylogenetic annotation of Gene Ontology terms: case study of the apoptosis and autophagy cellular processes. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw155.	1.4	12
23070	A High-Density Genetic Recombination Map of Sequence-Tagged Sites for <i>Sorghum</i> , as a Framework for Comparative Structural and Evolutionary Genomics of Tropical Grains and Grasses. Genetics, 2003, 165, 367-386.	1.2	185
23071	A network-based comparative framework to study conservation and divergence of proteomes in plant phylogenies. Nucleic Acids Research, 2021, 49, e3-e3.	6.5	5
23072	PANTHER version 16: a revised family classification, tree-based classification tool, enhancer regions and extensive API. Nucleic Acids Research, 2021, 49, D394-D403.	6.5	990
23073	Integration of single-cell datasets reveals novel transcriptomic signatures of β 2-cells in human type 2 diabetes. NAR Genomics and Bioinformatics, 2020, 2, lqaa097.	1.5	15
23074	Introduction to radiomics and radiogenomics in neuro-oncology: implications and challenges. Neuro-Oncology Advances, 2020, 2, iv3-iv14.	0.4	20
23075	Anno genominis XX: 20 years of Arabidopsis genomics. Plant Cell, 2021, 33, 832-845.	3.1	11
23076	Screening and identification of key biomarkers for retinoblastoma. Medicine (United States), 2020, 99, e19952.	0.4	3
23077	Modulation of Brain Transcriptome by Combined Histone Deacetylase Inhibition and Plasma Treatment Following Traumatic Brain Injury and Hemorrhagic Shock. Shock, 2021, 55, 110-120.	1.0	8
23078	Fatty acid bioconversion in harpacticoid copepods in a changing environment: a transcriptomic approach. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190645.	1.8	26
23079	Halobasidium xiangyangense gen. nov., sp. nov., a new xylose-utilizing yeast in the family Cystobasidiaceae, isolated from the pickling sauce used to make Datoucai, a high-salt fermented food. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 139-145.	0.8	5
23080	Capsulimonas corticalis gen. nov., sp. nov., an aerobic capsulated bacterium, of a novel bacterial order, Capsulimonadales ord. nov., of the class Armatimonadia of the phylum Armatimonadetes. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 220-226.	0.8	22

#	ARTICLE	IF	CITATIONS
23081	<i>Vibrio zhugei</i> sp. nov., a moderately halophilic bacterium isolated from pickling sauce. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1313-1319.	0.8	11
23082	<i>Gulosibacter macacae</i> sp. nov., a novel actinobacterium isolated from <i>Macaca mulatta</i> faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5115-5122.	0.8	12
23083	Imbalance between innate antiviral and pro-inflammatory immune responses may contribute to different outcomes involving low- and highly pathogenic avian influenza H5N3 infections in chickens. <i>Journal of General Virology</i> , 2017, 98, 1245-1258.	1.3	6
23084	Identification of a newly described OsHV-1 μ var from the North Adriatic Sea (Italy). <i>Journal of General Virology</i> , 2018, 99, 693-703.	1.3	41
23085	SynerClust: a highly scalable, synteny-aware orthologue clustering tool. <i>Microbial Genomics</i> , 2018, 4, .	1.0	18
23086	An in silico survey of <i>Clostridioides difficile</i> extrachromosomal elements. <i>Microbial Genomics</i> , 2019, 5, .	1.0	6
23087	Whole-genome analyses reveal gene content differences between nontypeable <i>Haemophilus influenzae</i> isolates from chronic obstructive pulmonary disease compared to other clinical phenotypes. <i>Microbial Genomics</i> , 2020, 6, .	1.0	10
23523	Prediction, Annotation, and Analysis of Human Promoters. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003, 68, 217-226.	2.0	7
23524	The Genome Knowledgebase: A Resource for Biologists and Bioinformaticists. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003, 68, 237-244.	2.0	45
23525	Genomic Perspective and Cancer. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2003, 68, 417-424.	2.0	2
23526	Sharing Big Data. <i>IUCr</i> , 2017, 4, 3-4.	1.0	2
23527	Tensor-based document retrieval over Neo4j with an application to PubMed mining. , 2016, , .		10
23528	A Feature Weighting-Assisted Approach for Cancer Subtypes Identification From Paired Expression Profiles. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 1403-1414.	1.9	1
23529	A chromosome-scale genome assembly of <i>Antheraea pernyi</i> (Saturniidae, Lepidoptera). <i>Molecular Ecology Resources</i> , 2020, 20, 1372-1383.	2.2	20
23530	Regulation of gene expression by MF63, a selective inhibitor of microsomal PGE synthase 1 (mPGES1) in human osteoarthritic chondrocytes. <i>British Journal of Pharmacology</i> , 2020, 177, 4134-4146.	2.7	6
23531	Disease swamps molecular signatures of genetic-environmental associations to abiotic factors in Tasmanian devil (<i>Sarcophilus harrisii</i>) populations. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 1392-1408.	1.1	18
23532	Hepatopancreatic multi-transcript expression patterns in the crayfish <i>Cherax quadricarinatus</i> during the moult cycle. <i>Insect Molecular Biology</i> , 2007, .	1.0	1
23533	A large-scale gene discovery for the red palm weevil <i>Rhynchophorus ferrugineus</i> (Coleoptera:) Tj ETQq1 1 0.784314 ggBT /Over 1.5 29	1.5	29

#	ARTICLE	IF	CITATIONS
23534	Pitfalls of ascertainment biases in genome annotationsâ€”computing comparable protein domain distributions in eukarya. Malaysian Journal of Fundamental and Applied Sciences, 2014, 10, .	0.4	3
23535	Navigation Over a Large Ontology for Industrial Web Applications. , 2009, , .		6
23536	VNB-mediated endosomal escape triggers robust gene silencing in human cell lines. , 2020, , .		1
23537	Functional Annotation of Mouse Genome Sequences. Science, 2001, 291, 1251-1255.	6.0	125
23538	Lignocellulosic Biomass Conversion to Ethanol by <i>Saccharomyces</i> , 0, , 17-36.		23
23539	Complete Genome Sequence of Bacteriocin-Producing <i>Enterococcus faecium</i> HY07. Microbiology Resource Announcements, 2019, 8, .	0.3	3
23540	Genome Sequence of <i>Lactobacillus futsaii</i> Y97, a Potential Probiotic Strain Isolated from Futsai of Taiwan. Microbiology Resource Announcements, 2019, 8, .	0.3	2
23541	Characterizing Uncertain Data using Compression. , 2011, , .		8
23542	Extending Consensus Clustering to Explore Multiple Clustering Views. , 2011, , .		5
23543	Query-based Biclustering using Formal Concept Analysis. , 2012, , .		7
23544	ESTIMATING SUPPORT FOR PROTEIN-PROTEIN INTERACTION DATA WITH APPLICATIONS TO FUNCTION PREDICTION. , 2008, , .		15
23545	ONBIRES: Ontology-Based Biological Relation Extraction System. , 2005, , .		5
23546	BAYESIAN DATA INTEGRATION: A FUNCTIONAL PERSPECTIVE. , 2006, , .		12
23547	A SYSTEMS BIOLOGY CASE STUDY OF OVARIAN CANCER DRUG RESISTANCE. , 2006, , .		13
23548	A NEW STRATEGY OF GEOMETRICAL BICLUSTERING FOR MICROARRAY DATA ANALYSIS. , 2007, , .		9
23549	MINING MOLECULAR CONTEXTS OF CANCER VIA IN-SILICO CONDITIONING. , 2007, , .		7
23550	GOTREES: PREDICTING GO ASSOCIATIONS FROM PROTEIN DOMAIN COMPOSITION USING DECISION TREES. , 2004, , .		15
23551	GO MOLECULAR FUNCTION TERMS ARE PREDICTIVE OF SUBCELLULAR LOCALIZATION. , 2004, , 151-61.		22

#	ARTICLE	IF	CITATIONS
23552	UNDERSTANDING THE GLOBAL PROPERTIES OF FUNCTIONALLY-RELATED GENE NETWORKS USING THE GENE ONTOLOGY. , 2004, , 209-20.		10
23553	AN EVIDENCE ONTOLOGY FOR USE IN PATHWAY/GENOME DATABASES. , 2003, , 190-201.		26
23554	THE COMPOSITIONAL STRUCTURE OF GENE ONTOLOGY TERMS. , 2003, , 214-25.		45
23555	Evolution and Classification of the Serpin Superfamily. , 2007, , 1-33.		4
23556	A FAULT MODEL FOR ONTOLOGY MAPPING, ALIGNMENT, AND LINKING SYSTEMS. , 2006, , .		8
23557	EXTRACTING GENE EXPRESSION PROFILES COMMON TO COLON AND PANCREATIC ADENOCARCINOMA USING SIMULTANEOUS NONNEGATIVE MATRIX FACTORIZATION. , 2007, , .		24
23558	EVALUATION OF ONTOLOGY MERGING TOOLS IN BIOINFORMATICS. , 2002, , 589-600.		24
23559	A METHODOLOGY TO MIGRATE THE GENE ONTOLOGY TO A DESCRIPTION LOGIC ENVIRONMENT USING DAML+OIL. , 2002, , 624-35.		69
23560	ONTOLOGY DEVELOPMENT FOR A PHARMACOGENETICS KNOWLEDGE BASE. , 2001, , .		11
23561	Emergence of pathway-level composite biomarkers from converging gene set signals of heterogeneous transcriptomic responses. , 2018, , .		10
23562	TOWARDS INTEGRATIVE GENE PRIORITIZATION IN ALZHEIMER'S DISEASE. , 2010, , 4-13.		3
23563	MINING FUNCTIONALLY RELEVANT GENE SETS FOR ANALYZING PHYSIOLOGICALLY NOVEL CLINICAL EXPRESSION DATA. , 2010, , 50-61.		3
23565	Rule responder HCLS eScience infrastructure. , 2008, , .		6
23566	Multi-way set enumeration in real-valued tensors. , 2009, , .		2
23567	A semantic annotation framework for retrieving and analyzing observational datasets. , 2010, , .		3
23568	Flexible and Robust Multi-Network Clustering. , 2015, , .		39
23570	Constructing Reliable Protein-Protein Interaction (PPI) Networks. , 2017, , 15.		4
23571	Gene Set Databases. , 2019, , .		4

#	ARTICLE	IF	CITATIONS
23572	Metabolic Pathway Membership Inference using an Ontology-based Similarity Approach. , 2019, , .		3
23573	Modeling with Node Popularities for Autonomous Overlapping Community Detection. ACM Transactions on Intelligent Systems and Technology, 2020, 11, 1-23.	2.9	9
23574	Developmental Mechanisms of Fleshy Fruit Diversity in Rosaceae. Annual Review of Plant Biology, 2020, 71, 547-573.	8.6	38
23575	Temporal patterns of gene expression in murine cutaneous burn wound healing. Physiological Genomics, 2004, 16, 341-348.	1.0	36
23577	MaizeGDB: The Maize Model Organism Database for Basic, Translational, and Applied Research. International Journal of Plant Genomics, 2008, 2008, 1-10.	2.2	95
23578	Elucidating the Mechanisms of Hagan Buzure Granule in the Treatment of Liver Fibrosis via Network Pharmacology. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-11.	0.5	28
23579	Monosomy X in Female Mice Influences the Regional Formation and Augments the Severity of Angiotensin II-Induced Aortopathies. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 269-283.	1.1	6
23580	Linking Lysosomal Enzyme Targeting Genes and Energy Metabolism with Altered Gray Matter Volume in Children with Persistent Stuttering. Neurobiology of Language (Cambridge, Mass), 2020, 1, 365-380.	1.7	20
23581	Concept Grounding to Multiple Knowledge Bases via Indirect Supervision. Transactions of the Association for Computational Linguistics, 2016, 4, 141-154.	3.2	7
23582	Vitreous Modulation of Gene Expression in Low-Passage Human Retinal Pigment Epithelial Cells. , 2007, 48, 1853.		15
23583	Acute Stress Responses Are Early Molecular Events of Retinal Degeneration in Abca4 ^{−/−} Rdh8 ^{−/−} Mice After Light Exposure. , 2016, 57, 3257.		26
23584	Transcriptome network analysis identifies protective role of the LXR/SREBP-1c axis in murine pulmonary fibrosis. JCI Insight, 2019, 4, .	2.3	33
23585	Transcriptional analysis of Foxp3+ Tregs and functions of two identified molecules during resolution of ALI. JCI Insight, 2019, 4, .	2.3	26
23586	Epigenetic loss of the endoplasmic reticulum-associated degradation inhibitor SVIP induces cancer cell metabolic reprogramming. JCI Insight, 2019, 4, .	2.3	14
23587	Proteasome inhibition preserves longitudinal growth of denervated muscle and prevents neonatal neuromuscular contractures. JCI Insight, 2019, 4, .	2.3	23
23588	Cell-specific ablation of Hsp47 defines the collagen-producing cells in the injured heart. JCI Insight, 2019, 4, e128722.	2.3	62
23589	Pulsed glucocorticoids enhance dystrophic muscle performance through epigenetic-metabolic reprogramming. JCI Insight, 2019, 4, .	2.3	32
23590	Humoral immune responses mediate the development of a restrictive phenotype of chronic lung allograft dysfunction. JCI Insight, 2020, 5, .	2.3	17

#	ARTICLE	IF	CITATIONS
23591	Integrated urine proteomics and renal single-cell genomics identify an IFN- λ 3 response gradient in lupus nephritis. <i>JCI Insight</i> , 2020, 5, .	2.3	57
23592	Transcriptional dissection of melanoma identifies a high-risk subtype underlying TP53 family genes and epigenome deregulation. <i>JCI Insight</i> , 2017, 2, .	2.3	48
23593	A peripheral blood transcriptomic signature predicts autoantibody development in infants at risk of type 1 diabetes. <i>JCI Insight</i> , 2018, 3, .	2.3	18
23594	BubR1 allelic effects drive phenotypic heterogeneity in mosaic-variegated aneuploidy progeria syndrome. <i>Journal of Clinical Investigation</i> , 2019, 130, 171-188.	3.9	8
23595	Concordant morphologic and gene expression data show that a vaccine halts HER-2/neu preneoplastic lesions. <i>Journal of Clinical Investigation</i> , 2004, 113, 709-717.	3.9	64
23596	Identification and validation of genes affecting aortic lesions in mice. <i>Journal of Clinical Investigation</i> , 2010, 120, 2414-2422.	3.9	49
23597	Intra-graft expression of genes involved in iron homeostasis predicts the development of operational tolerance in human liver transplantation. <i>Journal of Clinical Investigation</i> , 2012, 122, 368-382.	3.9	183
23598	Fibrotic extracellular matrix activates a profibrotic positive feedback loop. <i>Journal of Clinical Investigation</i> , 2014, 124, 1622-1635.	3.9	444
23599	Probing chromatin landscape reveals roles of endocardial TBX20 in septation. <i>Journal of Clinical Investigation</i> , 2016, 126, 3023-3035.	3.9	30
23600	Early pregnancy vitamin D status and risk of preeclampsia. <i>Journal of Clinical Investigation</i> , 2016, 126, 4702-4715.	3.9	160
23601	Ribonuclease inhibitor 1 regulates erythropoiesis by controlling GATA1 translation. <i>Journal of Clinical Investigation</i> , 2018, 128, 1597-1614.	3.9	20
23602	Insulin resistance causes inflammation in adipose tissue. <i>Journal of Clinical Investigation</i> , 2018, 128, 1538-1550.	3.9	303
23603	Expression and Possible Molecular Mechanisms of microRNA-205-5p in Patients With Head and Neck Squamous Cell Carcinoma. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303382098011.	0.8	5
23604	Epigenomic Evolution In Diffuse Large B-Cell Lymphomas. <i>Blood</i> , 2013, 122, 634-634.	0.6	2
23606	Proteome-Wide Analyses Reveal the Diverse Functions of Lysine 2-Hydroxyisobutyrylation in <i>Oryza sativa</i> . <i>Rice</i> , 2020, 13, 34.	1.7	17
23607	ARPIR: automatic RNA-Seq pipelines with interactive report. <i>BMC Bioinformatics</i> , 2020, 21, 574.	1.2	13
23608	A comparison of curated gene sets versus transcriptomics-derived gene signatures for detecting pathway activation in immune cells. <i>BMC Bioinformatics</i> , 2020, 21, 28.	1.2	4
23610	Effect of aging on the transcriptomic changes associated with the expression of the HERV-K (HML-2) provirus at 1q22. <i>Immunity and Ageing</i> , 2020, 17, 11.	1.8	11

#	ARTICLE	IF	CITATIONS
23611	Proteomic characterization of HaCaT keratinocytes provides new insights into changes associated with SDS exposure. <i>Biomedical Dermatology</i> , 2020, 4, .	7.6	8
23612	Eliciting expertise. , 2005, , 185-218.		17
23614	Advanced Bioinformatics Tools and Strategies. , 2010, , 447-493.		2
23615	Computational Phenotype Analysis in Human Medicine. , 2014, , 8-23.		3
23616	Systems Biology Application to Decipher Mechanisms and Novel Biomarkers in CNS Trauma. , 2015, , 448-461.		12
23617	A statistical framework for testing functional categories in microarray data. <i>Annals of Applied Statistics</i> , 2008, 2, .	0.5	56
23618	Estimating the proportion of differentially expressed genes in comparative DNA microarray experiments. , 2007, , 92-102.		1
23619	Adaptive estimation in structured factor models with applications to overlapping clustering. <i>Annals of Statistics</i> , 2020, 48, .	1.4	8
23620	Simultaneous high-probability bounds on the false discovery proportion in structured, regression and online settings. <i>Annals of Statistics</i> , 2020, 48, .	1.4	21
23621	Adaptive p -value weighting with power optimality. <i>Electronic Journal of Statistics</i> , 2019, 13, .	0.4	10
23622	A primer for generating and using transcriptome data and gene sets. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	6
23623	Potential Role of lncRNAs in Contributing to Pathogenesis of Intervertebral Disc Degeneration Based on Microarray Data. <i>Medical Science Monitor</i> , 2015, 21, 3449-3458.	0.5	43
23624	Personalized Identification of Differentially Expressed Modules in Osteosarcoma. <i>Medical Science Monitor</i> , 2017, 23, 774-779.	0.5	4
23625	RNA-Sequence Analysis Reveals Differentially Expressed Genes (DEGs) in Patients Exhibiting Different Risks of Tumor Metastasis. <i>Medical Science Monitor</i> , 2017, 23, 2842-2849.	0.5	6
23626	Identification of Biological Targets of Therapeutic Intervention for Hepatocellular Carcinoma by Integrated Bioinformatical Analysis. <i>Medical Science Monitor</i> , 2018, 24, 3450-3461.	0.5	10
23627	Both Peripheral Blood and Urinary miR-195-5p, miR-192-3p, miR-328-5p and Their Target Genes PPM1A, RAB1A and BRSK1 May Be Potential Biomarkers for Membranous Nephropathy. <i>Medical Science Monitor</i> , 2019, 25, 1903-1916.	0.5	16
23628	Use of Genome-Scale Integrated Analysis to Identify Key Genes and Potential Molecular Mechanisms in Recurrence of Lower-Grade Brain Glioma. <i>Medical Science Monitor</i> , 2019, 25, 3716-3727.	0.5	15
23629	Network Pharmacology Identifies the Mechanisms of Action of Shaoyao Gancao Decoction in the Treatment of Osteoarthritis. <i>Medical Science Monitor</i> , 2019, 25, 6051-6073.	0.5	40

#	ARTICLE	IF	CITATIONS
23630	Identification of Hub Genes and Pathways in Gastric Adenocarcinoma Based on Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2020, 26, e920261.	0.5	18
23631	SPP1 and FN1 associated with progression and prognosis of esophageal cancer identified by integrated expression profiles analysis. <i>Medical Science Monitor</i> , 2020, 26, e920355.	0.5	15
23632	POLE2 Serves as a Prognostic Biomarker and Is Associated with Immune Infiltration in Squamous Cell Lung Cancer. <i>Medical Science Monitor</i> , 2020, 26, e921430.	0.5	11
23633	Bioinformatics Analysis Identifies the Estrogen Receptor 1 (ESR1) Gene and hsa-miR-26a-5p as Potential Prognostic Biomarkers in Patients with Intrahepatic Cholangiocarcinoma. <i>Medical Science Monitor</i> , 2020, 26, e921815.	0.5	6
23634	Bioinformatics Analysis and High-Throughput Sequencing to Identify Differentially Expressed Genes in Nebulin Gene (NEB) Mutations Mice. <i>Medical Science Monitor</i> , 2020, 26, e922953.	0.5	2
23635	Screening and Identification of Potential Peripheral Blood Biomarkers for Alzheimer's Disease Based on Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2020, 26, e924263.	0.5	12
23636	A Systematic Pharmacology and In Vitro Study to Identify the Role of the Active Compounds of <i>Achyranthes bidentata</i> in the Treatment of Osteoarthritis. <i>Medical Science Monitor</i> , 2020, 26, e925545.	0.5	4
23637	Network Pharmacology to Uncover the Molecular Mechanisms of Action of LeiGongTeng for the Treatment of Nasopharyngeal Carcinoma. <i>Medical Science Monitor Basic Research</i> , 2020, 26, e923431.	2.6	9
23638	Progress and challenges in the computational prediction of gene function using networks. <i>F1000Research</i> , 2012, 1, 14.	0.8	19
23639	A Bioconductor workflow for processing and analysing spatial proteomics data. <i>F1000Research</i> , 2016, 5, 2926.	0.8	34
23640	A Bioconductor workflow for processing and analysing spatial proteomics data. <i>F1000Research</i> , 2016, 5, 2926.	0.8	26
23641	ELIXIR pilot action: Marine metagenomics – towards a domain specific set of sustainable services. <i>F1000Research</i> , 2017, 6, 70.	0.8	8
23642	Protein sites with more coevolutionary connections tend to evolve slower, while more variable protein families acquire higher coevolutionary connections. <i>F1000Research</i> , 2017, 6, 453.	0.8	3
23643	Protein sites with more coevolutionary connections tend to evolve slower, while more variable protein families acquire higher coevolutionary connections. <i>F1000Research</i> , 2017, 6, 453.	0.8	5
23644	Semantics for interoperability of distributed data and models: Foundations for better-connected information. <i>F1000Research</i> , 0, 6, 686.	0.8	19
23645	Using regulatory genomics data to interpret the function of disease variants and prioritise genes from expression studies. <i>F1000Research</i> , 2018, 7, 121.	0.8	4
23646	eXamine: Visualizing annotated networks in Cytoscape. <i>F1000Research</i> , 2018, 7, 519.	0.8	3
23647	autoHGPEC: Automated prediction of novel disease-gene and disease-disease associations and evidence collection based on a random walk on heterogeneous network. <i>F1000Research</i> , 0, 7, 658.	0.8	3

#	ARTICLE	IF	CITATIONS
23648	To select relevant features for longitudinal gene expression data by extending a pathway analysis method. F1000Research, 2018, 7, 1166.	0.8	3
23649	Large-scale protein function prediction using heterogeneous ensembles. F1000Research, 2018, 7, 1577.	0.8	12
23650	Expanding the Orthologous Matrix (OMA) programmatic interfaces: REST API and the OmaDB packages for R and Python. F1000Research, 2019, 8, 42.	0.8	11
23651	Detection and analysis of RNA methylation. F1000Research, 2019, 8, 559.	0.8	36
23652	Introducing high school students to the Gene Ontology classification system. F1000Research, 0, 8, 241.	0.8	1
23653	Introducing high school students to the Gene Ontology classification system. F1000Research, 0, 8, 241.	0.8	4
23654	BioHackathon 2015: Semantics of data for life sciences and reproducible research. F1000Research, 2020, 9, 136.	0.8	5
23655	A step-by-step guide to analyzing CAGE data using R/Bioconductor. F1000Research, 2019, 8, 886.	0.8	23
23656	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. F1000Research, 2019, 8, 296.	0.8	49
23657	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. F1000Research, 0, 8, 296.	0.8	2
23658	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. F1000Research, 2019, 8, 296.	0.8	45
23659	From zebrafish heart jogging genes to mouse and human orthologs: using Gene Ontology to investigate mammalian heart development.. F1000Research, 2013, 2, 242.	0.8	7
23660	From zebrafish heart jogging genes to mouse and human orthologs: using Gene Ontology to investigate mammalian heart development.. F1000Research, 2013, 2, 242.	0.8	6
23661	Construction and accessibility of a cross-species phenotype ontology along with gene annotations for biomedical research. F1000Research, 2013, 2, 30.	0.8	72
23662	Construction and accessibility of a cross-species phenotype ontology along with gene annotations for biomedical research. F1000Research, 2013, 2, 30.	0.8	64
23663	A p53-like transcription factor similar to Ndt80 controls the response to nutrient stress in the filamentous fungus, <i>Aspergillus nidulans</i> . F1000Research, 2013, 2, 72.	0.8	54
23664	gprofiler2 – an R package for gene list functional enrichment analysis and namespace conversion toolset g:Profiler. F1000Research, 2020, 9, 709.	0.8	128
23665	gprofiler2 – an R package for gene list functional enrichment analysis and namespace conversion toolset g:Profiler. F1000Research, 2020, 9, 709.	0.8	331

#	ARTICLE	IF	CITATIONS
23666	BioJS DAGViewer: A reusable JavaScript component for displaying directed graphs. F1000Research, 2014, 3, 51.	0.8	5
23667	Development and use of the Cytoscape app GFD-Net for measuring semantic dissimilarity of gene networks. F1000Research, 2014, 3, 142.	0.8	11
23668	AGA: Interactive pipeline for reproducible gene expression and DNA methylation data analyses. F1000Research, 2015, 4, 28.	0.8	4
23669	The unfolded protein response and its potential role in Huntington's disease elucidated by a systems biology approach. F1000Research, 2015, 4, 103.	0.8	32
23670	The unfolded protein response and its potential role in Huntington's disease elucidated by a systems biology approach. F1000Research, 2015, 4, 103.	0.8	29
23671	SwissPalm: Protein Palmitoylation database. F1000Research, 2015, 4, 261.	0.8	209
23672	PHENOstruct: Prediction of human phenotype ontology terms using heterogeneous data sources. F1000Research, 2015, 4, 259.	0.8	31
23673	FlyOde - a platform for community curation and interactive visualization of dynamic gene regulatory networks in Drosophila eye development. F1000Research, 2015, 4, 1484.	0.8	4
23674	An end to end workflow for differential gene expression using Affymetrix microarrays. F1000Research, 2016, 5, 1384.	0.8	36
23675	An end to end workflow for differential gene expression using Affymetrix microarrays. F1000Research, 2016, 5, 1384.	0.8	31
23676	AutoAnnotate: A Cytoscape app for summarizing networks with semantic annotations. F1000Research, 2016, 5, 1717.	0.8	249
23677	BgeeDB, an R package for retrieval of curated expression datasets and for gene list expression localization enrichment tests. F1000Research, 2016, 5, 2748.	0.8	23
23678	BgeeDB, an R package for retrieval of curated expression datasets and for gene list expression localization enrichment tests. F1000Research, 2016, 5, 2748.	0.8	27
23679	Progression of the canonical reference malaria parasite genome from 2002 to 2019. Wellcome Open Research, 2019, 4, 58.	0.9	51
23680	Progression of the canonical reference malaria parasite genome from 2002 to 2019. Wellcome Open Research, 2019, 4, 58.	0.9	47
23681	Genome-wide CRISPR screening identifies new regulators of glycoprotein secretion. Wellcome Open Research, 0, 4, 119.	0.9	4
23682	GeneDB and Wikidata. Wellcome Open Research, 2019, 4, 114.	0.9	2
23683	Representation of behaviour change interventions and their evaluation: Development of the Upper Level of the Behaviour Change Intervention Ontology. Wellcome Open Research, 2020, 5, 123.	0.9	41

#	ARTICLE	IF	CITATIONS
23684	Development of an Intervention Setting Ontology for behaviour change: Specifying where interventions take place. Wellcome Open Research, 2020, 5, 124.	0.9	26
23685	Delivering Behaviour Change Interventions: Development of a Mode of Delivery Ontology. Wellcome Open Research, 2020, 5, 125.	0.9	33
23686	Ontologies relevant to behaviour change interventions: a method for their development. Wellcome Open Research, 2020, 5, 126.	0.9	10
23687	Ontologies relevant to behaviour change interventions: a method for their development. Wellcome Open Research, 0, 5, 126.	0.9	7
23688	Ontologies relevant to behaviour change interventions: a method for their development. Wellcome Open Research, 2020, 5, 126.	0.9	18
23689	Feature Ranking for Hierarchical Multi-Label Classification with Tree Ensemble Methods. Acta Polytechnica Hungarica, 2020, 17, 129-148.	2.5	4
23690	HIV and innate immunity – a genomics perspective. F1000prime Reports, 2013, 5, 29.	5.9	10
23691	Which to use? - microarray data analysis in input and output data processing. Chem-Bio Informatics Journal, 2004, 4, 56-72.	0.1	3
23692	Knowledge Organization Systems for Systematic Chemical Assessments. Environmental Health Perspectives, 2020, 128, 125001.	2.8	21
23693	Discovery of Gene-disease Associations from Biomedical Texts. Computer Science and Information Technology, 2016, 4, 1-8.	0.1	8
23694	Ontologies in Quantitative Biology: A Basis for Comparison, Integration, and Discovery. PLoS Biology, 2010, 8, e1000374.	2.6	41
23695	YAP/TAZ deficiency reprograms macrophage phenotype and improves infarct healing and cardiac function after myocardial infarction. PLoS Biology, 2020, 18, e3000941.	2.6	78
23696	Inferring function using patterns of native disorder in proteins. PLoS Computational Biology, 2005, preprint, e162.	1.5	3
23697	Aggregation Propensity of the Human Proteome. PLoS Computational Biology, 2008, 4, e1000199.	1.5	81
23698	Directed Mammalian Gene Regulatory Networks Using Expression and Comparative Genomic Hybridization Microarray Data from Radiation Hybrids. PLoS Computational Biology, 2009, 5, e1000407.	1.5	17
23699	Single Sample Expression-Anchored Mechanisms Predict Survival in Head and Neck Cancer. PLoS Computational Biology, 2012, 8, e1002350.	1.5	75
23700	Alternative Protein-Protein Interfaces Are Frequent Exceptions. PLoS Computational Biology, 2012, 8, e1002623.	1.5	26
23701	Heterogeneous Network Edge Prediction: A Data Integration Approach to Prioritize Disease-Associated Genes. PLoS Computational Biology, 2015, 11, e1004259.	1.5	120

#	ARTICLE	IF	CITATIONS
23702	Finding New Order in Biological Functions from the Network Structure of Gene Annotations. PLoS Computational Biology, 2015, 11, e1004565.	1.5	11
23703	Erosion of Conserved Binding Sites in Personal Genomes Points to Medical Histories. PLoS Computational Biology, 2016, 12, e1004711.	1.5	7
23704	Fast and Rigorous Computation of Gene and Pathway Scores from SNP-Based Summary Statistics. PLoS Computational Biology, 2016, 12, e1004714.	1.5	330
23705	Ten Simple Rules for Selecting a Bio-ontology. PLoS Computational Biology, 2016, 12, e1004743.	1.5	29
23706	Computational Reconstruction of NF κ B Pathway Interaction Mechanisms during Prostate Cancer. PLoS Computational Biology, 2016, 12, e1004820.	1.5	27
23707	Network-Based Interpretation of Diverse High-Throughput Datasets through the Omics Integrator Software Package. PLoS Computational Biology, 2016, 12, e1004879.	1.5	123
23708	Learning from Heterogeneous Data Sources: An Application in Spatial Proteomics. PLoS Computational Biology, 2016, 12, e1004920.	1.5	47
23709	Novel Computational Protocols for Functionally Classifying and Characterising Serine Beta-Lactamases. PLoS Computational Biology, 2016, 12, e1004926.	1.5	24
23710	Reactome from a WikiPathways Perspective. PLoS Computational Biology, 2016, 12, e1004941.	1.5	35
23711	MEGAN Community Edition - Interactive Exploration and Analysis of Large-Scale Microbiome Sequencing Data. PLoS Computational Biology, 2016, 12, e1004957.	1.5	1,500
23712	An Asymmetrically Balanced Organization of Kinases versus Phosphatases across Eukaryotes Determines Their Distinct Impacts. PLoS Computational Biology, 2017, 13, e1005221.	1.5	31
23713	Identification of Entry Factors Involved in Hepatitis C Virus Infection Based on Host-Mimicking Short Linear Motifs. PLoS Computational Biology, 2017, 13, e1005368.	1.5	8
23714	Interrogating the topological robustness of gene regulatory circuits by randomization. PLoS Computational Biology, 2017, 13, e1005456.	1.5	161
23715	CLIC, a tool for expanding biological pathways based on co-expression across thousands of datasets. PLoS Computational Biology, 2017, 13, e1005653.	1.5	30
23716	Insight into glucocorticoid receptor signalling through interactome model analysis. PLoS Computational Biology, 2017, 13, e1005825.	1.5	7
23717	Automated visualization of rule-based models. PLoS Computational Biology, 2017, 13, e1005857.	1.5	12
23718	Improving pairwise comparison of protein sequences with domain co-occurrence. PLoS Computational Biology, 2018, 14, e1005889.	1.5	7
23719	LAILAPS-QSM: A RESTful API and JAVA library for semantic query suggestions. PLoS Computational Biology, 2018, 14, e1006058.	1.5	4

#	ARTICLE	IF	CITATIONS
23720	IL6-mediated HCoV-host interactome regulatory network and GO/Pathway enrichment analysis. PLoS Computational Biology, 2020, 16, e1008238.	1.5	3
23721	A semi-supervised Bayesian approach for simultaneous protein sub-cellular localisation assignment and novelty detection. PLoS Computational Biology, 2020, 16, e1008288.	1.5	16
23722	DeepPheno: Predicting single gene loss-of-function phenotypes using an ontology-aware hierarchical classifier. PLoS Computational Biology, 2020, 16, e1008453.	1.5	17
23723	Predictive network modeling in human induced pluripotent stem cells identifies key driver genes for insulin responsiveness. PLoS Computational Biology, 2020, 16, e1008491.	1.5	14
23724	Transcriptional profiling of aging in human muscle reveals a common aging signature. PLoS Genetics, 2005, preprint, e115.	1.5	208
23725	AGEMAP: a gene expression database for aging in mice. PLoS Genetics, 2005, preprint, e201.	1.5	3
23726	Genome-Wide Fitness and Expression Profiling Implicate Mga2 in Adaptation to Hydrogen Peroxide. PLoS Genetics, 2009, 5, e1000488.	1.5	51
23727	Accurately Assessing the Risk of Schizophrenia Conferred by Rare Copy-Number Variation Affecting Genes with Brain Function. PLoS Genetics, 2010, 6, e1001097.	1.5	134
23728	Analysis of the Basidiomycete Coprinopsis cinerea Reveals Conservation of the Core Meiotic Expression Program over Half a Billion Years of Evolution. PLoS Genetics, 2010, 6, e1001135.	1.5	38
23729	Systematic Detection of Polygenic cis-Regulatory Evolution. PLoS Genetics, 2011, 7, e1002023.	1.5	61
23730	The Human Blood Metabolome-Transcriptome Interface. PLoS Genetics, 2015, 11, e1005274.	1.5	99
23731	Strong Components of Epigenetic Memory in Cultured Human Fibroblasts Related to Site of Origin and Donor Age. PLoS Genetics, 2016, 12, e1005819.	1.5	20
23732	NUCLEAR FACTOR Y, Subunit C (NF-YC) Transcription Factors Are Positive Regulators of Photomorphogenesis in Arabidopsis thaliana. PLoS Genetics, 2016, 12, e1006333.	1.5	61
23733	Evolutionary history of Tibetans inferred from whole-genome sequencing. PLoS Genetics, 2017, 13, e1006675.	1.5	89
23734	Hereditary cancer genes are highly susceptible to splicing mutations. PLoS Genetics, 2018, 14, e1007231.	1.5	45
23735	Argonaute2 and LaminB modulate gene expression by controlling chromatin topology. PLoS Genetics, 2018, 14, e1007276.	1.5	20
23736	Inflammatory Manifestations of Experimental Lymphatic Insufficiency. PLoS Medicine, 2006, 3, e254.	3.9	182
23737	Bone marrow microenvironments that contribute to patient outcomes in newly diagnosed multiple myeloma: A cohort study of patients in the Total Therapy clinical trials. PLoS Medicine, 2020, 17, e1003323.	3.9	33

#	ARTICLE	IF	CITATIONS
23738	Needles in the EST Haystack: Large-Scale Identification and Analysis of Excretory-Secretory (ES) Proteins in Parasitic Nematodes Using Expressed Sequence Tags (ESTs). <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e301.	1.3	44
23739	The Effect of In Vitro Cultivation on the Transcriptome of Adult <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004311.	1.3	22
23740	<i>Ixodes scapularis</i> Tick Saliva Proteins Sequentially Secreted Every 24 h during Blood Feeding. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004323.	1.3	136
23741	Comprehensive Transcriptome Meta-analysis to Characterize Host Immune Responses in Helminth Infections. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004624.	1.3	30
23742	Time-resolved proteomic profile of <i>Amblyomma americanum</i> tick saliva during feeding. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0007758.	1.3	40
23743	Epigenetic Activation of a Subset of mRNAs by eIF4E Explains Its Effects on Cell Proliferation. <i>PLoS ONE</i> , 2007, 2, e242.	1.1	184
23744	Genome-Wide Analysis of Nucleotide-Level Variation in Commonly Used <i>Saccharomyces cerevisiae</i> Strains. <i>PLoS ONE</i> , 2007, 2, e322.	1.1	100
23745	Deductive Biocomputing. <i>PLoS ONE</i> , 2007, 2, e339.	1.1	12
23746	Microarray Expression Profiles of 20,000 Genes across 23 Healthy Porcine Tissues. <i>PLoS ONE</i> , 2007, 2, e1203.	1.1	33
23747	Predicted Functional RNAs within Coding Regions Constrain Evolutionary Rates of Yeast Proteins. <i>PLoS ONE</i> , 2008, 3, e1559.	1.1	15
23748	Protein Function Assignment through Mining Cross-Species Protein-Protein Interactions. <i>PLoS ONE</i> , 2008, 3, e1562.	1.1	21
23749	Evidence-Based Annotation of the Malaria Parasite's Genome Using Comparative Expression Profiling. <i>PLoS ONE</i> , 2008, 3, e1570.	1.1	78
23750	Sirt1 Deficiency Attenuates Spermatogenesis and Germ Cell Function. <i>PLoS ONE</i> , 2008, 3, e1571.	1.1	116
23751	A Visual Data Mining Tool that Facilitates Reconstruction of Transcription Regulatory Networks. <i>PLoS ONE</i> , 2008, 3, e1717.	1.1	23
23752	Mapping Genetically Compensatory Pathways from Synthetic Lethal Interactions in Yeast. <i>PLoS ONE</i> , 2008, 3, e1922.	1.1	41
23753	Functional Annotation and Identification of Candidate Disease Genes by Computational Analysis of Normal Tissue Gene Expression Data. <i>PLoS ONE</i> , 2008, 3, e2439.	1.1	20
23754	Genes to Diseases (G2D) Computational Method to Identify Asthma Candidate Genes. <i>PLoS ONE</i> , 2008, 3, e2907.	1.1	35
23755	Improved Elucidation of Biological Processes Linked to Diabetic Nephropathy by Single Probe-Based Microarray Data Analysis. <i>PLoS ONE</i> , 2008, 3, e2937.	1.1	69

#	ARTICLE	IF	CITATIONS
23756	Refinement of Light-Responsive Transcript Lists Using Rice Oligonucleotide Arrays: Evaluation of Gene-Redundancy. PLoS ONE, 2008, 3, e3337.	1.1	104
23757	Randomization in Laboratory Procedure Is Key to Obtaining Reproducible Microarray Results. PLoS ONE, 2008, 3, e3724.	1.1	33
23758	Comprehensive Dissection of PDGF-PDGFR Signaling Pathways in PDGFR Genetically Defined Cells. PLoS ONE, 2008, 3, e3794.	1.1	99
23759	Global Expression Profiling in Atopic Eczema Reveals Reciprocal Expression of Inflammatory and Lipid Genes. PLoS ONE, 2008, 3, e4017.	1.1	75
23760	Molecular Time-Course and the Metabolic Basis of Entry into Dauer in <i>Caenorhabditis elegans</i> . PLoS ONE, 2009, 4, e4162.	1.1	58
23761	Using Sequence Similarity Networks for Visualization of Relationships Across Diverse Protein Superfamilies. PLoS ONE, 2009, 4, e4345.	1.1	385
23762	An Attempt to Understand Kidney's Protein Handling Function by Comparing Plasma and Urine Proteomes. PLoS ONE, 2009, 4, e5146.	1.1	60
23763	A Sequence and Structure Based Method to Predict Putative Substrates, Functions and Regulatory Networks of Endo Proteases. PLoS ONE, 2009, 4, e5700.	1.1	8
23764	How Do Human Cells React to the Absence of Mitochondrial DNA?. PLoS ONE, 2009, 4, e5713.	1.1	31
23765	Local Network Topology in Human Protein Interaction Data Predicts Functional Association. PLoS ONE, 2009, 4, e6410.	1.1	21
23766	Apoptosis of CD4+CD25high T Cells in Type 1 Diabetes May Be Partially Mediated by IL-2 Deprivation. PLoS ONE, 2009, 4, e6527.	1.1	73
23767	Global Brain Gene Expression Analysis Links Glutamatergic and GABAergic Alterations to Suicide and Major Depression. PLoS ONE, 2009, 4, e6585.	1.1	333
23768	Butyrate-Induced Transcriptional Changes in Human Colonic Mucosa. PLoS ONE, 2009, 4, e6759.	1.1	149
23769	The FunGenES Database: A Genomics Resource for Mouse Embryonic Stem Cell Differentiation. PLoS ONE, 2009, 4, e6804.	1.1	54
23770	Systematic Characterisation of Cellular Localisation and Expression Profiles of Proteins Containing MHC Ligands. PLoS ONE, 2009, 4, e7448.	1.1	33
23771	A Statistical Model of Protein Sequence Similarity and Function Similarity Reveals Overly-Specific Function Predictions. PLoS ONE, 2009, 4, e7546.	1.1	26
23772	Exploiting Amino Acid Composition for Predicting Protein-Protein Interactions. PLoS ONE, 2009, 4, e7813.	1.1	61
23773	Discovery of Novel Serum Biomarkers for Prenatal Down Syndrome Screening by Integrative Data Mining. PLoS ONE, 2009, 4, e8010.	1.1	20

#	ARTICLE	IF	CITATIONS
23774	Spatial and Temporal Analysis of Gene Expression during Growth and Fusion of the Mouse Facial Prominences. PLoS ONE, 2009, 4, e8066.	1.1	71
23775	Effective Identification of Conserved Pathways in Biological Networks Using Hidden Markov Models. PLoS ONE, 2009, 4, e8070.	1.1	24
23776	An Epigenetic Signature in Peripheral Blood Predicts Active Ovarian Cancer. PLoS ONE, 2009, 4, e8274.	1.1	291
23777	Covariation of Branch Lengths in Phylogenies of Functionally Related Genes. PLoS ONE, 2009, 4, e8487.	1.1	5
23778	Identification of Novel Glial Genes by Single-Cell Transcriptional Profiling of Bergmann Glial Cells from Mouse Cerebellum. PLoS ONE, 2010, 5, e9198.	1.1	75
23779	Integrative Meta-Analysis of Differential Gene Expression in Acute Myeloid Leukemia. PLoS ONE, 2010, 5, e9466.	1.1	26
23780	A New Method for Predicting the Subcellular Localization of Eukaryotic Proteins with Both Single and Multiple Sites: Euk-mPloc 2.0. PLoS ONE, 2010, 5, e9931.	1.1	300
23781	Reconstruction of Gene Regulatory Modules in Cancer Cell Cycle by Multi-Source Data Integration. PLoS ONE, 2010, 5, e10268.	1.1	13
23782	Downregulation of Homologous Recombination DNA Repair Genes by HDAC Inhibition in Prostate Cancer Is Mediated through the E2F1 Transcription Factor. PLoS ONE, 2010, 5, e11208.	1.1	140
23783	Proteomics-Based Systems Biology Modeling of Bovine Germinal Vesicle Stage Oocyte and Cumulus Cell Interaction. PLoS ONE, 2010, 5, e11240.	1.1	42
23784	Plant-mPloc: A Top-Down Strategy to Augment the Power for Predicting Plant Protein Subcellular Localization. PLoS ONE, 2010, 5, e11335.	1.1	732
23785	Understanding PRRSV Infection in Porcine Lung Based on Genome-Wide Transcriptome Response Identified by Deep Sequencing. PLoS ONE, 2010, 5, e11377.	1.1	119
23786	Gene Promoter Evolution Targets the Center of the Human Protein Interaction Network. PLoS ONE, 2010, 5, e11476.	1.1	7
23787	Characterization and Comparison of the Tissue-Related Modules in Human and Mouse. PLoS ONE, 2010, 5, e11730.	1.1	4
23788	Comparative Membranome Expression Analysis in Primary Tumors and Derived Cell Lines. PLoS ONE, 2010, 5, e11742.	1.1	18
23789	A Genome-Wide Gene Function Prediction Resource for Drosophila melanogaster. PLoS ONE, 2010, 5, e12139.	1.1	17
23790	Adding a Little Reality to Building Ontologies for Biology. PLoS ONE, 2010, 5, e12258.	1.1	24
23791	Prediction and Testing of Biological Networks Underlying Intestinal Cancer. PLoS ONE, 2010, 5, e12497.	1.1	11

#	ARTICLE	IF	CITATIONS
23792	Temporal Gene Expression Profiling during Rat Femoral Marrow Ablation-Induced Intramembranous Bone Regeneration. PLoS ONE, 2010, 5, e12987.	1.1	45
23793	Identification of Novel p53 Pathway Activating Small-Molecule Compounds Reveals Unexpected Similarities with Known Therapeutic Agents. PLoS ONE, 2010, 5, e12996.	1.1	77
23794	Inference of Surface Membrane Factors of HIV-1 Infection through Functional Interaction Networks. PLoS ONE, 2010, 5, e13139.	1.1	7
23795	eXtraembryonic ENdoderm (XEN) Stem Cells Produce Factors that Activate Heart Formation. PLoS ONE, 2010, 5, e13446.	1.1	35
23796	The LARGE Principle of Cellular Reprogramming: Lost, Acquired and Retained Gene Expression in Foreskin and Amniotic Fluid-Derived Human iPS Cells. PLoS ONE, 2010, 5, e13703.	1.1	61
23797	Expanding the Landscape of Chromatin Modification (CM)-Related Functional Domains and Genes in Human. PLoS ONE, 2010, 5, e14122.	1.1	10
23798	Gene Expression Meta-Analysis Identifies VDAC1 as a Predictor of Poor Outcome in Early Stage Non-Small Cell Lung Cancer. PLoS ONE, 2011, 6, e14635.	1.1	60
23799	Analysis of Common and Specific Mechanisms of Liver Function Affected by Nitrotoluene Compounds. PLoS ONE, 2011, 6, e14662.	1.1	33
23800	ENCODE Tiling Array Analysis Identifies Differentially Expressed Annotated and Novel 5' Capped RNAs in Hepatitis C Infected Liver. PLoS ONE, 2011, 6, e14697.	1.1	16
23801	Named Entity Recognition for Bacterial Type IV Secretion Systems. PLoS ONE, 2011, 6, e14780.	1.1	17
23802	The PluriNetWork: An Electronic Representation of the Network Underlying Pluripotency in Mouse, and Its Applications. PLoS ONE, 2010, 5, e15165.	1.1	67
23803	Comprehensive Gene-Expression Survey Identifies Wif1 as a Modulator of Cardiomyocyte Differentiation. PLoS ONE, 2010, 5, e15504.	1.1	18
23804	A Key Role for Poly(ADP-Ribose) Polymerase 3 in Ectodermal Specification and Neural Crest Development. PLoS ONE, 2011, 6, e15834.	1.1	17
23805	An Integrated Pipeline for the Genome-Wide Analysis of Transcription Factor Binding Sites from ChIP-Seq. PLoS ONE, 2011, 6, e16432.	1.1	39
23806	Simultaneous Analysis of Proteome, Phospho- and Glycoproteome of Rat Kidney Tissue with Electrostatic Repulsion Hydrophilic Interaction Chromatography. PLoS ONE, 2011, 6, e16884.	1.1	54
23807	miRNA-mRNA Integrated Analysis Reveals Roles for miRNAs in Primary Breast Tumors. PLoS ONE, 2011, 6, e16915.	1.1	278
23808	The Impact of Multifunctional Genes on "Guilt by Association" Analysis. PLoS ONE, 2011, 6, e17258.	1.1	171
23809	Assessing the Biological Significance of Gene Expression Signatures and Co-Expression Modules by Studying Their Network Properties. PLoS ONE, 2011, 6, e17474.	1.1	24

#	ARTICLE	IF	CITATIONS
23810	Genome-Wide Identification of Molecular Mimicry Candidates in Parasites. PLoS ONE, 2011, 6, e17546.	1.1	49
23811	Do Two Machine-Learning Based Prognostic Signatures for Breast Cancer Capture the Same Biological Processes?. PLoS ONE, 2011, 6, e17795.	1.1	35
23812	TargetMine, an Integrated Data Warehouse for Candidate Gene Prioritisation and Target Discovery. PLoS ONE, 2011, 6, e17844.	1.1	115
23813	Systems-Scale Analysis Reveals Pathways Involved in Cellular Response to Methamphetamine. PLoS ONE, 2011, 6, e18215.	1.1	20
23814	iLoc-Euk: A Multi-Label Classifier for Predicting the Subcellular Localization of Singleplex and Multiplex Eukaryotic Proteins. PLoS ONE, 2011, 6, e18258.	1.1	298
23815	Functional Cohesion of Gene Sets Determined by Latent Semantic Indexing of PubMed Abstracts. PLoS ONE, 2011, 6, e18851.	1.1	28
23816	Consensus Pathways Implicated in Prognosis of Colorectal Cancer Identified Through Systematic Enrichment Analysis of Gene Expression Profiling Studies. PLoS ONE, 2011, 6, e18867.	1.1	31
23817	Genes Influencing Circadian Differences in Blood Pressure in Hypertensive Mice. PLoS ONE, 2011, 6, e19203.	1.1	26
23818	Signalogs: Orthology-Based Identification of Novel Signaling Pathway Components in Three Metazoans. PLoS ONE, 2011, 6, e19240.	1.1	22
23819	OrthoList: A Compendium of <i>C. elegans</i> Genes with Human Orthologs. PLoS ONE, 2011, 6, e20085.	1.1	378
23820	Rapid Evolution of Coral Proteins Responsible for Interaction with the Environment. PLoS ONE, 2011, 6, e20392.	1.1	114
23821	Why Is There a Lack of Consensus on Molecular Subgroups of Glioblastoma? Understanding the Nature of Biological and Statistical Variability in Glioblastoma Expression Data. PLoS ONE, 2011, 6, e20826.	1.1	14
23822	Loss of DNA Mismatch Repair Imparts a Selective Advantage in Planarian Adult Stem Cells. PLoS ONE, 2011, 6, e21808.	1.1	12
23823	HelmCoP: An Online Resource for Helminth Functional Genomics and Drug and Vaccine Targets Prioritization. PLoS ONE, 2011, 6, e21832.	1.1	17
23824	SNOSite: Exploiting Maximal Dependence Decomposition to Identify Cysteine S-Nitrosylation with Substrate Site Specificity. PLoS ONE, 2011, 6, e21849.	1.1	77
23825	The Collagen Chaperone HSP47 Is a New Interactor of APP that Affects the Levels of Extracellular Beta-Amyloid Peptides. PLoS ONE, 2011, 6, e22370.	1.1	11
23826	The Genome Sequence of the North-European Cucumber (<i>Cucumis sativus</i> L.) Unravels Evolutionary Adaptation Mechanisms in Plants. PLoS ONE, 2011, 6, e22728.	1.1	112
23827	Pathway Analysis for Genome-Wide Association Study of Basal Cell Carcinoma of the Skin. PLoS ONE, 2011, 6, e22760.	1.1	15

#	ARTICLE	IF	CITATIONS
23828	A Computational Method Based on the Integration of Heterogeneous Networks for Predicting Disease-Gene Associations. <i>PLoS ONE</i> , 2011, 6, e24171.	1.1	22
23829	Phospholipase C Isozymes Are Deregulated in Colorectal Cancer – Insights Gained from Gene Set Enrichment Analysis of the Transcriptome. <i>PLoS ONE</i> , 2011, 6, e24419.	1.1	58
23830	Disease Gene Interaction Pathways: A Potential Framework for How Disease Genes Associate by Disease-Risk Modules. <i>PLoS ONE</i> , 2011, 6, e24495.	1.1	7
23831	Gene Signatures Derived from a c-MET-Driven Liver Cancer Mouse Model Predict Survival of Patients with Hepatocellular Carcinoma. <i>PLoS ONE</i> , 2011, 6, e24582.	1.1	26
23832	The Chemical Information Ontology: Provenance and Disambiguation for Chemical Data on the Biological Semantic Web. <i>PLoS ONE</i> , 2011, 6, e25513.	1.1	86
23833	Expression and Localization of microRNAs in Perinatal Rat Pancreas: Role of miR-21 in Regulation of Cholesterol Metabolism. <i>PLoS ONE</i> , 2011, 6, e25997.	1.1	24
23834	An Interaction Network Predicted from Public Data as a Discovery Tool: Application to the Hsp90 Molecular Chaperone Machine. <i>PLoS ONE</i> , 2011, 6, e26044.	1.1	225
23835	Sialome of a Generalist Lepidopteran Herbivore: Identification of Transcripts and Proteins from <i>Helicoverpa armigera</i> Labial Salivary Glands. <i>PLoS ONE</i> , 2011, 6, e26676.	1.1	45
23836	A Point Mutation in Translation Initiation Factor eIF2B Leads to Function- and Time-Specific Changes in Brain Gene Expression. <i>PLoS ONE</i> , 2011, 6, e26992.	1.1	13
23837	Time-Resolved Transcriptomics and Bioinformatic Analyses Reveal Intrinsic Stress Responses during Batch Culture of <i>Bacillus subtilis</i> . <i>PLoS ONE</i> , 2011, 6, e27160.	1.1	47
23838	Transcriptional Profiling of Human Familial Longevity Indicates a Role for ASF1A and IL7R. <i>PLoS ONE</i> , 2012, 7, e27759.	1.1	39
23839	Transcriptomic Analyses during the Transition from Biomass Production to Lipid Accumulation in the Oleaginous Yeast <i>Yarrowia lipolytica</i> . <i>PLoS ONE</i> , 2011, 6, e27966.	1.1	117
23840	Microarray-Based Transcriptomic Analysis of Differences between Long-Term Gregarious and Solitary Desert Locusts. <i>PLoS ONE</i> , 2011, 6, e28110.	1.1	36
23841	Identification of Lactoferricin B Intracellular Targets Using an <i>Escherichia coli</i> Proteome Chip. <i>PLoS ONE</i> , 2011, 6, e28197.	1.1	33
23842	Gene Discovery in the Threatened Elkhorn Coral: 454 Sequencing of the <i>Acropora palmata</i> Transcriptome. <i>PLoS ONE</i> , 2011, 6, e28634.	1.1	58
23843	Metatranscriptomics Reveals the Diversity of Genes Expressed by Eukaryotes in Forest Soils. <i>PLoS ONE</i> , 2012, 7, e28967.	1.1	149
23844	A Case Study for Large-Scale Human Microbiome Analysis Using JCVI's Metagenomics Reports (METAREP). <i>PLoS ONE</i> , 2012, 7, e29044.	1.1	11
23845	Statistical Properties and Robustness of Biological Controller-Target Networks. <i>PLoS ONE</i> , 2012, 7, e29374.	1.1	13

#	ARTICLE	IF	CITATIONS
23846	Functional Categories Associated with Clusters of Genes That Are Co-Expressed across the NCI-60 Cancer Cell Lines. PLoS ONE, 2012, 7, e30317.	1.1	11
23847	Transcriptome Analysis of the Model Protozoan, <i>Tetrahymena thermophila</i> , Using Deep RNA Sequencing. PLoS ONE, 2012, 7, e30630.	1.1	111
23848	Identification of Candidate Susceptibility and Resistance Genes of Mice Infected with <i>Streptococcus suis</i> Type 2. PLoS ONE, 2012, 7, e32150.	1.1	11
23849	pcaGoPromoter - An R Package for Biological and Regulatory Interpretation of Principal Components in Genome-Wide Gene Expression Data. PLoS ONE, 2012, 7, e32394.	1.1	25
23850	Regular Patterns for Proteome-Wide Distribution of Protein Abundance across Species. PLoS ONE, 2012, 7, e32423.	1.1	12
23851	Reducing False-Positive Prediction of Minimotifs with a Genetic Interaction Filter. PLoS ONE, 2012, 7, e32630.	1.1	3
23852	microPIR: An Integrated Database of MicroRNA Target Sites within Human Promoter Sequences. PLoS ONE, 2012, 7, e33888.	1.1	34
23853	Systematic Identification of Spontaneous Preterm Birth-Associated RNA Transcripts in Maternal Plasma. PLoS ONE, 2012, 7, e34328.	1.1	43
23854	Learning Transcriptional Regulatory Relationships Using Sparse Graphical Models. PLoS ONE, 2012, 7, e35762.	1.1	3
23855	Digital Gene Expression Analysis Based on Integrated De Novo Transcriptome Assembly of Sweet Potato [<i>Ipomoea batatas</i> (L.) Lam.]. PLoS ONE, 2012, 7, e36234.	1.1	156
23856	A Multi-Label Predictor for Identifying the Subcellular Locations of Singleplex and Multiplex Eukaryotic Proteins. PLoS ONE, 2012, 7, e36317.	1.1	38
23857	Insecticide Resistance Mechanisms in the Green Peach Aphid <i>Myzus persicae</i> (Hemiptera: Aphididae) I: A Transcriptomic Survey. PLoS ONE, 2012, 7, e36366.	1.1	133
23858	Assessment Method for a Power Analysis to Identify Differentially Expressed Pathways. PLoS ONE, 2012, 7, e37510.	1.1	16
23859	Pyrosequencing-Based Comparative Genome Analysis of <i>Vibrio vulnificus</i> Environmental Isolates. PLoS ONE, 2012, 7, e37553.	1.1	64
23860	An Interferon-Related Signature in the Transcriptional Core Response of Human Macrophages to <i>Mycobacterium tuberculosis</i> Infection. PLoS ONE, 2012, 7, e38367.	1.1	29
23861	The Enzymatic and Metabolic Capabilities of Early Life. PLoS ONE, 2012, 7, e39912.	1.1	24
23862	Hox Gene Expression Leads to Differential Hind Leg Development between Honeybee Castes. PLoS ONE, 2012, 7, e40111.	1.1	17
23863	Hippocampal CA1 Transcriptional Profile of Sleep Deprivation: Relation to Aging and Stress. PLoS ONE, 2012, 7, e40128.	1.1	25

#	ARTICLE	IF	CITATIONS
23864	Genome-Wide Detection of Genes Targeted by Non-Ig Somatic Hypermutation in Lymphoma. PLoS ONE, 2012, 7, e40332.	1.1	44
23865	Molecular Resistance Fingerprint of Pemetrexed and Platinum in a Long-Term Survivor of Mesothelioma. PLoS ONE, 2012, 7, e40521.	1.1	35
23866	Regulation and Gene Expression Profiling of NKG2D Positive Human Cytomegalovirus-Primed CD4+ T-Cells. PLoS ONE, 2012, 7, e41577.	1.1	6
23867	Deep Sequencing-Based Transcriptome Analysis of Chicken Spleen in Response to Avian Pathogenic Escherichia coli (APEC) Infection. PLoS ONE, 2012, 7, e41645.	1.1	56
23868	Identifying Responsive Modules by Mathematical Programming: An Application to Budding Yeast Cell Cycle. PLoS ONE, 2012, 7, e41854.	1.1	8
23869	SIMPLEX: Cloud-Enabled Pipeline for the Comprehensive Analysis of Exome Sequencing Data. PLoS ONE, 2012, 7, e41948.	1.1	38
23870	Bovine ncRNAs Are Abundant, Primarily Intergenic, Conserved and Associated with Regulatory Genes. PLoS ONE, 2012, 7, e42638.	1.1	64
23871	Subcellular Localization of Extracytoplasmic Proteins in Monoderm Bacteria: Rational Secretomics-Based Strategy for Genomic and Proteomic Analyses. PLoS ONE, 2012, 7, e42982.	1.1	50
23872	Dysfunctions Associated with Methylation, MicroRNA Expression and Gene Expression in Lung Cancer. PLoS ONE, 2012, 7, e43441.	1.1	18
23873	Mechanisms of Dietary Response in Mice and Primates: A Role for EGR1 in Regulating the Reaction to Human-Specific Nutritional Content. PLoS ONE, 2012, 7, e43915.	1.1	3
23874	Distinct Functional Patterns of Gene Promoter Hypomethylation and Hypermethylation in Cancer Genomes. PLoS ONE, 2012, 7, e44822.	1.1	25
23875	Deep Sequencing of the Transcriptomes of Soybean Aphid and Associated Endosymbionts. PLoS ONE, 2012, 7, e45161.	1.1	44
23876	Achieving High Accuracy Prediction of Minimotifs. PLoS ONE, 2012, 7, e45589.	1.1	4
23877	Development, Characterization and Experimental Validation of a Cultivated Sunflower (Helianthus) Tj ETQq1 1 0.784314 rgBT / Overl... 28	1.1	28
23878	Met Kinetic Signature Derived from the Response to HGF/SF in a Cellular Model Predicts Breast Cancer Patient Survival. PLoS ONE, 2012, 7, e45969.	1.1	5
23879	miRNA Regulons Associated with Synaptic Function. PLoS ONE, 2012, 7, e46189.	1.1	39
23880	MK4MDD: A Multi-Level Knowledge Base and Analysis Platform for Major Depressive Disorder. PLoS ONE, 2012, 7, e46335.	1.1	14
23881	GenoSets: Visual Analytic Methods for Comparative Genomics. PLoS ONE, 2012, 7, e46401.	1.1	13

#	ARTICLE	IF	CITATIONS
23882	A Complex Set of Sex Pheromones Identified in the Cuttlefish <i>Sepia officinalis</i> . PLoS ONE, 2012, 7, e46531.	1.1	7
23883	Transcriptome Sequencing and De Novo Analysis for Ma Bamboo (<i>Dendrocalamus latiflorus</i> Munro) Using the Illumina Platform. PLoS ONE, 2012, 7, e46766.	1.1	104
23884	Identification of Global Alteration of Translational Regulation in Glioma In Vivo. PLoS ONE, 2012, 7, e46965.	1.1	21
23885	Combining Next-Generation Sequencing and Microarray Technology into a Transcriptomics Approach for the Non-Model Organism <i>Chironomus riparius</i> . PLoS ONE, 2012, 7, e48096.	1.1	32
23886	Genome-Wide Identification of Copy Number Variations in Chinese Holstein. PLoS ONE, 2012, 7, e48732.	1.1	62
23887	Predicting Secretory Proteins of Malaria Parasite by Incorporating Sequence Evolution Information into Pseudo Amino Acid Composition via Grey System Model. PLoS ONE, 2012, 7, e49040.	1.1	47
23888	Genome-Wide Expression Analysis in Down Syndrome: Insight into Immunodeficiency. PLoS ONE, 2012, 7, e49130.	1.1	13
23889	Formalization, Annotation and Analysis of Diverse Drug and Probe Screening Assay Datasets Using the BioAssay Ontology (BAO). PLoS ONE, 2012, 7, e49198.	1.1	49
23890	Transcriptome Analysis of Renal Ischemia/Reperfusion Injury and Its Modulation by Ischemic Pre-Conditioning or Hemin Treatment. PLoS ONE, 2012, 7, e49569.	1.1	45
23891	A Framework for Annotating Human Genome in Disease Context. PLoS ONE, 2012, 7, e49686.	1.1	13
23892	A Comparison of the Whole Genome Approach of MeDIP-Seq to the Targeted Approach of the Infinium HumanMethylation450 BeadChip® for Methylome Profiling. PLoS ONE, 2012, 7, e50233.	1.1	83
23893	PROSPER: An Integrated Feature-Based Tool for Predicting Protease Substrate Cleavage Sites. PLoS ONE, 2012, 7, e50300.	1.1	265
23894	The Duplicated Genes Database: Identification and Functional Annotation of Co-Localised Duplicated Genes across Genomes. PLoS ONE, 2012, 7, e50653.	1.1	54
23895	Genome-Wide Transcriptome and Proteome Analysis on Different Developmental Stages of <i>Cordyceps militaris</i> . PLoS ONE, 2012, 7, e51853.	1.1	78
23896	Inhibition of the Pim1 Oncogene Results in Diminished Visual Function. PLoS ONE, 2012, 7, e52177.	1.1	20
23897	Identifying In-Trans Process Associated Genes in Breast Cancer by Integrated Analysis of Copy Number and Expression Data. PLoS ONE, 2013, 8, e53014.	1.1	54
23898	Exome Capture Sequencing of Adenoma Reveals Genetic Alterations in Multiple Cellular Pathways at the Early Stage of Colorectal Tumorigenesis. PLoS ONE, 2013, 8, e53310.	1.1	37
23899	VennPlex—A Novel Venn Diagram Program for Comparing and Visualizing Datasets with Differentially Regulated Datapoints. PLoS ONE, 2013, 8, e53388.	1.1	97

#	ARTICLE	IF	CITATIONS
23900	Integration of Transcriptome, Proteome and Metabolism Data Reveals the Alkaloids Biosynthesis in <i>Macleaya cordata</i> and <i>Macleaya microcarpa</i> . PLoS ONE, 2013, 8, e53409.	1.1	61
23901	A Global Transcriptome Analysis Reveals Molecular Hallmarks of Neural Stem Cell Death, Survival, and Differentiation in Response to Partial FGF-2 and EGF Deprivation. PLoS ONE, 2013, 8, e53594.	1.1	28
23902	mirTarPri: Improved Prioritization of MicroRNA Targets through Incorporation of Functional Genomics Data. PLoS ONE, 2013, 8, e53685.	1.1	14
23903	Urinary MicroRNA Profiling in the Nephropathy of Type 1 Diabetes. PLoS ONE, 2013, 8, e54662.	1.1	139
23904	Whole Genome Gene Expression Analysis Reveals Casiopeína-Induced Apoptosis Pathways. PLoS ONE, 2013, 8, e54664.	1.1	32
23905	The 3D Organization of the Yeast Genome Correlates with Co-Expression and Reflects Functional Relations between Genes. PLoS ONE, 2013, 8, e54699.	1.1	54
23906	miRNA Expression Profile Analysis in Kidney of Different Porcine Breeds. PLoS ONE, 2013, 8, e55402.	1.1	23
23907	Transcriptome Profiling of the Goose (<i>Anser cygnoides</i>) Ovaries Identify Laying and Broodiness Phenotypes. PLoS ONE, 2013, 8, e55496.	1.1	66
23908	Integrative Analyses Identify Osteopontin, LAMB3 and ITGB1 as Critical Pro-Metastatic Genes for Lung Cancer. PLoS ONE, 2013, 8, e55714.	1.1	81
23909	Massive-Scale Gene Co-Expression Network Construction and Robustness Testing Using Random Matrix Theory. PLoS ONE, 2013, 8, e55871.	1.1	49
23910	Shotgun Proteomic Analysis of Plasma from Dairy Cattle Suffering from Footrot: Characterization of Potential Disease-Associated Factors. PLoS ONE, 2013, 8, e55973.	1.1	26
23911	Transcriptome and Proteome Exploration to Provide a Resource for the Study of <i>Agrocybe aegerita</i> . PLoS ONE, 2013, 8, e56686.	1.1	56
23912	Molecular Subtypes in Head and Neck Cancer Exhibit Distinct Patterns of Chromosomal Gain and Loss of Canonical Cancer Genes. PLoS ONE, 2013, 8, e56823.	1.1	263
23913	RNA-Seq Reveals Activation of Both Common and Cytokine-Specific Pathways following Neutrophil Priming. PLoS ONE, 2013, 8, e58598.	1.1	92
23914	A Genome-Wide Association Study for Primary Open Angle Glaucoma and Macular Degeneration Reveals Novel Loci. PLoS ONE, 2013, 8, e58657.	1.1	35
23915	Defining the Transcriptional and Cellular Landscape of Type 1 Diabetes in the NOD Mouse. PLoS ONE, 2013, 8, e59701.	1.1	101
23916	Sodium Laurate, a Novel Protease- and Mass Spectrometry-Compatible Detergent for Mass Spectrometry-Based Membrane Proteomics. PLoS ONE, 2013, 8, e59779.	1.1	44
23917	Hidden Information Revealed by Optimal Community Structure from a Protein-Complex Bipartite Network Improves Protein Function Prediction. PLoS ONE, 2013, 8, e60372.	1.1	28

#	ARTICLE	IF	CITATIONS
23918	De novo Sequence Assembly and Characterization of Lycoris aurea Transcriptome Using GS FLX Titanium Platform of 454 Pyrosequencing. PLoS ONE, 2013, 8, e60449.	1.1	33
23919	In-Depth Transcriptomic Analysis on Giant Freshwater Prawns. PLoS ONE, 2013, 8, e60839.	1.1	32
23920	From Data towards Knowledge: Revealing the Architecture of Signaling Systems by Unifying Knowledge Mining and Data Mining of Systematic Perturbation Data. PLoS ONE, 2013, 8, e61134.	1.1	11
23921	Differential Expression Profiles in the Midgut of Triatoma infestans Infected with Trypanosoma cruzi. PLoS ONE, 2013, 8, e61203.	1.1	39
23922	Effects of Guideline-Based Training on the Quality of Formal Ontologies: A Randomized Controlled Trial. PLoS ONE, 2013, 8, e61425.	1.1	4
23923	p.Arg82Leu von Hippel-Lindau (VHL) Gene Mutation among Three Members of a Family with Familial Bilateral Pheochromocytoma in India: Molecular Analysis and In Silico Characterization. PLoS ONE, 2013, 8, e61908.	1.1	10
23924	A Fourteen Gene GBM Prognostic Signature Identifies Association of Immune Response Pathway and Mesenchymal Subtype with High Risk Group. PLoS ONE, 2013, 8, e62042.	1.1	47
23925	Defining the Genomic Signature of Totipotency and Pluripotency during Early Human Development. PLoS ONE, 2013, 8, e62135.	1.1	27
23926	Protein Complex Detection via Weighted Ensemble Clustering Based on Bayesian Nonnegative Matrix Factorization. PLoS ONE, 2013, 8, e62158.	1.1	28
23927	A Multi-Platform Draft de novo Genome Assembly and Comparative Analysis for the Scarlet Macaw (Ara macao). PLoS ONE, 2013, 8, e62415.	1.1	51
23928	Structure and Non-Structure of Centrosomal Proteins. PLoS ONE, 2013, 8, e62633.	1.1	25
23929	Textrousl!: Extracting Semantic Textual Meaning from Gene Sets. PLoS ONE, 2013, 8, e62665.	1.1	23
23930	De Novo Assembly, Functional Annotation and Comparative Analysis of Withania somnifera Leaf and Root Transcriptomes to Identify Putative Genes Involved in the Withanolides Biosynthesis. PLoS ONE, 2013, 8, e62714.	1.1	95
23931	Semi-Supervised Prediction of SH2-Peptide Interactions from Imbalanced High-Throughput Data. PLoS ONE, 2013, 8, e62732.	1.1	27
23932	Suppression and Activation of the Malignant Phenotype by Extracellular Matrix in Xenograft Models of Bladder Cancer: A Model for Tumor Cell "Dormancy". PLoS ONE, 2013, 8, e64181.	1.1	15
23933	Identification of C/EBP β Target Genes in ALK+ Anaplastic Large Cell Lymphoma (ALCL) by Gene Expression Profiling and Chromatin Immunoprecipitation. PLoS ONE, 2013, 8, e64544.	1.1	28
23934	Identification of a Testis-Enriched Heat Shock Protein and Fourteen Members of Hsp70 Family in the Swamp Eel. PLoS ONE, 2013, 8, e65269.	1.1	25
23935	How to Make a Dolphin: Molecular Signature of Positive Selection in Cetacean Genome. PLoS ONE, 2013, 8, e65491.	1.1	38

#	ARTICLE	IF	CITATIONS
23936	ToP: A Trend-of-Disease-Progression Procedure Works Well for Identifying Cancer Genes from Multi-State Cohort Gene Expression Data for Human Colorectal Cancer. PLoS ONE, 2013, 8, e65683.	1.1	11
23937	Transcription Factors in Escherichia coli Prefer the Holo Conformation. PLoS ONE, 2013, 8, e65723.	1.1	23
23938	Cancer Subtype Discovery and Biomarker Identification via a New Robust Network Clustering Algorithm. PLoS ONE, 2013, 8, e66256.	1.1	26
23939	Complementing the Eukaryotic Protein Interactome. PLoS ONE, 2013, 8, e66635.	1.1	9
23940	Nodes Having a Major Influence to Break Cooperation Define a Novel Centrality Measure: Game Centrality. PLoS ONE, 2013, 8, e67159.	1.1	18
23941	Community Structure Analysis of Gene Interaction Networks in Duchenne Muscular Dystrophy. PLoS ONE, 2013, 8, e67237.	1.1	9
23942	Predicting and Analyzing Interactions between Mycobacterium tuberculosis and Its Human Host. PLoS ONE, 2013, 8, e67472.	1.1	34
23943	Gene Set Based Integrated Data Analysis Reveals Phenotypic Differences in a Brain Cancer Model. PLoS ONE, 2013, 8, e68288.	1.1	3
23944	Analysis of 953 Human Proteins from a Mitochondrial HEK293 Fraction by Complexome Profiling. PLoS ONE, 2013, 8, e68340.	1.1	51
23945	NanoMiner – Integrative Human Transcriptomics Data Resource for Nanoparticle Research. PLoS ONE, 2013, 8, e68414.	1.1	20
23946	Identification of Immunity Related Genes to Study the Physalis peruviana – Fusarium oxysporum Pathosystem. PLoS ONE, 2013, 8, e68500.	1.1	30
23947	Comparison of Profile Similarity Measures for Genetic Interaction Networks. PLoS ONE, 2013, 8, e68664.	1.1	31
23948	Identification of Genome-Wide Copy Number Variations among Diverse Pig Breeds Using SNP Genotyping Arrays. PLoS ONE, 2013, 8, e68683.	1.1	41
23949	A New Omics Data Resource of Pleurocybella porrigens for Gene Discovery. PLoS ONE, 2013, 8, e69681.	1.1	12
23950	Genes Dysregulated to Different Extent or Oppositely in Estrogen Receptor-Positive and Estrogen Receptor-Negative Breast Cancers. PLoS ONE, 2013, 8, e70017.	1.1	10
23951	A Possible Mechanism behind Autoimmune Disorders Discovered By Genome-Wide Linkage and Association Analysis in Celiac Disease. PLoS ONE, 2013, 8, e70174.	1.1	51
23952	A Comparative Analysis of Industrial Escherichia coli K12 and B Strains in High-Glucose Batch Cultivations on Process-, Transcriptome- and Proteome Level. PLoS ONE, 2013, 8, e70516.	1.1	77
23953	TrOn: An Anatomical Ontology for the Beetle Tribolium castaneum. PLoS ONE, 2013, 8, e70695.	1.1	15

#	ARTICLE	IF	CITATIONS
23954	Functional Comparison between Genes Dysregulated in Ulcerative Colitis and Colorectal Carcinoma. PLoS ONE, 2013, 8, e71989.	1.1	6
23955	Structural Phylogenomics Retrodicts the Origin of the Genetic Code and Uncovers the Evolutionary Impact of Protein Flexibility. PLoS ONE, 2013, 8, e72225.	1.1	61
23956	Functional Genomic Analyses of Two Morphologically Distinct Classes of Drosophila Sensory Neurons: Post-Mitotic Roles of Transcription Factors in Dendritic Patterning. PLoS ONE, 2013, 8, e72434.	1.1	69
23957	Atypical E2fs Control Lymphangiogenesis through Transcriptional Regulation of Ccbe1 and Flt4. PLoS ONE, 2013, 8, e73693.	1.1	30
23958	Cancer Stemness in Apc- vs. Apc/KRAS-Driven Intestinal Tumorigenesis. PLoS ONE, 2013, 8, e73872.	1.1	8
23959	CoCiter: An Efficient Tool to Infer Gene Function Co-Citation. PLoS ONE, 2013, 8, e74074.	1.1	36
23960	Specific Extracellular Matrix Remodeling Signature of Colon Hepatic Metastases. PLoS ONE, 2013, 8, e74599.	1.1	46
23961	Genome-Wide Copy Number Variations Inferred from SNP Genotyping Arrays Using a Large White and Minzhu Intercross Population. PLoS ONE, 2013, 8, e74879.	1.1	24
23962	Identification of Unstable Network Modules Reveals Disease Modules Associated with the Progression of Alzheimer's Disease. PLoS ONE, 2013, 8, e76162.	1.1	41
23963	Generation and Analysis of a Large-Scale Expressed Sequence Tag Database from a Full-Length Enriched cDNA Library of Developing Leaves of Gossypium hirsutum L. PLoS ONE, 2013, 8, e76443.	1.1	10
23964	Multi-Dimensional Prioritization of Dental Caries Candidate Genes and Its Enriched Dense Network Modules. PLoS ONE, 2013, 8, e76666.	1.1	24
23965	Transcriptome Analysis of Androgenic Gland for Discovery of Novel Genes from the Oriental River Prawn, Macrobrachium nipponense, Using Illumina Hiseq 2000. PLoS ONE, 2013, 8, e76840.	1.1	78
23966	Transcriptional Response to Deletion of the Phosphatidylserine Decarboxylase Psd1p in the Yeast Saccharomyces cerevisiae. PLoS ONE, 2013, 8, e77380.	1.1	23
23967	Inference of Gene-Phenotype Associations via Protein-Protein Interaction and Orthology. PLoS ONE, 2013, 8, e77478.	1.1	9
23968	Classification of α -Helical Membrane Proteins Using Predicted Helix Architectures. PLoS ONE, 2013, 8, e77491.	1.1	4
23969	Proteomic Changes during B Cell Maturation: 2D-DIGE Approach. PLoS ONE, 2013, 8, e77894.	1.1	7
23970	The Transcriptional Repressor TupA in Aspergillus niger Is Involved in Controlling Gene Expression Related to Cell Wall Biosynthesis, Development, and Nitrogen Source Availability. PLoS ONE, 2013, 8, e78102.	1.1	19
23971	Architecture and Gene Repertoire of the Flexible Genome of the Extreme Acidophile Acidithiobacillus caldus. PLoS ONE, 2013, 8, e78237.	1.1	68

#	ARTICLE	IF	CITATIONS
23972	SVD Identifies Transcript Length Distribution Functions from DNA Microarray Data and Reveals Evolutionary Forces Globally Affecting GBM Metabolism. PLoS ONE, 2013, 8, e78913.	1.1	13
23973	Discovering Transcription and Splicing Networks in Myelodysplastic Syndromes. PLoS ONE, 2013, 8, e79118.	1.1	11
23974	Development of Reference Transcriptomes for the Major Field Insect Pests of Cowpea: A Toolbox for Insect Pest Management Approaches in West Africa. PLoS ONE, 2013, 8, e79929.	1.1	23
23975	Candidate Gene Identification for Systemic Lupus Erythematosus Using Network Centrality Measures and Gene Ontology. PLoS ONE, 2013, 8, e81766.	1.1	17
23976	N-glycoproteome Analysis of the Secretome of Human Metastatic Hepatocellular Carcinoma Cell Lines Combining Hydrazide Chemistry, HILIC Enrichment and Mass Spectrometry. PLoS ONE, 2013, 8, e81921.	1.1	27
23977	A Genome-Wide Longitudinal Transcriptome Analysis of the Aging Model <i>Podospira anserine</i> . PLoS ONE, 2013, 8, e83109.	1.1	30
23978	Early Transcriptional Response of Soybean Contrasting Accessions to Root Dehydration. PLoS ONE, 2013, 8, e83466.	1.1	27
23979	Evolution of Human Longevity Uncoupled from Caloric Restriction Mechanisms. PLoS ONE, 2014, 9, e84117.	1.1	13
23980	Extracting Tag Hierarchies. PLoS ONE, 2013, 8, e84133.	1.1	18
23981	Clustering Gene Expression Regulators: New Approach to Disease Subtyping. PLoS ONE, 2014, 9, e84955.	1.1	32
23982	A Snapshot of a Coral "Holobiont": A Transcriptome Assembly of the Scleractinian Coral, <i>Porites</i> , Captures a Wide Variety of Genes from Both the Host and Symbiotic Zooxanthellae. PLoS ONE, 2014, 9, e85182.	1.1	95
23983	Robust Prognostic Gene Expression Signatures in Bladder Cancer and Lung Adenocarcinoma Depend on Cell Cycle Related Genes. PLoS ONE, 2014, 9, e85249.	1.1	26
23984	Genome-Wide Detection of Copy Number Variations among Diverse Horse Breeds by Array CGH. PLoS ONE, 2014, 9, e86860.	1.1	31
23985	SYK Allelic Loss and the Role of Syk-Regulated Genes in Breast Cancer Survival. PLoS ONE, 2014, 9, e87610.	1.1	29
23986	Single-Cell States in the Estrogen Response of Breast Cancer Cell Lines. PLoS ONE, 2014, 9, e88485.	1.1	4
23987	Transcriptome Profile of <i>Trichoderma harzianum</i> IOC-3844 Induced by Sugarcane Bagasse. PLoS ONE, 2014, 9, e88689.	1.1	41
23988	Evaluation of Sequence Features from Intrinsically Disordered Regions for the Estimation of Protein Function. PLoS ONE, 2014, 9, e89890.	1.1	19
23989	Transcriptomics of the Interaction between the Monopartite Phloem-Limited Geminivirus Tomato Yellow Leaf Curl Sardinia Virus and <i>Solanum lycopersicum</i> Highlights a Role for Plant Hormones, Autophagy and Plant Immune System Fine Tuning during Infection. PLoS ONE, 2014, 9, e89951.	1.1	77

#	ARTICLE	IF	CITATIONS
23990	Using Multi-Instance Hierarchical Clustering Learning System to Predict Yeast Gene Function. PLoS ONE, 2014, 9, e90962.	1.1	6
23991	Parallel Clustering Algorithm for Large-Scale Biological Data Sets. PLoS ONE, 2014, 9, e91315.	1.1	18
23992	Molecular Characterization of Adipose Tissue in the African Elephant (<i>Loxodonta africana</i>). PLoS ONE, 2014, 9, e91717.	1.1	3
23993	Global Changes in Gene Expression of Barrett's Esophagus Compared to Normal Squamous Esophagus and Gastric Cardia Tissues. PLoS ONE, 2014, 9, e93219.	1.1	27
23994	Proteomic Analysis of Cattle Tick <i>Rhipicephalus (Boophilus) microplus</i> Saliva: A Comparison between Partially and Fully Engorged Females. PLoS ONE, 2014, 9, e94831.	1.1	165
23995	The Epigenetic Bivalency of Core Pancreatic \hat{I}^2 -Cell Transcription Factor Genes within Mouse Pluripotent Embryonic Stem Cells Is Not Affected by Knockdown of the Polycomb Repressive Complex 2, SUZ12. PLoS ONE, 2014, 9, e97820.	1.1	7
23996	On the Crucial Cerebellar Wound Healing-Related Pathways and Their Cross-Talks after Traumatic Brain Injury in <i>Danio rerio</i> . PLoS ONE, 2014, 9, e97902.	1.1	20
23997	Genes Responsive to Elevated CO ₂ Concentrations in Triploid White Poplar and Integrated Gene Network Analysis. PLoS ONE, 2014, 9, e98300.	1.1	16
23998	Hypoxia-Induced miR-15a Promotes Mesenchymal Ablation and Adaptation to Hypoxia during Lung Development in Chicken. PLoS ONE, 2014, 9, e98868.	1.1	24
23999	CELLO2GO: A Web Server for Protein subCELLular LOCALization Prediction with Functional Gene Ontology Annotation. PLoS ONE, 2014, 9, e99368.	1.1	357
24000	Inferring Gene Family Histories in Yeast Identifies Lineage Specific Expansions. PLoS ONE, 2014, 9, e99480.	1.1	6
24001	Transcriptome Profiling of the Theca Interna from Bovine Ovarian Follicles during Atresia. PLoS ONE, 2014, 9, e99706.	1.1	39
24002	Comparison of the Transcriptomes of Ginger (<i>Zingiber officinale</i> Rosc.) and Mango Ginger (<i>Curcuma</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.1	19 / 50
24003	Exploring Function Prediction in Protein Interaction Networks via Clustering Methods. PLoS ONE, 2014, 9, e99755.	1.1	17
24004	Genetic Variation in DNA Repair Pathways and Risk of Non-Hodgkin's Lymphoma. PLoS ONE, 2014, 9, e101685.	1.1	19
24005	Serum miRNA Signature in Moyamoya Disease. PLoS ONE, 2014, 9, e102382.	1.1	46
24006	biDCC: A New Method for Discovering Global Features of DNA Microarray Data via an Iterative Re-Clustering Procedure. PLoS ONE, 2014, 9, e102445.	1.1	4
24007	Systems-Based Analyses of Brain Regions Functionally Impacted in Parkinson's Disease Reveals Underlying Causal Mechanisms. PLoS ONE, 2014, 9, e102909.	1.1	74

#	ARTICLE	IF	CITATIONS
24008	A Tri-Component Conservation Strategy Reveals Highly Confident MicroRNA-mRNA Interactions and Evolution of MicroRNA Regulatory Networks. <i>PLoS ONE</i> , 2014, 9, e103142.	1.1	3
24009	Wnt Pathway Activation Increases Hypoxia Tolerance during Development. <i>PLoS ONE</i> , 2014, 9, e103292.	1.1	8
24010	Molecular Characterization and Differential Expression of Olfactory Genes in the Antennae of the Black Cutworm Moth <i>Agrotis ipsilon</i> . <i>PLoS ONE</i> , 2014, 9, e103420.	1.1	66
24011	Identifying a Polymorphic "Switch"™ That Influences miRNAs' Regulation of a Myasthenia Gravis Risk Pathway. <i>PLoS ONE</i> , 2014, 9, e104827.	1.1	8
24012	Transcriptional Landscape of Glomerular Parietal Epithelial Cells. <i>PLoS ONE</i> , 2014, 9, e105289.	1.1	10
24013	Research Resources: Comparative MicroRNA Profiles in Human Corona Radiata Cells and Cumulus Oophorus Cells Detected by Next-Generation Small RNA Sequencing. <i>PLoS ONE</i> , 2014, 9, e106706.	1.1	22
24014	Analysis of Tumor Suppressor Genes Based on Gene Ontology and the KEGG Pathway. <i>PLoS ONE</i> , 2014, 9, e107202.	1.1	44
24015	Gene Expression and Pathway Analysis of Effects of the CMAH Deactivation on Mouse Lung, Kidney and Heart. <i>PLoS ONE</i> , 2014, 9, e107559.	1.1	15
24016	Enhancing the Functional Content of Eukaryotic Protein Interaction Networks. <i>PLoS ONE</i> , 2014, 9, e109130.	1.1	4
24017	Transcriptome Analysis of the <i>Trachinotus ovatus</i> : Identification of Reproduction, Growth and Immune-Related Genes and Microsatellite Markers. <i>PLoS ONE</i> , 2014, 9, e109419.	1.1	42
24018	Expression Profiling of Mitochondrial Voltage-Dependent Anion Channel-1 Associated Genes Predicts Recurrence-Free Survival in Human Carcinomas. <i>PLoS ONE</i> , 2014, 9, e110094.	1.1	28
24019	Relating Diseases by Integrating Gene Associations and Information Flow through Protein Interaction Network. <i>PLoS ONE</i> , 2014, 9, e110936.	1.1	18
24020	From Moderately Severe to Severe Hypertriglyceridemia Induced Acute Pancreatitis: Circulating MiRNAs Play Role as Potential Biomarkers. <i>PLoS ONE</i> , 2014, 9, e111058.	1.1	30
24021	MitProNet: A Knowledgebase and Analysis Platform of Proteome, Interactome and Diseases for Mammalian Mitochondria. <i>PLoS ONE</i> , 2014, 9, e111187.	1.1	4
24022	Identification of Under-Detected Periodicity in Time-Series Microarray Data by Using Empirical Mode Decomposition. <i>PLoS ONE</i> , 2014, 9, e111719.	1.1	2
24023	Computational Approaches for Predicting Biomedical Research Collaborations. <i>PLoS ONE</i> , 2014, 9, e111795.	1.1	6
24024	17 β -Estradiol Modulates Gene Expression in the Female Mouse Cerebral Cortex. <i>PLoS ONE</i> , 2014, 9, e111975.	1.1	18
24025	Exploring the Genetic Basis of Adaptation to High Elevations in Reptiles: A Comparative Transcriptome Analysis of Two Toad-Headed Agamas (Genus <i>Phrynocephalus</i>). <i>PLoS ONE</i> , 2014, 9, e112218.	1.1	27

#	ARTICLE	IF	CITATIONS
24026	Synergy: A Web Resource for Exploring Gene Regulation in <i>Synechocystis</i> sp. PCC6803. PLoS ONE, 2014, 9, e113496.	1.1	4
24027	Accounting for eXentricities: Analysis of the X Chromosome in GWAS Reveals X-Linked Genes Implicated in Autoimmune Diseases. PLoS ONE, 2014, 9, e113684.	1.1	100
24028	System-Level Insights into the Cellular Interactome of a Non-Model Organism: Inferring, Modelling and Analysing Functional Gene Network of Soybean (<i>Glycine max</i>). PLoS ONE, 2014, 9, e113907.	1.1	9
24029	Phylogenetic Profiling: How Much Input Data Is Enough?. PLoS ONE, 2015, 10, e0114701.	1.1	31
24030	The Transcriptomic and Proteomic Landscapes of Bone Marrow and Secondary Lymphoid Tissues. PLoS ONE, 2014, 9, e115911.	1.1	13
24031	Expression of Tumor Necrosis Factor-Alpha-Mediated Genes Predicts Recurrence-Free Survival in Lung Cancer. PLoS ONE, 2014, 9, e115945.	1.1	14
24032	Fetal-Adult Cardiac Transcriptome Analysis in Rats with Contrasting Left Ventricular Mass Reveals New Candidates for Cardiac Hypertrophy. PLoS ONE, 2015, 10, e0116807.	1.1	4
24033	Synergistic and Antagonistic Interplay between Myostatin Gene Expression and Physical Activity Levels on Gene Expression Patterns in Triceps Brachii Muscles of C57/BL6 Mice. PLoS ONE, 2015, 10, e0116828.	1.1	10
24034	A Hybrid Computational Method for the Discovery of Novel Reproduction-Related Genes. PLoS ONE, 2015, 10, e0117090.	1.1	13
24035	Gene Co-Expression Network Analysis Provides Novel Insights into Myostatin Regulation at Three Different Mouse Developmental Timepoints. PLoS ONE, 2015, 10, e0117607.	1.1	12
24036	An Ensemble Method with Hybrid Features to Identify Extracellular Matrix Proteins. PLoS ONE, 2015, 10, e0117804.	1.1	20
24037	Discovery of New Candidate Genes Related to Brain Development Using Protein Interaction Information. PLoS ONE, 2015, 10, e0118003.	1.1	12
24038	Proteome Exploration to Provide a Resource for the Investigation of <i>Ganoderma lucidum</i> . PLoS ONE, 2015, 10, e0119439.	1.1	24
24039	GRYFUN: A Web Application for GO Term Annotation Visualization and Analysis in Protein Sets. PLoS ONE, 2015, 10, e0119631.	1.1	3
24040	Transcriptome Sequencing and Positive Selected Genes Analysis of <i>Bombyx mandarina</i> . PLoS ONE, 2015, 10, e0122837.	1.1	25
24041	A De Novo Floral Transcriptome Reveals Clues into <i>Phalaenopsis</i> Orchid Flower Development. PLoS ONE, 2015, 10, e0123474.	1.1	34
24042	De Novo Assembly and Transcriptome Analysis of Wheat with Male Sterility Induced by the Chemical Hybridizing Agent SQ-1. PLoS ONE, 2015, 10, e0123556.	1.1	28
24043	Quantitative Proteomics of an Amphibian Pathogen, <i>Batrachochytrium dendrobatidis</i> , following Exposure to Thyroid Hormone. PLoS ONE, 2015, 10, e0123637.	1.1	4

#	ARTICLE	IF	CITATIONS
24044	piRNAs from Pig Testis Provide Evidence for a Conserved Role of the Piwi Pathway in Post-Transcriptional Gene Regulation in Mammals. PLoS ONE, 2015, 10, e0124860.	1.1	48
24045	Different Astrocytic Activation between Adult Gekko japonicus and Rats during Wound Healing In Vitro. PLoS ONE, 2015, 10, e0127663.	1.1	10
24046	PAND: A Distribution to Identify Functional Linkage from Networks with Preferential Attachment Property. PLoS ONE, 2015, 10, e0127968.	1.1	1
24047	Adaptation of a Bioinformatics Microarray Analysis Workflow for a Toxicogenomic Study in Rainbow Trout. PLoS ONE, 2015, 10, e0128598.	1.1	5
24048	Changes in Macrophage Gene Expression Associated with Leishmania (Viannia) braziliensis Infection. PLoS ONE, 2015, 10, e0128934.	1.1	34
24049	Association of Protein Translation and Extracellular Matrix Gene Sets with Breast Cancer Metastasis: Findings Uncovered on Analysis of Multiple Publicly Available Datasets Using Individual Patient Data Approach. PLoS ONE, 2015, 10, e0129610.	1.1	5
24050	Defining the Human Brain Proteome Using Transcriptomics and Antibody-Based Profiling with a Focus on the Cerebral Cortex. PLoS ONE, 2015, 10, e0130028.	1.1	44
24051	Asian Citrus Psyllid Expression Profiles Suggest Candidatus Liberibacter Asiaticus-Mediated Alteration of Adult Nutrition and Metabolism, and of Nymphal Development and Immunity. PLoS ONE, 2015, 10, e0130328.	1.1	85
24052	Global Gene-Expression Analysis to Identify Differentially Expressed Genes Critical for the Heat Stress Response in Brassica rapa. PLoS ONE, 2015, 10, e0130451.	1.1	44
24053	Genome Scan for Selection in Structured Layer Chicken Populations Exploiting Linkage Disequilibrium Information. PLoS ONE, 2015, 10, e0130497.	1.1	19
24054	A Comparative Transcriptome Analysis between Wild and Albino Yellow Catfish (Pelteobagrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342	1.1	33
24055	Prenatal Exposure to DEHP Affects Spermatogenesis and Sperm DNA Methylation in a Strain-Dependent Manner. PLoS ONE, 2015, 10, e0132136.	1.1	42
24056	Lung Transcriptomics during Protective Ventilatory Support in Sepsis-Induced Acute Lung Injury. PLoS ONE, 2015, 10, e0132296.	1.1	20
24057	Identification of MicroRNAs in Response to Different Day Lengths in Soybean Using High-Throughput Sequencing and qRT-PCR. PLoS ONE, 2015, 10, e0132621.	1.1	16
24058	A P-Norm Robust Feature Extraction Method for Identifying Differentially Expressed Genes. PLoS ONE, 2015, 10, e0133124.	1.1	11
24059	Genes Upregulated in Winter Wheat (Triticum aestivum L.) during Mild Freezing and Subsequent Thawing Suggest Sequential Activation of Multiple Response Mechanisms. PLoS ONE, 2015, 10, e0133166.	1.1	13
24060	Network-Based Analysis of Schizophrenia Genome-Wide Association Data to Detect the Joint Functional Association Signals. PLoS ONE, 2015, 10, e0133404.	1.1	38
24061	Optimal Threshold Determination for Interpreting Semantic Similarity and Particularity: Application to the Comparison of Gene Sets and Metabolic Pathways Using GO and ChEBI. PLoS ONE, 2015, 10, e0133579.	1.1	7

#	ARTICLE	IF	CITATIONS
24062	Quantitative Trait Loci Associated with the Tocochromanol (Vitamin E) Pathway in Barley. PLoS ONE, 2015, 10, e0133767.	1.1	14
24063	Genome-Wide Analyses Suggest Mechanisms Involving Early B-Cell Development in Canine IgA Deficiency. PLoS ONE, 2015, 10, e0133844.	1.1	14
24064	Characterization of the Cardiac Overexpression of HSPB2 Reveals Mitochondrial and Myogenic Roles Supported by a Cardiac HspB2 Interactome. PLoS ONE, 2015, 10, e0133994.	1.1	11
24065	A Methodology for the Development of RESTful Semantic Web Services for Gene Expression Analysis. PLoS ONE, 2015, 10, e0134011.	1.1	7
24066	Cox4i2, Ifit2, and Prdm11 Mutant Mice: Effective Selection of Genes Predisposing to an Altered Airway Inflammatory Response from a Large Compendium of Mutant Mouse Lines. PLoS ONE, 2015, 10, e0134503.	1.1	5
24067	Gene Function Prediction from Functional Association Networks Using Kernel Partial Least Squares Regression. PLoS ONE, 2015, 10, e0134668.	1.1	15
24068	Draft De Novo Transcriptome of the Rat Kangaroo Potorous tridactylus as a Tool for Cell Biology. PLoS ONE, 2015, 10, e0134738.	1.1	18
24069	Proteomic Analysis of Disease Stratified Human Pancreas Tissue Indicates Unique Signature of Type 1 Diabetes. PLoS ONE, 2015, 10, e0135663.	1.1	22
24070	A Catalog of Proteins Expressed in the AG Secreted Fluid during the Mature Phase of the Chinese Mitten Crabs (<i>Eriocheir sinensis</i>). PLoS ONE, 2015, 10, e0136266.	1.1	3
24071	A Survey of the ATP-Binding Cassette (ABC) Gene Superfamily in the Salmon Louse (<i>Lepeophtheirus</i>) Tj ETQq1 1 0.784314 rgBT /Overb 1.1 19	1.1	19
24072	Negative Regulation of p21Waf1/Cip1 by Human INO80 Chromatin Remodeling Complex Is Implicated in Cell Cycle Phase G2/M Arrest and Abnormal Chromosome Stability. PLoS ONE, 2015, 10, e0137411.	1.1	20
24073	Identification of Gene-Expression Signatures and Protein Markers for Breast Cancer Grading and Staging. PLoS ONE, 2015, 10, e0138213.	1.1	30
24074	Site-Specific Ser/Thr/Tyr Phosphoproteome of <i>Sinorhizobium meliloti</i> at Stationary Phase. PLoS ONE, 2015, 10, e0139143.	1.1	11
24075	Comparative Characterization of Cardiac Development Specific microRNAs: Fetal Regulators for Future. PLoS ONE, 2015, 10, e0139359.	1.1	11
24076	Gene-Set Local Hierarchical Clustering (GSLHC)â€”A Gene Set-Based Approach for Characterizing Bioactive Compounds in Terms of Biological Functional Groups. PLoS ONE, 2015, 10, e0139889.	1.1	8
24077	Increased Transcript Complexity in Genes Associated with Chronic Obstructive Pulmonary Disease. PLoS ONE, 2015, 10, e0140885.	1.1	18
24078	Transcriptional Profile of <i>Bacillus subtilis</i> sigF-Mutant during Vegetative Growth. PLoS ONE, 2015, 10, e0141553.	1.1	8
24079	From System-Wide Differential Gene Expression to Perturbed Regulatory Factors: A Combinatorial Approach. PLoS ONE, 2015, 10, e0142147.	1.1	2

#	ARTICLE	IF	CITATIONS
24080	Transcriptome Analysis of <i>Syringa oblata</i> Lindl. Inflorescence Identifies Genes Associated with Pigment Biosynthesis and Scent Metabolism. PLoS ONE, 2015, 10, e0142542.	1.1	34
24081	Bringing Down Cancer Aircraft: Searching for Essential Hypomutated Proteins in Skin Melanoma. PLoS ONE, 2015, 10, e0142819.	1.1	14
24082	Gonadal Transcriptome Analysis in Sterile Double Haploid Japanese Flounder. PLoS ONE, 2015, 10, e0143204.	1.1	10
24083	Detecting Protein Complexes in Protein Interaction Networks Modeled as Gene Expression Biclusters. PLoS ONE, 2015, 10, e0144163.	1.1	30
24084	Tissue Restricted Splice Junctions Originate Not Only from Tissue-Specific Gene Loci, but Gene Loci with a Broad Pattern of Expression. PLoS ONE, 2015, 10, e0144302.	1.1	20
24085	Label-Free Quantitative Proteomic Analysis of <i>Puccinia psidii</i> Uredospores Reveals Differences of Fungal Populations Infecting Eucalyptus and Guava. PLoS ONE, 2016, 11, e0145343.	1.1	18
24086	miRLAB: An R Based Dry Lab for Exploring miRNA-mRNA Regulatory Relationships. PLoS ONE, 2015, 10, e0145386.	1.1	33
24087	Brain Transcriptomic Response to Social Eavesdropping in Zebrafish (<i>Danio rerio</i>). PLoS ONE, 2015, 10, e0145801.	1.1	21
24088	Selecting Superior De Novo Transcriptome Assemblies: Lessons Learned by Leveraging the Best Plant Genome. PLoS ONE, 2016, 11, e0146062.	1.1	93
24089	Transcription Factors Exhibit Differential Conservation in Bacteria with Reduced Genomes. PLoS ONE, 2016, 11, e0146901.	1.1	19
24090	De Novo Transcriptome Assembly of the Chinese Swamp Buffalo by RNA Sequencing and SSR Marker Discovery. PLoS ONE, 2016, 11, e0147132.	1.1	43
24091	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
24092	Uncovering New Pathogen-Host Protein-Protein Interactions by Pairwise Structure Similarity. PLoS ONE, 2016, 11, e0147612.	1.1	13
24093	Transcriptomic Determinants of Scrapie Prion Propagation in Cultured Ovine Microglia. PLoS ONE, 2016, 11, e0147727.	1.1	13
24094	Identification of Genes Relevant to Pesticides and Biology from Global Transcriptome Data of <i>Monochamus alternatus</i> Hope (Coleoptera: Cerambycidae) Larvae. PLoS ONE, 2016, 11, e0147855.	1.1	19
24095	Characterising Complex Enzyme Reaction Data. PLoS ONE, 2016, 11, e0147952.	1.1	13
24096	Transcriptome and Expression Patterns of Chemosensory Genes in Antennae of the Parasitoid Wasp <i>Chouioia cunea</i> . PLoS ONE, 2016, 11, e0148159.	1.1	53
24097	Novel Biomarker Proteins in Chronic Lymphocytic Leukemia: Impact on Diagnosis, Prognosis and Treatment. PLoS ONE, 2016, 11, e0148500.	1.1	13

#	ARTICLE	IF	CITATIONS
24098	Muscle Logic: New Knowledge Resource for Anatomy Enables Comprehensive Searches of the Literature on the Feeding Muscles of Mammals. PLoS ONE, 2016, 11, e0149102.	1.1	5
24099	Analysis of the <i>Phialocephala subalpina</i> Transcriptome during Colonization of Its Host Plant <i>Picea abies</i> . PLoS ONE, 2016, 11, e0150591.	1.1	11
24100	ENTPRISE: An Algorithm for Predicting Human Disease-Associated Amino Acid Substitutions from Sequence Entropy and Predicted Protein Structures. PLoS ONE, 2016, 11, e0150965.	1.1	23
24101	Genetic Divergence between <i>Camellia sinensis</i> and Its Wild Relatives Revealed via Genome-Wide SNPs from RAD Sequencing. PLoS ONE, 2016, 11, e0151424.	1.1	72
24102	Proteomic Profiling of Mouse Liver following Acute <i>Toxoplasma gondii</i> Infection. PLoS ONE, 2016, 11, e0152022.	1.1	66
24103	Human Milk Cells and Lipids Conserve Numerous Known and Novel miRNAs, Some of Which Are Differentially Expressed during Lactation. PLoS ONE, 2016, 11, e0152610.	1.1	58
24104	Targeted Sequencing and Meta-Analysis of Preterm Birth. PLoS ONE, 2016, 11, e0155021.	1.1	13
24105	Independent Evolution of Winner Traits without Whole Genome Duplication in <i>Dekkera</i> Yeasts. PLoS ONE, 2016, 11, e0155140.	1.1	6
24106	Comparative Genomics of Pathogens Causing Brown Spot Disease of Tobacco: <i>Alternaria longipes</i> and <i>Alternaria alternata</i> . PLoS ONE, 2016, 11, e0155258.	1.1	42
24107	Generating Gene Ontology-Disease Inferences to Explore Mechanisms of Human Disease at the Comparative Toxicogenomics Database. PLoS ONE, 2016, 11, e0155530.	1.1	24
24108	Identifying Aspects of the Post-Transcriptional Program Governing the Proteome of the Green Alga <i>Micromonas pusilla</i> . PLoS ONE, 2016, 11, e0155839.	1.1	7
24109	Genomic Characteristics of Genetic Creutzfeldt-Jakob Disease Patients with V180I Mutation and Associations with Other Neurodegenerative Disorders. PLoS ONE, 2016, 11, e0157540.	1.1	7
24110	Comparative Digital Gene Expression Analysis of the <i>Arabidopsis</i> Response to Volatiles Emitted by <i>Bacillus amyloliquefaciens</i> . PLoS ONE, 2016, 11, e0158621.	1.1	41
24111	Comparative Transcriptome Analysis of Resistant and Susceptible Common Bean Genotypes in Response to Soybean Cyst Nematode Infection. PLoS ONE, 2016, 11, e0159338.	1.1	54
24112	SILAC-MS Based Characterization of LPS and Resveratrol Induced Changes in Adipocyte Proteomics – Resveratrol as Ameliorating Factor on LPS Induced Changes. PLoS ONE, 2016, 11, e0159747.	1.1	17
24113	Meta-Analysis of Parkinson's Disease Transcriptome Data Using TRAM Software: Whole Substantia Nigra Tissue and Single Dopamine Neuron Differential Gene Expression. PLoS ONE, 2016, 11, e0161567.	1.1	71
24114	Identification of Genes Potentially Associated with the Fertility Instability of S-Type Cytoplasmic Male Sterility in Maize via Bulk Segregant RNA-Seq. PLoS ONE, 2016, 11, e0163489.	1.1	37
24115	Changes to the Aqueous Humor Proteome during Glaucoma. PLoS ONE, 2016, 11, e0165314.	1.1	53

#	ARTICLE	IF	CITATIONS
24116	An Integrative Analysis of Preeclampsia Based on the Construction of an Extended Composite Network Featuring Protein-Protein Physical Interactions and Transcriptional Relationships. PLoS ONE, 2016, 11, e0165849.	1.1	13
24117	Transcriptome Profiling of Watermelon Root in Response to Short-Term Osmotic Stress. PLoS ONE, 2016, 11, e0166314.	1.1	20
24118	Global Deletion of TSPO Does Not Affect the Viability and Gene Expression Profile. PLoS ONE, 2016, 11, e0167307.	1.1	32
24119	Transcriptomic Changes in Liver of Young Bulls Caused by Diets Low in Mineral and Protein Contents and Supplemented with n-3 Fatty Acids and Conjugated Linoleic Acid. PLoS ONE, 2016, 11, e0167747.	1.1	8
24120	Integrity of Induced Pluripotent Stem Cell (iPSC) Derived Megakaryocytes as Assessed by Genetic and Transcriptomic Analysis. PLoS ONE, 2017, 12, e0167794.	1.1	9
24121	Functional Analyses of the Crohn's Disease Risk Gene LACC1. PLoS ONE, 2016, 11, e0168276.	1.1	24
24122	Integrated Analysis of Long Noncoding RNA and mRNA Expression Profile in Advanced Laryngeal Squamous Cell Carcinoma. PLoS ONE, 2016, 11, e0169232.	1.1	51
24123	Human Lacrimal Gland Gene Expression. PLoS ONE, 2017, 12, e0169346.	1.1	12
24124	Expression Quantitative Trait loci (QTL) in tumor adjacent normal breast tissue and breast tumor tissue. PLoS ONE, 2017, 12, e0170181.	1.1	12
24125	CyNetSVM: A Cytoscape App for Cancer Biomarker Identification Using Network Constrained Support Vector Machines. PLoS ONE, 2017, 12, e0170482.	1.1	5
24126	Transcriptome analysis of hexaploid hullless oat in response to salinity stress. PLoS ONE, 2017, 12, e0171451.	1.1	41
24127	Evolution of protein-protein interaction networks in yeast. PLoS ONE, 2017, 12, e0171920.	1.1	24
24128	Cyclin Y-mediated transcript profiling reveals several important functional pathways regulated by Cyclin Y in hippocampal neurons. PLoS ONE, 2017, 12, e0172547.	1.1	11
24129	Transcriptomes of three species of Tipuloidea (Diptera, Tipulomorpha) and implications for phylogeny of Tipulomorpha. PLoS ONE, 2017, 12, e0173207.	1.1	14
24130	Enhancement of Arabidopsis growth characteristics using genome interrogation with artificial transcription factors. PLoS ONE, 2017, 12, e0174236.	1.1	7
24131	Multiple components of PKA and TGF- β pathways are mutated in pseudomyxoma peritonei. PLoS ONE, 2017, 12, e0174898.	1.1	15
24132	Integrated network analysis reveals potentially novel molecular mechanisms and therapeutic targets of refractory epilepsies. PLoS ONE, 2017, 12, e0174964.	1.1	13
24133	Cyclosporine A alters expression of renal microRNAs: New insights into calcineurin inhibitor nephrotoxicity. PLoS ONE, 2017, 12, e0175242.	1.1	35

#	ARTICLE	IF	CITATIONS
24134	Genetic variant of miR-4293 rs12220909 is associated with susceptibility to non-small cell lung cancer in a Chinese Han population. PLoS ONE, 2017, 12, e0175666.	1.1	11
24135	Properties of genes essential for mouse development. PLoS ONE, 2017, 12, e0178273.	1.1	17
24136	De novo characterization of the pine aphid <i>Cinara pinitabulaeformis</i> Zhang et Zhang transcriptome and analysis of genes relevant to pesticides. PLoS ONE, 2017, 12, e0178496.	1.1	7
24137	Proteome profiling in IL-1 β and VEGF-activated human umbilical vein endothelial cells delineates the interlink between inflammation and angiogenesis. PLoS ONE, 2017, 12, e0179065.	1.1	64
24138	De novo transcriptomic analysis and development of EST-SSRs for <i>Sorbus pohuashanensis</i> (Hance) Hedl.. PLoS ONE, 2017, 12, e0179219.	1.1	16
24139	RBM10 promotes transformation-associated processes in small cell lung cancer and is directly regulated by RBM5. PLoS ONE, 2017, 12, e0180258.	1.1	25
24140	Affected pathways and transcriptional regulators in gene expression response to an ultra-marathon trail: Global and independent activity approaches. PLoS ONE, 2017, 12, e0180322.	1.1	7
24141	Enriching plausible new hypothesis generation in PubMed. PLoS ONE, 2017, 12, e0180539.	1.1	15
24142	Resequencing and variation identification of whole genome of the japonica rice variety "Longdao24" with high yield. PLoS ONE, 2017, 12, e0181037.	1.1	9
24143	The prediction of late-onset preeclampsia: Results from a longitudinal proteomics study. PLoS ONE, 2017, 12, e0181468.	1.1	84
24144	Novel and ultra-rare damaging variants in neuropeptide signaling are associated with disordered eating behaviors. PLoS ONE, 2017, 12, e0181556.	1.1	37
24145	Differential regulation of germ line apoptosis and germ cell differentiation by CPEB family members in <i>C. elegans</i> . PLoS ONE, 2017, 12, e0182270.	1.1	5
24146	Characterization of the genome of a phylogenetically distinct tospovirus and its interactions with the local lesion-induced host <i>Chenopodium quinoa</i> by whole-transcriptome analyses. PLoS ONE, 2017, 12, e0182425.	1.1	11
24147	Multi-tissue RNA-seq and transcriptome characterisation of the spiny dogfish shark (<i>Squalus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 osmoregulation. PLoS ONE, 2017, 12, e0182756.	1.1	22
24148	Genome-wide association analysis reveals genetic loci and candidate genes for feeding behavior and eating efficiency in Duroc boars. PLoS ONE, 2017, 12, e0183244.	1.1	34
24149	Proteome dynamics and physiological responses to short-term salt stress in <i>Leymus chinensis</i> leaves. PLoS ONE, 2017, 12, e0183615.	1.1	25
24150	Hsp70/J-protein machinery from <i>Glossina morsitans morsitans</i> , vector of African trypanosomiasis. PLoS ONE, 2017, 12, e0183858.	1.1	1
24151	Whole-genome sequencing reveals mutational landscape underlying phenotypic differences between two widespread Chinese cattle breeds. PLoS ONE, 2017, 12, e0183921.	1.1	33

#	ARTICLE	IF	CITATIONS
24152	De novo transcriptome assembly and analysis of differential gene expression in response to drought in European beech. PLoS ONE, 2017, 12, e0184167.	1.1	28
24153	Comparative proteomic analysis of pituitary glands from Huoyan geese between pre-laying and laying periods using an iTRAQ-based approach. PLoS ONE, 2017, 12, e0185253.	1.1	6
24154	A draft genome sequence of the rose black spot fungus <i>Diplocarpon rosae</i> reveals a high degree of genome duplication. PLoS ONE, 2017, 12, e0185310.	1.1	8
24155	A novel network analysis approach reveals DNA damage, oxidative stress and calcium/cAMP homeostasis-associated biomarkers in frontotemporal dementia. PLoS ONE, 2017, 12, e0185797.	1.1	21
24156	Hsp90-downregulation influences the heat-shock response, innate immune response and onset of oocyte development in nematodes. PLoS ONE, 2017, 12, e0186386.	1.1	15
24157	Insight into cordycepin biosynthesis of <i>Cordyceps militaris</i> : Comparison between a liquid surface culture and a submerged culture through transcriptomic analysis. PLoS ONE, 2017, 12, e0187052.	1.1	29
24158	Differential transcriptome analysis reveals genes related to cold tolerance in seabuckthorn carpenter moth, <i>Eogystia hippophaecolus</i> . PLoS ONE, 2017, 12, e0187105.	1.1	26
24159	Large-scale mapping of bioactive peptides in structural and sequence space. PLoS ONE, 2018, 13, e0191063.	1.1	18
24160	RNA-seq transcriptome analysis of the immature seeds of two <i>Brassica napus</i> lines with extremely different thousand-seed weight to identify the candidate genes related to seed weight. PLoS ONE, 2018, 13, e0191297.	1.1	13
24161	Cross-species multiple environmental stress responses: An integrated approach to identify candidate genes for multiple stress tolerance in sorghum (<i>Sorghum bicolor</i> (L.) Moench) and related model species. PLoS ONE, 2018, 13, e0192678.	1.1	24
24162	Why West? Comparisons of clinical, genetic and molecular features of infants with and without spasms. PLoS ONE, 2018, 13, e0193599.	1.1	28
24163	New drug candidates for treatment of atypical meningiomas: An integrated approach using gene expression signatures for drug repurposing. PLoS ONE, 2018, 13, e0194701.	1.1	18
24164	Burden of rare deleterious variants in WNT signaling genes among 511 myelomeningocele patients. PLoS ONE, 2020, 15, e0239083.	1.1	7
24165	Mining GWAS and eQTL data for CF lung disease modifiers by gene expression imputation. PLoS ONE, 2020, 15, e0239189.	1.1	9
24166	Transcriptomic signatures of cold adaptation and heat stress in the winter ant (<i>Prenolepis imparis</i>). PLoS ONE, 2020, 15, e0239558.	1.1	6
24167	Lipopolysaccharide triggers different transcriptional signatures in taurine and indicine cattle macrophages: Reactive oxygen species and potential outcomes to the development of immune response to infections. PLoS ONE, 2020, 15, e0241861.	1.1	5
24168	Genome-wide profiling of alternative splicing genes in hybrid poplar (<i>P.alba</i> — <i>P.glandulosa</i> cv.84K) leaves. PLoS ONE, 2020, 15, e0241914.	1.1	6
24169	A thorough analysis of the contribution of experimental, derived and sequence-based predicted protein-protein interactions for functional annotation of proteins. PLoS ONE, 2020, 15, e0242723.	1.1	2

#	ARTICLE	IF	CITATIONS
24170	Identifying transcriptomic correlates of histology using deep learning. PLoS ONE, 2020, 15, e0242858.	1.1	12
24171	Essential gene prediction using limited gene essentiality information—An integrative semi-supervised machine learning strategy. PLoS ONE, 2020, 15, e0242943.	1.1	8
24172	Composition and origin of lung fluid proteome in premature infants and relationship to respiratory outcome. PLoS ONE, 2020, 15, e0243168.	1.1	3
24173	PEREGRINE: A genome-wide prediction of enhancer to gene relationships supported by experimental evidence. PLoS ONE, 2020, 15, e0243791.	1.1	12
24174	CD39 Expression Identifies Terminally Exhausted CD8+ T Cells. PLoS Pathogens, 2015, 11, e1005177.	2.1	296
24175	Transcriptome Remodeling in Trypanosoma cruzi and Human Cells during Intracellular Infection. PLoS Pathogens, 2016, 12, e1005511.	2.1	157
24176	Overexpression of Differentially Expressed Genes Identified in Non-pathogenic and Pathogenic Entamoeba histolytica Clones Allow Identification of New Pathogenicity Factors Involved in Amoebic Liver Abscess Formation. PLoS Pathogens, 2016, 12, e1005853.	2.1	35
24177	Herpesvirus deconjugases inhibit the IFN response by promoting TRIM25 autoubiquitination and functional inactivation of the RIG-I signalosome. PLoS Pathogens, 2018, 14, e1006852.	2.1	56
24178	Epistatic and environmental control of genome-wide gene expression. Twin Research and Human Genetics, 2005, 8, 5-15.	0.3	7
24179	Phototransduction genes are up-regulated in a global gene expression study of Drosophila melanogaster selected for heat resistance. Cell Stress and Chaperones, 2006, 11, 325.	1.2	23
24180	Life-giving caspases: revealing new roles during mouse embryo preimplantation development. International Journal of Developmental Biology, 2010, 54, 857-865.	0.3	11
24181	Knowledge-based bioinformatics for the study of mammalian oocytes. International Journal of Developmental Biology, 2012, 56, 859-866.	0.3	1
24182	STSM: An Infrastructure for Unifying Steel Knowledge and Discovering New Knowledge. International Journal of Database Theory and Application, 2014, 7, 175-190.	0.2	6
24183	The Chromosomal and Functional Clustering of Markedly Divergent Human-Mouse Orthologs Run Parallel to their Compositional Features. Journal of DNA and RNA Research, 2016, 1, 31-49.	1.0	4
24184	Analysis of Genes with Alternatively Spliced Transcripts in the Leaf, Root, Panicle and Seed of Rice Using a Long Oligomer Microarray and RNA-Seq. Molecules and Cells, 2017, 40, 714-730.	1.0	28
24185	NGSEA: Network-Based Gene Set Enrichment Analysis for Interpreting Gene Expression Phenotypes with Functional Gene Sets. Molecules and Cells, 2019, 42, 579-588.	1.0	13
24186	Comparative Analysis of Methodologies for Domain Ontology Development: A Systematic Review. International Journal of Advanced Computer Science and Applications, 2020, 11, .	0.5	12
24187	A toxicology ontology roadmap. ALTEX: Alternatives To Animal Experimentation, 2012, 29, 129-137.	0.9	22

#	ARTICLE	IF	CITATIONS
24188	Bioinformatic analysis reveals CYP2C9 as a potential prognostic marker for HCC and liver cancer cell lines suitable for its mechanism study. Cellular and Molecular Biology, 2018, 64, 70-74.	0.3	20
24189	Possible key microRNAs and corresponding molecular mechanisms for atrial fibrillation. Anatolian Journal of Cardiology, 2020, 23, 324-333.	0.5	4
24190	RelB deficiency causes combined immunodeficiency. LymphoSign Journal, 2015, 2, 147-155.	0.1	21
24191	NEUROD2 Regulates <i>Stim1</i> Expression and Store-Operated Calcium Entry in Cortical Neurons. ENeuro, 2017, 4, ENEURO.0255-16.2017.	0.9	20
24192	Donor-Specific Transcriptomic Analysis of Alzheimer's Disease-Associated Hypometabolism Highlights a Unique Donor, Ribosomal Proteins and Microglia. ENeuro, 2020, 7, ENEURO.0255-20.2020.	0.9	5
24193	A stress-induced tyrosine-tRNA depletion response mediates codon-based translational repression and growth suppression. EMBO Journal, 2021, 40, e106696.	3.5	25
24194	The impact of the genetic background on gene deletion phenotypes in <i>Saccharomyces cerevisiae</i> . Molecular Systems Biology, 2019, 15, e8831.	3.2	44
24195	<i>SBML</i> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	3.2	178
24196	Mapping the nucleolar proteome reveals a spatiotemporal organization related to intrinsic protein disorder. Molecular Systems Biology, 2020, 16, e9469.	3.2	91
24197	Androgen deprivation therapy promotes an obesity-like microenvironment in periprostatic fat. Endocrine Connections, 2019, 8, 547-558.	0.8	16
24198	Generation and characterization of a mitotane-resistant adrenocortical cell line. Endocrine Connections, 2020, 9, 122-134.	0.8	11
24199	Circ-Tulp4 promotes β -cell adaptation to lipotoxicity by regulating <i>soat1</i> expression. Journal of Molecular Endocrinology, 2020, 65, 149-161.	1.1	21
24200	Uterine fluid proteome changes during diapause and resumption of embryo development in roe deer (<i>Capreolus capreolus</i>). Reproduction, 2019, 158, 13-24.	1.1	15
24201	Application of Transcriptional Gene Modules to Analysis of <i>Caenorhabditis elegans</i> Gene Expression Data. G3: Genes, Genomes, Genetics, 2020, 10, 3623-3638.	0.8	8
24202	Intronic miRNA miR-3666 Modulates its Host Gene FOXP2 Functions in Neurodevelopment and May Contribute to Pathogenesis of Neurological Disorders Schizophrenia and Autism. Journal of Applied Biotechnology & Bioengineering, 2017, 2, .	0.0	1
24203	Myths of the Baltic Sea eutrophication. Journal of Aquaculture & Marine Biology, 2018, 7, .	0.2	2
24204	Gene Ontology: A Resource for Analysis and Interpretation of Alzheimer's Disease Data. , 0, , 23-36.		9
24205	Construction and evaluation of yeast expression networks by database-guided predictions. Microbial Cell, 2016, 3, 236-247.	1.4	7

#	ARTICLE	IF	CITATIONS
24206	Genome-wide analysis of yeast expression data based on a priori generated co-regulation cliques. <i>Microbial Cell</i> , 2019, 6, 160-176.	1.4	2
24207	Integrative representations and analyses of vaccine-induced intended protective immunity and unintended adverse events using ontology-based and theory-guided approaches. <i>Global Vaccines and Immunology</i> , 2016, 1, 37-39.	0.2	3
24208	An overview of integrative analysis in cancer studies. <i>Integrative Cancer Science and Therapeutics</i> , 2016, 3, 484-485.	0.1	4
24209	Identification of the molecular mechanisms associated with acute type A aortic dissection through bioinformatics methods. <i>Brazilian Journal of Medical and Biological Research</i> , 2019, 52, e8950.	0.7	11
24210	Differential gene expression in response to water deficit in leaf and root tissues of soybean genotypes with contrasting tolerance profiles. <i>Genetics and Molecular Biology</i> , 2020, 43, e20180290.	0.6	5
24211	Integrated analysis of lncRNA-associated ceRNA network identified potential regulatory interactions in osteosarcoma. <i>Genetics and Molecular Biology</i> , 2020, 43, e20190090.	0.6	4
24212	A comparison of mRNA and circRNA expression between squamous cell carcinoma and adenocarcinoma of the lungs. <i>Genetics and Molecular Biology</i> , 2020, 43, e20200054.	0.6	7
24213	Protein identification from the parotoid macrogland secretion of <i>Duttaphrynus melanostictus</i> . <i>Journal of Venomous Animals and Toxins Including Tropical Diseases</i> , 2019, 25, e20190029.	0.8	8
24214	In-depth transcriptome reveals the potential biotechnological application of <i>Bothrops jararaca</i> venom gland. <i>Journal of Venomous Animals and Toxins Including Tropical Diseases</i> , 2020, 26, e20190058.	0.8	4
24215	Marcadores moleculares derivados de sequências expressas do genoma café potencialmente envolvidas na resistência à ferrugem. <i>Pesquisa Agropecuária Brasileira</i> , 2011, 46, 890-898.	0.9	6
24216	Expressed cDNAs from Embryonic and Larval Stages of the Horn Fly (Diptera: Muscidae). <i>Journal of Medical Entomology</i> , 2008, 45, 686-692.	0.9	6
24217	Automated Reasoning in Modal and Description Logics via SAT Encoding: the Case Study of K(m)/ALC-Satisfiability. <i>Journal of Artificial Intelligence Research</i> , 0, 35, 343-389.	7.0	17
24218	Semantic Similarity Measures Applied to an Ontology for Human-Like Interaction. <i>Journal of Artificial Intelligence Research</i> , 0, 44, 397-421.	7.0	6
24219	Combining Two and Three-Way Embedding Models for Link Prediction in Knowledge Bases. <i>Journal of Artificial Intelligence Research</i> , 0, 55, 715-742.	7.0	30
24220	Expression Level Dominance and Homeolog Expression Bias in Recurrent Origins of the Allopolyploid Fern <i>Polypodium hesperium</i> . <i>American Fern Journal</i> , 2019, 109, 224.	0.2	14
24221	Effect of Ionizing Radiation on Transcriptome during Neural Differentiation of Human Embryonic Stem Cells. <i>Radiation Research</i> , 2020, 193, 460.	0.7	5
24222	Computational Ontologies and Information Systems II: Formal Specification. <i>Communications of the Association for Information Systems</i> , 0, 14, .	0.7	13
24223	Improving Usability of Social and Behavioral Sciences™ Evidence: A Call to Action for a National Infrastructure Project for Mining Our Knowledge. <i>Communications of the Association for Information Systems</i> , 0, , 1-17.	0.7	5

#	ARTICLE	IF	CITATIONS
24224	Two new functions in the WormBase Enrichment Suite. <i>MicroPublication Biology</i> , 2018, 2018, .	0.1	45
24225	iTRAQ-based proteomics analysis of aqueous humor in patients with dry age-related macular degeneration. <i>International Journal of Ophthalmology</i> , 2019, 12, 1758-1766.	0.5	18
24226	Gene expression alterations induced by low molecular weight heparin during bowel anastomosis healing in rats.. <i>Acta Biochimica Polonica</i> , 2011, 58, .	0.3	3
24227	Detecting epistasis via Markov bases. <i>Journal of Algebraic Statistics</i> , 2015, 2, .	0.6	3
24228	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
24229	Molecular links between cellular senescence, longevity and age-related diseases – a systems biology perspective. <i>Aging</i> , 2011, 3, 1178-1191.	1.4	119
24230	Dietary switch reveals fast coordinated gene expression changes in <i>Drosophila melanogaster</i> . <i>Aging</i> , 2014, 6, 355-368.	1.4	47
24231	Higher expression of somatic repair genes in long-lived ant queens than workers. <i>Aging</i> , 2016, 8, 1940-1951.	1.4	28
24232	An intestinal microRNA modulates the homeostatic adaptation to chronic oxidative stress in <i>C. elegans</i> . <i>Aging</i> , 2016, 8, 1979-2005.	1.4	29
24233	Higher gene expression stability during aging in long-lived giant mole-rats than in short-lived rats. <i>Aging</i> , 2018, 10, 3938-3956.	1.4	16
24234	A novel alternative splicing-based prediction model for uteri corpus endometrial carcinoma. <i>Aging</i> , 2019, 11, 263-283.	1.4	16
24235	The acute transcriptional response to resistance exercise: impact of age and contraction mode. <i>Aging</i> , 2019, 11, 2111-2126.	1.4	14
24236	Prediction of competing endogenous RNA coexpression network as prognostic markers in AML. <i>Aging</i> , 2019, 11, 3333-3347.	1.4	43
24237	Prognostic value and immune infiltration of novel signatures in clear cell renal cell carcinoma microenvironment. <i>Aging</i> , 2019, 11, 6999-7020.	1.4	163
24238	Cognitive impairment and transcriptomic profile in hippocampus of young mice after multiple neonatal exposures to sevoflurane. <i>Aging</i> , 2019, 11, 8386-8417.	1.4	32
24239	Systematic identification of lncRNA-based prognostic biomarkers for glioblastoma. <i>Aging</i> , 2019, 11, 9405-9423.	1.4	13
24240	Screening, identification and validation of CCND1 and PECAM1/CD31 for predicting prognosis in renal cell carcinoma patients. <i>Aging</i> , 2019, 11, 12057-12079.	1.4	26
24241	Development and validation of a nomogram with an autophagy-related gene signature for predicting survival in patients with glioblastoma. <i>Aging</i> , 2019, 11, 12246-12269.	1.4	79

#	ARTICLE	IF	CITATIONS
24242	ASPM promotes glioblastoma growth by regulating G1 restriction point progression and Wnt- β -catenin signaling. <i>Aging</i> , 2020, 12, 224-241.	1.4	30
24243	Identification of 34 genes conferring genetic and pharmacological risk for the comorbidity of schizophrenia and smoking behaviors. <i>Aging</i> , 2020, 12, 2169-2225.	1.4	15
24244	ESHRD: deconvolution of brain homogenate RNA expression data to identify cell-type-specific alterations in Alzheimer's disease. <i>Aging</i> , 2020, 12, 4124-4162.	1.4	4
24245	Identification of frailty-associated genes by coordination analysis of gene expression. <i>Aging</i> , 2020, 12, 4222-4229.	1.4	9
24246	Comprehensive analysis of circular RNA profiles in skeletal muscles of aging mice and after aerobic exercise intervention. <i>Aging</i> , 2020, 12, 5071-5090.	1.4	20
24247	Identification of transforming growth factor beta induced (TGFB1) as an immune-related prognostic factor in clear cell renal cell carcinoma (ccRCC). <i>Aging</i> , 2020, 12, 8484-8505.	1.4	16
24248	Identification of potential novel differentially-expressed genes and their role in invasion and migration in renal cell carcinoma. <i>Aging</i> , 2020, 12, 9205-9223.	1.4	4
24249	Multi-omics network analysis reveals distinct stages in the human aging progression in epidermal tissue. <i>Aging</i> , 2020, 12, 12393-12409.	1.4	21
24250	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
24251	LINC01235-TWIST2 feedback loop facilitates epithelial-mesenchymal transition in gastric cancer by inhibiting THBS2. <i>Aging</i> , 2020, 12, 25060-25075.	1.4	19
24252	In-depth transcriptomic analyses of lncRNA and mRNA expression in the hippocampus of APP/PS1 mice by Danggui-Shaoyao-San. <i>Aging</i> , 2020, 12, 23945-23959.	1.4	9
24253	Identification and validation of an immune-related gene signature predictive of overall survival in colon cancer. <i>Aging</i> , 2020, 12, 26095-26120.	1.4	35
24254	Enhanced MYC association with the NuA4 histone acetyltransferase complex mediated by the adenovirus E1A N-terminal domain activates a subset of MYC target genes highly expressed in cancer cells. <i>Genes and Cancer</i> , 2017, 8, 752-761.	0.6	9
24255	Identification of a panel of MYC and Tip60 co-regulated genes functioning primarily in cell cycle and DNA replication. <i>Genes and Cancer</i> , 2018, 9, 101-113.	0.6	3
24256	Comprehensive analysis of lncRNAs microarray profile and mRNA-lncRNA co-expression in oncogenic HPV-positive cervical cancer cell lines. <i>Oncotarget</i> , 2016, 7, 49917-49929.	0.8	38
24257	Association of multiparametric MRI quantitative imaging features with prostate cancer gene expression in MRI-targeted prostate biopsies. <i>Oncotarget</i> , 2016, 7, 53362-53376.	0.8	90
24258	Identification of biomarkers for pseudo and true progression of GBM based on radiogenomics study. <i>Oncotarget</i> , 2016, 7, 55377-55394.	0.8	29
24259	Prelplantation factor (PIF) therapy provides comprehensive protection against radiation induced pathologies. <i>Oncotarget</i> , 2016, 7, 58975-58994.	0.8	17

#	ARTICLE	IF	CITATIONS
24260	Partial loss of interleukin 2 receptor gamma function in pigs provides mechanistic insights for the study of human immunodeficiency syndrome. <i>Oncotarget</i> , 2016, 7, 50914-50926.	0.8	8
24261	Repair of UVB-induced DNA damage is reduced in melanoma due to low XPC and global genome repair. <i>Oncotarget</i> , 2016, 7, 60940-60953.	0.8	28
24262	Constructing Bayesian networks by integrating gene expression and copy number data identifies <i>NLGN4Y</i> as a novel regulator of prostate cancer progression. <i>Oncotarget</i> , 2016, 7, 68688-68707.	0.8	10
24263	Proteomic analysis reveals diverse proline hydroxylation-mediated oxygen-sensing cellular pathways in cancer cells. <i>Oncotarget</i> , 2016, 7, 79154-79169.	0.8	26
24264	Identification of potential genes for human ischemic cardiomyopathy based on RNA-Seq data. <i>Oncotarget</i> , 2016, 7, 82063-82073.	0.8	7
24265	Altered microRNA profiles in plasma exosomes from mesial temporal lobe epilepsy with hippocampal sclerosis. <i>Oncotarget</i> , 2017, 8, 4136-4146.	0.8	105
24266	High throughput estimation of functional cell activities reveals disease mechanisms and predicts relevant clinical outcomes. <i>Oncotarget</i> , 2017, 8, 5160-5178.	0.8	66
24267	Talin-1 interaction network promotes hepatocellular carcinoma progression. <i>Oncotarget</i> , 2017, 8, 13003-13014.	0.8	13
24268	Clinical significance and effect of AEG-1 on the proliferation, invasion, and migration of NSCLC: a study based on immunohistochemistry, TCGA, bioinformatics, <i>in vitro</i> and <i>in vivo</i> verification. <i>Oncotarget</i> , 2017, 8, 16531-16552.	0.8	27
24269	Identification of driver modules in pan-cancer via coordinating coverage and exclusivity. <i>Oncotarget</i> , 2017, 8, 36115-36126.	0.8	19
24270	SEL120-34A is a novel CDK8 inhibitor active in AML cells with high levels of serine phosphorylation of STAT1 and STAT5 transactivation domains. <i>Oncotarget</i> , 2017, 8, 33779-33795.	0.8	70
24271	A subset of microRNAs defining the side population of a human malignant mesothelioma cell line. <i>Oncotarget</i> , 2017, 8, 42847-42856.	0.8	4
24272	Endoplasmic reticulum chaperone prolyl 4-hydroxylase, beta polypeptide (P4HB) promotes malignant phenotypes in glioma via MAPK signaling. <i>Oncotarget</i> , 2017, 8, 71911-71923.	0.8	21
24273	Genome-wide functional analysis on the molecular mechanism of specifically biosynthesized fluorescence Eu complex. <i>Oncotarget</i> , 2017, 8, 72082-72095.	0.8	3
24274	VEGF121, is predictor for survival in activated B-cell-like diffuse large B-cell lymphoma and is related to an immune response gene signature conserved in cancers. <i>Oncotarget</i> , 2017, 8, 90808-90824.	0.8	3
24275	Integrating omics data and protein interaction networks to prioritize driver genes in cancer. <i>Oncotarget</i> , 2017, 8, 58050-58060.	0.8	11
24276	RNA-seq based gene expression analysis of ovarian granulosa cells exposed to zearalenone <i>in vitro</i> : significance to steroidogenesis. <i>Oncotarget</i> , 2017, 8, 64001-64014.	0.8	23
24277	miR-101 is down-regulated in glioblastoma resulting in EZH2-induced proliferation, migration, and angiogenesis. <i>Oncotarget</i> , 2010, 1, 710-720.	0.8	217

#	ARTICLE	IF	CITATIONS
24278	PTEN regulates spindle assembly checkpoint timing through MAD1 in interphase. <i>Oncotarget</i> , 2017, 8, 98040-98050.	0.8	7
24279	Mutational analysis of primary central nervous system lymphoma. <i>Oncotarget</i> , 2014, 5, 5065-5075.	0.8	149
24280	MicroRNA-21 inhibits mitochondria-mediated apoptosis in keloid. <i>Oncotarget</i> , 2017, 8, 92914-92925.	0.8	26
24281	Differential prioritization of therapies to subtypes of triple negative breast cancer using a systems medicine method. <i>Oncotarget</i> , 2017, 8, 92926-92942.	0.8	6
24282	Proteome profiling of clear cell renal cell carcinoma in von Hippel-Lindau patients highlights upregulation of Xaa-Pro aminopeptidase-1, an anti-proliferative and anti-migratory exoprotease. <i>Oncotarget</i> , 2017, 8, 100066-100078.	0.8	13
24283	Differential gene expression profiles between two subtypes of ischemic stroke with blood stasis syndromes. <i>Oncotarget</i> , 2017, 8, 111608-111622.	0.8	6
24284	Identification of human age-associated gene co-expressions in functional modules using liquid association. <i>Oncotarget</i> , 2018, 9, 1063-1074.	0.8	16
24285	Identification and analysis of hub genes and networks related to hypoxia preconditioning in mice (No) Tj ETQq1 1 0,784314 rgBT /Over	0.8	9
24286	Analysis of a gene panel for targeted sequencing of colorectal cancer samples. <i>Oncotarget</i> , 2018, 9, 9043-9060.	0.8	8
24287	An integrative transcriptomic approach to identify depot differences in genes and microRNAs in adipose tissues from high fat fed mice. <i>Oncotarget</i> , 2018, 9, 9246-9261.	0.8	19
24288	Discovery and validation of a glioblastoma co-expressed gene module. <i>Oncotarget</i> , 2018, 9, 10995-11008.	0.8	15
24289	Identification of key pathways and genes in response to trastuzumab treatment in breast cancer using bioinformatics analysis. <i>Oncotarget</i> , 2018, 9, 32149-32160.	0.8	9
24290	Transcriptome profiling of anti-m β 4lllerian hormone treated preantral/small antral mouse ovary follicles. <i>Oncotarget</i> , 2018, 9, 30253-30267.	0.8	3
24291	A role for BMP-induced homeobox gene <i>MIXL1</i> in acute myelogenous leukemia and identification of type I BMP receptor as a potential target for therapy. <i>Oncotarget</i> , 2014, 5, 12675-12693.	0.8	19
24292	MicroRNA-based regulation of Aurora A kinase in breast cancer. <i>Oncotarget</i> , 2020, 11, 4306-4324.	0.8	11
24293	Gene expression profile predictive of response to chemotherapy in metastatic colorectal cancer. <i>Oncotarget</i> , 2015, 6, 6151-6159.	0.8	28
24294	BET inhibitor OTX015 targets BRD2 and BRD4 and decreases c-MYC in acute leukemia cells. <i>Oncotarget</i> , 2015, 6, 17698-17712.	0.8	225
24295	ErbB-3 activation by NRG-1 β sustains growth and promotes vemurafenib resistance in BRAF-V600E colon cancer stem cells (CSCs). <i>Oncotarget</i> , 2015, 6, 16902-16911.	0.8	29

#	ARTICLE	IF	CITATIONS
24296	LncRNA ontology: inferring lncRNA functions based on chromatin states and expression patterns. <i>Oncotarget</i> , 2015, 6, 39793-39805.	0.8	38
24297	A network-based method to evaluate quality of reproducibility of differential expression in cancer genomics studies. <i>Oncotarget</i> , 2015, 6, 44714-44727.	0.8	2
24298	The cytomegalovirus protein UL138 induces apoptosis of gastric cancer cells by binding to heat shock protein 70. <i>Oncotarget</i> , 2016, 7, 5630-5645.	0.8	10
24299	Cross-platform comparison of independent datasets identifies an immune signature associated with improved survival in metastatic melanoma. <i>Oncotarget</i> , 2016, 7, 14415-14428.	0.8	13
24300	Cinacalcet inhibits neuroblastoma tumor growth and upregulates cancer-testis antigens. <i>Oncotarget</i> , 2016, 7, 16112-16129.	0.8	19
24301	Common DNA methylation alterations of Alzheimer's disease and aging in peripheral whole blood. <i>Oncotarget</i> , 2016, 7, 19089-19098.	0.8	25
24302	In-depth analysis of secretome and N-glycosylome of human hepatocellular carcinoma metastatic cell lines shed light on metastasis correlated proteins. <i>Oncotarget</i> , 2016, 7, 22031-22049.	0.8	18
24303	ATG9A loss confers resistance to trastuzumab via c-Cbl mediated Her2 degradation. <i>Oncotarget</i> , 2016, 7, 27599-27612.	0.8	21
24304	Identification of a new gene regulatory circuit involving B cell receptor activated signaling using a combined analysis of experimental, clinical and global gene expression data. <i>Oncotarget</i> , 2016, 7, 47061-47081.	0.8	8
24305	Reprogramming human A375 amelanotic melanoma cells by catalase overexpression: Upregulation of antioxidant genes correlates with regression of melanoma malignancy and with malignant progression when downregulated. <i>Oncotarget</i> , 2016, 7, 41154-41171.	0.8	27
24306	Prospective evidence of a circulating microRNA signature as a non-invasive marker of hepatocellular carcinoma in HBV patients. <i>Oncotarget</i> , 2016, .	0.8	8
24307	Transcriptomic and proteomic analysis of mouse radiation-induced acute myeloid leukaemia (AML). <i>Oncotarget</i> , 2016, 7, 40461-40480.	0.8	6
24308	Genome-wide comparison of the transcriptomes of highly enriched normal and chronic myeloid leukemia stem and progenitor cell populations. <i>Oncotarget</i> , 2013, 4, 715-728.	0.8	92
24309	Knowledge Graph Embedding with Hierarchical Relation Structure. , 2018, , .		42
24310	CRAFT Shared Tasks 2019 Overview - Integrated Structure, Semantics, and Coreference. , 2019, , .		11
24311	Biomedical Event Extraction based on Knowledge-driven Tree-. , 2019, , .		21
24312	A Silver Standard Corpus of Human Phenotype-Gene Relations. , 2019, , .		19
24313	Inferring Concept Hierarchies from Text Corpora via Hyperbolic Embeddings. , 2019, , .		30

#	ARTICLE	IF	CITATIONS
24314	Complex Event Extraction using DRUM. , 2015, , .		12
24315	Proteomics Profiling of Chimeric-Truncated Tissue Plasminogen activator Producing- Chinese Hamster Ovary Cells Cultivated in a Chemically Defined Medium Supplemented with Protein Hydrolysates. Iranian Biomedical Journal, 2017, 21, 154-166.	0.4	4
24316	Genomic classification of protein-coding gene families. WormBook, 2005, , 1-23.	5.3	19
24317	From Markers to Molecular Mechanisms: Type 1 Diabetes in the Post-GWAS Era. Review of Diabetic Studies, 2012, 9, 201-223.	0.5	13
24318	A Pathway-based Gene Selection Method Provides Accurate Disease Classification. International Journal for Digital Society, 2011, 2, 571-578.	0.1	3
24319	Single-Cell RNA Sequencing of Visceral Adipose Tissue Leukocytes Reveals that Caloric Restriction Following Obesity Promotes the Accumulation of a Distinct Macrophage Population with Features of Phagocytic Cells. Immunometabolism, 2019, 1, .	0.7	63
24321	Blockade of AXL activation overcomes acquired resistance to EGFR tyrosine kinase inhibition in non-small cell lung cancer. Translational Cancer Research, 2019, 8, 2425-2438.	0.4	14
24322	A reusable tree-based web-visualization to browse EDAM ontology, and contribute to it.. Journal of Open Source Software, 2018, 3, 698.	2.0	2
24324	Identification of MicroRNAs and Their Targets Involved in Paeonia rockii Petal Variegation Using High-throughput Sequencing. Journal of the American Society for Horticultural Science, 2019, 144, 118-129.	0.5	5
24325	A Short Study on the Success of the Gene Ontology. SSRN Electronic Journal, 0, , .	0.4	3
24326	An Atlas of Protein-Protein Interactions Across Mammalian Tissues. SSRN Electronic Journal, 0, , .	0.4	8
24327	BNO - An Ontology for Understanding the Transittability of Complex Biomolecular Networks. SSRN Electronic Journal, 0, , .	0.4	1
24328	Pathogenic Tau Causes a Toxic Depletion of Nuclear Calcium Mediated by BK Channels. SSRN Electronic Journal, 0, , .	0.4	1
24329	Analysis of Differentially Expressed Genes in Necrotic Enteritis-infected Fayoumi Chickens using RNA Sequencing. Journal of Poultry Science, 2017, 54, 121-133.	0.7	5
24330	Assessing the Functional Bias of Commercial Microarrays Using the Onto-Compare Database. BioTechniques, 2003, 34, S55-S61.	0.8	13
24331	Evaluation of the proteomic profiles of ejaculated spermatozoa from Saanen bucks (Capra hircus). Animal Reproduction, 2019, 16, 902-913.	0.4	5
24332	A Novel Prediction of Quaternary Structural Type of Proteins with Gene Ontology. Protein and Peptide Letters, 2020, 27, 313-320.	0.4	2
24333	Ligand- and Structure-Based Drug Design and Optimization using KNIME. Current Medicinal Chemistry, 2020, 27, 6458-6479.	1.2	14

#	ARTICLE	IF	CITATIONS
24334	A Systems Medicine Clinical Platform for Understanding and Managing Non- Communicable Diseases. Current Pharmaceutical Design, 2014, 20, 5945-5956.	0.9	32
24335	RNAi-Based Functional Genomics in Caenorhabditis elegans. Current Genomics, 2002, 3, 69-81.	0.7	7
24336	A Systems Biology Study of Two Distinct Growth Phases of Saccharomyces cerevisiae Cultures. Current Genomics, 2004, 5, 649-663.	0.7	36
24337	System Level Meta-analysis of Microarray Datasets for Elucidation of Diabetes Mellitus Pathobiology. Current Genomics, 2017, 18, 298-304.	0.7	11
24338	Decoding Common Features of Neurodegenerative Disorders: From Differentially Expressed Genes to Pathways. Current Genomics, 2018, 19, 300-312.	0.7	21
24339	Computational Prediction of Ubiquitination Proteins Using Evolutionary Profiles and Functional Domain Annotation. Current Genomics, 2019, 20, 389-399.	0.7	11
24340	Comparative RNA-Seq Analysis of Differentially Expressed Genes in the Epididymides of Yak and Cattle. Current Genomics, 2019, 20, 293-305.	0.7	11
24341	Computational Methods for Identification of Functional Residues in Protein Structures. Current Protein and Peptide Science, 2011, 12, 456-469.	0.7	24
24342	Structure-Based Drug Discovery Accelerated by Many-Core Devices. Current Drug Targets, 2016, 17, 1595-1609.	1.0	6
24343	Integrated Analysis of mRNA-seq and miRNA-seq to Identify c-MYC, YAP1 and miR-3960 as Major Players in the Anticancer Effects of Caffeic Acid Phenethyl Ester in Human Small Cell Lung Cancer Cell Line. Current Gene Therapy, 2020, 20, 15-24.	0.9	34
24344	Diagnostic Value of MiR-125b as a Potential Biomarker for Stage I Lung Adenocarcinoma. Current Molecular Medicine, 2019, 19, 216-227.	0.6	23
24345	Ontologies in Medicinal Chemistry: Current Status and Future Challenges. Current Topics in Medicinal Chemistry, 2013, 13, 576-590.	1.0	2
24346	Bioinformatics Tools for the Functional Interpretation of Quantitative Proteomics Results. Current Topics in Medicinal Chemistry, 2014, 14, 435-449.	1.0	14
24347	Impacts of Bioinformatics to Medicinal Chemistry. Medicinal Chemistry, 2015, 11, 218-234.	0.7	496
24348	Computational RNA Structure Prediction. Current Bioinformatics, 2008, 3, 32-45.	0.7	37
24349	Predicting False Positives of Protein-Protein Interaction Data by Semantic Similarity Measures. Current Bioinformatics, 2013, 8, 339-346.	0.7	19
24350	Function Analysis of Human Protein Interactions Based on a Novel Minimal Loop Algorithm. Current Bioinformatics, 2019, 14, 164-173.	0.7	5
24351	The Regulation of Target Genes by Co-occupancy of Transcription Factors, c-Myc and Mxi1 with Max in the Mouse Cell Line. Current Bioinformatics, 2020, 15, 581-588.	0.7	9

#	ARTICLE	IF	CITATIONS
24352	Stability and Flexibility from a System Analysis of Gene Regulatory Networks Based on Ordinary Differential Equations. <i>Open Bioinformatics Journal</i> , 2011, 5, 26-33.	1.0	2
24353	Statistical Methods for Overdispersion in mRNA-Seq Count Data. <i>Open Bioinformatics Journal</i> , 2013, 7, 34-40.	1.0	8
24354	The Pathway Less Traveled: Moving from Candidate Genes to Candidate Pathways in the Analysis of Genome-Wide Data from Large Scale Pharmacogenetic Association Studies. <i>Current Pharmacogenomics and Personalized Medicine</i> , 2008, 6, 150-159.	0.2	42
24355	Alternatively Spliced Genes as Biomarkers for Schizophrenia, Bipolar Disorder and Psychosis: A Blood-Based Spliceome-Profiling Exploratory Study (Supplementary Table). <i>Current Pharmacogenomics and Personalized Medicine</i> , 2009, 7, 164-188.	0.2	44
24356	Gene Expression Under the Influence: Transcriptional Profiling of Ethanol in the Brain. <i>Current Psychopharmacology</i> , 2012, 1, 301-314.	0.1	41
24357	The Genome of Model Malaria Parasites, and Comparative Genomics. <i>Current Issues in Molecular Biology</i> , 2005, , .	1.0	22
24358	Murine interfollicular epidermal differentiation is gradualistic with GRHL3 controlling progression from stem to transition cell states. <i>Nature Communications</i> , 2020, 11, .	5.8	1
24359	Detection of Distinct Changes in Gene-expression Profiles in Specimens of Tumors and Transition Zones of Tenascinpositive/- negative Head and Neck Squamous Cell Carcinoma. <i>Anticancer Research</i> , 2018, 38, 1279-1290.	0.5	8
24360	Transcriptomic Profiling of MDA-MB-231 Cells Exposed to <i>Boswellia Serrata</i> and 3-O-Acetyl- β -Boswellic Acid; ER/UPR Mediated Programmed Cell Death. <i>Cancer Genomics and Proteomics</i> , 2017, 14, 409-425.	1.0	12
24361	The Anatomy of the SARS-CoV-2 Biomedical Literature: Introducing the CovidX Network Algorithm for Drug Repurposing Recommendation. <i>Journal of Medical Internet Research</i> , 2020, 22, e21169.	2.1	16
24362	A Querying Method over RDF-ized Health Level Seven v2.5 Messages Using Life Science Knowledge Resources. <i>JMIR Medical Informatics</i> , 2016, 4, e12.	1.3	17
24363	Knowledge Management Framework for Emerging Infectious Diseases Preparedness and Response: Design and Development of Public Health Document Ontology. <i>JMIR Research Protocols</i> , 2017, 6, e196.	0.5	5
24364	Microarray missing values imputation methods: Critical analysis review. <i>Computer Science and Information Systems</i> , 2009, 6, 165-190.	0.7	8
24365	An integrated information-based similarity measurement of gene ontology terms. <i>Computer Science and Information Systems</i> , 2015, 12, 1235-1253.	0.7	2
24366	Graph-based sequence annotation using a data integration approach. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.0	4
24367	An ontology for description of drug discovery investigations. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	22
24368	BacillOndex: an integrated data resource for systems and synthetic biology. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 224.	1.0	4
24369	Chromosomal level assembly and population sequencing of the Chinese tree shrew genome. <i>Zoological Research</i> , 2019, 40, 506-521.	0.9	43

#	ARTICLE	IF	CITATIONS
24370	Neuroprotectants attenuate hypobaric hypoxia-induced brain injuries in cynomolgus monkeys. <i>Zoological Research</i> , 2020, 41, 3-19.	0.9	19
24371	Improving Publication Pipeline with Automated Biological Entity Detection and Validation Service. <i>Data and Information Management</i> , 2019, 3, 3-17.	0.7	2
24372	lpEdit: an editor to facilitate reproducible analysis via literate programming. , 2013, , .		1
24373	Small RNA-Seq reveals novel miRNAs shaping the transcriptomic identity of rat brain structures. <i>Life Science Alliance</i> , 2018, 1, e201800018.	1.3	6
24374	An integrative machine learning approach for prediction of toxicity-related drug safety. <i>Life Science Alliance</i> , 2018, 1, e201800098.	1.3	44
24375	A role for MED14 and UVH6 in heterochromatin transcription upon destabilization of silencing. <i>Life Science Alliance</i> , 2018, 1, e201800197.	1.3	14
24376	Dependence on Myb expression is attenuated in myeloid leukaemia with N-terminal CEBPA mutations. <i>Life Science Alliance</i> , 2019, 2, e201800207.	1.3	6
24377	CLIC4 and CLIC1 bridge plasma membrane and cortical actin network for a successful cytokinesis. <i>Life Science Alliance</i> , 2020, 3, e201900558.	1.3	23
24378	An Integrative Genomics Approach for Associating Genetic Susceptibility with the Tumor Immune Microenvironment in Triple Negative Breast Cancer. <i>Biomedical Journal of Scientific & Technical Research</i> , 2019, 15, .	0.0	1
24379	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
24380	Integration of bioinformatics resources for functional analysis of gene expression and proteomic data. <i>Frontiers in Bioscience - Landmark</i> , 2007, 12, 5071.	3.0	30
24381	A ground truth based comparative study on clustering of gene expression data. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 3839.	3.0	5
24382	[Special Issue: Fact Databases and Freewares] RIKEN Natural Products Encyclopedia (RIKEN NPedia), a Chemical Database of RIKEN Natural Products Depository (RIKEN NPDepo). <i>Journal of Computer Aided Chemistry</i> , 2006, 7, 157-162.	0.3	23
24383	Protein name tagging for biomedical annotation in text. , 2003, , .		31
24384	Extracting regulatory gene expression networks from PubMed. , 2004, , .		10
24385	Integrating co-occurrence statistics with information extraction for robust retrieval of protein interactions from Medline. , 2006, , .		14
24386	Selecting an ontology for biomedical text mining. , 2009, , .		10
24387	BioNoculars. , 2007, , .		6

#	ARTICLE	IF	CITATIONS
24388	What's in a gene name?. , 2007, , .		3
24389	Using biomedical literature mining to consolidate the set of known human protein-protein interactions. , 2005, , .		7
24390	The impact of near domain transfer on biomedical named entity recognition. , 2014, , .		2
24391	A System for Building FrameNet-like Corpus for the Biomedical Domain. , 2014, , .		2
24392	Identification of Key Candidate Genes and Pathways for Relationship between Ovarian Cancer and Diabetes Mellitus Using Bioinformatical Analysis. Asian Pacific Journal of Cancer Prevention, 2019, 20, 145-155.	0.5	5
24393	The case for development of an E-cigarette Ontology (E-CigO) to improve quality, efficiency and clarity in the conduct and interpretation of research. Qeios, 0, , .	0.0	7
24394	Addiction Ontology: Applying Basic Formal Ontology in the Addiction domain. Qeios, 0, , .	0.0	8
24395	Comparative analysis of complete chloroplast genomes sequences of <i>Arctium lappa</i> and <i>A. tomentosum</i> . Biologia Plantarum, 0, , .	1.9	4
24396	Baseline SUV_{max} is related to tumor cell proliferation and patient outcome in follicular lymphoma. Haematologica, 2022, 107, 221-230.	1.7	17
24397	Deciphering diatom biochemical pathways via whole-cell proteomics. Aquatic Microbial Ecology, 2009, 55, 241-253.	0.9	48
24398	Differences in Protein Profiles in Schizophrenia Prefrontal Cortex Compared to Other Major Brain Disorders. Clinical Schizophrenia and Related Psychoses, 2007, 1, 73-91.	1.4	8
24399	Predict New Therapeutic Drugs for Hepatocellular Carcinoma Based on Gene Mutation and Expression. Frontiers in Bioengineering and Biotechnology, 2020, 8, 8.	2.0	52
24401	Hub Genes Identification in a Murine Model of Allergic Rhinitis Based on Bioinformatics Analysis. Frontiers in Genetics, 2020, 11, 970.	1.1	5
24402	Silent Witness: Dual-Species Transcriptomics Reveals Epithelial Immunological Quiescence to Helminth Larval Encounter and Fostered Larval Development. Frontiers in Immunology, 2018, 9, 1868.	2.2	13
24403	Proteome of the Triatomine Digestive Tract: From Catalytic to Immune Pathways; Focusing on Annexin Expression. Frontiers in Molecular Biosciences, 2020, 7, 589435.	1.6	8
24404	Integration of Transcriptome and Metabolome Provides Unique Insights to Pathways Associated With Obese Breast Cancer Patients. Frontiers in Oncology, 2020, 10, 804.	1.3	36
24405	Transcriptome Analysis of Juvenile <i>Tilapia</i> (<i>Oreochromis niloticus</i>) Blood, Fed With Different Concentrations of Resveratrol. Frontiers in Physiology, 2020, 11, 600730.	1.3	10
24406	The Interactome of Cancer-Related Lysyl Oxidase and Lysyl Oxidase-Like Proteins. Cancers, 2021, 13, 71.	1.7	20

#	ARTICLE	IF	CITATIONS
24407	Application of Biological Domain Knowledge Based Feature Selection on Gene Expression Data. Entropy, 2021, 23, 2.	1.1	34
24408	Transcriptomic and Metabolomic Changes Triggered by Fusarium solani in Common Bean (Phaseolus Tj ETQq1 1 0.784314 rgBT /Overl	1.0	25
24409	Transcriptomic Analysis of a Diabetic Skin-Humanized Mouse Model Dissects Molecular Pathways Underlying the Delayed Wound Healing Response. Genes, 2021, 12, 47.	1.0	6
24410	Whole-Transcriptome RNA Sequencing Reveals the Global Molecular Responses and CeRNA Regulatory Network of mRNAs, lncRNAs, miRNAs and circRNAs in Response to Salt Stress in Sugar Beet (Beta Tj ETQq1 1 0.784314 rgBT /Overl	1.0	25
24411	Accumulation of the Auxin Precursor Indole-3-Acetamide Curtails Growth through the Repression of Ribosome-Biogenesis and Development-Related Transcriptional Networks. International Journal of Molecular Sciences, 2021, 22, 2040.	1.8	6
24412	Complete Genome Sequence Reveals Evolutionary and Comparative Genomic Features of Xanthomonas albilineans Causing Sugarcane Leaf Scald. Microorganisms, 2020, 8, 182.	1.6	17
24413	DNA MICROARRAY DATA ANALYSIS: A NEW SURVEY ON BICLUSTERING. International Journal for Computational Biology, 2014, 4, 21.	0.1	17
24414	Bioinformatic detection of horizontally transferred DNA in bacterial genomes. F1000 Biology Reports, 2009, 1, 25.	4.0	9
24415	Genome-wide Analysis of μDR-related Transposable Elements Insertion Population in Maize. Acta Agronomica Sinica(China), 2011, 37, 772-777.	0.1	1
24416	Predicting Disease Genes of Coronary Artery Disease Based on Functional Consistency and Network Topological Features*. Progress in Biochemistry and Biophysics, 2009, 2009, 781-786.	0.3	1
24417	A Review on The Processing and Analysis of Next-generation RNA-seq Data*. Progress in Biochemistry and Biophysics, 2010, 37, 834-846.	0.3	8
24418	Discovering Active Subnetwork in Protein Interaction Network*. Progress in Biochemistry and Biophysics, 2010, 37, 208-217.	0.3	2
24419	Human Protein Structural Interaction Network: Domain Effects on Network Topology and Protein Function*. Progress in Biochemistry and Biophysics, 2010, 37, 517-526.	0.3	2
24420	Gene expression arrays as a tool to unravel mechanisms of normal tissue radiation injury and prediction of response. World Journal of Gastroenterology, 2007, 13, 2669.	1.4	34
24421	Natural taurine promotes apoptosis of human hepatic stellate cells in proteomics analysis. World Journal of Gastroenterology, 2010, 16, 1916.	1.4	18
24422	Probiotic Lactobacillus rhamnosus downregulates FCER1 and HRH4 expression in human mast cells. World Journal of Gastroenterology, 2011, 17, 750.	1.4	63
24423	Identification of deregulated miRNAs and their targets in hepatitis B virus-associated hepatocellular carcinoma. World Journal of Gastroenterology, 2012, 18, 5442.	1.4	93
24424	Early dynamic transcriptomic changes during preoperative radiotherapy in patients with rectal cancer: A feasibility study. World Journal of Gastroenterology, 2013, 19, 3249.	1.4	31

#	ARTICLE	IF	CITATIONS
24425	Clinical applications of next-generation sequencing in colorectal cancers. <i>World Journal of Gastroenterology</i> , 2013, 19, 6784.	1.4	29
24426	Long noncoding RNAs in hepatitis B virus-related hepatocellular carcinoma. <i>World Journal of Gastroenterology</i> , 2015, 21, 7208-7217.	1.4	25
24427	Integrated analysis of microRNA and mRNA expression profiles in HBx-expressing hepatic cells. <i>World Journal of Gastroenterology</i> , 2017, 23, 1787.	1.4	9
24429	Abiotic Stress-Related Expressed Sequence Tags from the Diploid Strawberry <i>Fragaria vesca</i> f. <i>semperflorens</i> . <i>Plant Genome</i> , 2011, 4, .	1.6	7
24430	OntoCell: An ontology of Cellular Biology. <i>Journal of Computer Science</i> , 2005, 1, 445-449.	0.5	4
24431	Identification of potential key genes in gastric cancer using bioinformatics analysis. <i>Biomedical Reports</i> , 2020, 12, 178-192.	0.9	18
24432	Identification of prognostic gene biomarkers for metastatic skin cancer using data mining. <i>Biomedical Reports</i> , 2020, 13, 22-30.	0.9	5
24433	Bioinformatics analysis shows that TOP2A functions as a key candidate gene in the progression of cervical cancer. <i>Biomedical Reports</i> , 2020, 13, 21.	0.9	11
24434	Expression and potential prognostic value of histone family gene signature in breast cancer. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 4893-4903.	0.8	17
24435	Identification of differentially expressed genes and signaling pathways involved in endometriosis by integrated bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2020, 19, 264-272.	0.8	7
24436	Integrative module analysis of HCC gene expression landscapes. <i>Experimental and Therapeutic Medicine</i> , 2020, 19, 1779-1788.	0.8	20
24437	Complete genome sequences of two <i>Enterococcus faecium</i> strains and comparative genomic analysis. <i>Experimental and Therapeutic Medicine</i> , 2020, 19, 2019-2028.	0.8	4
24438	Anti-inflammatory activity of <i>Radix Angelicae biseratae</i> in the treatment of osteoarthritis determined by systematic pharmacology and in vitro experiments. <i>Experimental and Therapeutic Medicine</i> , 2020, 21, 5.	0.8	5
24439	Prediction of crucial epigenetically-associated, differentially expressed genes by integrated bioinformatics analysis and the identification of S100A9 as a novel biomarker in psoriasis. <i>International Journal of Molecular Medicine</i> , 2020, 45, 93-102.	1.8	16
24440	Weighted gene co-expression network analysis to identify key modules and hub genes associated with atrial fibrillation. <i>International Journal of Molecular Medicine</i> , 2020, 45, 401-416.	1.8	23
24441	MicroRNA-449a regulates the progression of brain aging by targeting SCN2B in SAMP8 mice. <i>International Journal of Molecular Medicine</i> , 2020, 45, 1091-1102.	1.8	11
24442	Altered expression of glycoprotein non-metastatic melanoma protein B in the distal sciatic nerve following injury. <i>International Journal of Molecular Medicine</i> , 2020, 45, 1909-1917.	1.8	3
24443	Placental exosomes isolated from urine of patients with gestational diabetes exhibit a differential profile expression of microRNAs across gestation. <i>International Journal of Molecular Medicine</i> , 2020, 46, 546-560.	1.8	49

#	ARTICLE	IF	CITATIONS
24444	Bufalin exerts antitumor effects in neuroblastoma via the induction of reactive oxygen species-mediated apoptosis by targeting the electron transport chain. <i>International Journal of Molecular Medicine</i> , 2020, 46, 2137-2149.	1.8	16
24445	Resveratrol modulates the apoptosis and autophagic death of human lung adenocarcinoma A549 cells via a p53-dependent pathway: Integrated bioinformatics analysis and experimental validation. <i>International Journal of Oncology</i> , 2020, 57, 925-938.	1.4	18
24446	Comprehensive expression profiles and bioinformatics analysis reveal special circular RNA expression and potential predictability in the peripheral blood of humans with idiopathic membranous nephropathy. <i>Molecular Medicine Reports</i> , 2019, 20, 4125-4139.	1.1	6
24447	Phosphoproteomic profiling of oxycodone-treated spinal cord of rats with cancer-induced bone pain. <i>Molecular Medicine Reports</i> , 2019, 20, 4695-4705.	1.1	1
24448	Comparative proteomic and genomic analyses of <i>Brucella abortus</i> biofilm and planktonic cells. <i>Molecular Medicine Reports</i> , 2020, 21, 731-743.	1.1	6
24449	Global pathway view analysis of microRNA clusters in myasthenia gravis. <i>Molecular Medicine Reports</i> , 2019, 19, 2350-2360.	1.1	3
24450	Application of weighted gene co-expression network analysis to explore the potential diagnostic biomarkers for colorectal cancer. <i>Molecular Medicine Reports</i> , 2020, 21, 2533-2543.	1.1	8
24451	A novel plasma lncRNA ENST00000416361 is upregulated in coronary artery disease and is related to inflammation and lipid metabolism. <i>Molecular Medicine Reports</i> , 2020, 21, 2375-2384.	1.1	12
24452	Expression profile of circular RNAs in the peripheral blood of neonates with hypoxic-ischemic encephalopathy. <i>Molecular Medicine Reports</i> , 2020, 22, 87-96.	1.1	6
24453	Key miRNAs associated with memory and learning disorder upon exposure to sevoflurane determined by RNA sequencing. <i>Molecular Medicine Reports</i> , 2020, 22, 1567-1575.	1.1	6
24454	Genome-wide analysis of DNA methylation and gene expression changes in an ovalbumin-induced asthma mouse model. <i>Molecular Medicine Reports</i> , 2020, 22, 1709-1716.	1.1	7
24455	Expression profiling of circular RNAs and their potential role in early-stage diabetic cardiomyopathy. <i>Molecular Medicine Reports</i> , 2020, 22, 1958-1968.	1.1	12
24456	miR-592 acts as an oncogene and promotes medullary thyroid cancer tumorigenesis by targeting cyclin-dependent kinase 8. <i>Molecular Medicine Reports</i> , 2020, 22, 3316-3326.	1.1	6
24457	Uncovering potential differentially expressed miRNAs and targeted mRNAs in myocardial infarction based on integrating analysis. <i>Molecular Medicine Reports</i> , 2020, 22, 4383-4395.	1.1	6
24458	Identification of inflammation-associated circulating long non-coding RNAs and genes in intracranial aneurysm rupture-induced subarachnoid hemorrhage. <i>Molecular Medicine Reports</i> , 2020, 22, 4541-4550.	1.1	9
24459	Co-expression network analysis identified specific miRNAs and genes in association with slow-transit constipation. <i>Molecular Medicine Reports</i> , 2020, 22, 4696-4706.	1.1	6
24460	Anti-inflammatory mechanism of berberine on lipopolysaccharide-induced IEC-18 models based on comparative transcriptomics. <i>Molecular Medicine Reports</i> , 2020, 22, 5163-5180.	1.1	11
24461	Four targeted genes for predicting the prognosis of colorectal cancer: A bioinformatics analysis case. <i>Oncology Letters</i> , 2019, 18, 5043-5054.	0.8	18

#	ARTICLE	IF	CITATIONS
24462	Screening and identification of key biomarkers in lung squamous cell carcinoma by bioinformatics analysis. <i>Oncology Letters</i> , 2019, 18, 5185-5196.	0.8	10
24463	Bioinformatics analysis of Ewing's sarcoma: Seeking key candidate genes and pathways. <i>Oncology Letters</i> , 2019, 18, 6008-6016.	0.8	28
24464	Identification of core differentially methylated genes in glioma. <i>Oncology Letters</i> , 2019, 18, 6033-6045.	0.8	31
24465	Five extracellular matrix-associated genes upregulated in oral tongue squamous cell carcinoma: An integrated bioinformatics analysis. <i>Oncology Letters</i> , 2019, 18, 5959-5967.	0.8	5
24466	Identification of key candidate genes for colorectal cancer by bioinformatics analysis. <i>Oncology Letters</i> , 2019, 18, 6583-6593.	0.8	14
24467	Identification of hub genes and key pathways associated with the progression of gynecological cancer. <i>Oncology Letters</i> , 2019, 18, 6516-6524.	0.8	25
24468	Association between breast cancer cell migration and radiosensitivity <i>in vitro</i> . <i>Oncology Letters</i> , 2019, 18, 6877-6884.	0.8	4
24469	Identification of key candidate genes and pathways in endometrial cancer: Evidence from bioinformatics analysis. <i>Oncology Letters</i> , 2019, 18, 6679-6689.	0.8	5
24470	Identification of key genes for predicting colorectal cancer prognosis by integrated bioinformatics analysis. <i>Oncology Letters</i> , 2020, 19, 388-398.	0.8	29
24471	Integrated bioinformatics analysis of the association between apolipoprotein E expression and patient prognosis in papillary thyroid carcinoma. <i>Oncology Letters</i> , 2020, 19, 2295-2305.	0.8	3
24472	Identification of hub genes associated with outcome of clear cell renal cell carcinoma. <i>Oncology Letters</i> , 2020, 19, 2846-2860.	0.8	6
24473	A putative competing endogenous RNA network in cisplatin-resistant lung adenocarcinoma cells identifying potentially rewarding research targets. <i>Oncology Letters</i> , 2020, 19, 4040-4052.	0.8	4
24474	Comprehensive characterization of driver genes in diffuse large B-cell lymphoma. <i>Oncology Letters</i> , 2020, 20, 382-390.	0.8	11
24475	GGCT promotes colorectal cancer migration and invasion via epithelial-mesenchymal transition. <i>Oncology Letters</i> , 2020, 20, 1063-1070.	0.8	9
24476	Mechanistic studies of cytotoxic activity of the mesoionic compound MIH2.4BI in MCF7 breast cancer cells. <i>Oncology Letters</i> , 2020, 20, 2291-2301.	0.8	4
24477	Circular RNA profiling in plasma exosomes from patients with gastric cancer. <i>Oncology Letters</i> , 2020, 20, 2199-2208.	0.8	14
24478	Immunotyping of tumor-infiltrating lymphocytes in triple-negative breast cancer and genetic characterization. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	12
24479	TMEM206 is a potential prognostic marker of hepatocellular carcinoma. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	12

#	ARTICLE	IF	CITATIONS
24480	Involvement of the Wnt/β-Catenin signaling pathway in the heterogenous nuclear ribonucleoprotein-driven inhibition of proliferation and migration in head and neck squamous cell carcinoma. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	3
24481	Polyphyllin VII suppresses cell proliferation, the cell cycle and cell migration in colorectal cancer. <i>Oncology Letters</i> , 2020, 21, 1-1.	0.8	7
24482	Effect of let-7c on the PI3K/Akt/FoxO signaling pathway in hepatocellular carcinoma. <i>Oncology Letters</i> , 2020, 21, 96.	0.8	24
24483	LncRNA ROR1AS1 high expression and its prognostic significance in liver cancer. <i>Oncology Reports</i> , 2020, 43, 55-74.	1.2	20
24484	Integrative analysis of mRNA and miRNA expression profiles reveals seven potential diagnostic biomarkers for non-small cell lung cancer. <i>Oncology Reports</i> , 2020, 43, 99-112.	1.2	20
24485	Patient-derived orthotopic xenograft glioma models fail to replicate the magnetic resonance imaging features of the original patient tumor. <i>Oncology Reports</i> , 2020, 43, 1619-1629.	1.2	7
24486	Principal component analysis on LC-MS/MS and 2DE-MALDI-TOF in glioblastoma cell lines reveals that mitochondria act as organelle sensors of the metabolic state in glioblastoma. <i>Oncology Reports</i> , 2020, 44, 661-673.	1.2	8
24487	Human milk proteins: strides in proteomics and benefits in nutrition research. <i>Human Health Handbooks</i> , 2013, , 249-292.	0.1	2
24488	Microarray evaluation of bovine hepatic gene response to fescue toxicosis. <i>World Mycotoxin Journal</i> , 2013, 6, 419-426.	0.8	2
24489	Understanding potato with the help of genomics. <i>AIMS Agriculture and Food</i> , 2017, 2, 16-39.	0.8	10
24490	What's the big deal about big data?. <i>Big Data & Information Analytics</i> , 2015, 1, 31-79.	1.3	5
24491	Characteristics of Atmospheric Fine Particulate Matter (PM) Induced Differentially Expressed Proteins Determined by Proteomics and Bioinformatics Analyses. <i>Biomedical and Environmental Sciences</i> , 2020, 33, 583-592.	0.2	4
24492	MIR-182 is up-regulated and targeting Cebpa in hepatocellular carcinoma. <i>Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association</i> , Beijing Institute for Cancer Research, 2014, 26, 17-29.	0.7	36
24493	Outer Membrane Vesicles Derived from Salmonella Enteritidis Protect against the Virulent Wild-Type Strain Infection in a Mouse Model. <i>Journal of Microbiology and Biotechnology</i> , 2017, 27, 1519-1528.	0.9	22
24494	Genomics and LC-MS Reveal Diverse Active Secondary Metabolites in Bacillus amyloliquefaciens WS-8. <i>Journal of Microbiology and Biotechnology</i> , 2020, 30, 417-426.	0.9	7
24495	A Semantic Framework for Cloud Learning Environments. , 2012, , 17-31.		13
24496	On the Integration of Clinical Archetypes with Ontologies and Rules. <i>Advances in Healthcare Information Systems and Administration Book Series</i> , 2013, , 82-147.	0.2	2
24497	Text Mining on Big and Complex Biomedical Literature. <i>Advances in Bioinformatics and Biomedical Engineering Book Series</i> , 2015, , 21-45.	0.2	4

#	ARTICLE	IF	CITATIONS
24498	Function and Homology of Proteins Similar in Sequence. , 2009, , 143-166.		1
24499	High-Throughput GRID Computing for Life Sciences. , 2009, , 187-205.		1
24500	Discovering Network Motifs in Protein Interaction Networks. , 2009, , 117-143.		3
24501	Discovering Protein Complexes in Protein Interaction Networks. , 2009, , 144-168.		3
24502	An Integrated Framework for Fuzzy Classification and Analysis of Gene Expression Data. , 0, , 151-177.		1
24503	Stepwise Semantic Enrichment in Health-Related Public Management by Using Semantic Information Models. , 0, , 195-212.		3
24504	Biclustering of DNA Microarray Data. , 2011, , 148-186.		8
24505	Pathway Resources at the Rat Genome Database. , 2011, , 316-336.		1
24506	GO-Based Term Semantic Similarity. , 2011, , 174-185.		2
24507	Improving Ontology Alignment through Genetic Algorithms. , 2010, , 240-259.		26
24508	Wave-SOM. International Journal of Knowledge Discovery in Bioinformatics, 2010, 1, 50-73.	0.8	2
24509	New Trends in Graph Mining. International Journal of Knowledge Discovery in Bioinformatics, 2010, 1, 81-99.	0.8	6
24510	Search for Protein Sequence Homologues that Display Considerable Domain Length Variations. International Journal of Knowledge Discovery in Bioinformatics, 2011, 2, 55-77.	0.8	4
24511	BioTextRetriever. International Journal of Knowledge Discovery in Bioinformatics, 2011, 2, 21-36.	0.8	2
24512	Improved Feature Selection by Incorporating Gene Similarity into the LASSO. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 1-22.	0.8	1
24513	Complete genome sequence of <i>Sulfurimonas autotrophica</i> type strain (OK10T). Standards in Genomic Sciences, 2010, 3, 194-202.	1.5	37
24514	Complete genome sequence of <i>Methanoplanus petrolearius</i> type strain (SEBR 4847T). Standards in Genomic Sciences, 2010, 3, 203-211.	1.5	14
24515	Complete genome sequence of <i>Riemerella anatipestifer</i> type strain (ATCC 11845). Standards in Genomic Sciences, 2011, 4, 144-53.	1.5	20

#	ARTICLE	IF	CITATIONS
24516	Non-contiguous finished genome sequence and description of <i>Alistipes timonensis</i> sp. nov.. Standards in Genomic Sciences, 2012, 6, 315-324.	1.5	8
24517	Non-contiguous finished genome sequence and description of <i>Paenibacillus senegalensis</i> sp. nov.. Standards in Genomic Sciences, 2012, 7, 70-81.	1.5	47
24518	Metagenomes of tropical soil-derived anaerobic switchgrass-adapted consortia with and without iron. Standards in Genomic Sciences, 2013, 7, 382-398.	1.5	12
24519	Genome sequence of <i>Phaeobacter caeruleus</i> type strain (DSM 24564(T)), a surface-associated member of the marine <i>Roseobacter</i> clade. Standards in Genomic Sciences, 2013, 8, 403-19.	1.5	12
24520	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093T). Standards in Genomic Sciences, 2012, 7, 44-58.	1.5	19
24521	Differential Gene Expression Common to Acquired and Intrinsic Resistance to BRAF Inhibitor Revealed by RNA-Seq Analysis. Biomolecules and Therapeutics, 2019, 27, 302-310.	1.1	19
24522	Combining differential expression and differential coexpression analysis identifies optimal gene and gene set in cervical cancer. Journal of Cancer Research and Therapeutics, 2018, 14, 201-207.	0.3	9
24523	Identification of key genes related to high-risk gastrointestinal stromal tumors using bioinformatics analysis. Journal of Cancer Research and Therapeutics, 2018, 14, S243-S247.	0.3	8
24524	Systematic enrichment analysis of gene expression profiling studies identifies consensus pathways implicated in colorectal cancer development. Journal of Carcinogenesis, 2011, 10, 7.	2.5	25
24525	miRNA targeted signaling pathway in the early stage of denervated fast and slow muscle atrophy. Neural Regeneration Research, 2016, 11, 1293.	1.6	23
24526	Differential gene and protein expression between rat tibial nerve and common peroneal nerve during Wallerian degeneration. Neural Regeneration Research, 2019, 14, 2183.	1.6	11
24527	Bioinformatic identification of key candidate genes and pathways in axon regeneration after spinal cord injury in zebrafish. Neural Regeneration Research, 2020, 15, 103.	1.6	5
24528	Biomedical imaging ontologies: A survey and proposal for future work. Journal of Pathology Informatics, 2015, 6, 37.	0.8	24
24529	Comprehensive transcriptome analysis based on RNA sequencing identifies critical genes for lipopolysaccharide-induced epididymitis in a rat model. Asian Journal of Andrology, 2019, 21, 605.	0.8	12
24530	Altered microRNA profiles of testicular biopsies from patients with nonobstructive azoospermia. Asian Journal of Andrology, 2020, 22, 100.	0.8	25
24531	Predictive Modeling of Drug Treatment in the Area of Personalized Medicine. Cancer Informatics, 2015, 14, 95-103.	0.9	17
24532	Use of Proteomics Analysis for Molecular Precision Approaches in Cancer Therapy. Drug Target Insights, 2008, 3, DTI.S649.	0.9	2
24533	Serum proteomics analysis of feline mammary carcinoma based on label-free and PRM techniques. Journal of Veterinary Science, 2020, 21, e45.	0.5	5

#	ARTICLE	IF	CITATIONS
24534	New Approaches to Functional Process Discovery in HPV 16-Associated Cervical Cancer Cells by Gene Ontology. <i>Cancer Research and Treatment</i> , 2003, 35, 304-313.	1.3	2
24535	cDNA Microarray Analysis of Gene Expression Profiles Associated with Cervical Cancer. <i>Cancer Research and Treatment</i> , 2003, 35, 451-459.	1.3	19
24536	Chitinase 3-Like 1 Contributes to Food Allergy via M2 Macrophage Polarization. <i>Allergy, Asthma and Immunology Research</i> , 2020, 12, 1012.	1.1	31
24537	Characterization of <i>Clostridium acetobutylicum</i> Protein Interaction Network from Butanol Fermentation. <i>Journal of Analytical & Bioanalytical Techniques</i> , 2013, 04, .	0.6	1
24538	New Era of Developing and Using Ontologies for Microbiology Research and Diagnosis. , 2012, 01, .		20
24539	Using Host-Pathogen Functional Interactions for Filtering Potential Drug Targets in <i>Mycobacterium tuberculosis</i> . <i>Mycobacterial Diseases: Tuberculosis & Leprosy</i> , 2013, 03, .	0.1	11
24540	Alternations in miRNA Expression in Chronic Stress-Induced Ageing of Leydig Cells. , 2017, 06, .		1
24541	Identification of Stress Related Molecular Biomarkers in Zebrafish Employing an In-Silico Approach to Access Toxicity based Risks in Aquaculture. <i>Poultry Fisheries & Wildlife Sciences</i> , 2015, 03, .	0.1	3
24542	Role of a Web-based Software Platform for Systems Biology. <i>Journal of Computer Science and Systems Biology</i> , 2011, 04, .	0.0	9
24543	Global Proteomics: Pharmacodynamic Decision Making via Geometric Interpretations of Proteomic Analyses. <i>Journal of Proteomics and Bioinformatics</i> , 2008, 01, 315-328.	0.4	6
24544	Functional Insights from Computational Modeling of Orphan Proteins Expressed in a Microbial Community. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, 266-274.	0.4	2
24545	Tissue-Specific Protein Expression in Human Cells, Tissues and Organs. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, .	0.4	7
24546	Integrated Bioinformatics Analysis of the Publicly Available Protein Data Shows Evidence for 96% of the Human Proteome. <i>Journal of Proteomics and Bioinformatics</i> , 2014, 07, .	0.4	6
24548	Computing a Predictor Set Influence Zone through a Multi-Layer Genetic Network to Explore the Role of Estrogen in Breast Cancer. <i>Advances in Breast Cancer Research</i> , 2012, 01, 21-29.	0.1	1
24549	Transcriptome Analysis of Ten-DPA Fiber in an Upland Cotton (&i>Gossypium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 American Journal of Plant Sciences, 2017, 08, 2530-2553.	0.3	8
24550	Transcriptome Analysis of Ten Days Post Anthesis Elongating Fiber in the Upland Cotton (&i>Gossypium hirsutum</i>) Chromosome Substitution Line CS-B25. <i>American Journal of Plant Sciences</i> , 2018, 09, 1334-1361.	0.3	2
24551	Comparative cytogenetics of spiny rats of the genus <i>Proechimys</i> (Rodentia, Echimyidae) from the Amazon region. <i>Genetics and Molecular Research</i> , 2012, 11, 830-846.	0.3	14
24552	The full Bayesian significance test for mixture models: results in gene expression clustering. <i>Genetics and Molecular Research</i> , 2008, 7, 883-897.	0.3	2

#	ARTICLE	IF	CITATIONS
24553	Constructing human phenome-interactome networks for the prioritization of candidate genes. <i>Statistics and Its Interface</i> , 2012, 5, 137-148.	0.2	6
24554	Synthetic kinds. , 2019, , 78-96.		20
24555	Top-Down Causation in Biology and Neuroscience. , 2017, , 203-224.		18
24556	"Stop Ne(c)king around": How interactomics contributes to functionally characterize Nek family kinases. <i>World Journal of Biological Chemistry</i> , 2014, 5, 141-60.	1.7	52
24557	Yeast require an Intact Tryptophan Biosynthesis Pathway and Exogenous Tryptophan for Resistance to Sodium Dodecyl Sulfate. <i>Journal of Student Research</i> , 2015, 4, 74-82.	0.0	2
24558	Analysis of Gene Expression Profile of AGS Cells Stimulated by Helicobacter pylori Adhesion. <i>Gut and Liver</i> , 2007, 1, 040-048.	1.4	13
24559	Comparison of transcriptome analysis between red flash peach cultivar and white flash peach cultivar using next generation sequencing. <i>Journal of Plant Biotechnology</i> , 2012, 39, 273-280.	0.1	2
24560	Effect of LED mixed light conditions on the glucosinolate pathway in brassica rapa. <i>Journal of Plant Biotechnology</i> , 2015, 42, 245-256.	0.1	11
24561	A New Survey on Biclustering of MicroArray Data. , 2014, , .		1
24562	Mechanistic insight into the progressive retinal atrophy disease in dogs via pathway-based genome-wide association analysis. <i>Journal of Animal Science and Technology</i> , 2020, 62, 765-776.	0.8	3
24563	Sculpting the UMLS Refined Semantic Network. <i>Online Journal of Public Health Informatics</i> , 2014, 6, e181.	0.4	10
24566	Functional relationship and gene ontology classification of breast cancer biomarkers. <i>International Journal of Biological Markers</i> , 2003, 18, 241-272.	0.7	20
24567	Activation of IL5R and CRTH2 on Human Eosinophils Elicit a Similar Molecular Response and Reveal a Synergistic Effect. <i>European Journal of Molecular and Clinical Medicine</i> , 2018, 5, 1-11.	0.5	1
24568	Transcriptome Analysis of the Small Brown Planthopper, <i>Laodelphax striatellus</i> Carrying Rice stripe virus. <i>Plant Pathology Journal</i> , 2013, 29, 330-337.	0.7	17
24569	Statistical modeling for differential transcriptome analysis using RNA-Seq technology. <i>Journal of Solid Tumors</i> , 2012, 2, .	0.1	3
24571	KNApSAck gene classification system for <i>Arabidopsis thaliana</i> : Comparative genomic analysis of unicellular to seed plants. <i>Plant Biotechnology</i> , 2009, 26, 509-516.	0.5	3
24572	Mechanism of Statin-Induced Myopathy Investigated Using Microarray Technology. <i>Journal of Atherosclerosis and Thrombosis</i> , 2009, 16, 30-32.	0.9	4
24575	Genomic and Proteomic Databases: Foundations, Current Status and Future Applications. <i>Journal of Computing Science and Engineering</i> , 2007, 1, 1-30.	0.3	4

#	ARTICLE	IF	CITATIONS
24576	A New Information Criterion Based on Langevin Mixture Distribution for Clustering Circular Data with Application to Time Course Genomic Data. <i>Statistica Sinica</i> , 2015, , .	0.2	2
24577	Detection of copy number variation and selection signatures on the X chromosome in Chinese indigenous sheep with different types of tail. <i>Asian-Australasian Journal of Animal Sciences</i> , 2020, 33, 1378-1386.	2.4	8
24578	Paradigm of Time-sequence Development of the Intestine of Suckling Piglets with Microarray. <i>Asian-Australasian Journal of Animal Sciences</i> , 2012, 25, 1481-1492.	2.4	3
24579	A systems biological approach to identify key transcription factors and their genomic neighborhoods in human sarcomas. <i>Chinese Journal of Cancer</i> , 2011, 30, 27-40.	4.9	6
24580	GOMA: functional enrichment analysis tool based on GO modules. <i>Chinese Journal of Cancer</i> , 2013, 32, 195-204.	4.9	15
24581	Microarray Analysis of Undifferentiated and Differentiated Human Pluripotent Stem Cells. , 0, , .		3
24582	Prioritising Genes with an Artificial Neural Network Comprising Medical Documents to Accelerate Positional Cloning in Biological Research. , 0, , .		1
24583	Computational Approaches to Predict Protein Interaction. , 0, , .		1
24584	Bioinformatics as a Tool for the Structural and Evolutionary Analysis of Proteins. , 0, , .		7
24585	Mesenchymal Stem Cells Isolated from the Anterior Cruciate Ligament: Characterization and Comparison of Cells from Young and Old Donors. <i>Knee Surgery and Related Research</i> , 2018, 30, 193-205.	1.8	13
24586	Performance Comparison of Two Gene Set Analysis Methods for Genome-wide Association Study Results: GSA-SNP vs i-GSEA4GWAS. <i>Genomics and Informatics</i> , 2012, 10, 123.	0.4	4
24587	An Ontology-Based GIS for Genomic Data Management of Rumen Microbes. <i>Genomics and Informatics</i> , 2015, 13, 7.	0.4	2
24588	Mutational Analysis of Extranodal NK/T-Cell Lymphoma Using Targeted Sequencing with a Comprehensive Cancer Panel. <i>Genomics and Informatics</i> , 2016, 14, 78.	0.4	17
24589	Integrated Analysis of Gene Expression Profiles Reveals Deregulation of the Immune Response Genes during Different Phases of Chronic Hepatitis B Infection. <i>Hepatitis Monthly</i> , 2017, 17, .	0.1	1
24590	Laboratory-Guided Detection of Disease Outbreaks: Three Generations of Surveillance Systems. <i>Archives of Pathology and Laboratory Medicine</i> , 2009, 133, 916-925.	1.2	33
24591	Molecular Classification of Human Cancers Using a 92-Gene Real-Time Quantitative Polymerase Chain Reaction Assay. <i>Archives of Pathology and Laboratory Medicine</i> , 2006, 130, 465-473.	1.2	192
24592	On gene ontology and function annotation. <i>Bioinformation</i> , 2006, 1, 97-98.	0.2	21
24593	FGO: A novel ontology for identification of ligand functional group. <i>Bioinformation</i> , 2007, 2, 113-118.	0.2	4

#	ARTICLE	IF	CITATIONS
24594	GS2PATH: A web-based integrated analysis tool for finding functional relationships using gene ontology and biochemical pathway data. <i>Bioinformatics</i> , 2007, 2, 194-196.	0.2	2
24595	A tool for the prediction of functionally important sites in proteins using a library of functional templates. <i>Bioinformatics</i> , 2008, 2, 279-283.	0.2	3
24596	GeneComps and ChemComps: a new CTD metric to identify genes and chemicals with shared toxicogenomic profiles. <i>Bioinformatics</i> , 2009, 4, 173-174.	0.2	13
24597	The capsicum transcriptome DB: a "hot" tool for genomic research. <i>Bioinformatics</i> , 2012, 8, 43-47.	0.2	22
24598	TPX: Biomedical literature search made easy. <i>Bioinformatics</i> , 2012, 8, 578-580.	0.2	9
24599	Computer aided gene mining for gingerol biosynthesis. <i>Bioinformatics</i> , 2015, 11, 316-321.	0.2	3
24600	Genes2GO: A web application for querying gene sets for specific GO terms. <i>Bioinformatics</i> , 2016, 12, 231-232.	0.2	4
24601	Analysis of MAP kinase MPK4/MEKK1/MKK genes of <i>Carica papaya</i> L. comparative to other plant homologues. <i>Bioinformatics</i> , 2017, 13, 31-41.	0.2	2
24602	Identification and prioritization of macrolideresistance genes with hypothetical annotation in <i>Streptococcus pneumoniae</i> . <i>Bioinformatics</i> , 2018, 14, 488-498.	0.2	6
24603	DAGmaps: Space Filling Visualization of Directed Acyclic Graphs. <i>Journal of Graph Algorithms and Applications</i> , 2009, 13, 319-347.	0.4	8
24604	Construction of cDNA Library and EST Analysis Related to Seed-hair Characteristics in Carrot. <i>Horticultural Science and Technology</i> , 2013, 31, 782-789.	0.9	1
24605	Business intelligence strategies enables rapid analysis of quantitative proteomics data. <i>Journal of Proteome Science and Computational Biology</i> , 2012, 1, 5.	1.0	3
24606	MiRNA Synergistic Network Construction and Enrichment Analysis for Common Target Genes in Small-cell Lung Cancer. <i>Asian Pacific Journal of Cancer Prevention</i> , 2012, 13, 6375-6378.	0.5	7
24607	Identification of Genes and MicroRNAs Involved in Ovarian Carcinogenesis. <i>Asian Pacific Journal of Cancer Prevention</i> , 2012, 13, 3997-4000.	0.5	10
24608	Partial Least Squares Based Gene Expression Analysis in EBV-Positive and EBV-Negative Posttransplant Lymphoproliferative Disorders. <i>Asian Pacific Journal of Cancer Prevention</i> , 2013, 14, 6347-6350.	0.5	3
24609	Pathway and Network Analysis in Glioma with the Partial Least Squares Method. <i>Asian Pacific Journal of Cancer Prevention</i> , 2014, 15, 3145-3149.	0.5	2
24610	Analysis of Molecular Pathways in Pancreatic Ductal Adenocarcinomas with a Bioinformatics Approach. <i>Asian Pacific Journal of Cancer Prevention</i> , 2015, 16, 2561-2567.	0.5	14
24611	Microarray Analysis of Long Non-coding RNA Expression Profile Associated with 5-Fluorouracil-Based Chemoradiation Resistance in Colorectal Cancer Cells. <i>Asian Pacific Journal of Cancer Prevention</i> , 2015, 16, 3395-3402.	0.5	30

#	ARTICLE	IF	CITATIONS
24612	Age- and diet-associated metabolome remodeling characterizes the aging process driven by damage accumulation. <i>ELife</i> , 2014, 3, e02077.	2.8	56
24613	Mapping and analysis of <i>Caenorhabditis elegans</i> transcription factor sequence specificities. <i>ELife</i> , 2015, 4, .	2.8	85
24614	Viruses are a dominant driver of protein adaptation in mammals. <i>ELife</i> , 2016, 5, .	2.8	267
24615	PDZD7-MYO7A complex identified in enriched stereocilia membranes. <i>ELife</i> , 2016, 5, .	2.8	40
24616	Selecting the most appropriate time points to profile in high-throughput studies. <i>ELife</i> , 2017, 6, .	2.8	27
24617	A computational interactome and functional annotation for the human proteome. <i>ELife</i> , 2016, 5, .	2.8	58
24618	Ongoing resolution of duplicate gene functions shapes the diversification of a metabolic network. <i>ELife</i> , 2016, 5, .	2.8	29
24619	Unconventional secretory processing diversifies neuronal ion channel properties. <i>ELife</i> , 2016, 5, .	2.8	92
24620	Systematic bacterialization of yeast genes identifies a near-universally swappable pathway. <i>ELife</i> , 2017, 6, .	2.8	32
24621	The DREAM complex through its subunit Lin37 cooperates with Rb to initiate quiescence. <i>ELife</i> , 2017, 6, .	2.8	41
24622	Live-cell mapping of organelle-associated RNAs via proximity biotinylation combined with protein-RNA crosslinking. <i>ELife</i> , 2017, 6, .	2.8	143
24623	Metabolic co-dependence drives the evolutionarily ancient <i>Hydra</i> – <i>Chlorella</i> symbiosis. <i>ELife</i> , 2018, 7, .	2.8	47
24624	Inhibiting the integrated stress response pathway prevents aberrant chondrocyte differentiation thereby alleviating chondrodysplasia. <i>ELife</i> , 2018, 7, .	2.8	59
24625	Mapping the transcriptional diversity of genetically and anatomically defined cell populations in the mouse brain. <i>ELife</i> , 2019, 8, .	2.8	59
24626	The cargo receptor SURF4 promotes the efficient cellular secretion of PCSK9. <i>ELife</i> , 2018, 7, .	2.8	72
24627	Glucose intake hampers PKA-regulated HSP90 chaperone activity. <i>ELife</i> , 2018, 7, .	2.8	16
24628	Time-resolved mapping of genetic interactions to model rewiring of signaling pathways. <i>ELife</i> , 2018, 7, .	2.8	21
24629	Human pancreatic cancer cell exosomes, but not human normal cell exosomes, act as an initiator in cell transformation. <i>ELife</i> , 2019, 8, .	2.8	63

#	ARTICLE	IF	CITATIONS
24630	Single cell RNA-seq identifies the origins of heterogeneity in efficient cell transdifferentiation and reprogramming. <i>ELife</i> , 2019, 8, .	2.8	44
24631	Determination of host proteins composing the microenvironment of coronavirus replicase complexes by proximity-labeling. <i>ELife</i> , 2019, 8, .	2.8	157
24632	Quantitative insights into the cyanobacterial cell economy. <i>ELife</i> , 2019, 8, .	2.8	82
24633	eIF2B activator prevents neurological defects caused by a chronic integrated stress response. <i>ELife</i> , 2019, 8, .	2.8	124
24634	The genomes of polyextremophilic cyanidiales contain 1% horizontally transferred genes with diverse adaptive functions. <i>ELife</i> , 2019, 8, .	2.8	50
24635	Genetic interactions of G-quadruplexes in humans. <i>ELife</i> , 2019, 8, .	2.8	91
24636	Evolution of C4 photosynthesis predicted by constraint-based modelling. <i>ELife</i> , 2019, 8, .	2.8	46
24637	Stereotyped transcriptomic transformation of somatosensory neurons in response to injury. <i>ELife</i> , 2019, 8, .	2.8	75
24638	Duodenum Intestine-Chip for preclinical drug assessment in a human relevant model. <i>ELife</i> , 2020, 9, .	2.8	143
24639	Comprehensive transcriptome analysis of cochlear spiral ganglion neurons at multiple ages. <i>ELife</i> , 2020, 9, .	2.8	52
24640	Endogenous siRNAs promote proteostasis and longevity in germline-less <i>Caenorhabditis elegans</i> . <i>ELife</i> , 2020, 9, .	2.8	13
24641	Dynamic post-translational modification profiling of <i>Mycobacterium tuberculosis</i> -infected primary macrophages. <i>ELife</i> , 2020, 9, .	2.8	44
24642	The transcriptomic response of cells to a drug combination is more than the sum of the responses to the monotherapies. <i>ELife</i> , 2020, 9, .	2.8	21
24643	A fully automated high-throughput workflow for 3D-based chemical screening in human midbrain organoids. <i>ELife</i> , 2020, 9, .	2.8	117
24644	Skd3 (human ClpB) is a potent mitochondrial protein disaggregase that is inactivated by 3-methylglutaconic aciduria-linked mutations. <i>ELife</i> , 2020, 9, .	2.8	44
24645	DAZL mediates a broad translational program regulating expansion and differentiation of spermatogonial progenitors. <i>ELife</i> , 2020, 9, .	2.8	28
24646	Localized inhibition in the <i>Drosophila</i> mushroom body. <i>ELife</i> , 2020, 9, .	2.8	29
24647	A cross-kingdom conserved ER-phagy receptor maintains endoplasmic reticulum homeostasis during stress. <i>ELife</i> , 2020, 9, .	2.8	139

#	ARTICLE	IF	CITATIONS
24648	The leukocyte non-coding RNA landscape in critically ill patients with sepsis. <i>ELife</i> , 2020, 9, .	2.8	36
24649	Evolved bacterial resistance against fluoropyrimidines can lower chemotherapy impact in the <i>Caenorhabditis elegans</i> host. <i>ELife</i> , 2020, 9, .	2.8	19
24650	Reprogramming of bone marrow myeloid progenitor cells in patients with severe coronary artery disease. <i>ELife</i> , 2020, 9, .	2.8	23
24652	Global gene expression analyses of the alkamide-producing plant <i>Heliopsis longipes</i> supports a polyketide synthase-mediated biosynthesis pathway. <i>PeerJ</i> , 2020, 8, e10074.	0.9	7
24653	Constitution of a comprehensive phytochemical profile and network pharmacology based investigation to decipher molecular mechanisms of <i>Teucrium polium</i> L. in the treatment of type 2 diabetes mellitus. <i>PeerJ</i> , 2020, 8, e10111.	0.9	6
24654	MutRank: an R shiny web-application for exploratory targeted mutual rank-based coexpression analyses integrated with user-provided supporting information. <i>PeerJ</i> , 2020, 8, e10264.	0.9	7
24655	Identification of significant genes signatures and prognostic biomarkers in cervical squamous carcinoma via bioinformatic data. <i>PeerJ</i> , 2020, 8, e10386.	0.9	10
24656	Comprehensive analysis of circRNA expression profiles and circRNA-associated competing endogenous RNA networks in IgA nephropathy. <i>PeerJ</i> , 2020, 8, e10395.	0.9	7
24657	Unbiased high-throughput characterization of mussel transcriptomic responses to sublethal concentrations of the biotoxin okadaic acid. <i>PeerJ</i> , 2015, 3, e1429.	0.9	15
24658	Emerging semantics to link phenotype and environment. <i>PeerJ</i> , 2015, 3, e1470.	0.9	15
24659	BD-Func: a streamlined algorithm for predicting activation and inhibition of pathways. <i>PeerJ</i> , 2013, 1, e159.	0.9	10
24660	The Iflaviruses Sacbrood virus and Deformed wing virus evoke different transcriptional responses in the honeybee which may facilitate their horizontal or vertical transmission. <i>PeerJ</i> , 2016, 4, e1591.	0.9	59
24661	<i>De novo</i> assembly and characterization of the Chinese three-keeled pond turtle (<i>Mauremys</i>) Tj ETQq0 0 0 rgBT /Overlock 10 TF	0.9	19
24662	Transcriptome analysis of immature xylem in the Chinese fir at different developmental phases. <i>PeerJ</i> , 2016, 4, e2097.	0.9	16
24663	Transcriptional similarity in couples reveals the impact of shared environment and lifestyle on gene regulation through modified cytosines. <i>PeerJ</i> , 2016, 4, e2123.	0.9	4
24664	Pathway-GPS and SIGORA: identifying relevant pathways based on the over-representation of their gene-pair signatures. <i>PeerJ</i> , 2013, 1, e229.	0.9	64
24665	Transcriptome analysis of colored calla lily (<i>Zantedeschia rehmannii</i> Engl.) by Illumina sequencing: <i>de novo</i> assembly, annotation and EST-SSR marker development. <i>PeerJ</i> , 2016, 4, e2378.	0.9	38
24666	Genomic and transcriptomic resources for assassin flies including the complete genome sequence of <i>Proctacanthus coquillettii</i> (Insecta: Diptera: Asilidae) and 16 representative transcriptomes. <i>PeerJ</i> , 2017, 5, e2951.	0.9	23

#	ARTICLE	IF	CITATIONS
24667	Transcriptome analyses provide insights into the difference of alkaloids biosynthesis in the Chinese goldthread (<i>Coptis chinensis</i> Franch.) from different biotopes. PeerJ, 2017, 5, e3303.	0.9	19
24668	Comparative transcriptome analysis of isonuclear-alloplasmic lines unmask key transcription factor genes and metabolic pathways involved in sterility of maize CMS-C. PeerJ, 2017, 5, e3408.	0.9	22
24669	GeNNet: an integrated platform for unifying scientific workflows and graph databases for transcriptome data analysis. PeerJ, 2017, 5, e3509.	0.9	11
24670	Onset of human preterm and term birth is related to unique inflammatory transcriptome profiles at the maternal fetal interface. PeerJ, 2017, 5, e3685.	0.9	62
24671	A practical guide to build <i>de-novo</i> assemblies for single tissues of non-model organisms: the example of a Neotropical frog. PeerJ, 2017, 5, e3702.	0.9	16
24672	Gene expression profiling and functional analysis reveals that p53 pathway-related gene expression is highly activated in cancer cells treated by cold atmospheric plasma-activated medium. PeerJ, 2017, 5, e3751.	0.9	31
24673	Characterisation of the horse transcriptome from immunologically active tissues. PeerJ, 2014, 2, e382.	0.9	6
24674	Increasing the precision of orthology-based complex prediction through network alignment. PeerJ, 2014, 2, e413.	0.9	1
24675	Biotea: semantics for Pubmed Central. PeerJ, 2018, 6, e4201.	0.9	5
24676	RBiomirGS: an all-in-one miRNA gene set analysis solution featuring target mRNA mapping and expression profile integration. PeerJ, 2018, 6, e4262.	0.9	18
24677	Evaluating the adaptive evolutionary convergence of carnivorous plant taxa through functional genomics. PeerJ, 2018, 6, e4322.	0.9	6
24678	miRNAome expression profiles in the gonads of adult <i>Melopsittacus undulatus</i> . PeerJ, 2018, 6, e4615.	0.9	17
24679	Candidate genes associated with red colour formation revealed by comparative genomic variant analysis of red- and green-skinned fruits of Japanese apricot (<i>Prunus mume</i>). PeerJ, 2018, 6, e4625.	0.9	13
24680	Divergent and convergent evolution of housekeeping genes in human-pig lineage. PeerJ, 2018, 6, e4840.	0.9	19
24681	Identification of SNPs potentially related to immune responses and growth performance in <i>Litopenaeus vannamei</i> by RNA-seq analyses. PeerJ, 2018, 6, e5154.	0.9	13
24682	Gonadal transcriptome sequencing of the critically endangered <i>Acipenser dabryanus</i> to discover candidate sex-related genes. PeerJ, 2018, 6, e5389.	0.9	20
24683	Comparison of gene expression profiles between human erythroid cells derived from fetal liver and adult peripheral blood. PeerJ, 2018, 6, e5527.	0.9	16
24684	CMTCN: a web tool for investigating cancer-specific microRNA and transcription factor co-regulatory networks. PeerJ, 2018, 6, e5951.	0.9	9

#	ARTICLE	IF	CITATIONS
24685	The identification of gene signature and critical pathway associated with childhood-onset type 2 diabetes. PeerJ, 2019, 7, e6343.	0.9	4
24686	Detection of condition-specific marker genes from RNA-seq data with MGFR. PeerJ, 2019, 7, e6970.	0.9	8
24687	Partial defoliation of <i>Brachypodium distachyon</i> plants grown in petri dishes under low light increases P and other nutrient levels concomitantly with transcriptional changes in the roots. PeerJ, 2019, 7, e7102.	0.9	2
24688	Comprehensive analysis of an lncRNA-miRNA-mRNA competing endogenous RNA network in pulpitis. PeerJ, 2019, 7, e7135.	0.9	34
24689	Identification of crucial genes based on expression profiles of hepatocellular carcinomas by bioinformatics analysis. PeerJ, 2019, 7, e7436.	0.9	48
24690	Integrated mRNA and miRNA profiling in NIH/3T3 cells in response to bovine papillomavirus E6 gene expression. PeerJ, 2019, 7, e7442.	0.9	4
24691	Network-based approach to identify biomarkers predicting response and prognosis for HER2-negative breast cancer treatment with taxane-anthracycline neoadjuvant chemotherapy. PeerJ, 2019, 7, e7515.	0.9	7
24692	Identification of lncRNAs associated with lung squamous cell carcinoma prognosis in the competitive endogenous RNA network. PeerJ, 2019, 7, e7727.	0.9	17
24693	Computational analysis of the LRRK2 interactome. PeerJ, 2015, 3, e778.	0.9	48
24694	Identification of key genes and pathways associated with cholangiocarcinoma development based on weighted gene correlation network analysis. PeerJ, 2019, 7, e7968.	0.9	18
24695	Transcriptome profiling analysis reveals key genes of different coat color in sheep skin. PeerJ, 2019, 7, e8077.	0.9	14
24696	Comprehensive analysis of differentially expressed microRNAs and mRNAs in MDBK cells expressing bovine papillomavirus E5 oncogene. PeerJ, 2019, 7, e8098.	0.9	6
24697	Navigating oxygen deprivation: liver transcriptomic responses of the red eared slider turtle to environmental anoxia. PeerJ, 2019, 7, e8144.	0.9	11
24698	DNA methylation profiling in recurrent miscarriage. PeerJ, 2020, 8, e8196.	0.9	5
24699	Comparative analysis of primary metabolites and transcriptome changes between ungrafted and pumpkin-grafted watermelon during fruit development. PeerJ, 2020, 8, e8259.	0.9	21
24700	The complete chloroplast genome of <i>Microcycas calocoma</i> (Miq.) A. DC. (Zamiaceae, Cycadales) and evolution in Cycadales. PeerJ, 2020, 8, e8305.	0.9	6
24701	Genome-wide analysis of lncRNAs, miRNAs, and mRNAs forming a prognostic scoring system in esophageal squamous cell carcinoma. PeerJ, 2020, 8, e8368.	0.9	13
24702	Comparative transcriptome analysis revealed genes involved in the fruiting body development of <i>Ophiocordyceps sinensis</i> . PeerJ, 2020, 8, e8379.	0.9	13

#	ARTICLE	IF	CITATIONS
24703	Detection and characterization of microRNA expression profiling and its target genes in response to canine parvovirus in Crandell Reese Feline Kidney cells. PeerJ, 2020, 8, e8522.	0.9	8
24704	Co-expression network analysis reveals the pivotal role of mitochondrial dysfunction and interferon signature in juvenile dermatomyositis. PeerJ, 2020, 8, e8611.	0.9	7
24705	Identification and validation of HELLS (Helicase, Lymphoid-Specific) and ICAM1 (Intercellular adhesion) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.9	17
24706	Transcriptome sequencing and analysis reveals the molecular response to selenium stimuli in <i>Pueraria lobata</i> (willd.) Ohwi. PeerJ, 2020, 8, e8768.	0.9	8
24707	Identification of core genes associated with prostate cancer progression and outcome via bioinformatics analysis in multiple databases. PeerJ, 2020, 8, e8786.	0.9	20
24708	Draft genome of <i>Rosenbergiella nectarea</i> strain 8N4 ^T provides insights into the potential role of this species in its plant host. PeerJ, 2020, 8, e8822.	0.9	7
24709	Post-transcriptional regulation of several biological processes involved in latex production in <i>Hevea brasiliensis</i> . PeerJ, 2020, 8, e8932.	0.9	9
24710	High expression of stromal signatures correlated with macrophage infiltration, angiogenesis and poor prognosis in glioma microenvironment. PeerJ, 2020, 8, e9038.	0.9	29
24711	SMRT sequencing of the full-length transcriptome of the <i>Rhynchophorus ferrugineus</i> (Coleoptera: Curculionidae). PeerJ, 2020, 8, e9133.	0.9	17
24712	GFVO: the Genomic Feature and Variation Ontology. PeerJ, 2015, 3, e933.	0.9	3
24713	Method of Retrieving Articles on Protein Structure Analysis from User Intention. International Journal of Bioscience, Biochemistry, Bioinformatics (IJBBB), 2013, , 182-186.	0.2	2
24714	Analysis of Population Based Metaheuristic Used for Gene Clustering. International Journal of Computer and Communication Engineering, 2013, , 174-178.	0.2	2
24715	UV-B Resistant Yeast Inhabit the Phyllosphere of Strawberry. British Microbiology Research Journal, 2014, 4, 1105-1117.	0.2	1
24716	Grafting-Induced Gene Expression Change in Brassica rapa Leaves is Different from Fruit Trees. Plant Breeding and Biotechnology, 2015, 3, 67-76.	0.3	2
24717	Differential Expression of Flowering Genes between Rapid- and Slow-Cycling <i>Brassica rapa</i> . Plant Breeding and Biotechnology, 2016, 4, 145-157.	0.3	4
24718	The human telomeric proteome during telomere replication. Nucleic Acids Research, 2021, 49, 12119-12135.	6.5	15
24719	Network analytics for drug repurposing in COVID-19. Briefings in Bioinformatics, 2022, 23, .	3.2	16
24720	Hymenoptera Genome Database: new genomes and annotation datasets for improved go enrichment and orthologue analyses. Nucleic Acids Research, 2022, 50, D1032-D1039.	6.5	19

#	ARTICLE	IF	CITATIONS
24721	CompoDynamics: a comprehensive database for characterizing sequence composition dynamics. <i>Nucleic Acids Research</i> , 2022, 50, D962-D969.	6.5	6
24722	CircleBase: an integrated resource and analysis platform for human eccDNAs. <i>Nucleic Acids Research</i> , 2022, 50, D72-D82.	6.5	20
24723	Bioinspired NO release coating enhances endothelial cells and inhibits smooth muscle cells. <i>Journal of Materials Chemistry B</i> , 2022, 10, 2454-2462.	2.9	9
24724	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. <i>Nucleic Acids Research</i> , 2022, 50, D898-D911.	6.5	277
24725	Multiple regression analysis of a comprehensive transcriptomic data assembly elucidates mechanically- and biochemically-driven responses to focused ultrasound blood-brain barrier disruption. <i>Theranostics</i> , 2021, 11, 9847-9858.	4.6	8
24726	Complex Portal 2022: new curation frontiers. <i>Nucleic Acids Research</i> , 2022, 50, D578-D586.	6.5	27
24727	Hepatic lysosomal acid lipase overexpression worsens hepatic inflammation in mice fed a Western diet. <i>Journal of Lipid Research</i> , 2021, 62, 100133.	2.0	8
24728	POU class 2 homeobox associating factor 1 (POU2AF1) participates in abdominal aortic aneurysm enlargement based on integrated bioinformatics analysis. <i>Bioengineered</i> , 2021, 12, 8980-8993.	1.4	3
24729	Graphical Modeling of Multiple Biological Pathways in Genomic Studies. <i>Emerging Topics in Statistics and Biostatistics</i> , 2021, , 431-459.	0.1	0
24730	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	6.5	117
24731	High Expression of ERK-related RASGRF2 predicts Poor prognosis in patients with Stomach Adenocarcinoma and correlates with M2 macrophage. <i>Journal of Cancer</i> , 2021, 12, 7177-7189.	1.2	4
24732	Five genes involved in circular RNA-associated competitive endogenous RNA network correlates with metastasis in papillary thyroid carcinoma. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 9016-9032.	1.0	3
24733	EWAS Open Platform: integrated data, knowledge and toolkit for epigenome-wide association study. <i>Nucleic Acids Research</i> , 2022, 50, D1004-D1009.	6.5	57
24734	A Genome-Wide Association Study Reveals New Genes in a Molecular Network Associated with Alcohol Dependence and Related Clinical Measures. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
24735	Exploration the potential mechanism of the SIRT1 and its target gene FOXO1/PPARGC1A in uteropelvic junction obstruction. <i>Translational Andrology and Urology</i> , 2021, 10, 4192-4205.	0.6	0
24736	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. <i>Nature Communications</i> , 2021, 12, 5647.	5.8	61
24737	Investigation of the active components and mechanism of Sanao Decoction in treating chronic cough by network pharmacology and molecular docking. <i>Digital Chinese Medicine</i> , 2021, 4, 191-201.	0.5	0
24738	Aberrantly reduced expression of miR-342-5p contributes to CCND1-associated chronic myeloid leukemia progression and imatinib resistance. <i>Cell Death and Disease</i> , 2021, 12, 908.	2.7	8

#	ARTICLE	IF	CITATIONS
24739	Neurogenomic divergence during speciation by reinforcement of mating behaviors in chorus frogs (<i>Pseudacris</i>). <i>BMC Genomics</i> , 2021, 22, 711.	1.2	3
24741	Proteomic and electron microscopy study of myogenic differentiation of alveolar mucosa multipotent mesenchymal stromal cells in three-dimensional culture. <i>Proteomics</i> , 2021, , 2000304.	1.3	2
24742	Genome Resource for <i>Elsinoë batatas</i> , the Causal Agent of Stem and Foliage Scab Disease of Sweet Potato. <i>Phytopathology</i> , 2022, 112, 973-975.	1.1	4
24743	Agent Repurposing for the Treatment of Advanced Stage Diffuse Large B-Cell Lymphoma Based on Gene Expression and Network Perturbation Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 756784.	1.1	3
24744	Transcriptomic Analysis of Polyhexamethyleneguanidine-Induced Lung Injury in Mice after a Long-Term Recovery. <i>Toxics</i> , 2021, 9, 253.	1.6	4
24745	Prioritization of Diagnostic and Prognostic Biomarkers for Lupus Nephritis Based on Integrated Bioinformatics Analyses. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 717234.	2.0	7
24746	Neutrophil Pathways of Inflammation Characterize the Blood Transcriptomic Signature of Patients with Psoriasis and Cardiovascular Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10818.	1.8	18
24747	Clarifying the molecular mechanism of tomentosin-induced antiproliferative and proapoptotic effects in human multiple myeloma via gene expression profile and genetic interaction network analysis. <i>International Journal of Molecular Medicine</i> , 2021, 48, .	1.8	2
24748	Three chromosome-level duck genome assemblies provide insights into genomic variation during domestication. <i>Nature Communications</i> , 2021, 12, 5932.	5.8	27
24749	Genomic insights into biocontrol potential of <i>Bacillus stercoris</i> LJBS06. <i>3 Biotech</i> , 2021, 11, 458.	1.1	3
24750	Identification of Novel Biomarkers Related to Lung Squamous Cell Carcinoma Using Integrated Bioinformatics Analysis. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-18.	0.7	4
24751	Differential expression profile of gluten-specific T cells identified by single-cell RNA-seq. <i>PLoS ONE</i> , 2021, 16, e0258029.	1.1	4
24752	Clustering spatial transcriptomics data. <i>Bioinformatics</i> , 2022, 38, 997-1004.	1.8	25
24753	The Genomic and Transcriptomic Analyses of <i>Floccularia luteovirens</i> , a Rare Edible Fungus in the Qinghai-Tibet Plateau, Provide Insights into the Taxonomy Placement and Fruiting Body Formation. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 887.	1.5	4
24754	A method of mechanism analysis about a traditional chinese medicine prescription on a disease based on PageRank algorithm and network pharmacology. <i>Pharmacological Research Modern Chinese Medicine</i> , 2022, 3, 100016.	0.5	3
24755	Computational methods for protein localization prediction. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5834-5844.	1.9	12
24757	Differential transcriptome analysis and identification of genes related to resistance to blight in three varieties of <i>Bambusa pervariabilis</i> – <i>Dendrocalamopsis grandis</i> . <i>PeerJ</i> , 2021, 9, e12301.	0.9	5
24758	Text mining-based word representations for biomedical data analysis and protein-protein interaction networks in machine learning tasks. <i>PLoS ONE</i> , 2021, 16, e0258623.	1.1	6

#	ARTICLE	IF	CITATIONS
24759	Mitochondrial translation is required for sustained killing by cytotoxic T cells. <i>Science</i> , 2021, 374, eabe9977.	6.0	55
24760	A comparative analysis of differentially expressed mRNAs, miRNAs and circRNAs provides insights into the key genes involved in the high-altitude adaptation of yaks. <i>BMC Genomics</i> , 2021, 22, 744.	1.2	7
24761	Reduced expression of OXPHOS and DNA damage genes is linked to protection from microvascular complications in long-term type 1 diabetes: the PROLONG study. <i>Scientific Reports</i> , 2021, 11, 20735.	1.6	7
24762	<i>Bacteroides</i> spp. promotes branched-chain amino acid catabolism in brown fat and inhibits obesity. <i>IScience</i> , 2021, 24, 103342.	1.9	58
24763	Upregulation of cathepsin L gene under mild cold conditions in young Japanese male adults. <i>Journal of Physiological Anthropology</i> , 2021, 40, 16.	1.0	3
24764	Analysing the fitness cost of antibiotic resistance to identify targets for combination antimicrobials. <i>Nature Microbiology</i> , 2021, 6, 1410-1423.	5.9	16
24766	Identification of a Prognosis-Related Risk Signature for Bladder Cancer to Predict Survival and Immune Landscapes. <i>Journal of Immunology Research</i> , 2021, 2021, 1-26.	0.9	14
24768	Mass Spectrometry-Based Phosphoproteomics and Systems Biology: Approaches to Study T Lymphocyte Activation and Exhaustion. <i>Journal of Molecular Biology</i> , 2021, 433, 167318.	2.0	5
24769	De novo transcriptome analysis provides insights into the salt tolerance of <i>Podocarpus macrophyllus</i> under salinity stress. <i>BMC Plant Biology</i> , 2021, 21, 489.	1.6	9
24771	Neuronal activity regulates the nuclear proteome to promote activity-dependent transcription. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	4
24773	Genetic and epigenetic characterization of posterior pituitary tumors. <i>Acta Neuropathologica</i> , 2021, 142, 1025-1043.	3.9	7
24774	Integrated bioinformatics analysis of core regulatory elements involved in keloid formation. <i>BMC Medical Genomics</i> , 2021, 14, 239.	0.7	6
24775	Chromosome-scale genome assembly of <i>Castanopsis tibetana</i> provides a powerful comparative framework to study the evolution and adaptation of Fagaceae trees. <i>Molecular Ecology Resources</i> , 2022, 22, 1178-1189.	2.2	6
24776	Transcriptome Analysis of <i>Lolium temulentum</i> Exposed to a Combination of Drought and Heat Stress. <i>Plants</i> , 2021, 10, 2247.	1.6	3
24777	Single-Cell RNA Sequencing in Multiple Pathologic Types of Renal Cell Carcinoma Revealed Novel Potential Tumor-Specific Markers. <i>Frontiers in Oncology</i> , 2021, 11, 719564.	1.3	47
24778	Identification of candidate genes on the basis of SNP by time-lagged heat stress interactions for milk production traits in German Holstein cattle. <i>PLoS ONE</i> , 2021, 16, e0258216.	1.1	10
24779	Distinct Mitochondrial Remodeling During Mesoderm Differentiation in a Human-Based Stem Cell Model. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 744777.	1.8	5
24780	A global screening identifies chromatin-enriched RNA-binding proteins and the transcriptional regulatory activity of QKI5 during monocytic differentiation. <i>Genome Biology</i> , 2021, 22, 290.	3.8	13

#	ARTICLE	IF	CITATIONS
24781	Context-aware multi-token concept recognition of biological entities. BMC Bioinformatics, 2021, 22, 337.	1.2	2
24782	Imaging Transcriptomics of Brain Disorders. Biological Psychiatry Global Open Science, 2022, 2, 319-331.	1.0	22
24783	Comprehensive landscape and interference of clonal haematopoiesis mutations for liquid biopsy: A Chinese pan-cancer cohort. Journal of Cellular and Molecular Medicine, 2021, 25, 10279-10290.	1.6	4
24784	Chromosome-level genome assembly reveals genomic architecture of northern range expansion in the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins (Coleoptera: Curculionidae). Molecular Ecology Resources, 2022, 22, 1149-1167.	2.2	11
24785	Description and genome analysis of <i>Microvirga antarctica</i> sp. nov., a novel pink-pigmented psychrotolerant bacterium isolated from Antarctic soil. Antonie Van Leeuwenhoek, 2021, 114, 2219-2228.	0.7	3
24787	Student biocuration projects as a learning environment. F1000Research, 2021, 10, 1023.	0.8	0
24788	RabA2b Overexpression Alters the Plasma-Membrane Proteome and Improves Drought Tolerance in Arabidopsis. Frontiers in Plant Science, 2021, 12, 738694.	1.7	5
24789	Tracing protein and proteome history with chronologies and networks: folding recapitulates evolution. Expert Review of Proteomics, 2021, 18, 863-880.	1.3	9
24790	OnTheFly2.0: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis. NAR Genomics and Bioinformatics, 2021, 3, lqab090.	1.5	10
24791	Exploring the Freedoms in Data Mining: Why the Trustworthiness and Integrity of the Findings are the Casualties, and How to Resolve These?. Lecture Notes in Networks and Systems, 2022, , 616-635.	0.5	1
24792	Arabidopsis bioinformatics: tools and strategies. Plant Journal, 2021, 108, 1585-1596.	2.8	9
24793	TIGER: The gene expression regulatory variation landscape of human pancreatic islets. Cell Reports, 2021, 37, 109807.	2.9	45
24794	GNG7 and ADCY1 as diagnostic and prognostic biomarkers for pancreatic adenocarcinoma through bioinformatic-based analyses. Scientific Reports, 2021, 11, 20441.	1.6	10
24795	Complete Genome Sequence Resource for <i>Xanthomonas fragariae</i> Causing Crown Infection Pockets in Strawberry. Molecular Plant-Microbe Interactions, 2022, 35, 170-173.	1.4	5
24796	Effects of Lingonberry (<i>Vaccinium vitis-idaea</i> L.) Supplementation on Hepatic Gene Expression in High-Fat Diet Fed Mice. Nutrients, 2021, 13, 3693.	1.7	8
24798	Transcriptomic profiling of neonatal mouse granulosa cells reveals new insights into primordial follicle activation. Biology of Reproduction, 2022, 106, 503-514.	1.2	5
24799	Genome-wide distribution of 5hmC in the dental pulp of mouse molars and incisors. Journal of Biochemistry, 2022, 171, 123-129.	0.9	2
24800	Computational repurposing of therapeutic small molecules from cancer to pulmonary hypertension. Science Advances, 2021, 7, eabh3794.	4.7	16

#	ARTICLE	IF	CITATIONS
24801	Urinary extracellular vesicles: Assessment of pre-analytical variables and development of a quality control with focus on transcriptomic biomarker research. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12158.	5.5	26
24802	IL12 integrated into the CAR exodomain converts CD8+ T cells to poly-functional NK-like cells with superior killing of antigen-loss tumors. <i>Molecular Therapy</i> , 2022, 30, 593-605.	3.7	18
24803	Identification of Novel Endogenous Controls for qPCR Normalization in SK-BR-3 Breast Cancer Cell Line. <i>Genes</i> , 2021, 12, 1631.	1.0	2
24804	Transcriptome analysis reveals differing response and tolerance mechanism of EPSPS and GAT genes among transgenic soybeans. <i>Molecular Biology Reports</i> , 2021, 48, 7351-7360.	1.0	2
24805	Investigation of the transcriptomic response in Atlantic salmon (<i>Salmo salar</i>) gill exposed to <i>Paramoeba perurans</i> during early onset of disease. <i>Scientific Reports</i> , 2021, 11, 20682.	1.6	4
24806	The Genetic and Environmental Adaptation of the Associated Liana Species <i>Derris trifoliata</i> Lour. (Leguminosae) in Mangroves. <i>Forests</i> , 2021, 12, 1375.	0.9	2
24807	Revealing Pathways Associated with Feed Efficiency and Meat Quality Traits in Slow-Growing Chickens. <i>Animals</i> , 2021, 11, 2977.	1.0	7
24808	The chromosome-scale genome assembly, annotation and evolution of <i>Rhododendron henanense</i> subsp. <i>lingbaoense</i> . <i>Molecular Ecology Resources</i> , 2022, 22, 988-1001.	2.2	14
24809	Formalization of gene regulation knowledge using ontologies and gene ontology causal activity models. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194766.	0.9	6
24810	Gene Ontology curation of the blood-brain barrier to improve the analysis of Alzheimer's and other neurological diseases. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	6
24811	RNF2 ablation reprograms the tumor-immune microenvironment and stimulates durable NK and CD4+ T-cell-dependent antitumor immunity. <i>Nature Cancer</i> , 2021, 2, 1018-1038.	5.7	11
24812	Comparative genomics reveals molecular mechanisms underlying health and reproduction in cryptorchid mammals. <i>BMC Genomics</i> , 2021, 22, 763.	1.2	2
24813	Chromatin accessibility and gene expression during adipocyte differentiation identify context-dependent effects at cardiometabolic GWAS loci. <i>PLoS Genetics</i> , 2021, 17, e1009865.	1.5	9
24815	Adaptive translational pausing is a hallmark of the cellular response to severe environmental stress. <i>Molecular Cell</i> , 2021, 81, 4191-4208.e8.	4.5	18
24816	Host genetic factors associated with the range limit of a European hantavirus. <i>Molecular Ecology</i> , 2022, 31, 252-265.	2.0	6
24817	The KRAS-regulated kinome identifies WEE1 and ERK coinhibition as a potential therapeutic strategy in KRAS-mutant pancreatic cancer. <i>Journal of Biological Chemistry</i> , 2021, 297, 101335.	1.6	14
24818	Contextualizing Genes by Using Text-Mined Co-Occurrence Features for Cancer Gene Panel Discovery. <i>Frontiers in Genetics</i> , 2021, 12, 771435.	1.1	3
24819	Regulation of 5-Hydroxymethylcytosine by TET2 Contributes to Squamous Cell Carcinoma Tumorigenesis. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1270-1279.e2.	0.3	8

#	ARTICLE	IF	CITATIONS
24820	Dissecting the molecular mechanism of russeting in sand pear (<i>Pyrus pyrifolia</i> Nakai) by metabolomics, transcriptomics, and proteomics. <i>Plant Journal</i> , 2021, 108, 1644-1661.	2.8	17
24821	Drug Repurposing for Atopic Dermatitis by Integration of Gene Networking and Genomic Information. <i>Frontiers in Immunology</i> , 2021, 12, 724277.	2.2	18
24822	Optical Coherence Tomography Angiography Characteristics Serve as Retinal Vein Occlusion Therapeutic Biomarkers for Dexamethasone Intravitreal Implant. <i>Disease Markers</i> , 2021, 2021, 1-21.	0.6	1
24823	Transcriptome Analysis of <i>Zygophyllum xanthoxylum</i> Adaptation Strategies to Phosphate Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 723595.	1.7	4
24824	Hybrid Sequencing in Different Types of Goat Skeletal Muscles Reveals Genes Regulating Muscle Development and Meat Quality. <i>Animals</i> , 2021, 11, 2906.	1.0	4
24825	In-depth cell-free DNA sequencing reveals genomic landscape of Hodgkin's lymphoma and facilitates ultrasensitive residual disease detection. <i>Med</i> , 2021, 2, 1171-1193.e11.	2.2	24
24826	A Polycomb domain found in committed cells impairs differentiation when introduced into PRC1 in pluripotent cells. <i>Molecular Cell</i> , 2021, 81, 4677-4691.e8.	4.5	20
24829	Alterations in HLA Class I-Presented Immunopeptidome and Class I-Interactome upon Osimertinib Resistance in EGFR Mutant Lung Adenocarcinoma. <i>Cancers</i> , 2021, 13, 4977.	1.7	5
24831	Genome-wide associations for immune traits in two maternal pig lines. <i>BMC Genomics</i> , 2021, 22, 717.	1.2	11
24832	An updated SYSCILIA gold standard (SCGSv2) of known ciliary genes, revealing the vast progress that has been made in the cilia research field. <i>Molecular Biology of the Cell</i> , 2021, 32, br13.	0.9	23
24834	Proteomic profiling reveals engineered chitosan nanoparticles mediated cellular crosstalk and immunomodulation for therapeutic application in apical periodontitis. <i>Bioactive Materials</i> , 2022, 11, 77-89.	8.6	10
24835	Comparative RNA-Seq Analyses of <i>Solenopsis japonica</i> (Hymenoptera: Formicidae) Reveal Gene in Response to Cold Stress. <i>Genes</i> , 2021, 12, 1610.	1.0	10
24836	Deep post-GWAS analysis identifies potential risk genes and risk variants for Alzheimer's disease, providing new insights into its disease mechanisms. <i>Scientific Reports</i> , 2021, 11, 20511.	1.6	16
24837	Loss of the wild-type KRAS allele promotes pancreatic cancer progression through functional activation of YAP1. <i>Oncogene</i> , 2021, 40, 6759-6771.	2.6	13
24839	Protein function prediction using functional inter-relationship. <i>Computational Biology and Chemistry</i> , 2021, 95, 107593.	1.1	4
24840	Chromosome-scale assembly and high-density genetic map of the yellow drum, <i>Nibea albiflora</i> . <i>Scientific Data</i> , 2021, 8, 268.	2.4	5
24841	Downregulation of mitochondrial biogenesis by virus infection triggers antiviral responses by cyclic GMP-AMP synthase. <i>PLoS Pathogens</i> , 2021, 17, e1009841.	2.1	24
24842	Comparative Transcriptome Sequencing of Taro Corm Development With a Focus on the Starch and Sucrose Metabolism Pathway. <i>Frontiers in Genetics</i> , 2021, 12, 771081.	1.1	5

#	ARTICLE	IF	CITATIONS
24843	Evidence for Lignocellulose-Decomposing Enzymes in the Genome and Transcriptome of the Aquatic Hyphomycete <i>Clavariopsis aquatica</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 854.	1.5	6
24844	Development and Validation of a Prognostic Model of RNA-Binding Proteins in Colon Adenocarcinoma: A Study Based on TCGA and GEO Databases. <i>Cancer Management and Research</i> , 2021, Volume 13, 7709-7722.	0.9	4
24845	iMPT-FDNPL: Identification of Membrane Protein Types with Functional Domains and a Natural Language Processing Approach. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-10.	0.7	31
24846	Genome-wide phenotypic RNAi screen in the <i>Drosophila</i> wing: phenotypic description of functional classes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	7
24848	Network Pharmacology-Based Study of the Underlying Mechanisms of Huangqi Sijunzi Decoction for Alzheimer's Disease. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-13.	0.5	5
24849	SCovid: single-cell atlases for exposing molecular characteristics of COVID-19 across 10 human tissues. <i>Nucleic Acids Research</i> , 2022, 50, D867-D874.	6.5	28
24850	Identification of candidate genes from androgenic gland in <i>Macrobrachium nipponense</i> regulated by eyestalk ablation. <i>Scientific Reports</i> , 2021, 11, 19855.	1.6	19
24853	Genome and transcriptome analysis to understand the role diversification of cytochrome P450 gene under excess nitrogen treatment. <i>BMC Plant Biology</i> , 2021, 21, 447.	1.6	7
24854	Arabidopsis MED18 Interaction With RNA Pol IV and V Subunit NRPD2a in Transcriptional Regulation of Plant Immune Responses. <i>Frontiers in Plant Science</i> , 2021, 12, 692036.	1.7	7
24855	A Systems Approach Dissociates Fructose-Induced Liver Triglyceride from Hypertriglyceridemia and Hyperinsulinemia in Male Mice. <i>Nutrients</i> , 2021, 13, 3642.	1.7	3
24856	An Atypical Autoinflammatory Disease Due to an LRR Domain NLRP3 Mutation Enhancing Binding to NEK7. <i>Journal of Clinical Immunology</i> , 2022, 42, 158-170.	2.0	8
24857	Disrupted circadian oscillations in type 2 diabetes are linked to altered rhythmic mitochondrial metabolism in skeletal muscle. <i>Science Advances</i> , 2021, 7, eabi9654.	4.7	44
24858	Identification of Gene-Set Signature in Early-Stage Hepatocellular Carcinoma and Relevant Immune Characteristics. <i>Frontiers in Oncology</i> , 2021, 11, 740484.	1.3	2
24859	Epididymal mRNA and miRNA transcriptome analyses reveal important genes and miRNAs related to sperm motility in roosters. <i>Poultry Science</i> , 2022, 101, 101558.	1.5	8
24860	Identification and genomic analysis of <i>Mycobacterium ulcerans</i> ecovar <i>Liflandii</i> from the farmed Chinese tongue sole, <i>Cynoglossus semilaevis</i> G&Afrac14nther. <i>Aquaculture</i> , 2022, 548, 737614.	1.7	4
24861	Evolutionary divergence in embryo and seed coat development of U&Afrac14n Triangle <i>Brassica</i> species illustrated by a spatiotemporal transcriptome atlas. <i>New Phytologist</i> , 2022, 233, 30-51.	3.5	16
24862	Novel Enzymes From the Red Sea Brine Pools: Current State and Potential. <i>Frontiers in Microbiology</i> , 2021, 12, 732856.	1.5	3
24864	Transcriptomics Reveals the Putative Mycoparasitic Strategy of the Mushroom <i>Entoloma abortivum</i> on Species of the Mushroom Genus <i>Armillaria</i> . <i>MSystems</i> , 2021, 6, e0054421.	1.7	3

#	ARTICLE	IF	CITATIONS
24865	Screening of differentially expressed proteins in placentas from patients with late-onset preeclampsia. <i>Proteomics - Clinical Applications</i> , 2022, 16, e2100053.	0.8	5
24867	A metric for evaluating biological information in gene sets and its application to identify co-expressed gene clusters in PBMC. <i>PLoS Computational Biology</i> , 2021, 17, e1009459.	1.5	2
24868	Trends in biological data integration for the selection of enzymes and transcription factors related to cellulose and hemicellulose degradation in fungi. <i>3 Biotech</i> , 2021, 11, 475.	1.1	3
24869	Tlr2/4 Double Knockout Attenuates the Degeneration of Primary Auditory Neurons: Potential Mechanisms From Transcriptomic Perspectives. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 750271.	1.8	1
24870	Metabolic gene regulation by <i>Drosophila</i> GATA transcription factor Grain. <i>PLoS Genetics</i> , 2021, 17, e1009855.	1.5	2
24871	HPODNets: deep graph convolutional networks for predicting human protein-phenotype associations. <i>Bioinformatics</i> , 2022, 38, 799-808.	1.8	5
24872	Nkx3-1 and Fech genes might be switch genes involved in pituitary non-functioning adenoma invasiveness. <i>Scientific Reports</i> , 2021, 11, 20943.	1.6	3
24873	Multi-Omics-Based Identification and Functional Characterization of Ch_A06G1257 Proves Its Potential Role in Drought Stress Tolerance in <i>Gossypium hirsutum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 746771.	1.7	13
24874	DNA crosslinking and recombination-activating genes 1/2 (RAG1/2) are required for oncogenic splicing in acute lymphoblastic leukemia. <i>Cancer Communications</i> , 2021, 41, 1116-1136.	3.7	7
24875	Transcriptome profile of <i>Haemaphysalis longicornis</i> (Acari: Ixodidae) exposed to <i>Cymbopogon citratus</i> essential oil and citronella suggest a cytotoxic mode of action involving mitochondrial Ca ²⁺ overload and depolarization. <i>Pesticide Biochemistry and Physiology</i> , 2021, 179, 104971.	1.6	6
24876	Myogenin controls via AKAP6 non-centrosomal microtubule-organizing center formation at the nuclear envelope. <i>ELife</i> , 2021, 10, .	2.8	6
24877	Type 2 Diabetes Modifies Skeletal Muscle Gene Expression Response to Gastric Bypass Surgery. <i>Frontiers in Endocrinology</i> , 2021, 12, 728593.	1.5	6
24878	Are There Limits in Explainability of Prognostic Biomarkers? Scrutinizing Biological Utility of Established Signatures. <i>Cancers</i> , 2021, 13, 5087.	1.7	1
24879	Assessing Host-Pathogen Interaction Networks via RNA-Seq Profiling: A Systems Biology Approach. , 0, , .		1
24880	Integrated analysis of dysregulated microRNA and mRNA expression in intestinal epithelial cells following ethanol intoxication and burn injury. <i>Scientific Reports</i> , 2021, 11, 20213.	1.6	5
24881	Draft genome sequence of <i>Diaporthe batatatis</i> causing dry rot disease in sweetpotato. <i>Plant Disease</i> , 2021, , .	0.7	2
24883	A GO catalogue of human DNA-binding transcription factors. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194765.	0.9	15
24884	Establishment of a prognostic model of ten transcription factors in gastric cancer. <i>Genomics</i> , 2021, 113, 4075-4087.	1.3	2

#	ARTICLE	IF	CITATIONS
24885	Attention to time-of-day variability improves the reproducibility of gene expression patterns in multiple sclerosis. <i>IScience</i> , 2021, 24, 103247.	1.9	2
24886	Genome-wide association studies (GWAS) and post-GWAS analyses for technological traits in Assaf and Churra dairy breeds. <i>Journal of Dairy Science</i> , 2021, 104, 11850-11866.	1.4	11
24887	A review on omics-based biomarkers discovery for Alzheimer's disease from the bioinformatics perspectives: Statistical approach vs machine learning approach. <i>Computers in Biology and Medicine</i> , 2021, 139, 104947.	3.9	29
24888	Title is missing!. <i>Hikaku Seiri Seikagaku(Comparative Physiology and Biochemistry)</i> , 2000, 17, 146-154.	0.0	0
24889	Extending a Multi-agent System for Genomic Annotation. <i>Lecture Notes in Computer Science</i> , 2001, , 106-117.	1.0	5
24891	STRUCTURE-BASED COMPARISON OF FOUR EUKARYOTIC GENOMES. , 2001, , .		2
24893	BIKMAS: A Knowledge Engineering System for Bioinformatics. <i>Lecture Notes in Computer Science</i> , 2002, , 435-440.	1.0	0
24894	Protein Interaction Databases and Its Application. <i>Immune Network</i> , 2002, 2, 125.	1.6	0
24895	Complex Model Organism Genome Databases. , 2002, , 120-131.		0
24896	Database Systems for the Analysis of Biochemical Pathways. , 2002, , 201-220.		6
24897	GeneAround: A Browsing System for Gene Annotation Using XML Technologies. <i>Lecture Notes in Computer Science</i> , 2002, , 236-246.	1.0	0
24898	Using Perceptrons for Supervised Classification of DNA Microarray Samples: Obtaining the Optimal Level of Information and Finding Differentially Expressed Genes. <i>Lecture Notes in Computer Science</i> , 2002, , 577-582.	1.0	1
24899	FUNCTIONAL DISCRIMINATION OF GENE EXPRESSION PATTERNS IN TERMS OF THE GENE ONTOLOGY. , 2002, , .		11
24900	LINKING MOLECULAR IMAGING TERMINOLOGY TO THE GENE ONTOLOGY (GO). , 2002, , 613-23.		7
24901	A Virtual Approach to Integrating Biomedical Databases and Terminologies. <i>Lecture Notes in Computer Science</i> , 2003, , 31-38.	1.0	1
24902	ã,ãfSã, ã,ãfSã, ãfã,ã«ãSããã,ã“æœÿçš,,éª¼ãç™ºç³¼ã®ç¶²ç³¼...çš,,è\$£æž. <i>Hikaku Seiri Seikagaku(Comparative Physiology and Biochemistry)</i>		
24903	Experimental Design and Data Analysis. , 2003, , 179-241.		1
24904	Knowledge Discovery from the Human Transcriptome. , 2003, , 693-710.		1

#	ARTICLE	IF	CITATIONS
24905	Integrating Biological Process Modelling with Gene Expression Data and Ontologies for Functional Genomics (Position Paper). Lecture Notes in Computer Science, 2003, , 187-193.	1.0	0
24906	Microarrays. , 2003, , 665-692.		0
24907	Bioinformatics, Genomics, and Antimicrobial Drug Discovery. , 2003, , 27-42.		0
24908	Dynamic Visualization of Expressed Gene Networks. , 2003, , 277-298.		0
24909	Information economics and the Internet. , 2003, , 347-356.		0
24910	TERMINOLOGICAL MAPPING FOR HIGH THROUGHPUT COMPARATIVE BIOLOGY OF PHENOTYPES. , 2003, , 202-13.		20
24911	BUILDING MOUSE PHENOTYPE ONTOLOGIES. , 2003, , 178-89.		33
24912	Protein Data Resources. , 2004, , 478-483.		0
24913	Incorporation of quantitative knowledge into genetic information systems. , 2004, , 557-564.		0
24914	Database Challenges in the Integration of Biomedical Data Sets. , 2004, , 1202-1213.		3
24915	Discovery of the Î±-1 Microglobulin Complex in Urine Sample Patients with Cadmium Intoxication. Journal of Medical Sciences (Faisalabad, Pakistan), 2004, 4, 198-202.	0.0	2
24917	Methods of Computational Genomics. , 2004, , 279-342.		0
24918	Bioinformatics Tools. Nutrition and Disease Prevention, 2004, , 449-472.	0.1	0
24919	Metabolomics. , 2004, , 616-653.		0
24920	IMPLICATIONS OF COMPOSITIONALITY IN THE GENE ONTOLOGY FOR ITS CURATION AND USAGE. , 2004, , .		14
24921	SPARSE FACTORIZATIONS OF GENE EXPRESSION DATA GUIDED BY BINDING DATA. , 2004, , .		3
24922	MULTI-ASPECT GENE RELATION ANALYSIS. , 2004, , 233-44.		2
24924	GENESTRACE: PHENOMIC KNOWLEDGE DISCOVERY VIA STRUCTURED TERMINOLOGY. , 2004, , .		9

#	ARTICLE	IF	CITATIONS
24925	Gene Duplication and Adaptive Evolution of Digestive Proteases in <i>Drosophila arizonae</i> Female Reproductive Tracts. <i>PLoS Genetics</i> , 2005, preprint, e148.	1.5	0
24926	Cluster Based Integration of Heterogeneous Biological Databases Using the AutoMed Toolkit. <i>Lecture Notes in Computer Science</i> , 2005, , 191-207.	1.0	7
24928	Hybrid Integration of Molecular-Biological Annotation Data. <i>Lecture Notes in Computer Science</i> , 2005, , 208-223.	1.0	3
24929	Functional Coverage of the Human Genome by Existing Structures, Structural Genomics Targets and Homology Models. <i>PLoS Computational Biology</i> , 2005, preprint, e31.	1.5	0
24930	Elucidating the Altered Transcriptional Programs in Breast Cancer using Independent Component Analysis. <i>PLoS Computational Biology</i> , 2005, preprint, e161.	1.5	0
24931	Where have all the interactions gone? Estimating the coverage of two-hybrid protein interaction maps. <i>PLoS Computational Biology</i> , 2005, preprint, e214.	1.5	0
24932	Predicting Protein Function With Hierarchical Phylogenetic Profiles: the Gene3D Phylo-Tuner Method Applied to Eukaryotic Genomes. <i>PLoS Computational Biology</i> , 2005, preprint, e237.	1.5	0
24934	Subsumption in \mathcal{EL} w.r.t. Hybrid TBoxes. <i>Lecture Notes in Computer Science</i> , 2005, , 34-48.	1.0	4
24935	Visualizing the Science of Genomics. , 2005, , 217-251.		6
24936	Creating Ontologies for Content Representation – The OntoSeed Suite. <i>Lecture Notes in Computer Science</i> , 2005, , 1296-1313.	1.0	5
24937	Generation of Glyphs for Conveying Complex Information, with Application to Protein Representations. <i>Lecture Notes in Computer Science</i> , 2005, , 90-102.	1.0	1
24940	Flux-Based vs. Topology-Based Similarity of Metabolic Genes. <i>Lecture Notes in Computer Science</i> , 2006, , 274-285.	1.0	0
24942	Grid-Enabled Metropolis Shared Research Platform. <i>Lecture Notes in Computer Science</i> , 2006, , 477-485.	1.0	0
24944	Optimizing Monitoring Queries over Distributed Data. <i>Lecture Notes in Computer Science</i> , 2006, , 829-846.	1.0	4
24946	A Novel Method for Expanding Current Annotations in Gene Ontology. <i>Lecture Notes in Computer Science</i> , 2006, , 747-756.	1.0	0
24947	Ontology Guided Data Integration for Computational Prioritization of Disease Genes. <i>Lecture Notes in Computer Science</i> , 2006, , 689-698.	1.0	1
24948	A Computer Visualization Model for the De Novo Sphingolipid Biosynthetic Pathway. , 2006, , 493-508.		0
24949	A priority model for named entities. , 2006, , .		3

#	ARTICLE	IF	CITATIONS
24950	Term generalization and synonym resolution for biological abstracts. , 2006, , .		1
24951	GOHSE: Ontology Driven Linking of Biology Resources. SSRN Electronic Journal, 0, , .	0.4	1
24952	The Distinctiveness of Individuals: Using Knowledge Structures To Represent Research Focuses; The Field of Stem Cell Research. , 0, , .		0
24953	Genome Resources and Comparative Analysis Tools for Cardiovascular Research. Methods in Molecular Medicine, 2006, 128, 101-123.	0.8	0
24954	SWAN: A Distributed Knowledge Infrastructure for Alzheimer Disease Research. SSRN Electronic Journal, 0, , .	0.4	1
24955	A Method for Similarity-Based Grouping of Biological Data. Lecture Notes in Computer Science, 2006, , 136-151.	1.0	2
24956	Optimal Selection of Microarray Analysis Methods Using a Conceptual Clustering Algorithm. Lecture Notes in Computer Science, 2006, , 172-183.	1.0	2
24957	Bioinformatics Data Source Integration Based on Semantic Relationships Across Species. Lecture Notes in Computer Science, 2006, , 78-93.	1.0	1
24958	S-Adenosylmethionine and Methionine Adenosyltransferase Genes. , 2006, , 93-111.		0
24959	Condition Transition Analysis Reveals TF Activity Related to Nutrient-Limitation-Specific Effects of Oxygen Presence in Yeast. Lecture Notes in Computer Science, 2006, , 271-284.	1.0	0
24960	Contribution to Gene Expression Data Analysis by Means of Set Pattern Mining. Lecture Notes in Computer Science, 2006, , 328-347.	1.0	0
24961	Ontologies and Text Mining as a Basis for a Semantic Web for the Life Sciences. Lecture Notes in Computer Science, 2006, , 164-183.	1.0	2
24962	Tree-Dependent Components of Gene Expression Data for Clustering. Lecture Notes in Computer Science, 2006, , 837-846.	1.0	2
24964	Semantic Web Reasoning for Analyzing Gene Expression Profiles. Lecture Notes in Computer Science, 2006, , 78-89.	1.0	2
24965	Web-Based Genomic Information Integration with Gene Ontology. Lecture Notes in Computer Science, 2006, , 812-817.	1.0	0
24967	Advanced Prototype Machines: Exploring Prototypes for Classification. , 2006, , .		0
24968	BIOMEDIATOR DATA INTEGRATION AND INFERENCE FOR FUNCTIONAL ANNOTATION OF ANONYMOUS SEQUENCES. , 2006, , .		9
24969	Inference of Gene Coexpression Networks by Integrative Analysis across Microarray Experiments. Journal of Integrative Bioinformatics, 2006, 3, 137-147.	1.0	0

#	ARTICLE	IF	CITATIONS
24970	Omics Approaches in the Context of Environmental Toxicology. , 2006, , 1-31.		0
24971	Protein-Protein Interaction Reliability Enhancement System based on Feature Selection and Classification Technique. The KIPS Transactions PartB, 2006, 13B, 679-688.	0.1	0
24972	Information Bottleneck for Non Co-Occurrence Data. , 2007, , 1241-1248.		4
24973	Blind Matrix Decomposition Via Genetic Optimization of Sparseness and Nonnegativity Constraints. Lecture Notes in Computer Science, 2007, , 799-808.	1.0	1
24974	GoSh: a goat and sheep ESTs database. Italian Journal of Animal Science, 2007, 6, 60-62.	0.8	0
24975	BioPAX: A Standard Data Format for Pathway Data Exchange. Seibutsu Butsuri, 2007, 47, 179-184.	0.0	0
24976	Comparison of Protein-Protein Interaction Confidence Assignment Schemes. Lecture Notes in Computer Science, 2007, , 39-50.	1.0	1
24977	Protein Classification from Protein-Domain and Gene-Ontology Annotation Information Using Formal Concept Analysis. Lecture Notes in Computer Science, 2007, , 347-354.	1.0	0
24978	Cross-Species Comparison Using Expression Data. , 2007, , 147-159.		1
24979	A Multi-site Subcellular Localizer for Fungal Proteins. Lecture Notes in Computer Science, 2007, , 73-85.	1.0	0
24980	Validating Gene Clusterings by Selecting Informative Gene Ontology Terms with Mutual Information. Lecture Notes in Computer Science, 2007, , 81-92.	1.0	0
24981	Causal Inference of Regulator-Target Pairs by Gene Mapping of Expression Phenotypes. Lecture Notes in Computer Science, 2007, , 95-106.	1.0	0
24982	Unsupervised Decision Trees Structured by Gene Ontology (GO-UDTs) for the Interpretation of Microarray Data. Studies in Classification, Data Analysis, and Knowledge Organization, 2007, , 585-592.	0.1	0
24983	Extending the Interpretation of Gene Profiling Microarray Experiments to Pathway Analysis Through the Use of Gene Ontology Terms. , 2007, , 55-61.		0
24984	An automated protein annotation filter for integrating web-based annotation tools. Bioinformation, 2007, 2, 76-77.	0.2	0
24985	Large-scale EST Sequencing. CGB Technical Report, 2007, 2007, .	1.5	0
24986	SEMANTIC SIMILARITY DEFINITION OVER GENE ONTOLOGY BY FURTHER MINING OF THE INFORMATION CONTENT. , 2007, , .		2
24987	IDENTIFICATION OF ACTIVATED TRANSCRIPTION FACTORS FROM MICROARRAY GENE EXPRESSION DATA OF KAMPO MEDICINE-TREATED MICE. , 2007, , .		2

#	ARTICLE	IF	CITATIONS
24988	CONTEXT SPECIFIC PROTEIN FUNCTION PREDICTION. , 2007, , .		2
24989	Matching Spatial Regions with Combinations of Interacting Gene Expression Patterns. Communications in Computer and Information Science, 2008, , 347-361.	0.4	1
24990	New Trends in the Analysis of Functional Genomic Data. Mathematics in Industry, 2008, , 576-580.	0.1	1
24991	Predicting Protein Subcellular Localization using PsePSSM and Support Vector Machines. , 2008, , .		0
24992	Clustering Analysis for Combining Multiple Genomic Data. Seibutsu Butsuri, 2008, 48, 190-194.	0.0	0
24993	Online Resources for the Molecular Contextualization of Disease. Methods in Molecular Medicine, 2008, 141, 287-308.	0.8	0
24994	Image Data and Workflow Management. , 2008, , 499-530.		0
24995	A Tutorial on Hierarchical Classification with Applications in Bioinformatics. , 2008, , 114-140.		14
24996	Integration of Brain-Gene Ontology and Simulation Systems for Learning, Modelling and Discovery. Studies in Computational Intelligence, 2008, , 221-234.	0.7	0
24997	Knowledge Acquisition Focused Cooperative Development of Bio-ontologies " A Case Study with BIO2Me. Communications in Computer and Information Science, 2008, , 258-272.	0.4	1
24998	The Amine System Project: Systems Biology in Practice. Studies in Computational Intelligence, 2008, , 277-292.	0.7	0
24999	A Systems Approach Demonstrating Sphingolipid-Dependent Transcription in Stress Responses. Methods in Molecular Biology, 2008, 477, 369-381.	0.4	0
25000	ProtocolDB. , 2008, , .		5
25001	Linking Biological Databases Semantically for Knowledge Discovery. Lecture Notes in Computer Science, 2008, , 22-32.	1.0	0
25002	A Proof-Theoretic Approach to Deciding Subsumption and Computing Least Common Subsumer in \$cal EL\$ w.r.t. Hybrid TBoxes. Lecture Notes in Computer Science, 2008, , 311-323.	1.0	4
25003	Functional Classification of Genes Using Non-Negative Independent Component Analysis. Mathematics in Industry, 2008, , 571-575.	0.1	0
25004	Assays of MSCs with Microarrays. , 2008, 449, 133-151.		3
25005	Gene Ontology Assisted Exploratory Microarray Clustering and Its Application to Cancer. Lecture Notes in Computer Science, 2008, , 400-411.	1.0	0

#	ARTICLE	IF	CITATIONS
25006	Event frame extraction based on a gene regulation corpus. , 2008, , .		2
25007	From Protein Interaction Networks to Protein Function. Computational Biology, 2008, , 139-162.	0.1	0
25008	Structure to function. , 2008, , 239-262.		0
25009	GeneFAS: GeneFAS: A Tool for the Prediction of Gene function Using Multiple Sources of Data. Methods in Molecular Biology, 2008, 439, 369-386.	0.4	1
25010	A Deductive Approach for Resource Interoperability and Well-Defined Workflows. Lecture Notes in Computer Science, 2008, , 998-1009.	1.0	6
25016	XYLab: an interactive plotting tool for mixed multivariate data observation and interpretation. Bioinformatics, 2008, 2, 392-394.	0.2	0
25017	Ontologies and Life Science Data Management. , 2009, , 1960-1963.		1
25018	DCGene: A Novel Predicting Approach of the Disease Related Genes on Functional Annotation. Lecture Notes in Computer Science, 2009, , 956-964.	1.0	0
25019	Ontology Driven Semantic Profiling and Retrieval in Medical Information Systems. SSRN Electronic Journal, 0, , .	0.4	0
25021	A Bioinformatics Resource for Crop Functional Genomics: GFSelector Module in Automated Annotation System, RiceGAAS. Japan Agricultural Research Quarterly, 2009, 43, 103-113.	0.1	0
25022	Data Mining in Proteomics Using Grid Computing. , 2009, , 245-267.		0
25023	Clinical and Biomolecular Ontologies for E-Health. , 2009, , 165-179.		1
25024	Discovering Lethal Proteins in Protein Interaction Networks. , 2009, , 183-202.		0
25025	Incorporating Graph Features for Predicting Protein-Protein Interactions. , 2009, , 45-63.		0
25026	Network Querying Techniques for PPI Network Comparison. , 2009, , 312-334.		0
25027	Using Gene Expression Modeling to Determine Biological Relevance of Putative Regulatory Networks. Lecture Notes in Computer Science, 2009, , 40-51.	1.0	0
25028	GREAT: Gene Regulation EvAluation Tool. Lecture Notes in Computer Science, 2009, , 930-933.	1.0	0
25030	Biomedical Data/Content Acquisition, Curation. , 2009, , 224-229.		0

#	ARTICLE	IF	CITATIONS
25031	Transcription Factor Binding Probabilities in Orthologous Promoters: An Alignment-Free Approach to the Inference of Functional Regulatory Targets. Lecture Notes in Computer Science, 2009, , 229-240.	1.0	0
25032	AN ONTOLOGY FOR SUPPORTING CLINICAL RESEARCH ON CERVICAL CANCER. , 2009, , .		1
25033	Experiences with Industrial Ontology Engineering. Lecture Notes in Business Information Processing, 2009, , 61-72.	0.8	3
25034	Bridging the gap between domain-oriented and linguistically-oriented semantics. , 2009, , .		1
25035	Ontology Development for the Immune Epitope Database. , 2009, , 47-56.		1
25036	Pattern Discovery in Gene Expression Data. , 2009, , 45-64.		0
25037	Detecting and Characterizing the Modular Structure of the Yeast Transcription Network. Studies in Computational Intelligence, 2009, , 35-46.	0.7	0
25040	Learning Kernel Matrix from Gene Ontology and Annotation Data for Protein Function Prediction. Lecture Notes in Computer Science, 2009, , 694-703.	1.0	0
25041	Protein Function Prediction from Structure in Structural Genomics and its Contribution to the Study of Health and Disease. NATO Science for Peace and Security Series A: Chemistry and Biology, 2009, , 201-215.	0.5	0
25042	Ontology: Footstone for Strong Artificial Intelligence. Chinese Medical Sciences Journal, 2009, 34, 277-280.	0.2	0
25043	Identification of Lung Cancer Metastasis Related Gene Expression Profile Using Combined Transcriptome Analysis. Japanese Journal of Lung Cancer, 2009, 49, 902-909.	0.0	0
25044	Untangling BioOntologies for Mining Biomedical Information. , 2009, , 314-330.		0
25045	Bioinformatic and Computational Analysis for Genomic Medicine. , 2009, , 206-225.		0
25046	Biomedical Text Data Mining: Recent Patents. Recent Patents on Computer Science, 2009, 2, 59-67.	0.5	0
25047	Annotating Atomic Components of Papers in Digital Libraries: The Semantic and Social Web Heading towards a Living Document Supporting eSciences. Lecture Notes in Computer Science, 2009, , 287-301.	1.0	0
25048	Symbolic Biomedical Knowledge. , 2009, , 99-184.		0
25049	Remote Sensing Ontology Development for Earth Observation Data. Journal of the Japan Society of Photogrammetry and Remote Sensing, 2009, 48, 32-40.	0.0	0
25050	Graphical Analysis and Visualization Tools for Protein Interaction Networks. , 2009, , 286-311.		0

#	ARTICLE	IF	CITATIONS
25051	The Cultural History of Medical Classifications. , 2009, , 48-83.		0
25052	Discovering Interaction Motifs from Protein Interaction Networks. , 2009, , 99-116.		2
25053	Bioinformatics and Computational Biology. , 2009, , 160-165.		0
25054	Integration of Molecular and Cellular Pathogenesis: A Bioinformatics Approach. , 2009, , 219-224.		0
25055	Cooperative Medical Diagnosis Elaboration by Physicians and Artificial Agents. Understanding Complex Systems, 2009, , 315-339.	0.3	4
25056	Literature Databases. , 2009, , 331-345.		0
25057	An Empirical Evaluation of the Effectiveness of Different Types of Predictor Attributes in Protein Function Prediction. Studies in Computational Intelligence, 2009, , 339-357.	0.7	0
25058	Genetics of Abdominal Aortic Aneurysms. , 2009, , 1-26.		0
25060	Biomedical Information Access. , 2009, , 223-250.		0
25061	Protein Sequence Databases. , 2009, , 209-223.		0
25062	The Bioverse API and Web Application. Methods in Molecular Biology, 2009, 541, 511-534.	0.4	2
25063	Linking Life Sciences Data Using Graph-Based Mapping. Lecture Notes in Computer Science, 2009, , 16-30.	1.0	2
25064	Detecting Inconsistencies in the Gene Ontology Using Ontology Databases with Not-gadgets. Lecture Notes in Computer Science, 2009, , 948-965.	1.0	1
25065	Distal Tumors Elicit Distinctive Gene Expression Changes in Mouse Brain, Different from Those Induced by Arthritis. The Open Neuroscience Journal, 2009, 3, 13-25.	0.8	0
25066	Integrative Analysis of Microarray Data with Gene Ontology to Select Perturbed Molecular Functions using Gene Ontology Functional Code. Genomics and Informatics, 2009, 7, 122-130.	0.4	0
25067	Discovery of Regulatory Mechanisms from Gene Expression Variation by eQTL Analysis. Chapman & Hall/CRC Data Mining and Knowledge Discovery Series, 2009, , 205-228.	0.2	0
25070	The Frontiers of Computational Phenomics in Cancer Research. , 2010, , 201-210.		0
25071	An Integrated Oncogenomic Approach: From Genes to Pathway Analyses. , 2010, , 31-50.		0

#	ARTICLE	IF	CITATIONS
25072	Rapamycin-Induced Abundance Changes in the Proteome of Budding Yeast. Genomics and Informatics, 2009, 7, 203-207.	0.4	0
25073	Practical Guide: Genomic Techniques and How to Apply Them to Marine Questions. , 2010, , 315-378.		0
25074	Computational Methods for Predicting Domain- ² Domain Interactions. Computational Biology, 2010, , 157-173.	0.1	0
25075	Introduction and Overview of Technological Advances and Predictive Assays. , 2010, , 623-640.		0
25076	Combining Subgroup Discovery and Permutation Testing to Reduce Reduncancy. Lecture Notes in Computer Science, 2010, , 285-300.	1.0	0
25077	Multilinear Decomposition and Topographic Mapping of Binary Tensors. Lecture Notes in Computer Science, 2010, , 317-326.	1.0	0
25078	Prediction of Protein-Protein Interactions Using Subcellular and Functional Localizations. Lecture Notes in Computer Science, 2010, , 282-290.	1.0	0
25079	Logical Knowledge Representation of Regulatory Relations in Biomedical Pathways. Lecture Notes in Computer Science, 2010, , 186-200.	1.0	1
25080	VisualisationVISUALISATION of Transcriptomic TRANSCRIPTOMICS s Data in Metabolic Pathways. , 2010, , 335-342.		0
25081	Discovering biological processes and side effects relationship using the process-drug-side effect network. , 2010, , .		0
25082	Gene Expression Arrays in Pancreatic Cancer Drug Discovery Research. , 2010, , 113-134.		0
25083	Bioinformatics in Allergy: A Powerful Tool Joining Science and Clinical Applications. , 2010, , 19-30.		0
25084	A Data Warehousing Approach for Genomics Data Meta-Analysis. , 2010, , 129-161.		0
25085	An Agglomerate Algorithm for Mining Overlapping and Hierarchical Functional Modules in Protein Interaction Networks. Lecture Notes in Computer Science, 2010, , 140-151.	1.0	2
25086	Semantic Information Processing of Physical Simulation Based on Scientific Concept Vocabulary Model. IEEJ Transactions on Electronics, Information and Systems, 2010, 130, 1228-1237.	0.1	0
25087	âœ“Omicâœ“Technologies and Their Input for the Comprehension of Metabolic Systems Particularly Pertaining to Yeast Organisms. Progress in Botany Fortschritte Der Botanik, 2010, , 105-122.	0.1	0
25088	Semantic Web and Social Web Heading Towards Living Documents in the Life Sciences. SSRN Electronic Journal, 0, , .	0.4	2
25089	Integration of Molecular and Cellular Pathogenesis. , 2010, , 153-158.		0

#	ARTICLE	IF	CITATIONS
25090	Extracting Between-Pathway Models from E-MAP Interactions Using Expected Graph Compression. Lecture Notes in Computer Science, 2010, , 248-262.	1.0	1
25091	Forgetting Fragments from Evolving Ontologies. Lecture Notes in Computer Science, 2010, , 582-597.	1.0	1
25092	Hierarchical Classification with Dynamic-Threshold SVM Ensemble for Gene Function Prediction. Lecture Notes in Computer Science, 2010, , 336-347.	1.0	0
25093	Computational Identification of Cancer Susceptibility Loci. Methods in Molecular Biology, 2010, 653, 87-103.	0.4	0
25094	Meta-Analysis Approach for the Identification of Molecular Networks Related to Infections of the Oral Cavity. , 2010, , 237-250.		0
25095	Semantic Interoperability Issue of Standardizing Medical Vocabularies. , 2010, , 19-42.		0
25096	Data Integration and Knowledge Discovery in Life Sciences. Lecture Notes in Computer Science, 2010, , 102-111.	1.0	3
25097	Cellular Response Networks. , 2010, , 233-252.		0
25098	Identification of Modules in Protein-Protein Interaction Networks. , 2010, , 253-267.		0
25099	Genomics Data Analysis Pipelines. , 2010, , 117-137.		0
25100	Gene-Pair Representation and Incorporation of GO-based Semantic Similarity into Classification of Gene Expression Data. Lecture Notes in Computer Science, 2010, , 217-226.	1.0	0
25101	Systems-Level Analyses of the Mammalian Innate Immune Response. Systems Biology, 2010, , 531-560.	0.1	1
25102	Organization and Management of Large Categorical Systems. , 2010, , 67-100.		0
25103	Systems Biology of the \hat{I}^2 -Cell "Revisited". , 2011, , 3-23.		0
25104	An Evaluation of Gene Module Concepts in the Interpretation of Gene Expression Data. Computational Biology, 2010, , 331-349.	0.1	1
25105	Using Enriched Ontology Structure for Improving Statistical Models of Gene Annotation Sets. Communications in Computer and Information Science, 2010, , 55-64.	0.4	1
25106	Ontologies in Biology. , 2010, , 347-371.		3
25107	Linear Coherent Bi-cluster Discovery via Beam Detection and Sample Set Clustering. Lecture Notes in Computer Science, 2010, , 85-103.	1.0	2

#	ARTICLE	IF	CITATIONS
25108	Structural Learning of Genetic Regulatory Networks Based on Prior Biological Knowledge and Microarray Gene Expression Measurements. , 2010, , 289-309.		0
25109	Focusing Informatics Methods in Clinical Medicine and Biomedical Challenges. International Journal of Computer Applications, 2010, 1, 25-32.	0.2	8
25112	Efficient functional bioinformatics tools: towards understanding biological processes. EMBnet Journal, 2011, 16, 31.	0.2	0
25114	Role of Bioinformatics as a Tool. , 2010, , 263-289.		2
25115	BioVLAB. , 2010, , 309-327.		1
25116	Scale-Out RDF Molecule Store for Efficient, Scalable Data Integration and Querying. , 2010, , 343-368.		0
25117	Scale-Out RDF Molecule Store for Efficient, Scalable Data Integration and Querying. , 2010, , 329-354.		0
25118	A Novel Weighted Functional Similarity Algorithm Applied to Analyze the Protein-protein Interaction*. Ying Yong Yu Huan Jing Sheng Wu Xue Bao = Chinese Journal of Applied and Environmental Biology, 2010, 16, 420-423.	0.1	0
25120	Inference of Protein Function from the Structure of Interaction Networks. , 2011, , 439-461.		2
25121	Uncovering Atherosclerotic Risk Disease Gene Based on Expression and Network Topological Structure*. Progress in Biochemistry and Biophysics, 2010, 37, 916-922.	0.3	0
25122	Functional Pathway Analysis for Understanding Immunologic Signature of Rejection: Current Approaches and Outstanding Challenges. , 2011, , 239-256.		0
25123	Mutational Data Loading Routines for Human Genome Databases: the BRCA1 Case. Journal of Computing Science and Engineering, 2010, 4, 291-312.	0.3	2
25124	Text Mining for the Semantic Web. , 2011, , 978-980.		0
25125	A Framework for Lipoprotein Ontology. Advances in Experimental Medicine and Biology, 2011, 696, 547-553.	0.8	0
25126	Similarity of Transcription Profiles for Genes in Gene Sets. Lecture Notes in Computer Science, 2011, , 393-399.	1.0	0
25127	Functional Inference in Microbial Genomics Based on Large-Scale Comparative Analysis. , 2011, , 55-92.		0
25128	Towards Elucidation of the Escherichia coli K-12 Unknownome. , 2011, , 289-305.		0
25129	Describing knowledge domains: a case study of biological ontologies. , 2011, , 289-301.		1

#	ARTICLE	IF	CITATIONS
25130	Exploiting Inter-Sample Information and Exploring Visualization in Data Mining: from Bioinformatics to Anthropology and Aesthetics Disciplines. , 0, , .		0
25131	A Conceptual Modeling Approach To Improve Human Genome Understanding. , 2011, , 517-541.		4
25132	Modules in Biological Networks. , 2011, , 248-274.		0
25133	The Informatics of High-Throughput Mouse Phenotyping: EUMODIC and Beyond. , 2011, , 77-87.		1
25134	Facing the Challenges of Genome Information Systems: A Variation Analysis Prototype. Lecture Notes in Computer Science, 2011, , 222-237.	1.0	3
25135	Ontology-Driven Method for Integrating Biomedical Repositories. Lecture Notes in Computer Science, 2011, , 473-482.	1.0	0
25136	Selection of GO-Based Semantic Similarity Measures through AMDE for Predicting Protein-Protein Interactions. Lecture Notes in Computer Science, 2011, , 55-62.	1.0	1
25137	Protein Function Prediction by Spectral Clustering of Protein Interaction Network. Communications in Computer and Information Science, 2011, , 108-117.	0.4	0
25138	Clustering with Overlap for Genetic Interaction Networks via Local Search Optimization. Lecture Notes in Computer Science, 2011, , 326-338.	1.0	0
25139	Correlation of Genes Similarity Measures Based on GO Terms Similarity and Gene Expression Values. Advances in Intelligent and Soft Computing, 2011, , 137-144.	0.2	2
25140	Describing the Orthology Signal in a PPI Network at a Functional, Complex Level. Lecture Notes in Computer Science, 2011, , 209-226.	1.0	4
25141	Time Series Analysis Of Cancer Metastasis Gene Expression Data Using Predictive Clustering Trees (PCT). International Journal on Applied Bio-Engineering, 2011, 5, 20-24.	0.2	0
25142	Visual Gene Ontology Based Knowledge Discovery in Functional Genomics. , 0, , .		1
25143	The Next Generation of ALI Genetics: Insights into Pathophysiology. Annual Update in Intensive Care and Emergency Medicine, 2011, , 97-108.	0.1	0
25144	Criteria-Based Approximate Matching of Large-Scale Ontologies. Advances in Intelligent and Soft Computing, 2011, , 283-288.	0.2	0
25146	Network-Driven Analysis Methods and their Application to Drug Discovery. , 2011, , 294-315.		0
25148	Integrating Medical Patient Data with Family Trees to Improve the Quality of Information. Advances in Intelligent and Soft Computing, 2011, , 17-22.	0.2	0
25149	Baiacu: A Tool for the Visual Analysis of the Saccharomyces Cerevisiae Regulatory Network. Advances in Intelligent and Soft Computing, 2011, , 49-56.	0.2	0

#	ARTICLE	IF	CITATIONS
25150	Knowledge-Driven, Data-Assisted Integrative Pathway Analytics. , 2011, , 225-247.		0
25151	Prediction of Transitive Co-expressed Genes Function by Shortest-Path Algorithm. Lecture Notes in Electrical Engineering, 2011, , 79-87.	0.3	0
25153	Gene Ontology Based Automated Annotation: Why It Isn't Working. Lecture Notes in Computer Science, 2011, , 203-209.	1.0	1
25154	Investigating the Biological Significance of Metallointercalators with cDNA Microarrays. , 2011, , 325-359.		0
25155	Incorporating Correlations among Gene Ontology Terms into Predicting Protein Functions. , 2011, , 154-173.		0
25157	'Deep insight' into microarray technology. Atlas of Genetics and Cytogenetics in Oncology and Haematology, 2011, , .	0.1	1
25158	Bioinformatics Approach to Direct Target Prediction for RNAi Function and Non-specific Cosuppression in Caenorhabditis elegans. KSBB Journal, 2011, 26, 131-138.	0.1	0
25162	Statistical and Knowledge Supported Visualization of Multivariate Data. Springer Proceedings in Mathematics, 2012, , 143-173.	0.5	0
25164	Operon Prediction Based On an Iterative Self-learning Algorithm*. Progress in Biochemistry and Biophysics, 2011, 38, 642-651.	0.3	0
25165	Data-Driven Evaluation of Ontologies Using Machine Learning Algorithms. , 2011, , 211-273.		0
25166	BiCross : A Biclustering Technique for Gene Expression Data using One Layer Fixed Weighted Bipartite Graph Crossing Minimization. International Journal of Computer Applications, 2011, 29, 28-34.	0.2	20
25167	Functional Context Network of T2DM. , 0, , .		0
25171	Disease Gene Prioritization. , 0, , .		0
25174	Translational Oncogenomics and Human Cancer Interactomics: Advanced Techniques and Complex System Dynamic Approaches. , 0, , .		3
25175	Ontologies. Springer Briefs in Electrical and Computer Engineering, 2012, , 45-64.	0.3	0
25178	Prostate Cancer Dephosphorylation Atlas. , 0, , .		0
25179	Visual Data Mining of Coexpression Data to Set Research Priorities in Cardiac Development Research. Methods in Molecular Biology, 2012, 843, 291-307.	0.4	1
25180	Hierarchical Classification of Gene Ontology with Learning Classifier Systems. Lecture Notes in Computer Science, 2012, , 120-129.	1.0	2

#	ARTICLE	IF	CITATIONS
25181	Sparse Learning Based Linear Coherent Bi-clustering. Lecture Notes in Computer Science, 2012, , 346-364.	1.0	2
25182	A Method for the Detection of Meaningful and Reproducible Group Signatures from Gene Expression Profiles. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2012, , 387-401.	0.2	0
25183	Iteratively Predict Protein Functions from Protein-Protein Interactions. Advances in Intelligent and Soft Computing, 2012, , 771-778.	0.2	0
25184	Clinical Research in the Postgenomic Era. Computers in Health Care, 2012, , 113-131.	0.2	1
25185	Gene By Environment Interaction. , 2012, , 189-206.		0
25186	Clinical Trials in Cancer and Pharmacogenomics: A Critical Evaluation. Journal of Clinical Trials, 2012, 02, .	0.1	1
25187	Identification of the Compound Subjective Rule Interestingness Measure for Rule-Based Functional Description of Genes. Lecture Notes in Computer Science, 2012, , 125-134.	1.0	0
25188	Analysis and visualization of gene expression data using biclustering: A comparative study. African Journal of Biotechnology, 2012, 11, .	0.3	1
25189	Analysis of Labeled Quantitative Mass Spectrometry Proteomics Data. , 2012, , 79-91.		0
25190	How Bioinformatics Enables Livestock Applied Sciences in the Genomic Era. Lecture Notes in Computer Science, 2012, , 192-201.	1.0	1
25191	Facilitating and Augmenting Collaboration in the Biomedical Domain. International Journal of Systems Biology and Biomedical Technologies, 2012, 1, 52-65.	0.2	2
25192	Ontology Based Statistical Automated Inference - New Approach to Artificial Intelligence. International Journal of Statistics in Medical Research, 0, , .	0.5	0
25193	High-Throughput GRID Computing for Life Sciences. , 2012, , 821-840.		2
25194	Toward a Translational Medicine Approach for Hypertrophic Cardiomyopathy. Lecture Notes in Computer Science, 2012, , 151-165.	1.0	0
25195	InterOnto â€œ Ranking Inter-Ontology Links. Lecture Notes in Computer Science, 2012, , 5-20.	1.0	1
25196	Genome Mapping and Genomics in Drosophila. , 2012, , 31-86.		1
25197	Data Mining in Proteomics Using Grid Computing. , 2012, , 918-940.		0
25198	Clustering GO Terms Applied to Differential Gene Expression Detection*. Ying Yong Yu Huan Jing Sheng Wu Xue Bao = Chinese Journal of Applied and Environmental Biology, 2012, 17, 422-426.	0.1	0

#	ARTICLE	IF	CITATIONS
25199	LONETSSOM Platform: Enabling Distributed Processing, Managing and Mining of Biological Data through Fusion of Logical Network and Web Technologies in NETWORK Infrastructure. International Journal of Computer Applications, 2012, 39, 23-31.	0.2	4
25200	Reverse Engineering Gene Regulatory Networks by Integrating Multi-Source Biological Data. , 0, , .		0
25201	Role of Bioinformatics as a Tool. , 2012, , 194-216.		0
25202	Protein Interactome and Its Application to Protein Function Prediction. , 0, , .		0
25203	Scalable, Integrative Analysis and Visualization of Protein Interactions. , 0, , .		1
25204	Predicting Aging-Genes in Drosophila Melanogaster by Integrating Network Topological Features and Functional Categories. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 16-26.	0.8	0
25205	Data Mining and Meta-Analysis on DNA Microarray Data. International Journal of Systems Biology and Biomedical Technologies, 2012, 1, 1-39.	0.2	0
25206	BiRange:An Efficient Framework for Biclustering of Gene Expression Data Using Range Bipartite Graph. American Journal of Bioinformatics Research, 2012, 2, 40-46.	0.3	0
25207	Bioinformatics as a Tool for Stone Fruit Research. , 2012, , 355-377.		1
25208	Visualization Techniques and Tools for Genomic Data. Chapman & Hall/CRC Mathematical and Computational Biology Series, 2012, , .	0.1	0
25209	Prioritizing Disease Genes and Understanding Disease Pathways. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 31-49.	0.8	0
25210	Protein Interactions for Functional Genomics. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 15-30.	0.8	0
25211	Predicting Protein Functions from Protein Interaction Networks. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 50-70.	0.8	4
25212	The integration of microRNA target data by biclustering techniques opens new roads for signaling networks analysis. EMBnet Journal, 2012, 18, 142.	0.2	1
25213	StRAP: An Integrated Resource for Profiling High-Throughput Cancer Genomic Data from Stress Response Studies. PLoS ONE, 2012, 7, e51693.	1.1	0
25214	Identification of Antiviral-related Genes Up-regulated in Response to Bombyx mori Nucleopolyhedrovirus. Journal of Sericultural and Entomological Science, 2012, 50, 53-62.	0.1	0
25215	Visualization of Large Ontologies with Landmarks. , 2013, , .		0
25217	A Semantic-Based Platform for Medical Image Storage and Sharing Using the Grid. Communications in Computer and Information Science, 2013, , 353-364.	0.4	1

#	ARTICLE	IF	CITATIONS
25218	Probabilistic Graphical Modeling in Systems Biology: A Framework for Integrative Approaches. , 2013, , 241-272.		0
25219	On the Hybrid Composition and Simulation of Heterogeneous Biochemical Models. Lecture Notes in Computer Science, 2013, , 192-205.	1.0	1
25220	A Formal Ontology of Interactions with Intensional Quantitative Semantics. Proceedings in Information and Communications Technology, 2013, , 13-33.	0.2	0
25221	Relationship Type Ontology. , 2013, , 1839-1840.		0
25222	Biological Applications of Network Modules. , 2013, , 110-112.		0
25223	2-D Thresholding of the Connectivity Map Following the Multiple Sequence Alignments of Diverse Datasets. , 2013, , .		0
25224	Analysis of the Membrane Proteins in Human Serum. Journal of Proteomics and Bioinformatics, 2013, 06, .	0.4	0
25225	Gene Ontology. , 2013, , 797-797.		1
25226	METAREP, Overview. , 2013, , 1-17.		0
25227	Applications of Intelligent Data Analysis for the Discovery of Gene Regulatory Networks. Studies in Computational Intelligence, 2013, , 251-262.	0.7	0
25228	Automatically Language Patterns Elicitation from Biomedical Literature. Advances in Intelligent Systems and Computing, 2013, , 149-158.	0.5	0
25229	Generalized Additive Models. , 2013, , 814-815.		3
25230	Retrieving and Extracting Entity Relations from EBIMed. , 2013, , 1852-1855.		0
25231	Improving the Semantics of a Conceptual Schema of the Human Genome by Incorporating the Modeling of SNPs. Communications in Computer and Information Science, 2013, , 23-37.	0.4	0
25232	BioModels Database: a public repository for sharing models of biological processes. , 2013, , 1-5.		0
25233	Linked Open Webble: Connecting Webbles to the World Wide Web. Communications in Computer and Information Science, 2013, , 66-78.	0.4	0
25234	Statistical Analysis of Patient-Specific Pathway Activities via Mixed Models. Journal of Biometrics & Biostatistics, 2013, 04, 7313.	4.0	1
25235	Database Systems in Biology. , 2013, , 80-96.		0

#	ARTICLE	IF	CITATIONS
25236	Metadata Inference for Description Authoring in a Document Composition Environment. Communications in Computer and Information Science, 2013, , 69-80.	0.4	2
25237	Knowledge Extraction and Mining in Biomedical Research Using Rule Network Model. Lecture Notes in Computer Science, 2013, , 506-515.	1.0	0
25238	World Wide Web. , 2013, , 2356-2361.		0
25239	Ontology Analysis of Biological Networks. , 2013, , 1561-1562.		0
25240	Automated Term Recognition. , 2013, , 57-59.		0
25241	Improving Classification Accuracy Using Gene Ontology Information. Communications in Computer and Information Science, 2013, , 171-176.	0.4	0
25243	Representative methods for genomic prediction and current status of the approaches using biological knowledge. Journal of Animal Genetics, 2013, 41, 93-99.	0.5	0
25244	Target Identification and Target-centered Network Construction from Biomedical Literature. Journal of Software, 2013, 8, .	0.6	1
25245	Computational Discovery of Transcriptional Regulatory Modules in Fungal Ribosome Biogenesis Genes Reveals Novel Sequence and Function Patterns. PLoS ONE, 2013, 8, e59851.	1.1	0
25246	Pitfalls in Experimental Designs for Characterizing the Transcriptional, Methylation and Copy Number Changes of Oncogenes and Tumor Suppressor Genes. PLoS ONE, 2013, 8, e58163.	1.1	1
25247	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
25249	Semi-supervised ensemble learning to boost miRNA target predictions.. EMBnet Journal, 2013, 19, 74.	0.2	0
25250	Ontology-based Semantic Similarity Transfer Algorithm. Journal of Software, 2013, 8, .	0.6	1
25251	Gene expression profiles of <i>Litopenaeus vannamei</i> in response to carbonate alkalinity stress. Journal of Fishery Sciences of China, 2013, 19, 1-12.	0.2	0
25252	Simple Sequence Repeats in 5' and 3' Flanking Sequences of Cell Cycle Genes. , 2014, , 89-101.		0
25253	HOMO: A novel script for data mining of micro arrays. Bioinformatics, 2013, 9, 748-749.	0.2	0
25254	C-element: A New Clustering Algorithm to Find High Quality Functional Modules in PPI Networks. PLoS ONE, 2013, 8, e72366.	1.1	1
25255	An ontology describing congenital heart defects data. EMBnet Journal, 2013, 19, 76.	0.2	0

#	ARTICLE	IF	CITATIONS
25257	Network Analysis and Integration in a Virtual Cell Environment. , 2014, , 275-297.		1
25258	Bioinformatics Approaches to the Study of MicroRNAs. , 2014, , 165-245.		0
25259	Staphylococcus aureus subsp. anaerobius strain ST1464 genome sequence. Standards in Genomic Sciences, 2013, 9, 1-11.	1.5	0
25260	Investigation of lifespan related genes of the silkworm, Bombyx mori L. Journal of Sericultural and Entomological Science, 2013, 51, 211-217.	0.1	1
25261	Translate gene sequence into gene ontology terms based on statistical machine translation. F1000Research, 0, 2, 231.	0.8	0
25262	METHODOLOGIES FOR THE CREATION OF SEMANTIC DATA. , 2014, , 185-215.		1
25263	Protein Network for Associating Genes with Dementia. International Journal of Computer Applications, 2013, 83, 29-35.	0.2	0
25264	Expression of Reactive Oxygen Species in Junctional and Pocket Epithelium. Oxidative Stress in Applied Basic Research and Clinical Practice, 2014, , 53-75.	0.4	2
25265	Complete genome sequence of Mesorhizobium australicum type strain (WSM2073T). Standards in Genomic Sciences, 2013, 9, 1-15.	1.5	1
25266	METADATA AND ONTOLOGIES FOR BIOINFORMATICS. , 2014, , 297-314.		0
25267	Whole Blood Transcriptomic Analysis to Identify Clinical Biomarkers of Drug Response. Methods in Molecular Biology, 2014, 1175, 35-43.	0.4	1
25269	Annotation-Based Feature Extraction from Sets of SBML Models. Lecture Notes in Computer Science, 2014, , 81-95.	1.0	1
25270	Mining Linked Open Data: A Case Study with Genes Responsible for Intellectual Disability. Lecture Notes in Computer Science, 2014, , 16-31.	1.0	0
25271	Ontology Translation: A Case Study on Translating the Gene Ontology from English to German. Lecture Notes in Computer Science, 2014, 8455, 33-38.	1.0	0
25272	13 Functional Genomics to Characterize Opportunistic Pathogens. , 2014, , 321-347.		0
25273	A New Framework for Bridging the Gap from Protein-Protein Interactions to Biological Process Interactions. IFIP Advances in Information and Communication Technology, 2014, , 196-204.	0.5	0
25274	BioMetaDB: Ontology-based Classification and Extension of Biodatabases. , 2014, , .		0
25275	A Comparative Study of Improvements Filter Methods Bring on Feature Selection Using Microarray Data. Lecture Notes in Computer Science, 2014, , 55-62.	1.0	0

#	ARTICLE	IF	CITATIONS
25276	Functional Annotation of Proteins by a Novel Method Using Weight and Feature Selection. Lecture Notes in Electrical Engineering, 2014, , 785-797.	0.3	0
25278	Pichia pastoris Aft1 - a novel transcription factor, enhancing recombinant protein secretion. Microbial Cell Factories, 2014, 13, 120.	1.9	1
25279	Transparent Incremental Updates for Genomics Data Analysis Pipelines. Lecture Notes in Computer Science, 2014, , 311-320.	1.0	5
25280	Statistical Data Mining for Symbol Associations in Genomic Databases. International Journal of Genetics and Genomics, 2014, 2, 97.	0.1	0
25281	CoffeebEST: an integrated resource for Coffea spp expressed sequence tags. Genetics and Molecular Research, 2014, 13, 10913-10920.	0.3	0
25282	Imputation of Quantitative Genetic Interactions in Epistatic MAPs by Interaction Propagation Matrix Completion. Lecture Notes in Computer Science, 2014, , 448-462.	1.0	0
25284	Identification of Co-regulated Gene Network by Using Path Consistency Algorithm Based on Gene Ontology. Lecture Notes in Computer Science, 2014, , 278-283.	1.0	0
25285	Bayesian Systems-Based Genetic Association Analysis with Effect Strength Estimation and Omic Wide Interpretation: A Case Study in Rheumatoid Arthritis. Methods in Molecular Biology, 2014, 1142, 143-176.	0.4	0
25286	Complex Networksâ€™ Analysis Using an Ontology-Based Approach: Initial Steps. Lecture Notes in Computer Science, 2014, , 326-337.	1.0	3
25287	Overexpression of the soybean transcription factor GmDof4 significantly enhances the lipid content of. Biotechnology for Biofuels, 2014, 7, 128.	6.2	50
25288	Ontologies and Machine Learning Systems. , 2014, , 865-872.		0
25289	The Ontology of the genetics. Transactions of the Japanese Society for Artificial Intelligence, 2014, 29, 311-327.	0.1	0
25290	Human Genome Network Platform: A Resource for TFRN Analysis. Methods in Molecular Biology, 2014, 1164, 147-162.	0.4	0
25291	Identification of Pathway Signatures in Parkinsonâ€™s Disease with Gene Ontology and Sparse Regularization. Lecture Notes in Computer Science, 2014, , 259-273.	1.0	0
25292	A Tutorial on Lotus japonicus Transcriptomic Tools. Compendium of Plant Genomes, 2014, , 183-199.	0.3	0
25294	Gene Expression in HNC. , 2014, , 325-341.		1
25295	Improvement of FP-Growth Algorithm for Mining Description-Oriented Rules. Advances in Intelligent Systems and Computing, 2014, , 183-192.	0.5	3
25296	Significance of Non-edge Priors in Gene Regulatory Network Reconstruction. Lecture Notes in Computer Science, 2014, , 446-453.	1.0	1

#	ARTICLE	IF	CITATIONS
25297	Authoring Composite Documents and Their Descriptions. Communications in Computer and Information Science, 2014, , 18-30.	0.4	0
25298	Accelerating Biomedical Research through Semantic Web Services. International Journal of Reliable and Quality E-Healthcare, 2014, 3, 32-48.	1.0	0
25300	Bioinformatics Analysis of Diguanylate Cyclases and c-di-GMP-Specific Phosphodiesterases from Xanthomonas Species. Hans Journal of Computational Biology, 2014, 04, 68-82.	0.0	0
25301	Comparative Analysis of 3D-Culture System for Murine Neonatal Heart Regeneration: A Systematic Approach for Big Gene Expression Data. Lecture Notes in Computer Science, 2014, , 754-764.	1.0	1
25304	Analysis of Gene Expression in <i>Legionella</i> during Axenic Growth and Infection. , 0, , 343-346.		1
25306	The Evolution of Information Resource Allocation Research based on Knowledge Mapping. International Journal of Database Theory and Application, 2014, 7, 109-120.	0.2	0
25308	Genomics and Proteomics of Foodborne Microorganisms. , 0, , 973-996.		0
25312	Building a Hierarchical Organization of Protein Complexes Out of Protein Association Data. PLoS ONE, 2014, 9, e100098.	1.1	0
25314	Subspace Clustering of DNA Microarray Data. International Journal of Computational Models and Algorithms in Medicine, 2014, 4, 1-52.	0.4	1
25315	Identification of Synchronized Role of Transcription Factors, Genes, and Enzymes in Arabidopsis thaliana under Four Abiotic Stress Responsive Pathways. Computational Biology Journal, 2014, 2014, 1-13.	0.6	1
25317	Speeding Up Iterative Ontology Alignment using Block-Coordinate Descent. Journal of Artificial Intelligence Research, 0, 50, 805-845.	7.0	0
25319	Network based meta-analysis prediction of microenvironmental relays involved in stemness of human embryonic stem cells. PeerJ, 2014, 2, e618.	0.9	2
25326	Neurodegenerative Diseases: Phenome to Genome Analysis. MOJ Proteomics & Bioinformatics, 2014, 2, .	0.1	2
25328	A Two-Stage Sparse Selection Method for Extracting Characteristic Genes. Lecture Notes in Computer Science, 2015, , 577-588.	1.0	0
25331	A Method of Retrieving Articles on Protein Structure Analysis from Query Articles Using a Concept Graph. IEEJ Transactions on Electronics, Information and Systems, 2015, 135, 340-348.	0.1	0
25332	Protein Function Prediction Using Neighbor Counting with Dynamic Threshold from Protein-Protein Interaction Network. Computational Biology and Bioinformatics, 2015, 3, 1.	0.3	0
25333	Atlas of the Open Reading Frames in Human Diseases: Dark Matter of the Human Genome. MOJ Proteomics & Bioinformatics, 2015, 2, .	0.1	1
25334	Targeting Foodome-Metabolome Interactions: A Combined Modeling Approach. , 2015, , 181-204.		0

#	ARTICLE	IF	CITATIONS
25335	Enrichment set cover problem. , 2015, , .		0
25336	A Method of Automatic Annotation for Medical Record Text Based on Latent Dirichlet Allocation. , 2015, , .		0
25339	AGA: Interactive pipeline for reproducible genomics analyses. F1000Research, 0, 4, 28.	0.8	2
25341	Evaluating the Robustness of Correlation Network Analysis in the Aging Mouse Hypothalamus. Communications in Computer and Information Science, 2015, , 224-238.	0.4	0
25342	Assessing Toxicity of Nanoparticles: In Vitro and In Vivo Assays. , 2015, , 1-15.		1
25343	Predicting Protein Functions Based on Dynamic Protein Interaction Networks. Lecture Notes in Computer Science, 2015, , 390-401.	1.0	1
25344	Pathway Analysis and Machine Learning as Tools in Systems Toxicology. Methods in Pharmacology and Toxicology, 2015, , 209-222.	0.1	0
25345	The Usage of the Agent Modeling Language for Modeling Complexity of the Immune System. Studies in Computational Intelligence, 2015, , 323-332.	0.7	2
25346	Computational Data Integration in Toxicogenomics. Methods in Pharmacology and Toxicology, 2015, , 371-392.	0.1	0
25348	Holistic Ontology-Based Assistance System for Efficient Process Model Parameter Identification. Journal of Computational Engineering, 2015, 2015, 1-14.	0.8	1
25349	Identification of prognosis-specific network and prediction for estrogen receptor-negative breast cancer using microarray data and PPI data. Journal of the Korea Society of Computer and Information, 2015, 20, 137-147.	0.0	0
25351	Analysis of Pharmacogenomic Variants Associated with Population Differentiation. PLoS ONE, 2015, 10, e0119994.	1.1	3
25352	Genetic make-up of arthropod vectors. OIE Revue Scientifique Et Technique, 2015, 34, 113-122.	0.5	0
25353	Lexical Characterisation of Bio-Ontologies by the Inspection of Regularities in Labels. Current Bioinformatics, 2015, 10, 165-176.	0.7	1
25354	Epitope specificity and protein signaling interactions driving epidemic occurrences of Ebola disease. F1000Research, 0, 4, 166.	0.8	2
25356	Â«NEXT GENERATION SEQUENCINGÂ» FOR STUDYING TRANSCRIPTOME PROFILES OF TISSUES AND ORGANS OF GARDEN PEA (Pisum sativum L.) (review). Sel'skokhozyaistvennaya Biologiya, 2015, 50, 278-287.	0.1	0
25360	Text Mining Approach to Analyse the Relation between Obesity and Breast Cancer Data. International Letters of Natural Sciences, 0, 44, 1-9.	1.0	1
25363	Modeling of Gene Regulatory Networks: A Literature Review. Journal of Computational Systems Biology, 2015, 1, .	0.8	8

#	ARTICLE	IF	CITATIONS
25364	Integration of OMICS Data for Obesity. Journal of Diabetes and Obesity, 2015, 2, 67-75.	0.2	0
25365	Integrative Construction of Gene Signatures Based on Fusion of Expression and Ontology Information. Advances in Intelligent Systems and Computing, 2016, , 237-249.	0.5	0
25367	Identifying the missing protein in human proteome by structure and function prediction. , 2015, , 19-26.		0
25368	Gene Expression Models of Signaling Pathways. Translational Bioinformatics, 2016, , 99-113.	0.0	0
25371	Structural Annotation of the Mycobacterium tuberculosis Proteome. , 0, , 261-280.		0
25373	SEPARATING THE CAUSES AND CONSEQUENCES IN DISEASE TRANSCRIPTOME. , 2016, , .		0
25374	Protein disorder reduced in Saccharomyces cerevisiae to survive heat shock. F1000Research, 2015, 4, 1222.	0.8	2
25375	Gene Ontology Analysis on Behalf of Improved Classification of Different Colorectal Cancer Stages. Studies in Computational Intelligence, 2016, , 487-500.	0.7	0
25377	Corn Gluten Hydrolysate Affects the Time-Course of Metabolic Changes Through Appetite Control in High-Fat Diet-Induced Obese Rats. Molecules and Cells, 2015, 38, 1044-1053.	1.0	1
25384	Characterization of the Alzheimer's disease-related network based on the dynamic network approach. Journal of Korean Institute of Intelligent Systems, 2015, 25, 529-535.	0.0	1
25387	Detecting Meaningful Compounds in Complex Class Labels. Lecture Notes in Computer Science, 2016, , 621-635.	1.0	1
25388	Morphological Ontology Design Engineering. Advances in Knowledge Acquisition, Transfer and Management Book Series, 2016, , 262-291.	0.1	2
25390	Conclusion: Implications for Psychiatry and Neuropsychology. Innovations in Cognitive Neuroscience, 2016, , 283-296.	0.3	0
25392	Gene Expression Analysis: Current Methods. , 2016, , 107-136.		2
25393	Accelerating Biomedical Research through Semantic Web Services. , 2016, , 2385-2401.		0
25394	Accelerating Biomedical Research through Semantic Web Services. , 2016, , 2199-2214.		0
25395	The SDREM Method for Reconstructing Signaling and Regulatory Response Networks: Applications for Studying Disease Progression. Methods in Molecular Biology, 2016, 1303, 493-506.	0.4	4
25396	Research into Methods to Construct Software Engineering Knowledge Database Based on Ontology. , 0, , .		0

#	ARTICLE	IF	CITATIONS
25397	Chapter 4. PSM Scoring and Validation. New Developments in Mass Spectrometry, 2016, , 69-92.	0.2	1
25398	Text Mining for the Semantic Web. , 2016, , 1-3.		0
25399	Ontology Construction of Crop Germplasm Resources. Acta Agronomica Sinica(China), 2016, 42, 407.	0.1	0
25400	Ontologies and Life Science Data Management. , 2016, , 1-5.		0
25402	Predicting Potential Functional Modules in Biological Networks Through Context-Sensitive Random Walk Based Network Querying. , 2016, , .		0
25403	Ontologies in Cheminformatics. , 2016, , 1-19.		0
25404	IFGFA: Identification of featured genes from genomic data using factor analysis. Genetics and Molecular Research, 2016, 15, .	0.3	0
25406	Strategies to avoid drowning in the deep sequencing data flood. Animal Reproduction, 2016, 13, 153-159.	0.4	0
25407	Assessing Toxicity of Nanoparticles: In Vitro and In Vivo Assays. , 2016, , 923-940.		0
25408	Highly Bi-Connected Subgraphs for Computational Protein Function Annotation. Lecture Notes in Computer Science, 2016, , 573-584.	1.0	0
25409	Transcriptional Analysis of Maize Resistance against Fusarium graminearum. Acta Agronomica Sinica(China), 2016, 42, 1122.	0.1	0
25410	Gene Expression Analysis: Applications. , 2016, , 137-149.		0
25411	The Role of Community Acceptance in Assessing Ontology Quality. Lecture Notes in Computer Science, 2016, , 24-36.	1.0	4
25412	Special Section on Enterprise Ontologies. Journal of Information Systems, 2016, 30, 1-3.	0.5	6
25418	Phenotyping Zebrafish. , 2016, , 75-95.		0
25424	A Latent Feature Model Approach to Biclustering. International Journal of Knowledge Discovery in Bioinformatics, 2016, 6, 11-28.	0.8	0
25425	Evaluation of protein clustering of pancreatic cancer. Arvand Journal of Health and Medical Sciences, 2016, 1, 0-0.	0.1	0
25429	Silicon Era of Carbon-Based Life: Application of Genomics and Bioinformatics in Crop Stress Research. , 2016, , 137-165.		0

#	ARTICLE	IF	CITATIONS
25430	Semantic Mining based on graph theory and ontologies. Case Study: Cell Signaling Pathways. CLEI Electronic Journal, 0, , .	0.2	2
25431	Proteomic Analysis Reveals GLUT1 to be a Novel Discriminating Marker of Human Arterial Endothelium In vivo and loss of Venous Identity in Cell Culture. , 2016, 1, 001-007.		0
25435	Studying Microarray Gene Expression Data of Schizophrenic Patients for Derivation of a Diagnostic Signature through the Aid of Machine Learning. Biometrics & Biostatistics International Journal, 2016, 4, .	0.2	1
25440	Self-Contained Statistical Analysis of Gene Sets. PLoS ONE, 2016, 11, e0163918.	1.1	0
25444	Whole-genome Transcriptional Responses to Hypoxia in Respiration-proficient and Respiration-deficient Yeasts: Implication of the Mitochondrial Respiratory Chain in Oxygen-regulated Gene Expression. Journal of Life Science, 2016, 26, 1137-1152.	0.2	1
25452	Marine Genomics: Recent Advancement and Wide-Area Applications. , 2016, , 117-128.		0
25453	Mechanism-based disease similarity. Journal of Rare Diseases Research & Treatment, 2016, 1, 1-4.	1.1	3
25465	Glycobiology Meets the Semantic Web. , 2017, , 351-370.		1
25468	A Comparative Study of Clustering and Biclustering of Microarray Data. Journal of Engineering Technology, 2016, 6, 239-257.	0.1	0
25470	Role of Bioinformatics in Nanotechnology. Advances in Medical Technologies and Clinical Practice Book Series, 2017, , 293-317.	0.3	0
25471	Estimating the Empirical Null Distribution of Maxmean Statistics in Gene Set Analysis. Open Journal of Statistics, 2017, 07, 761-767.	0.3	0
25472	Differentially Expressed Genes in Varicose Veins Disease: Current State of the Problem, Analysis of the Published Data. Flebologiya, 2017, 11, 190.	0.2	2
25473	Systems Biology: Salivary Gland Development, Disease, and Regenerative Medicine. , 2017, , 23-44.		0
25474	Relating Diseases Based on Disease Module Theory. Lecture Notes in Computer Science, 2017, , 24-33.	1.0	1
25477	Machine Learning in Computational Biology. , 2017, , 1-6.		0
25478	Finding Genes. , 2017, , 127-141.		0
25480	Text Mining for the Semantic Web. , 2017, , 1262-1263.		0
25481	Validity of Automated Inferences in Mapping of Anatomical Ontologies. Lecture Notes in Computer Science, 2017, , 251-260.	1.0	0

#	ARTICLE	IF	CITATIONS
25483	“Big Data and Dynamics” The Mathematical Toolkit Towards Personalized Medicine. Springer Proceedings in Mathematics and Statistics, 2017, , 338-369.	0.1	0
25484	Semantic Clustering for Identifying Overlapping Biological Communities. Lecture Notes in Computer Science, 2017, , 235-247.	1.0	0
25499	The Application of Genetic Tests in an Assisted Reproduction Unit: mRNA Microarrays. , 2017, , 71-94.		0
25500	SysFinder: A customized platform for search, comparison and assisted design of appropriate animal models based on systematic similarity. Journal of Genetics and Genomics, 2017, 44, 251-258.	1.7	0
25512	Bioinformatic Analysis of Genes Functioning in Salt Tolerance from Genomes of Two Bacillus Cereus Strains. DEStech Transactions on Environment Energy and Earth Science, 2017, , .	0.0	0
25523	Community detection in sequence similarity networks based on attribute clustering. PLoS ONE, 2017, 12, e0178650.	1.1	2
25531	A Novel Measure for Semantic Similarity Computation of Gene Ontology Terms Using Weighted Aggregation of Information Contents. Zahedan Journal of Researches in Medical Sciences, 2017, 19, .	0.1	0
25534	Similarities between plant traits based on their connection to underlying gene functions. PLoS ONE, 2017, 12, e0182097.	1.1	0
25537	Semantic Biomarker Selection for Functional Genomics of Heart Failure Model Organisms. , 0, , .		0
25539	Nanoparticles as Nitroso-Glutathion Vehicles. , 2017, , 223-234.		0
25543	Interplay between Brassinosteroid and ABA signaling during early seedling development. Journal of Plant Biotechnology, 2017, 44, 264-270.	0.1	1
25546	Metabolomics and Proteomics. Oxidative Stress and Disease, 2017, , 473-484.	0.3	0
25548	Integrating Association Rules Mined from Health-Care Data with Ontological Information for Automated Knowledge Generation. Advances in Intelligent Systems and Computing, 2018, , 3-16.	0.5	1
25551	A framework for exploring associations between biomedical terms in PubMed. Oncotarget, 2017, 8, 103100-103107.	0.8	0
25554	geneXplainR: An R interface for the geneXplain platform. Journal of Open Source Software, 2017, 2, 412.	2.0	3
25560	Single subject transcriptome analysis to identify functionally signed gene set or pathway activity. , 2018, , .		0
25561	Gene expression profiling and construction of a putative gene regulatory network of bladder cancer tumor-initiating cells. Oncotarget, 2017, 8, 111271-111280.	0.8	0
25563	Discovering Interesting Biological Patterns in the Context of Human Protein-Protein Interaction Network and Gene Disease Profile Data. Advances in Science, Technology and Engineering Systems, 2017, 2, 87-93.	0.4	0

#	ARTICLE	IF	CITATIONS
25575	Ontologies and Life Science Data Management. , 2018, , 2570-2574.		0
25577	Multi-Omics Insights into Functional Alterations of the Liver in Insulin-Deficient Diabetes Mellitus. SSRN Electronic Journal, 0, , .	0.4	0
25579	BioBroker: Knowledge Discovery Framework for Heterogeneous Biomedical Ontologies and Data. Journal of Intelligent Learning Systems and Applications, 2018, 10, 1-20.	0.4	5
25580	Macromolecular Connectivity Landscape of Mammalian Brain. SSRN Electronic Journal, 0, , .	0.4	1
25581	Targeting miRNAs in Osteoblast Differentiation under Malnutrition Conditions. Journal of Biosciences and Medicines, 2018, 06, 111-119.	0.1	0
25582	Incorporating Gene Ontology Information in Gene Expression Data Clustering Using Multiobjective Evolutionary Optimization: Application in Yeast Cell Cycle Data. , 2018, , 55-78.		1
25583	The properties of property alignment on the semantic web. International Journal of Metadata, Semantics and Ontologies, 2018, 13, 42.	0.2	1
25584	Machine Learning in Computational Biology. , 2018, , 2157-2162.		0
25585	A Cell Atlas of the Adult Drosophila Midgut. SSRN Electronic Journal, 0, , .	0.4	1
25586	Biomedical Data/Content Acquisition, Curation. , 2018, , 288-293.		0
25588	Exploring key genes and pathways underlying metastasis endometrial cancer based on gene expression microarray. Biomedical Research (Aligarh, India), 2018, 29, .	0.1	0
25590	A Wolfram Language Primer for Bioinformaticians. , 2018, , 7-65.		0
25591	Are Radiosensitive and Regular Response Cells Homogeneous in Their Correlations Between Copy Number State and Surviving Fraction After Irradiation?. Lecture Notes in Computer Science, 2018, , 197-208.	1.0	1
25595	The Receptor Tyrosine Kinase AXL Is Required at Multiple Steps of the Metastatic Cascade During HER2-Positive Breast Cancer Progression. SSRN Electronic Journal, 0, , .	0.4	0
25596	Neural Precursor Cell-Derived Pleiotrophin Mediates Glioma Invasion of the Subventricular Zone. SSRN Electronic Journal, 0, , .	0.4	0
25599	The Use of Distributed Data Storage and Processing Systems in Bioinformatic Data Analysis. Communications in Computer and Information Science, 2018, , 18-32.	0.4	0
25601	Latent Model-Based Clustering for Biological Discovery. SSRN Electronic Journal, 0, , .	0.4	0
25602	Text Mining on Big and Complex Biomedical Literature. , 2018, , 129-154.		0

#	ARTICLE	IF	CITATIONS
25603	Identifying the dynamic gene regulatory network during latent HIV-1 reactivation using high-dimensional ordinary differential equations. <i>International Journal of Computational Biology and Drug Design</i> , 2018, 11, 135.	0.3	0
25604	De Novo Sequence and Copy Number Variants are Strongly Associated with Tourette Disorder and Implicate Cell Polarity in Pathogenesis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
25606	Using regulatory genomics data to interpret the function of disease variants and prioritise genes from expression studies. <i>F1000Research</i> , 2018, 7, 121.	0.8	3
25612	Invited review: Genetic and genomic mouse models for livestock research. <i>Archives Animal Breeding</i> , 2018, 61, 87-98.	0.5	2
25620	Similarity of regulatory network between leukemia stem cells and normal hemopoietic stem cells. <i>Infection International</i> , 2018, 6, 129-140.	0.1	0
25629	Genomic and Transcriptomic Sequencing and Analysis Approaches. <i>Middle Black Sea Journal of Health Science</i> , 0, , 34-42.	0.2	0
25631	eXamine: Visualizing annotated networks in Cytoscape. <i>F1000Research</i> , 2018, 7, 519.	0.8	2
25634	Evolution of Conducting Cells in Plants; a Perspective from Key Transcription Factors of Conducting Cell Differentiation: From Recent Studies on Master Regulatory Transcription Factors for the Differentiation of Tracheary Elements and Sieve Element. <i>Kagaku To Seibutsu</i> , 2018, 56, 353-363.	0.0	0
25645	TRANSCRIPTOMICS RESEARCH IN THE CLINICAL AND EXPERIMENTAL INVESTIGATION OF PATHOGENETIC MECHANISMS OF ALIMENTARY OBESITY. <i>Vestnik Rossiiskoi Akademii Meditsinskikh Nauk</i> , 2018, 73, 172-180.	0.2	0
25675	TEMPO. , 2018, , .		1
25703	Statistical Models to Explore the Exposome: From OMICs Profiling to "Mechanome"™ Characterization. , 2019, , 279-314.		0
25706	The draft genome sequence of the Japanese honey bee, <i>Apis cerana japonica</i> (Hymenoptera: Apidae). <i>European Journal of Entomology</i> , 0, 115, 650-657.	1.2	6
25707	SNPs2ChIP: Latent Factors of ChIP-seq to infer functions of non-coding SNPs. , 2018, , .		0
25708	Precision drug repurposing via convergent eQTL-based molecules and pathway targeting independent disease-associated polymorphisms. , 2018, , .		3
25722	Identifying Principles for the Construction of an Ontology-Based Knowledge Base: A Case Study Approach. <i>JMIR Medical Informatics</i> , 2018, 6, e52.	1.3	2
25724	Inherited Properties of $\{FL\}_0$ Concept Similarity Measure Under Preference Profile. <i>Lecture Notes in Computer Science</i> , 2019, , 343-360.	1.0	1
25731	Dental Stem Cells in Regenerative Medicine: Emerging Trends and Prospects in the Era of Bioinformatics. , 2019, , 119-150.		0
25733	Single-Cell RNA-Seq of the Developing Cardiac Outflow Tract Reveals Convergent Development of the Vascular Smooth Muscle Cells at the Base of the Great Arteries. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
25737	Analysis of Novel Annotations in the Gene Ontology for Boosting the Selection of Negative Examples. , 2019, , .		0
25738	Using Ontologies to Express Prior Knowledge for Genetic Programming. Lecture Notes in Computer Science, 2019, , 362-376.	1.0	1
25741	Microbial Genome Diversity and Microbial Genome Sequencing. , 2019, , 175-201.		0
25742	Construction of Microbial Cell Factories by Systems and Synthetic Biotechnology. , 2019, , 9-43.		1
25744	Protein Function Prediction: Combining Statistical Features with Deep Learning. SSRN Electronic Journal, 0, , .	0.4	0
25745	Profiling of the Muscle-Specific Dystroglycan Complexome Identifies Novel Muscular Dystrophy Factors. SSRN Electronic Journal, 0, , .	0.4	0
25746	A Protocol to Map the Spatial Proteome Using HyperLOPIT in Saccharomyces cerevisiae. Bio-protocol, 2019, 9, e3303.	0.2	2
25747	Domain-Based Approaches to Prediction and Analysis of Protein-Protein Interactions. , 2019, , 406-427.		0
25748	Identification of Prognostic and Heterogeneous Breast Cancer Biomarkers Based on Fusion Network and Multiple Scoring Strategies. Lecture Notes in Computer Science, 2019, , 529-534.	1.0	2
25749	Bi-clustering by Multi-objective Evolutionary Algorithm for Multimodal Analytics and Big Data. , 2019, , 125-150.		1
25751	Data Management in Computational Systems Biology: Exploring Standards, Tools, Databases, and Packaging Best Practices. Methods in Molecular Biology, 2019, 2049, 285-314.	0.4	3
25752	Protein Secondary Structure Graphs as Predictors for Protein Function. Communications in Computer and Information Science, 2019, , 187-201.	0.4	0
25753	Guidelines for Bioinformatics and the Statistical Analysis of Omic Data. , 2019, , 45-75.		0
25754	RNA-Seq and Bulk Segregant Analysis of Genes Related to High Growth in <i>Ginkgo biloba</i> Half-Sibling Families. American Journal of Plant Sciences, 2019, 10, 79-100.	0.3	2
25756	Expanding the Orthologous Matrix (OMA) programmatic interfaces: REST API and the OmaDB packages for R and Python. F1000Research, 2019, 8, 42.	0.8	9
25759	Migratory Neural Crest Cells Phagocytose Cellular Debris in the Developing Nervous System. SSRN Electronic Journal, 0, , .	0.4	0
25760	Big Semantic Data Processing in the Life Sciences Domain. , 2019, , 351-358.		0
25762	DNA hypermethylation of Fgf16 and Tbx22 associated with cleft palate during palatal fusion. Journal of Applied Oral Science, 2019, 27, e20180649.	0.7	4

#	ARTICLE	IF	CITATIONS
25764	Comparative Analyses of 35 Marine Mammal Genomes Provide Insights into the Evolution of Aquatic Life. SSRN Electronic Journal, 0, , .	0.4	0
25765	Applications of Microarray in Cancer Cell Signaling Pathways. , 2019, , 369-387.		0
25766	Subspace Clustering of DNA Microarray Data. , 2019, , 210-264.		0
25767	Generating Knowledge Graph Paths from Textual Definitions using Sequence-to-Sequence Models. , 2019, , .		3
25768	Avian Abundance, Diversity and Conservation Status in Etago Sub-County Kisii County Kenya. Open Journal of Ecology, 2019, 09, 157-170.	0.4	3
25772	Understanding the Regulatory Features of Co-regulated Genes Using Distant Regulatory Elements (DiRE) Genomic Tool in Health and Disease. , 2019, , 283-299.		0
25773	The analysis of a time-course transcriptome profile by systems biology approaches reveals key molecular processes in acute kidney injury. Journal of Research in Medical Sciences, 2019, 24, 3.	0.4	2
25775	Semantic Integration and Enrichment of Heterogeneous Biological Databases. Methods in Molecular Biology, 2019, 1910, 655-690.	0.4	10
25777	Inference of Gene Regulatory Networks by Topological Prior Information and Data Integration. , 2019, , 265-304.		1
25778	Development and Genome Sequence of a Laboratory-Inbred Miniature Pig Facilitate Study of Human Diabetic Disease. SSRN Electronic Journal, 0, , .	0.4	0
25779	Resources. Advances in Experimental Medicine and Biology, 2019, 1137, 9-15.	0.8	1
25780	RetroSpect, a New Method of Measuring Gene Regulatory Evolution Rates Using Co-mapping of Genomic Functional Features with Transposable Elements. , 2019, , 85-111.		0
25781	Applications of Supercomputers in Sequence Analysis and Genome Annotation. , 2019, , 625-652.		0
25791	TFutils: Data structures for transcription factor bioinformatics. F1000Research, 2019, 8, 152.	0.8	1
25801	Machine learning techniques combined with dose profiles indicate radiation response biomarkers. International Journal of Applied Mathematics and Computer Science, 2019, 29, 169-178.	1.5	0
25802	Introducing high school students to the Gene Ontology classification system. F1000Research, 2019, 8, 241.	0.8	4
25817	Digital gene expression analysis of the hop (<i>Humulus lupulus</i> L.) transcriptome. Acta Horticulturae, 2019, , 135-144.	0.1	2
25819	Phenylobacterium soli sp. nov., isolated from arsenic and cadmium contaminated farmland soil. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1398-1403.	0.8	17

#	ARTICLE	IF	CITATIONS
25827	Identification of pathogenic genes and transcription factors in glaucoma. <i>Molecular Medicine Reports</i> , 2019, 20, 216-224.	1.1	22
25830	TFutils: Data structures for transcription factor bioinformatics. <i>F1000Research</i> , 2019, 8, 152.	0.8	3
25835	maGUI: A Graphical User Interface for Analysis and Annotation of DNA Microarray Data. <i>Open Bioinformatics Journal</i> , 2019, 12, 40-44.	1.0	2
25844	TENDENCIAS ACTUALES EN EL MANEJO DE DATOS DE INVESTIGACIÓN. <i>BIOCYT Biología Ciencia Y Tecnología</i> , 2019, 12, .	0.1	0
25846	Identification of Key Genes and Pathway for Ovarian Neoplasms Using the OVDM1 Cell Line Based on Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2019, 25, 4305-4313.	0.5	0
25854	RNA Sequencing of Osteosarcoma Gene Expression Profile Revealed that miR-214-3p Facilitates Osteosarcoma Cell Proliferation via Targeting Ubiquinol-Cytochrome c Reductase Core Protein 1 (UQCRC1). <i>Medical Science Monitor</i> , 2019, 25, 4982-4991.	0.5	7
25877	Introducing high school students to the Gene Ontology classification system. <i>F1000Research</i> , 2019, 8, 241.	0.8	5
25878	The Protozoan Tetrahymena: Cellular Model for Biological Studies. <i>Annual Research & Review in Biology</i> , 0, , 1-12.	0.4	0
25881	In Silico Prediction of Cell Wall Remodeling Genes in Tomato, Banana, Melon and Grape. <i>International Journal of Life Sciences and Biotechnology</i> , 2019, 2, 108-121.	0.2	2
25884	GeneDB and Wikidata. <i>Wellcome Open Research</i> , 2019, 4, 114.	0.9	0
25894	In silico approach to calculate the transcript capacity. <i>Genomics and Informatics</i> , 2019, 17, e31.	0.4	0
25899	PLCB4 upregulation is associated with unfavorable prognosis in pediatric acute myeloid leukemia. <i>Oncology Letters</i> , 2019, 18, 6057-6065.	0.8	6
25904	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , 0, 8, 1677.	0.8	0
25907	miRDriver. , 2019, , .		4
25908	Identification of prognostic biomarkers for malignant melanoma using microarray datasets. <i>Oncology Letters</i> , 2019, 18, 5243-5254.	0.8	3
25913	Majority Vote Cascading. , 2019, , .		1
25917	Exosome complex genes mediate RNA degradation and predict survival in mantle cell lymphoma. <i>Oncology Letters</i> , 2019, 18, 5119-5128.	0.8	8
25918	Fundamentals of Drug Metabolism and Pharmacogenomics Within a Learning Healthcare System Workflow Perspective. <i>Computers in Health Care</i> , 2020, , 59-80.	0.2	0

#	ARTICLE	IF	CITATIONS
25921	Biological networks analysis, analytical approaches and use case on protein-protein network interactions. , 2019, , .		1
25923	iMTBGO: An Algorithm for Integrating Metabolic Networks with Transcriptomes Based on Gene Ontology Analysis. Current Genomics, 2019, 20, 252-259.	0.7	2
25936	Proteome Bioinformatics Methods for Studying Histidine Phosphorylation. Methods in Molecular Biology, 2020, 2077, 237-250.	0.4	0
25937	Screening and identification of key biomarkers in prostate cancer using bioinformatics. Molecular Medicine Reports, 2020, 21, 311-319.	1.1	3
25941	aTEMPO: Pathway-Specific Temporal Anomalies for Precision Therapeutics. , 2019, , .		0
25959	Expression of a novel gene encoding protease inhibitor from metagenome of sponge in Vietnam. Academia Journal of Biology, 2019, 40, .	0.0	0
25960	Identification of key candidate tumor biomarkers in non-small cell lung cancer by in silico analysis. Oncology Letters, 2020, 19, 1008-1016.	0.8	4
25962	Expression profile of miRNA in NSCLC tissues in middle altitude area. Oncology Letters, 2020, 19, 783-794.	0.8	0
25963	Sparse Regression Models for Unraveling Group and Individual Associations in eQTL Mapping. Methods in Molecular Biology, 2020, 2082, 105-121.	0.4	0
25965	Reduction of the Saccharomyces cerevisiae Genome: Challenges and Perspectives. , 2020, , 117-139.		1
25967	Identification for Exploring Underlying Pathogenesis and Therapy Strategy of Oral Squamous Cell Carcinoma by Bioinformatics Analysis. Medical Science Monitor, 2019, 25, 9216-9226.	0.5	1
25972	Analysis of circular RNA-associated competing endogenous RNA network in breast cancer. Oncology Letters, 2020, 19, 1619-1634.	0.8	3
25973	Mixed Compensation Multidimensional Item Response Theory. Lecture Notes in Computer Science, 2020, , 132-141.	1.0	0
25974	Bioinformatics Analysis of Gene Expression and Signaling Pathways in Basal Cell Carcinoma. Advances in Clinical Medicine, 2020, 10, 1782-1790.	0.0	1
25975	Toward Development of Climate-Resilient Citrus. , 2020, , 117-134.		1
25976	Multitask Hopfield Networks. Lecture Notes in Computer Science, 2020, , 349-365.	1.0	0
25977	Conceptualization of Indian Biodiversity by Using Semantic Web Technologies. , 2020, , 1445-1453.		0
25979	Pan-Cancer Analysis of Pathway-Based Gene Expression Pattern at the Individual Level Reveals Novel Biomarkers of Clinical Prognosis. SSRN Electronic Journal, 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
25984	Hierarchical Canonical Correlation Analysis Reveals Phenotype, Genotype, and Geoclimate Associations in Plants. <i>Plant Phenomics</i> , 2020, 2020, 1969142.	2.5	1
25990	Abnormal DNA methylation patterns in patients with infectionâ€caused leukocytopenia based on methylation microarrays. <i>Molecular Medicine Reports</i> , 2020, 21, 2335-2348.	1.1	1
25998	IPDS: A semantic mediatorâ€based system using Spark for the integration of heterogeneous proteomics data sources. <i>Concurrency Computation Practice and Experience</i> , 2021, 33, .	1.4	5
26007	Automated ontology-based annotation of scientific literature using deep learning. , 2020, , .		6
26013	The identification of gene ontologies and candidate genes for digital dermatitis in beef cattle from a genome-wide association study. <i>International Journal of Veterinary Science and Research</i> , 2020, 6, 027-037.	0.1	3
26014	A transcriptomic map of murine and human alopecia areata. <i>JCI Insight</i> , 2020, 5, .	2.3	7
26015	Drug screening and identification of key candidate genes and pathways of rheumatoid arthritis. <i>Molecular Medicine Reports</i> , 2020, 22, 986-996.	1.1	2
26016	Computing on Phenotypic Descriptions for Candidate Gene Discovery and Crop Improvement. <i>Plant Phenomics</i> , 2020, 2020, 1963251.	2.5	5
26020	Mining Top- <i>k</i> pairs of correlated subgraphs in a large network. <i>Proceedings of the VLDB Endowment</i> , 2020, 13, 1511-1524.	2.1	10
26025	Identification of Target Genes and Transcription Factors in Mice with LMNA-Related Dilated Cardiomyopathy by Integrated Bioinformatic Analyses. <i>Medical Science Monitor</i> , 2020, 26, e924576.	0.5	1
26026	Use of Chouâ€™s 5-steps rule to predict the subcellular localization of gram-negative and gram-positive bacterial proteins by multi-label learning based on gene ontology annotation and profile alignment. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, 51-79.	1.0	7
26034	MicroRNAs de plantas sob estresses tÃpicos da caatinga. <i>Revista UNIARA</i> , 2020, 23, .	0.1	0
26035	Impaired Metabolic Pathways Related to Colorectal Cancer Progression and Therapeutic Implications. <i>Iranian Journal of Public Health</i> , 0, , .	0.3	1
26037	Identifying key genes and drug screening for preeclampsia based on gene expression profiles. <i>Oncology Letters</i> , 2020, 20, 1585-1596.	0.8	5
26040	Risk gene identification and support vector machine learning to construct an early diagnosis model of myocardial infarction. <i>Molecular Medicine Reports</i> , 2020, 22, 1775-1782.	1.1	4
26046	SMRT sequencing of the full-length transcriptome of the white-backed planthopper <i>Sogatella furcifera</i> . <i>PeerJ</i> , 2020, 8, e9320.	0.9	7
26047	Stress response in periodontal ligament stem cells may contribute to bisphosphonateâ€associated osteonecrosis of the jaw: A gene expression array analysis. <i>Molecular Medicine Reports</i> , 2020, 22, 2043-2051.	1.1	2
26055	WTO, an ontology for wheat traits and phenotypes in scientific publications. <i>Genomics and Informatics</i> , 2020, 18, e14.	0.4	2

#	ARTICLE	IF	CITATIONS
26060	Expression profiling of small intestinal neuroendocrine tumors identified pathways and gene networks linked to tumorigenesis and metastasis. <i>Bioscience Reports</i> , 2020, 40, .	1.1	6
26063	Role of CYP4F2 as a novel biomarker regulating malignant phenotypes of liver cancer cells via the Nrf2 signaling axis. <i>Oncology Letters</i> , 2020, 20, 13.	0.8	4
26064	Identification of key genes of human bone marrow stromal cells adipogenesis at an early stage. <i>PeerJ</i> , 2020, 8, e9484.	0.9	3
26071	Applications of Community Detection Algorithms to Large Biological Datasets. <i>Methods in Molecular Biology</i> , 2021, 2243, 59-80.	0.4	2
26078	iNOA. , 2020, , .		0
26087	Genes for defense response to <i>Plasmodiophora brassicae</i> during late infection in small spheroid galls of <i>Brassica rapa</i> . <i>Biologia Plantarum</i> , 0, 64, 551-560.	1.9	0
26094	Cellular expression profiles of Epstein-Barr virus-transformed B-lymphoblastoid cell lines. <i>Biomedical Reports</i> , 2020, 13, 1-1.	0.9	2
26098	Genetic Mutations That Drive Evolutionary Rescue to Lethal Temperature in <i>Escherichia coli</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 2029-2044.	1.1	3
26100	Using bioinformatics and metabolomics to identify altered granulosa cells in patients with diminished ovarian reserve. <i>PeerJ</i> , 2020, 8, e9812.	0.9	9
26102	MicroRNA expression profiles of the cuttlefish (<i>Sepiella japonica</i>) during embryonic development. <i>Animal Biology</i> , 2020, 71, 37-47.	0.6	0
26107	Identification of key differentially expressed mRNAs and microRNAs in non-small cell lung cancer using bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2020, 20, 3720-3732.	0.8	5
26111	Identification of fertility-related genes for maize CMS-S via Bulk Segregant RNA-Seq. <i>PeerJ</i> , 2020, 8, e10015.	0.9	2
26112	Microproteins: a 3D protein structure prediction analysis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-9.	2.0	1
26113	BCG vaccination and the risk of COVID 19: A possible correlation. <i>Virology</i> , 2022, 565, 73-81.	1.1	6
26114	Whole genome sequence data of <i>Chromobacterium violaceum</i> WCH4, a human pathogenic strain from Sabah, Malaysia. <i>Data in Brief</i> , 2021, 39, 107533.	0.5	1
26115	The transcriptome of neuronal cell bodies, dendrites, and axons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	65
26116	<sc>PANTHER</sc>: Making genome-scale phylogenetics accessible to all. <i>Protein Science</i> , 2022, 31, 8-22.	3.1	467
26117	The gene regulation knowledge commons: the action area of GREEKC. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194768.	0.9	3

#	ARTICLE	IF	CITATIONS
26118	Proteomic Response to Environmental Stresses in the Stolon of a Highly Invasive Fouling Ascidian. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	5
26119	Pathway-targeting gene matrix for <i>Drosophila</i> gene set enrichment analysis. <i>PLoS ONE</i> , 2021, 16, e0259201.	1.1	6
26120	Comparative RNA-Seq Analysis Reveals Potentially Resistance-Related Genes in Response to Bacterial Canker of Tomato. <i>Genes</i> , 2021, 12, 1745.	1.0	5
26121	Proteomics Profiling with SWATH-MS Quantitative Analysis of Changes in the Human Brain with HIV Infection Reveals a Differential Impact on the Frontal and Temporal Lobes. <i>Brain Sciences</i> , 2021, 11, 1438.	1.1	1
26122	Full-Length Transcriptomics Reveal the Gene Expression Profiles of Reef-Building Coral <i>Pocillopora damicornis</i> and Symbiont <i>Zooxanthellae</i> . <i>Diversity</i> , 2021, 13, 543.	0.7	1
26123	The <i>Melastoma dodecandrum</i> genome and the evolution of Myrtales. <i>Journal of Genetics and Genomics</i> , 2022, 49, 120-131.	1.7	14
26124	Genomics analysis of hexanoic acid exposure in <i>Drosophila</i> species. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	5
26125	Identification of Novel Kinase-Transcription Factor-mRNA-miRNA Regulatory Network in Nasopharyngeal Carcinoma by Bioinformatics Analysis. <i>International Journal of General Medicine</i> , 2021, Volume 14, 7453-7469.	0.8	2
26126	Crowdsourcing biocuration: The Community Assessment of Community Annotation with Ontologies (CACAO). <i>PLoS Computational Biology</i> , 2021, 17, e1009463.	1.5	7
26127	Whole-exome analysis in Tunisian Imazighen and Arabs shows the impact of demography in functional variation. <i>Scientific Reports</i> , 2021, 11, 21125.	1.6	4
26128	p21 produces a bioactive secretome that places stressed cells under immunosurveillance. <i>Science</i> , 2021, 374, eabb3420.	6.0	112
26131	Maternal methionine supplementation during gestation alters alternative splicing and DNA methylation in bovine skeletal muscle. <i>BMC Genomics</i> , 2021, 22, 780.	1.2	9
26132	Genome-wide association study of susceptibility to hospitalised respiratory infections. <i>Wellcome Open Research</i> , 0, 6, 290.	0.9	3
26133	Trichoderma-Induced Ethylene Responsive Factor MsERF105 Mediates Defense Responses in <i>Malus sieversii</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 708010.	1.7	9
26134	Selecting Hub Genes and Predicting Target Genes of microRNAs in Tuberculosis via the Bioinformatics Analysis. <i>Genetical Research</i> , 2021, 2021, 1-11.	0.3	3
26135	Distinct Exosomal miRNA Profiles from BALF and Lung Tissue of COPD and IPF Patients. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11830.	1.8	33
26136	ParsVNN: parsimony visible neural networks for uncovering cancer-specific and drug-sensitive genes and pathways. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab097.	1.5	12
26137	Transcriptome analysis of the effect of a novel human serine protease inhibitor SPINK13 on gene expression in MHCC97-H cells. <i>Translational Cancer Research</i> , 2021, 10, 4464-4477.	0.4	0

#	ARTICLE	IF	CITATIONS
26139	Transcriptome analysis of <i>Elymus breviaristatus</i> cv. Tongde under different nitrogen treatment. <i>Agronomy Journal</i> , 0, , .	0.9	1
26140	Integrated bioinformatics analysis of the anti-atherosclerotic mechanisms of the polysaccharide CM1 from <i>Cordyceps militaris</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 193, 1274-1285.	3.6	8
26142	Quantitative trait locus mapping and genomic selection of tobacco (<i>Nicotiana tabacum</i> L.) based on high-density genetic map. <i>Plant Biotechnology Reports</i> , 2021, 15, 845-854.	0.9	6
26143	Hypothalamic Transcriptome Analysis Reveals the Crucial MicroRNAs and mRNAs Affecting Litter Size in Goats. <i>Frontiers in Veterinary Science</i> , 2021, 8, 747100.	0.9	10
26146	Integrating full-length transcriptomics and metabolomics reveals the regulatory mechanisms underlying yellow pigmentation in tree peony (<i>Paeonia suffruticosa</i> Andr.) flowers. <i>Horticulture Research</i> , 2021, 8, 235.	2.9	26
26147	USH2A Mutation is Associated With Tumor Mutation Burden and Antitumor Immunity in Patients With Colon Adenocarcinoma. <i>Frontiers in Genetics</i> , 2021, 12, 762160.	1.1	9
26148	Spatially resolved transcriptomics reveals the architecture of the tumor-microenvironment interface. <i>Nature Communications</i> , 2021, 12, 6278.	5.8	112
26149	Nitecap: An Exploratory Circadian Analysis Web Application. <i>Journal of Biological Rhythms</i> , 2022, 37, 43-52.	1.4	18
26150	Transcriptome and Exome Analyses of Hepatocellular Carcinoma Reveal Patterns to Predict Cancer Recurrence in Liver Transplant Patients. <i>Hepatology Communications</i> , 2022, 6, 710-727.	2.0	9
26151	Pan-cancer analysis reveals the expression, genetic alteration and prognosis of pyroptosis key gene GSDMD. <i>International Immunopharmacology</i> , 2021, 101, 108270.	1.7	27
26152	Community-acquired methicillin-resistant <i>Staphylococcus aureus</i> provoked cytokine storm causing severe infection on BALB/c mice. <i>Molecular Immunology</i> , 2021, 140, 167-174.	1.0	4
26153	How to Annotate and Submit a Short Linear Motif to the Eukaryotic Linear Motif Resource. <i>Methods in Molecular Biology</i> , 2020, 2141, 73-102.	0.4	3
26154	Techniques for Small Non-Coding RNA Analysis in Seeds of Forest Tree Species. <i>Methods in Molecular Biology</i> , 2020, 2093, 217-225.	0.4	0
26155	Correlated Protein Function Prediction with Robust Feature Selection. <i>Communications in Computer and Information Science</i> , 2020, , 3-17.	0.4	0
26157	Functional Gene Networks and Their Applications. <i>Computational Biology</i> , 2020, , 31-43.	0.1	0
26158	Local Adaptation in the Interior Spruce Hybrid Complex. <i>Compendium of Plant Genomes</i> , 2020, , 155-176.	0.3	5
26159	HoSeln: A Workflow for Integrating Various Homology Search Results from Metagenomic and Metatranscriptomic Sequence Datasets. <i>Bio-protocol</i> , 2020, 10, e3679.	0.2	0
26162	Identification of long non-coding RNA signatures for squamous cell carcinomas and adenocarcinomas. <i>Aging</i> , 2021, 13, 2459-2479.	1.4	1

#	ARTICLE	IF	CITATIONS
26166	Identification of adriamycin resistance genes in breast cancer based on microarray data analysis. <i>Translational Cancer Research</i> , 2020, 9, 7486-7494.	0.4	1
26167	Identification of Core Genes Involved in the Metastasis of Clear Cell Renal Cell Carcinoma. <i>Cancer Management and Research</i> , 2020, Volume 12, 13437-13449.	0.9	8
26168	GONET: A Deep Network to Annotate Proteins via Recurrent Convolution Networks. , 2020, , .		2
26169	Novel therapeutic compounds for prostate adenocarcinoma treatment. <i>Medicine (United States)</i> , 2020, 99, e23768.	0.4	2
26171	High levels of glucose alter <i>Physcomitrella patens</i> metabolism and trigger a differential proteomic response. <i>PLoS ONE</i> , 2020, 15, e0242919.	1.1	0
26173	SNPViz v2.0: A web-based tool for enhanced haplotype analysis using large scale resequencing datasets and discovery of phenotypes causative gene using allelic variations. , 2020, , .		2
26175	Microarray Analysis for Differentially Expressed Genes Between Stromal and Epithelial Cells in Development and Metastasis of Invasive Breast Cancer. <i>Journal of Computational Biology</i> , 2020, 27, 1631-1643.	0.8	8
26176	Downregulation of miR-146a inhibits osteoporosis in the jaws of ovariectomized rats by regulating the Wnt/ β -catenin signaling pathway. <i>International Journal of Molecular Medicine</i> , 2020, 47, .	1.8	4
26177	Probabilistic graphlets capture biological function in probabilistic molecular networks. <i>Bioinformatics</i> , 2020, 36, i804-i812.	1.8	4
26178	Upregulation of 5'-terminal oligopyrimidine mRNA translation upon loss of the ARF tumor suppressor. <i>Scientific Reports</i> , 2020, 10, 22276.	1.6	5
26179	Identifying an Eight-Gene Signature to Optimize Overall Survival Prediction of Esophageal Adenocarcinoma Using Bioinformatics Analysis of ceRNA Network. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 13041-13054.	1.0	7
26180	Characterisation of gene and pathway expression in stabilised blood from children with coeliac disease. <i>BMJ Open Gastroenterology</i> , 2020, 7, e000536.	1.1	2
26181	Metric Labeling and Semimetric Embedding for Protein Annotation Prediction. <i>Journal of Computational Biology</i> , 2021, 28, 514-525.	0.8	1
26182	NCR: A novel method for measuring disease similarity based on non-coding RNA regulation. , 2020, , .		1
26183	Analysis of the Endometrial Transcriptome at the Time of Implantation in Women Receiving a Single Post-Ovulatory Dose of Levonorgestrel or Mifepristone. <i>Revista De Investigacion Clinica</i> , 2021, 72, 363-371.	0.2	0
26185	MUC4 is a novel mediator in <i>H. Pylori</i> infection-related pancreatic cancer. <i>Oncology Letters</i> , 2020, 21, 123.	0.8	2
26186	Relationships Between Vitamin D Status and Cytokine: Results from Interferon-Based Therapy in Non-Cirrhotic, Treatment-Naïve Patients with Chronic Hepatitis C Infection. <i>Journal of Inflammation Research</i> , 2020, Volume 13, 1207-1218.	1.6	1
26187	Personalized beyond Precision: Designing Unbiased Gold Standards to Improve Single-Subject Studies of Personal Genome Dynamics from Gene Products. <i>Journal of Personalized Medicine</i> , 2021, 11, 24.	1.1	3

#	ARTICLE	IF	CITATIONS
26188	Knowledge-aware Few-shot Learning Framework for Biomedical Event Trigger Identification. , 2020, , .		5
26189	Extending import detection algorithms for concept import from two to three biomedical terminologies. BMC Medical Informatics and Decision Making, 2020, 20, 272.	1.5	2
26191	Transcriptional profiles of human islet and exocrine endothelial cells in subjects with or without impaired glucose metabolism. Scientific Reports, 2020, 10, 22315.	1.6	3
26194	Genome analysis of <i>Plectes murrayi</i> , a nematode from continental Antarctica. G3: Genes, Genomes, Genetics, 2021, 11, 1-9.	0.8	4
26196	Multi-resolution visualization and analysis of biomolecular networks through hierarchical community detection and web-based graphical tools. PLoS ONE, 2020, 15, e0244241.	1.1	5
26198	Draft Genome Sequence of <i>Lactobacillus salivarius</i> KZ-NCB, Isolated from Chicken Cecum. Microbiology Resource Announcements, 2020, 9, .	0.3	0
26199	Concurrent Evolution of Antiaging Gene Duplications and Cellular Phenotypes in Long-Lived Turtles. Genome Biology and Evolution, 2021, 13, .	1.1	6
26200	Variation of biomolecules in plant species. , 2022, , 81-99.		2
26201	Evaluation of early post-natal pig mammary gland development and human breast cancer gene expression. Developmental Biology, 2022, 481, 95-103.	0.9	4
26202	High ORAI3 expression correlates with good prognosis in human muscle-invasive bladder cancer. Gene, 2022, 808, 145994.	1.0	4
26203	Bioinformatic tools for research in CRC. , 2022, , 231-247.		0
26204	The protease web. , 2022, , 229-250.		0
26205	Whole genome sequencing of an edible and medicinal mushroom, <i>Russula griseocarnosa</i> , and its association with mycorrhizal characteristics. Gene, 2022, 808, 145996.	1.0	4
26206	Complete genome sequence of <i>Polaribacter sejongensis</i> NJDZ03 exhibiting diverse macroalgal polysaccharide-degrading activity. Marine Genomics, 2022, 61, 100913.	0.4	1
26207	Bioinformatic Analysis of Potential Pathogenicity Effectors of <i>Candidatus Liberibacter asiaticus</i> , Causal Agent of Citrus Huanglongbing. American Journal of Plant Sciences, 2020, 11, 1319-1330.	0.3	0
26208	Predicting Associations Between Proteins and Multiple Diseases. Lecture Notes in Computer Science, 2020, , 383-392.	1.0	0
26209	A Collection of Benchmark Data Sets for Knowledge Graph-Based Similarity in the Biomedical Domain. Lecture Notes in Computer Science, 2020, , 50-55.	1.0	1
26210	Formalizing Graphical Modularization Approaches for Ontologies and the Knowledge Loss. Communications in Computer and Information Science, 2020, , 388-412.	0.4	3

#	ARTICLE	IF	CITATIONS
26211	Refactoring and optimization of metabolic network. , 2020, , 77-105.		2
26212	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	1
26213	Muscle biopsies differ in relation to expression of fiber-type specific genes. Journal of Diabetology, 2020, 11, 198.	0.1	0
26217	Transcriptomic analysis of Medicago truncatula calli with MtWOX9-1 overexpression. Vavilovskii Zhurnal Genetiki i Seleksii, 2019, 23, 691-699.	0.4	5
26220	Gene transcription profiling of astheno- and normo-zoospermic sperm subpopulations. Asian Journal of Andrology, 2020, 22, 608.	0.8	8
26221	Liver Disease Modelling. Learning Materials in Biosciences, 2020, , 189-207.	0.2	0
26226	Assessing Protein Function Through Structural Similarities with CATH. Methods in Molecular Biology, 2020, 2112, 43-57.	0.4	2
26227	Design of a Biochemistry Procedure-Oriented Ontology. Communications in Computer and Information Science, 2020, , 365-387.	0.4	0
26228	Opportunities and Challenges Provided by Boolean Modelling of Cancer Signalling Pathways. Computational Biology, 2020, , 199-216.	0.1	0
26229	Orthology: Promises and Challenges. , 2020, , 203-228.		10
26230	Novel Driver Synonymous Mutations in the Coding Regions of GCB Lymphoma Patients Improve the Transcription Levels of BCL2. Lecture Notes in Computer Science, 2020, , 108-118.	1.0	1
26231	Multi-label Learning with a Cone-Based Geometric Model. Lecture Notes in Computer Science, 2020, , 177-185.	1.0	3
26232	Committee-Based Active Learning to Select Negative Examples for Predicting Protein Functions. Lecture Notes in Computer Science, 2020, , 80-87.	1.0	0
26233	Identification of Potential Key Genes Involved in Progression of Gastric Cancer Using Bioinformatics Analysis. Diagnostics and Therapeutic Advances in GI Malignancies, 2020, , 101-114.	0.2	0
26234	Modelling Oxidative Stress Pathways. Computational Biology, 2020, , 277-300.	0.1	0
26236	Guide and legend. , 2020, , xxi-xxviii.		0
26238	Genome-wide CRISPR screening identifies new regulators of glycoprotein secretion. Wellcome Open Research, 2019, 4, 119.	0.9	3
26239	Analytical Approaches and Use Case on Network Interactions. Lecture Notes in Intelligent Transportation and Infrastructure, 2020, , 523-530.	0.3	0

#	ARTICLE	IF	CITATIONS
26240	An In Silico Approach for Function Prediction of Hypothetical Proteins of Mycobacterium laprae TN. SSRN Electronic Journal, 0, , .	0.4	2
26241	Graph Based Automatic Protein Function Annotation Improved by Semantic Similarity. Lecture Notes in Computer Science, 2020, , 261-272.	1.0	1
26242	Artificial Intelligence in Biological Modelling. , 2020, , 265-302.		1
26243	Hierarchy Decomposition Pipeline: A Toolbox for Comparison of Model Induction Algorithms on Hierarchical Multi-label Classification Problems. Lecture Notes in Computer Science, 2020, , 486-501.	1.0	0
26244	Computational Methods for Predicting Autism Spectrum Disorder from Gene Expression Data. Lecture Notes in Computer Science, 2020, , 395-409.	1.0	0
26245	Mapping the Patient's Experience: An Applied Ontological Framework for Phenomenological Psychopathology. Phenomenology and Mind, 0, , 200.	0.0	1
26246	Role of Bioinformatics in Nanotechnology. , 2020, , 1875-1894.		1
26247	Strategies and Resources for the Identification of microRNAs in Non-model Plants. Concepts and Strategies in Plant Sciences, 2020, , 45-55.	0.6	0
26248	Practice and Analysis of Knowledge Construction using a Domain Ontology and Procedural Knowledge. Transactions of the Japanese Society for Artificial Intelligence, 2020, 35, A-J44_1-12.	0.1	0
26250	Concept Similarity Under the Agent's Preferences for the Description Logic \mathcal{ALH} . Communications in Computer and Information Science, 2020, , 34-42.	0.4	0
26251	How does secondary hypogonadism affect the spermatozoa proteome? Lessons from a porcine animal model. Reproduction, Fertility and Development, 2020, , .	0.1	0
26252	Exploring lncRNA-MRNA Regulatory Modules Based on lncRNA Similarity in Breast Cancer. Lecture Notes in Computer Science, 2020, , 57-66.	1.0	0
26253	9 Fungal Genomics. , 2020, , 207-224.		0
26259	Genome sequencing of <i>Aspergillus glaucus</i> provides insights into salt-stress adaptation. PeerJ, 2020, 8, e8609.	0.9	4
26262	Pilot study and bioinformatics analysis of differentially expressed genes in adipose tissues of rats with excess dietary intake. Molecular Medicine Reports, 2020, 21, 2063-2072.	1.1	2
26264	OUP accepted manuscript. Tree Physiology, 2021, , .	1.4	2
26265	IID 2021: towards context-specific protein interaction analyses by increased coverage, enhanced annotation and enrichment analysis. Nucleic Acids Research, 2022, 50, D640-D647.	6.5	38
26266	An Integrative Data Mining Approach to Identify Purinergic Signaling Genes and Associated Neurodegenerative Diseases. , 2021, , .		0

#	ARTICLE	IF	CITATIONS
26269	Functional Annotations of Single-Nucleotide Polymorphism (SNP)-Based and Gene-Based Genome-Wide Association Studies Show Genes Affecting Keratitis Susceptibility. <i>Medical Science Monitor</i> , 2020, 26, e922710.	0.5	3
26284	Identification of key miRNAs and genes for mouse retinal development using a linear model. <i>Molecular Medicine Reports</i> , 2020, 22, 494-506.	1.1	8
26287	Candidate genes for predicting the survival of patients with gastric cancer: a study based on The Cancer Genome Atlas (TCGA) database. <i>Translational Cancer Research</i> , 2020, 9, 2599-2608.	0.4	2
26300	Integrative genomics analysis of eQTL and GWAS summary data identifies <i>PPP1CB</i> as a novel bone mineral density risk genes. <i>Bioscience Reports</i> , 2020, 40, .	1.1	0
26302	Identification of Key Differentially Methylated/Expressed Genes and Pathways for Ovarian Endometriosis by Bioinformatics Analysis. <i>Reproductive Sciences</i> , 2022, 29, 1630-1643.	1.1	7
26303	Platelet proteome dynamics in hibernating 13-lined ground squirrels. <i>Physiological Genomics</i> , 2021, 53, 473-485.	1.0	8
26304	A Novel Three-LncRNA Signature Predicting Tumor Recurrence in Nonfunctioning Pituitary Adenomas. <i>Frontiers in Genetics</i> , 2021, 12, 754503.	1.1	6
26305	Low-Level Laser Therapy Effects on Rat Blood Hemostasis Via Significant Alteration in Fibrinogen and Plasminogen Expression Level. <i>Journal of Lasers in Medical Sciences</i> , 2021, 12, e59-e59.	0.4	1
26306	Genome Instability and Long Noncoding RNA Reveal Biomarkers for Immunotherapy and Prognosis and Novel Competing Endogenous RNA Mechanism in Colon Adenocarcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 740455.	1.8	6
26307	Bioinformatic analysis of key pathways and genes shared between endometriosis and ovarian cancer. <i>Archives of Gynecology and Obstetrics</i> , 2022, 305, 1329-1342.	0.8	5
26308	Establishment and characterization of prostate organoids from treatment-naïve patients with prostate cancer. <i>Oncology Letters</i> , 2021, 23, 6.	0.8	12
26309	Co-evolution based machine-learning for predicting functional interactions between human genes. <i>Nature Communications</i> , 2021, 12, 6454.	5.8	12
26310	Network analysis reveals rare disease signatures across multiple levels of biological organization. <i>Nature Communications</i> , 2021, 12, 6306.	5.8	36
26311	A new trauma frontier: Exploratory pilot study of platelet transcriptomics in trauma patients. <i>Journal of Trauma and Acute Care Surgery</i> , 2022, 92, 313-322.	1.1	3
26312	Integrative analysis of Iso-Seq and RNA-seq data reveals transcriptome complexity and differentially expressed transcripts in sheep tail fat. <i>PeerJ</i> , 2021, 9, e12454.	0.9	16
26313	Phenotype-tissue expression and exploration (PTEE) resource facilitates the choice of tissue for RNA-seq-based clinical genetics studies. <i>BMC Genomics</i> , 2021, 22, 802.	1.2	8
26314	Single-cell analysis of arthritogenic alphavirus-infected human synovial fibroblasts links low abundance of viral RNA to induction of innate immunity and arthralgia-associated gene expression. <i>Emerging Microbes and Infections</i> , 2021, 10, 2151-2168.	3.0	11
26315	Edgetic Perturbations Contribute to Phenotypic Variability in PEX26 Deficiency. <i>Frontiers in Genetics</i> , 2021, 12, 726174.	1.1	2

#	ARTICLE	IF	CITATIONS
26316	RNA-seq library preparation for comprehensive transcriptome analysis in cancer cells: The impact of insert size. <i>Genomics</i> , 2021, 113, 4149-4162.	1.3	6
26317	Looking deeper into ocular surface health: an introduction to clinical tear proteomics analysis. <i>Acta Ophthalmologica</i> , 2022, 100, 486-498.	0.6	11
26318	High-dose dexamethasone injection disordered metabolism and multiple protein kinases expression in the mouse kidney. <i>Bioscience Reports</i> , 2021, 41, .	1.1	1
26319	GPRuler: Metabolic gene-protein-reaction rules automatic reconstruction. <i>PLoS Computational Biology</i> , 2021, 17, e1009550.	1.5	11
26320	Tumour DDR1 promotes collagen fibre alignment to instigate immune exclusion. <i>Nature</i> , 2021, 599, 673-678.	13.7	139
26321	Withering syndrome induced gene expression changes and a de-novo transcriptome for the Pinto abalone, <i>Haliotis kamtschatkana</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 41, 100930.	0.4	2
26322	Multidimensional Analysis of the Role of Charged Multivesicular Body Protein 7 in Pan-Cancer. <i>International Journal of General Medicine</i> , 2021, Volume 14, 7907-7923.	0.8	6
26323	Computationally Reconstructed Interactome of <i>Bradyrhizobium diazoefficiens</i> USDA110 Reveals Novel Functional Modules and Protein Hubs for Symbiotic Nitrogen Fixation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11907.	1.8	0
26324	Cross-platform transcriptomic profiling of the response to recombinant human erythropoietin. <i>Scientific Reports</i> , 2021, 11, 21705.	1.6	5
26325	Genome-wide CRISPR interference screen identifies long non-coding RNA loci required for differentiation and pluripotency. <i>PLoS ONE</i> , 2021, 16, e0252848.	1.1	12
26326	Broad Spectrum Antiviral Properties of Cardiotonic Steroids Used as Potential Therapeutics for Emerging Coronavirus Infections. <i>Pharmaceutics</i> , 2021, 13, 1839.	2.0	13
26327	Signaling pathways of heat- and hypersalinity-induced polyp bailout in <i>Pocillopora acuta</i> . <i>Coral Reefs</i> , 2021, 40, 1713-1728.	0.9	5
26328	Transcriptome Analysis Reveals Different Responsive Patterns to Nitrogen Deficiency in Two Wheat Near-Isogenic Lines Contrasting for Nitrogen Use Efficiency. <i>Biology</i> , 2021, 10, 1126.	1.3	6
26329	Cigarette smoking-associated isoform switching and 3' UTR lengthening via alternative polyadenylation. <i>Genomics</i> , 2021, 113, 4184-4195.	1.3	3
26330	Deciphering Genomic Heterogeneity and the Internal Composition of Tumour Activities through a Hierarchical Factorisation Model. <i>Mathematics</i> , 2021, 9, 2833.	1.1	0
26331	Single-cell profiling of T lymphocytes in deficiency of adenosine deaminase 2. <i>Journal of Leukocyte Biology</i> , 2022, 111, 301-312.	1.5	12
26332	Î²-Glucan Induces Distinct and Protective Innate Immune Memory in Differentiated Macrophages. <i>Journal of Immunology</i> , 2021, 207, 2785-2798.	0.4	29
26333	Pairwise Biological Network Alignment Based on Discrete Bat Algorithm. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-12.	0.7	1

#	ARTICLE	IF	CITATIONS
26335	Development of a bioinformatics platform for analysis of quantitative transcriptomics and proteomics data: the OMnalysis. <i>PeerJ</i> , 2021, 9, e12415.	0.9	2
26337	Proximity labeling identifies LOTUS domain proteins that promote the formation of perinuclear germ granules in <i>C. elegans</i> . <i>ELife</i> , 2021, 10, .	2.8	9
26338	Synergistic alterations in the multilevel chromatin structure anchor dysregulated genes in small cell lung cancer. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5946-5959.	1.9	6
26339	<i>Plasmodium falciparum</i> Calcium-Dependent Protein Kinase 4 is Critical for Male Gametogenesis and Transmission to the Mosquito Vector. <i>MBio</i> , 2021, 12, e0257521.	1.8	26
26340	Patch-seq of mouse DRG neurons reveals candidate genes for specific mechanosensory functions. <i>Cell Reports</i> , 2021, 37, 109914.	2.9	40
26341	Human transcriptional gene regulatory network compiled from 14 data resources. <i>Biochimie</i> , 2022, 193, 115-125.	1.3	4
26343	TORPEDO: witnessing model correctness with topological proofs. <i>Formal Aspects of Computing</i> , 2021, 33, 1039-1066.	1.4	2
26344	Transcriptome profiling reveals the developmental regulation of NaCl-treated <i>Forcipomyia taiwana</i> eggs. <i>BMC Genomics</i> , 2021, 22, 792.	1.2	2
26345	Passages in culture and stimulation conditions influence protein expression of primary fibroblasts. <i>Proteomics</i> , 2021, , 2100116.	1.3	0
26346	Dysregulated expression levels of APH1B in peripheral blood are associated with brain atrophy and amyloid- β deposition in Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 183.	3.0	13
26347	Proteogenomic discovery of sORF-encoded peptides associated with bacterial virulence in <i>Yersinia pestis</i> . <i>Communications Biology</i> , 2021, 4, 1248.	2.0	10
26348	Fibromine is a multi-omics database and mining tool for target discovery in pulmonary fibrosis. <i>Scientific Reports</i> , 2021, 11, 21712.	1.6	11
26349	The Rat Genome Database (RGD) facilitates genomic and phenotypic data integration across multiple species for biomedical research. <i>Mammalian Genome</i> , 2022, 33, 66-80.	1.0	14
26350	Genome Sequence Data of <i>Leptosphaerulina arachidicola</i> , a Causal Agent of Peanut Scorch Spot in China. <i>Plant Disease</i> , 2022, 106, 748-750.	0.7	1
26352	The long-read genome assembly of hop (<i>Humulus lupulus</i>) uncovers the pseudoautosomal region and other genomic features. <i>Acta Horticulturae</i> , 2021, , 1-16.	0.1	2
26353	Comparison of the Proteomes of Porcine Macrophages and a Stable Porcine Cell Line after Infection with African Swine Fever Virus. <i>Viruses</i> , 2021, 13, 2198.	1.5	15
26354	Immune Characteristics Analysis and Transcriptional Regulation Prediction Based on Gene Signatures of Chronic Obstructive Pulmonary Disease. <i>International Journal of COPD</i> , 2021, Volume 16, 3027-3039.	0.9	5
26355	Structure-Aware <i>Mycobacterium tuberculosis</i> Functional Annotation Uncloaks Resistance, Metabolic, and Virulence Genes. <i>MSystems</i> , 2021, , e0067321.	1.7	4

#	ARTICLE	IF	CITATIONS
26356	Transcriptomic analyses reveal variegation-induced metabolic changes leading to high L-theanine levels in albino sectors of variegated tea (<i>Camellia sinensis</i>). <i>Plant Physiology and Biochemistry</i> , 2021, 169, 29-39.	2.8	8
26361	Effects of Egr1 on pancreatic acinar intracellular trypsinogen activation and the associated ceRNA network. <i>Molecular Medicine Reports</i> , 2020, 22, 2496-2506.	1.1	3
26364	Atherosclerosis prediction by microarray-based DNA methylation analysis. <i>Experimental and Therapeutic Medicine</i> , 2020, 20, 2863-2869.	0.8	3
26366	Hyperbolic Distance Matrices. , 2020, , .		12
26370	Efficient Calculation of Empirical P-values for Association Testing of Binary Classifications. , 2020, , .		0
26372	Key genes involved in cell cycle arrest and DNA damage repair identified in anaplastic thyroid carcinoma using integrated bioinformatics analysis. <i>Translational Cancer Research</i> , 2020, 9, 4188-4203.	0.4	4
26373	Screening and Interaction Analysis of Key Genes in miR-542-3p Over- Expressed Osteosarcoma Cells by Bioinformatics. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 411-418.	0.6	0
26374	High-Throughput GRID Computing for Life Sciences. , 0, , 821-840.		0
26375	Data Mining in Proteomics Using Grid Computing. , 0, , 918-940.		0
26376	Wave-SOM. , 0, , 104-126.		0
26377	New Trends in Graph Mining. , 0, , 259-278.		0
26378	GO-Based Term Semantic Similarity. , 0, , 93-104.		0
26379	Knowledge-Driven, Data-Assisted Integrative Pathway Analytics. , 0, , 173-194.		0
26380	Biclustering of DNA Microarray Data. , 0, , 513-551.		3
26381	Modules in Biological Networks. , 0, , 637-663.		0
26382	Incorporating Correlations among Gene Ontology Terms into Predicting Protein Functions. , 0, , 831-850.		0
26383	Data Mining and Meta-Analysis on DNA Microarray Data. , 0, , 1196-1236.		0
26384	Applications of Supercomputers in Sequence Analysis and Genome Annotation. <i>Advances in Systems Analysis, Software Engineering, and High Performance Computing Book Series</i> , 0, , 149-175.	0.5	2

#	ARTICLE	IF	CITATIONS
26385	Inference of Gene Regulatory Networks by Topological Prior Information and Data Integration. Advances in Medical Technologies and Clinical Practice Book Series, 0, , 1-51.	0.3	0
26386	Evolving-pattern analysis of transient and long-term biomarkers for cancers: Hepatocellular carcinoma as a case. Interdisciplinary Sciences, Computational Life Sciences, 2015, , .	2.2	0
26387	Analysis of the real EADGENE data set: Multivariate approaches and post analysis (<i><i>Open Access</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	1
26391	On External Indices for Mixtures: Validating Mixtures of Genes. , 2006, , 662-669.		0
26393	Linking Gene Expression Patterns and Transcriptional Regulation in Plasmodium falciparum. , 2007, , 137-156.		1
26396	Functional Genomics and Bioinformatics of the Phytophthora sojae Soybean Interaction. , 2008, , 67-78.		6
26399	Integrated Servers for Structure-Informed Function Prediction. , 2009, , 251-272.		0
26400	The Relevance of Epigenetics to Major Psychosis. , 2009, , 411-434.		0
26401	Magnaporthe grisea Oryza sativa (MGOS) Interaction Database: Community Annotation. , 2009, , 405-415.		0
26404	Handling and Interpreting Gene Groups. , 2007, , 69-84.		0
26405	COBrA and COBrA-CT: Ontology Engineering Tools. , 2008, , 151-162.		1
26406	SYMBIOS: A Semantic Pervasive Services Platform for Biomedical Information Integration. Lecture Notes in Computer Science, 2008, , 951-962.	1.0	0
26407	A Tree Index to Support Clustering Based Exploratory Data Analysis. Communications in Computer and Information Science, 2008, , 1-15.	0.4	1
26408	Combining Protein-Protein Interaction (PPI) Network and Sequence Attributes for Predicting Hypertension Related Proteins. Communications in Computer and Information Science, 2008, , 377-391.	0.4	1
26409	Multi-represented Classification Based on Confidence Estimation. , 2007, , 23-34.		5
26410	Modeling Genetic Networks: Comparison of Static and Dynamic Models. , 2007, , 78-89.		1
26413	Creating Ontologies for Content Representationâ€™The OntoSeed Suite. Lecture Notes in Computer Science, 2007, , 141-166.	1.0	0
26414	Automated Methods of Predicting the Function of Biological Sequences Using GO and Rough Set. Lecture Notes in Computer Science, 2007, , 1-10.	1.0	0

#	ARTICLE	IF	CITATIONS
26415	Gene Arrays for Gene Discovery. , 2008, , 23-36.		0
26416	Matching in Hybrid Terminologies. , 2007, , 166-180.		0
26418	Concept Lattice Representations of Annotated Taxonomies. , 2006, , 214-225.		5
26419	Dynamic Problem Solving in the Semantic Grid. Advanced Topics in Science and Technology in China, 2008, , 48-78.	0.0	0
26422	The Relation between Indel Length and Functional Divergence: A Formal Study. Lecture Notes in Computer Science, 2008, , 330-341.	1.0	1
26423	Gene Interactions Sub-networks and Soft Computing. Studies in Computational Intelligence, 2009, , 313-327.	0.7	0
26424	Clustering Using Multi-objective Differential Evolution Algorithms. Studies in Computational Intelligence, 2009, , 213-238.	0.7	2
26425	Identifying Functional miRNA Targets Using Overexpression and Knockdown Methods. , 2012, , 295-317.		0
26426	<i>Nitrincola iocasae</i> sp. nov., a bacterium isolated from sediment collected at a cold seep field in the South China Sea. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4897-4902.	0.8	7
26427	Sox9 promotes renal tubular epithelialâ€mesenchymal transition and extracellular matrix aggregation via the PI3K/AKT signaling pathway. Molecular Medicine Reports, 2020, 22, 4017-4030.	1.1	5
26428	Altered expression of genes regulating inflammation and synaptogenesis during regrowth of afferent neurons to cochlear hair cells. PLoS ONE, 2020, 15, e0238578.	1.1	7
26429	Exploration of ovine milk whey proteome during postnatal development using an iTRAQ approach. PeerJ, 2020, 8, e10105.	0.9	9
26430	Integrated transcriptome meta-analysis of pancreatic ductal adenocarcinoma and matched adjacent pancreatic tissues. PeerJ, 2020, 8, e10141.	0.9	34
26453	Study of the differentially abundant proteins among <i>Leishmania amazonensis</i> , <i>L. braziliensis</i> , and <i>L. infantum</i> . PLoS ONE, 2020, 15, e0240612.	1.1	3
26454	Transcriptome analysis revealed misregulated gene expression in blastoderms of interspecific chicken and Japanese quail F1 hybrids. PLoS ONE, 2020, 15, e0240183.	1.1	0
26455	Dual genome-wide CRISPR knockout and CRISPR activation screens identify mechanisms that regulate the resistance to multiple ATR inhibitors. PLoS Genetics, 2020, 16, e1009176.	1.5	17
26456	Differential transcript usage in the Parkinsonâ€™s disease brain. PLoS Genetics, 2020, 16, e1009182.	1.5	15
26464	TriRNSC: triclustering of gene expression microarray data using restricted neighbourhood search. IET Systems Biology, 2020, 14, 323-333.	0.8	3

#	ARTICLE	IF	CITATIONS
26477	Genome-Wide Analyses Provide Insights into the Scavenging Lifestyle of the Striped Hyena (<i>Hyaena</i>)	0.9	3
26478	Global insights to drought stress perturbed genes in oat (<i>Avena sativa</i> L.) seedlings using RNA sequencing. <i>Plant Signaling and Behavior</i> , 2021, 16, 1845934.	1.2	2
26498	Bioinformatic Tools in Arabidopsis Research. <i>Methods in Molecular Biology</i> , 2021, 2200, 25-89.	0.4	4
26499	Data Analysis for Antibody Arrays. <i>Methods in Molecular Biology</i> , 2021, 2237, 263-276.	0.4	0
26500	Predicting Dihydroartemisinin Resistance in <i>Plasmodium falciparum</i> using Pathway Activity Inference. , 2020, , .		0
26501	In Silico Docking of Vitamin E Isomers on Transport Proteins. <i>Current Computer-Aided Drug Design</i> , 2020, 16, 467-472.	0.8	1
26502	Epigenome-wide association scan identifies methylation sites associated with HIV infection. <i>Epigenomics</i> , 2020, 12, 1917-1927.	1.0	7
26503	Effective Random Walk Models for Comparative Network Analysis. , 2021, , 27-44.		0
26504	BioFabric Visualization of Network Alignments. , 2021, , 65-97.		0
26505	Protein-Protein Interaction Network Analysis for a Biomarker Panel Related to Human Esophageal Adenocarcinoma. <i>Asian Pacific Journal of Cancer Prevention</i> , 2017, 18, 3357-3363.	0.5	35
26506	Deep-coverage rhesus red blood cell proteome: a first comparison with the human and mouse red blood cell. <i>Blood Transfusion</i> , 2010, 8 Suppl 3, s126-39.	0.3	10
26508	Development of gene ontology tool for biological interpretation of genomic and proteomic data. <i>AMIA ... Annual Symposium proceedings</i> , 2003, , 839.	0.2	8
26509	The ontology of the gene ontology. <i>AMIA ... Annual Symposium proceedings</i> , 2003, , 609-13.	0.2	32
26510	Evaluation of lexical methods for detecting relationships between concepts from multiple ontologies. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006, , 28-39.	0.7	14
26511	Using web ontology language to integrate heterogeneous databases in the neurosciences. <i>AMIA ... Annual Symposium proceedings</i> , 2006, , 464-8.	0.2	11
26512	SemCat: semantically categorized entities for genomics. <i>AMIA ... Annual Symposium proceedings</i> , 2006, , 754-8.	0.2	5
26513	Discovering biological guilds through topological abstraction. <i>AMIA ... Annual Symposium proceedings</i> , 2006, , 1-5.	0.2	4
26514	A metadata framework for interoperating heterogeneous genome data using XML. <i>Proceedings</i> , 2001, , 110-4.	0.6	1

#	ARTICLE	IF	CITATIONS
26515	Making a new technology work: the standardization and regulation of microarrays. <i>Yale Journal of Biology and Medicine</i> , 2007, 80, 165-78.	0.2	31
26516	Public databases and software for the pathway analysis of cancer genomes. <i>Cancer Informatics</i> , 2007, 3, 379-97.	0.9	6
26518	NEIBank: genomics and bioinformatics resources for vision research. <i>Molecular Vision</i> , 2008, 14, 1327-37.	1.1	30
26520	Transcriptional regulatory network analysis during epithelial-mesenchymal transformation of retinal pigment epithelium. <i>Molecular Vision</i> , 2008, 14, 1414-28.	1.1	23
26521	A fault model for ontology mapping, alignment, and linking systems. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2007, , 233-44.	0.7	7
26522	Assessing and combining reliability of protein interaction sources. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2007, , 433-44.	0.7	4
26523	Accessing and integrating data and knowledge for biomedical research. <i>Yearbook of Medical Informatics</i> , 2008, , 91-101.	0.8	24
26524	From "glycosyltransferase" to "congenital muscular dystrophy": integrating knowledge from NCBI Entrez Gene and the Gene Ontology. <i>Studies in Health Technology and Informatics</i> , 2007, 129, 1260-4.	0.2	6
26525	Using metabolomics to estimate unintended effects in transgenic crop plants: problems, promises, and opportunities. <i>Journal of Biomolecular Techniques</i> , 2008, 19, 159-66.	0.8	29
26526	Biomedical ontologies in action: role in knowledge management, data integration and decision support. <i>Yearbook of Medical Informatics</i> , 2008, , 67-79.	0.8	134
26527	Gene expression profiling reveals a diverse array of pathways inhibited by nuclear receptor SHP during adipogenesis. <i>International Journal of Clinical and Experimental Pathology</i> , 2009, 2, 275-85.	0.5	8
26528	Differential expression of anti-angiogenic factors and guidance genes in the developing macula. <i>Molecular Vision</i> , 2009, 15, 45-59.	1.1	48
26530	Finding GeneRIFs via gene ontology annotations. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006, , 52-63.	0.7	15
26531	Adaptive classifiers, topic drifts and GO annotations. <i>AMIA ... Annual Symposium proceedings</i> , 2007, , 681-5.	0.2	3
26532	Magellan: a web based system for the integrated analysis of heterogeneous biological data and annotations; application to DNA copy number and expression data in ovarian cancer. <i>Cancer Informatics</i> , 2007, 2, 10-21.	0.9	7
26533	Integrative analysis of gene expression data including an assessment of pathway enrichment for predicting prostate cancer. <i>Cancer Informatics</i> , 2007, 2, 289-300.	0.9	3
26535	Discovery of Recurrent Sequence Motifs in <i>Saccharomyces cerevisiae</i> Cell Wall Proteins. <i>Match</i> , 2007, 58, 281-299.	0.8	3
26536	Dissecting the interface between signaling and transcriptional regulation in human B cells. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2009, , 264-75.	0.7	14

#	ARTICLE	IF	CITATIONS
26537	From gene expression profiles to biological validation in enteroviral heart disease. <i>Experimental and Clinical Cardiology</i> , 2003, 8, 125-30.	1.3	0
26538	Do sex steroids exert sex-specific and/or opposite effects on gene expression in lacrimal and meibomian glands?. <i>Molecular Vision</i> , 2009, 15, 1553-72.	1.1	82
26540	Gene set enrichment analyses revealed differences in gene expression patterns between males and females. <i>In Silico Biology</i> , 2009, 9, 55-63.	0.4	15
26541	Variability of DNA microarray gene expression profiles in cultured rat primary hepatocytes. <i>Gene Regulation and Systems Biology</i> , 2007, 1, 235-49.	2.3	2
26542	Developing a systems biology approach to study disease progression caused by <i>Heterodera glycines</i> in <i>Glycine max.</i> <i>Gene Regulation and Systems Biology</i> , 2007, 1, 17-33.	2.3	5
26543	A systems biology approach to study the phagosomal proteome modulated by mycobacterial infections. <i>International Journal of Clinical and Experimental Medicine</i> , 2009, 2, 233-47.	1.3	16
26544	Expression analysis of human pterygium shows a predominance of conjunctival and limbal markers and genes associated with cell migration. <i>Molecular Vision</i> , 2009, 15, 2421-34.	1.1	37
26545	Including Functional Annotations and Extending the Collection of Structural Classifications of Protein Loops (ArchDB). <i>Bioinformatics and Biology Insights</i> , 2009, 1, 77-90.	1.0	1
26546	Influence of sex on gene expression in human corneal epithelial cells. <i>Molecular Vision</i> , 2009, 15, 2554-69.	1.1	20
26547	Acid stress response of a mycobacterial proteome: insight from a gene ontology analysis. <i>International Journal of Clinical and Experimental Medicine</i> , 2009, 2, 309-28.	1.3	10
26550	Discovery of protein interaction networks shared by diseases. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2007, , 76-87.	0.7	25
26552	Genetrace: phenomic knowledge discovery via structured terminology. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005, , 103-14.	0.7	9
26553	PhenoGO: assigning phenotypic context to gene ontology annotations with natural language processing. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006, , 64-75.	0.7	28
26554	Semantic webs for life sciences. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006, , 112-5.	0.7	2
26557	The Pitfalls of Thesaurus Ontologization - the Case of the NCI Thesaurus. <i>AMIA ... Annual Symposium proceedings</i> , 2010, 2010, 727-31.	0.2	5
26558	Biomolecular Systems of Disease Buried Across Multiple GWAS Unveiled by Information Theory and Ontology. <i>Summit on Translational Bioinformatics</i> , 2010, 2010, 31-5.	0.7	5
26559	Modeling and characterization of disease associated subnetworks in the human interactome using machine learning. <i>Summit on Translational Bioinformatics</i> , 2009, 2009, 1-28.	0.7	0
26561	Effect of PITX2 knockdown on transcriptome of primary human trabecular meshwork cell cultures. <i>Molecular Vision</i> , 2011, 17, 1209-21.	1.1	22

#	ARTICLE	IF	CITATIONS
26562	Mixed Membership Stochastic Blockmodels. <i>Journal of Machine Learning Research</i> , 2008, 9, 1981-2014.	62.4	515
26563	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FLGlyR). <i>Standards in Genomic Sciences</i> , 2011, 4, 371-80.	1.5	4
26565	Methods, challenges, and promise of next-generation sequencing in cancer biology. <i>Yale Journal of Biology and Medicine</i> , 2011, 84, 439-46.	0.2	13
26566	Mapping annotations with textual evidence using an scLDA model. <i>AMIA ... Annual Symposium proceedings</i> , 2011, 2011, 834-42.	0.2	1
26567	Similarity-based disease risk assessment for personal genomes: proof of concept. <i>AMIA ... Annual Symposium proceedings</i> , 2011, 2011, 1524-31.	0.2	0
26568	Drug repositioning using disease associated biological processes and network analysis of drug targets. <i>AMIA ... Annual Symposium proceedings</i> , 2011, 2011, 305-11.	0.2	10
26569	Prediction of interactions between HIV-1 and human proteins by information integration. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2009, , 516-27.	0.7	45
26570	Non-housekeeping genes expressed in human trabecular meshwork cell cultures. <i>Molecular Vision</i> , 2012, 18, 241-54.	1.1	28
26571	Gaining confidence in cross-species annotation transfer: from simple molecular function to complex phenotypic traits. <i>Aspects of Applied Biology</i> , 2011, 107, 79-87.	0.0	4
26572	Predicting the effects of copy-number variation in double and triple mutant combinations. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012, , 19-30.	0.7	2
26573	Androgen regulation of gene expression in human meibomian gland and conjunctival epithelial cells. <i>Molecular Vision</i> , 2012, 18, 1055-67.	1.1	44
26575	Integrating genome and functional genomics data to reveal perturbed signaling pathways in ovarian cancers. <i>AMIA Summits on Translational Science Proceedings</i> , 2012, 2012, 72-8.	0.4	5
26577	OPIC: Ontology-driven Patient Information Capturing system for epilepsy. <i>AMIA ... Annual Symposium proceedings</i> , 2012, 2012, 799-808.	0.2	13
26579	Next-generation analysis of cataracts: determining knowledge driven gene-gene interactions using Biofilter, and gene-environment interactions using the PhenX Toolkit. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2013, , 147-58.	0.7	13
26580	Detection of protein catalytic sites in the biomedical literature. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2013, , 433-44.	0.7	6
26581	The Profile of Human Sperm Proteome; A Mini-review. <i>Journal of Reproduction and Infertility</i> , 2011, 12, 193-9.	1.0	12
26582	Non contiguous-finished genome sequence and description of <i>Peptoniphilus obesi</i> sp. nov. <i>Standards in Genomic Sciences</i> , 2013, 7, 357-69.	1.5	24
26584	THE INTERACTIVE DECISION COMMITTEE FOR CHEMICAL TOXICITY ANALYSIS. <i>Journal of Statistical Research</i> , 2012, 46, 157-186.	0.0	0

#	ARTICLE	IF	CITATIONS
26585	Dissection of complex gene expression using the combined analysis of pleiotropy and epistasis. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 200-11.	0.7	2
26586	Matrix factorization-based data fusion for gene function prediction in baker's yeast and slime mold. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 400-11.	0.7	14
26587	In silico functional profiling of individual prostate cancer tumors: many genes, few functions. Cancer Genomics and Proteomics, 2012, 9, 109-14.	1.0	2
26588	Identifying mutation specific cancer pathways using a structurally resolved protein interaction network. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 84-95.	0.7	7
26589	Biological mechanism analysis of acute renal allograft rejection: integrated of mRNA and microRNA expression profiles. International Journal of Clinical and Experimental Medicine, 2014, 7, 5170-80.	1.3	2
26590	Genomic analysis of drug resistant pancreatic cancer cell line by combining long non-coding RNA and mRNA expression profiling. International Journal of Clinical and Experimental Pathology, 2015, 8, 38-52.	0.5	18
26591	Identification of B cells participated in the mechanism of postmenopausal women osteoporosis using microarray analysis. International Journal of Clinical and Experimental Medicine, 2015, 8, 1027-34.	1.3	11
26592	Expression profile of mitogen-activated protein kinase (MAPK) signaling genes in the skeletal muscle & liver of rat with type 2 diabetes: role in disease pathology. Indian Journal of Medical Research, 2014, 140, 744-55.	0.4	1
26593	Evaluation of need for ontologies to manage domain content for the Reportable Conditions Knowledge Management System. AMIA ... Annual Symposium proceedings, 2014, 2014, 496-505.	0.2	1
26594	An empirically derived taxonomy of errors in SNOMED CT. AMIA ... Annual Symposium proceedings, 2014, 2014, 899-906.	0.2	4
26595	Biomarkers of erlotinib response in non-small cell lung cancer tumors that do not harbor the more common epidermal growth factor receptor mutations. International Journal of Clinical and Experimental Pathology, 2015, 8, 2888-98.	0.5	9
26597	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
26598	Differentially expressed genes and microRNAs in bladder carcinoma cell line 5637 and T24 detected by RNA sequencing. International Journal of Clinical and Experimental Pathology, 2015, 8, 12678-87.	0.5	17
26599	Dysregulated expression of microRNAs and mRNAs in myocardial infarction. American Journal of Translational Research (discontinued), 2015, 7, 2291-304.	0.0	25
26600	Differences in gene expression profiles and signaling pathways in rhabdomyolysis-induced acute kidney injury. International Journal of Clinical and Experimental Pathology, 2015, 8, 14087-98.	0.5	6
26601	SEPARATING THE CAUSES AND CONSEQUENCES IN DISEASE TRANSCRIPTOME. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 381-92.	0.7	0
26603	Drug-drug Interaction Discovery Using Abstraction Networks for "National Drug File - Reference Terminology" Chemical Ingredients. AMIA ... Annual Symposium proceedings, 2015, 2015, 973-82.	0.2	7
26604	Successful establishment of patient-derived tumor xenografts from gastrointestinal stromal tumor-a single center experience. American Journal of Cancer Research, 2016, 6, 533-43.	1.4	0

#	ARTICLE	IF	CITATIONS
26606	Transient resistance to DNA damaging agents is associated with expression of microRNAs-135b and -196b in human leukemia cell lines. <i>International Journal of Biochemistry and Molecular Biology</i> , 2016, 7, 27-47.	0.1	11
26607	Ion Channel ElectroPhysiology Ontology (ICEPO) - a case study of text mining assisted ontology development. <i>AMIA Summits on Translational Science Proceedings</i> , 2016, 2016, 42-51.	0.4	0
26608	Community-based Ontology Development, Annotation and Discussion with MediaWiki extension Ontokiwi and Ontokiwi-based Ontobedia. <i>AMIA Summits on Translational Science Proceedings</i> , 2016, 2016, 65-74.	0.4	2
26609	Discovering regulated networks during HIV-1 latency and reactivation. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006, , 354-66.	0.7	13
26610	Tracking the Remodeling of SNOMED CT's Bacterial Infectious Diseases. <i>AMIA ... Annual Symposium proceedings</i> , 2016, 2016, 974-983.	0.2	5
26611	Meta-Analysis of Gene Expression Profiles in Acute Promyelocytic Leukemia Reveals Involved Pathways. <i>International Journal of Hematology-Oncology and Stem Cell Research</i> , 2017, 11, 1-12.	0.3	8
26612	Introducing crucial protein panel of gastric adenocarcinoma disease. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2017, 10, 21-28.	0.6	13
26613	Bioinformatics and co-expression network analysis of differentially expressed lncRNAs and mRNAs in hippocampus of APP/PS1 transgenic mice with Alzheimer disease. <i>American Journal of Translational Research (discontinued)</i> , 2017, 9, 1381-1391.	0.0	13
26615	Comprehensive analysis of long non-coding RNA PVT1 gene interaction regulatory network in hepatocellular carcinoma using gene microarray and bioinformatics. <i>American Journal of Translational Research (discontinued)</i> , 2017, 9, 3904-3917.	0.0	23
26616	Quantitative proteomics analysis of mitochondrial proteins in lung adenocarcinomas and normal lung tissue using iTRAQ and tandem mass spectrometry. <i>American Journal of Translational Research (discontinued)</i> , 2017, 9, 3918-3934.	0.0	13
26617	Extracting a biologically relevant latent space from cancer transcriptomes with variational autoencoders. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018, 23, 80-91.	0.7	66
26618	Convergent downstream candidate mechanisms of independent intergenic polymorphisms between co-classified diseases implicate epistasis among noncoding elements. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018, 23, 524-535.	0.7	1
26619	Single subject transcriptome analysis to identify functionally signed gene set or pathway activity. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018, 23, 400-411.	0.7	1
26620	Emergence of pathway-level composite biomarkers from converging gene set signals of heterogeneous transcriptomic responses. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018, 23, 484-495.	0.7	7
26621	MIRNA Signaling in Viral Myocarditis Novel and Unique Pathological Features. <i>Acta Cardiologica Sinica</i> , 2018, 34, 77-86.	0.1	1
26622	Annotating gene sets by mining large literature collections with protein networks. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018, 23, 602-613.	0.7	6
26623	The chemokine receptor CCR1 is identified in mast cell-derived exosomes. <i>American Journal of Translational Research (discontinued)</i> , 2018, 10, 352-367.	0.0	14
26624	Evaluation of involved proteins in colon adenocarcinoma: an interactome analysis. <i>Gastroenterology and Hepatology From Bed To Bench</i> , 2017, 10, S129-S138.	0.6	6

#	ARTICLE	IF	CITATIONS
26625	Leveraging Collaborative Filtering to Accelerate Rare Disease Diagnosis. AMIA ... Annual Symposium proceedings, 2017, 2017, 1554-1563.	0.2	11
26626	Deep Learning Meets Biomedical Ontologies: Knowledge Embeddings for Epilepsy. AMIA ... Annual Symposium proceedings, 2017, 2017, 1233-1242.	0.2	7
26627	The Ontology of Biological and Clinical Statistics (OBCS)-based statistical method standardization and meta-analysis of host responses to yellow fever vaccines. Quantitative Biology, 2017, 5, 291-301.	0.3	2
26628	A comprehensive investigation using meta-analysis and bioinformatics on miR-34a-5p expression and its potential role in head and neck squamous cell carcinoma. American Journal of Translational Research (discontinued), 2018, 10, 2246-2263.	0.0	5
26629	Transcriptomic profile analysis of brain microvascular pericytes in spontaneously hypertensive rats by RNA-Seq. American Journal of Translational Research (discontinued), 2018, 10, 2372-2386.	0.0	13
26630	PRECISION MEDICINE: FROM DIPTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 389-399.	0.7	1
26631	EFNB2 acts as the target of miR-557 to facilitate cell proliferation, migration and invasion in pancreatic ductal adenocarcinoma by bioinformatics analysis and verification. American Journal of Translational Research (discontinued), 2018, 10, 3514-3528.	0.0	11
26632	Barrett's esophagus network analysis revealed that arginine, alanine, aspartate, glutamate, valine, leucine and isoleucine can be biomarkers. Gastroenterology and Hepatology From Bed To Bench, 2018, 11, S98-S104.	0.6	1
26633	FAIRness and Usability for Open-access Omics Data Systems. AMIA ... Annual Symposium proceedings, 2018, 2018, 232-241.	0.2	7
26634	How Sustainable are Biomedical Ontologies?. AMIA ... Annual Symposium proceedings, 2018, 2018, 470-479.	0.2	1
26635	Overlapping Complex Concepts Have More Commission Errors, Especially in Intensive Terminology Auditing. AMIA ... Annual Symposium proceedings, 2018, 2018, 1157-1166.	0.2	0
26636	SNPs2ChIP: Latent Factors of ChIP-seq to infer functions of non-coding SNPs. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 184-195.	0.7	0
26637	Precision drug repurposing via convergent eQTL-based molecules and pathway targeting independent disease-associated polymorphisms. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 308-319.	0.7	5
26638	Protein-Protein Interaction Analysis of Common Top Genes in Obsessive-Compulsive Disorder (OCD) and Schizophrenia: Towards New Drug Approach Obsessive-Compulsive disorder (OCD) and Schizophrenia Comorbidity Gene Analysis. Iranian Journal of Pharmaceutical Research, 2018, 17, 173-186.	0.3	9
26639	Protein Interaction Mapping related to Becker Muscular Dystrophy. Iranian Journal of Child Neurology, 2019, 13, 125-134.	0.2	1
26640	Buyang Huanwu Tang alleviates inflammation and improves motor endplate functions in DSMA rat models by activating several biological molecules and associated signaling pathways. American Journal of Translational Research (discontinued), 2019, 11, 3056-3068.	0.0	2
26641	RNA sequencing profiling of the retina in C57BL/6J and DBA/2J mice: Enhancing the retinal microarray data sets from GeneNetwork. Molecular Vision, 2019, 25, 345-358.	1.1	13
26642	Replication and transcriptionomic analysis of human noroviruses in human intestinal enteroids. American Journal of Translational Research (discontinued), 2019, 11, 3365-3374.	0.0	8

#	ARTICLE	IF	CITATIONS
26643	Detecting the long non-coding RNA signature related to spinal cord ependymal tumor subtype using a genome-wide methylome analysis approach. <i>Molecular Medicine Reports</i> , 2019, 20, 1531-1540.	1.1	2
26646	Identification of potential core genes in metastatic renal cell carcinoma using bioinformatics analysis. <i>American Journal of Translational Research (discontinued)</i> , 2019, 11, 6812-6825.	0.0	4
26647	From genome to phenome: Predicting multiple cancer phenotypes based on somatic genomic alterations via the genomic impact transformer. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2020, 25, 79-90.	0.7	7
26648	Exploring Relationships between the Density of Charged Tracts within Disordered Regions and Phase Separation. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2020, 25, 207-218.	0.7	0
26649	Bioinformatic analysis of differential expression and core GENEs in breast cancer. <i>International Journal of Clinical and Experimental Pathology</i> , 2018, 11, 1146-1156.	0.5	3
26650	Effects of prenatal hypoxia on fetal sheep heart development and proteomics analysis. <i>International Journal of Clinical and Experimental Pathology</i> , 2018, 11, 1909-1922.	0.5	1
26651	Whole Genome Analysis of the Red-Crowned Crane Provides Insight into Avian Longevity. <i>Molecules and Cells</i> , 2020, 43, 86-95.	1.0	6
26652	Gambogenic acid exerts anticancer effects in cisplatin-resistant non-small cell lung cancer cells. <i>Molecular Medicine Reports</i> , 2020, 21, 1267-1275.	1.1	7
26653	Tip of the iceberg: roles of circRNAs in hematological malignancies. <i>American Journal of Cancer Research</i> , 2020, 10, 367-382.	1.4	5
26654	Impaired Metabolic Pathways Related to Colorectal Cancer Progression and Therapeutic Implications. <i>Iranian Journal of Public Health</i> , 2020, 49, 56-67.	0.3	0
26655	Identification of biomarkers for the transition from low-grade glioma to secondary glioblastoma by an integrated bioinformatic analysis. <i>American Journal of Translational Research (discontinued)</i> , 2020, 12, 1222-1238.	0.0	3
26656	Comprehensive identification of a two-genesignature as a novel potential prognostic model for patients with medulloblastoma. <i>American Journal of Translational Research (discontinued)</i> , 2020, 12, 1600-1613.	0.0	1
26657	Identification of transcriptomic markers for developing idiopathic pulmonary fibrosis: an integrative analysis of gene expression profiles. <i>International Journal of Clinical and Experimental Pathology</i> , 2020, 13, 1698-1706.	0.5	4
26658	Phenotypic Analysis of Clinical Narratives Using Human Phenotype Ontology. <i>Studies in Health Technology and Informatics</i> , 2017, 245, 581-585.	0.2	14
26659	Identification and validation of novel metastasis-related signatures of clear cell renal cell carcinoma using gene expression databases. <i>American Journal of Translational Research (discontinued)</i> , 2020, 12, 4108-4126.	0.0	4
26660	Association of tricellulin expression with poor colorectal cancer prognosis and metastasis. <i>Oncology Reports</i> , 2020, 44, 2174-2184.	1.2	0
26661	The efficacy of chemotherapeutic drug combinations may be predicted by concordance of gene response to the single agents. <i>Oncology Letters</i> , 2020, 20, 321.	0.8	0
26662	Towards a foundational representation of potential drug-drug interaction knowledge. <i>CEUR Workshop Proceedings</i> , 2014, 1309, 16-31.	2.3	3

#	ARTICLE	IF	CITATIONS
26663	Using mRNA deep sequencing to analyze differentially expressed genes during <i>Panax notoginseng</i> saponin treatment of ischemic stroke. <i>Molecular Medicine Reports</i> , 2020, 22, 4743-4753.	1.1	0
26664	Integrated microarray analysis of key genes and a miRNA-mRNA regulatory network of early-onset preeclampsia. <i>Molecular Medicine Reports</i> , 2020, 22, 4772-4782.	1.1	0
26665	Upregulated lncHRK2:1 prompts nucleus pulposus cell senescence in intervertebral disc degeneration. <i>Molecular Medicine Reports</i> , 2020, 22, 5251-5261.	1.1	1
26666	Integrated Bioinformatics Analysis of Hub Genes and Pathways Associated with a Compression Model of Spinal Cord Injury in Rats. <i>Medical Science Monitor</i> , 2020, 26, e927107.	0.5	3
26667	aTEMPO: Pathway-Specific Temporal Anomalies for Precision Therapeutics. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2020, 25, 683-694.	0.7	0
26668	Exploring biomarkers and therapeutic targets for pressure overload induced heart failure based on microarray data. <i>Cardiovascular Diagnosis and Therapy</i> , 2020, 10, 1226-1237.	0.7	0
26669	Identification of Dysregulated Genes for Late-Onset Alzheimer's Disease Using Gene Expression Data in Brain. , 2020, 10, .		0
26670	Free Wanderer Powder regulates AMPA receptor homeostasis in chronic restraint stress-induced rat model of depression with liver-depression and spleen-deficiency syndrome. <i>Aging</i> , 2020, 12, 19563-19584.	1.4	1
26671	Semantic Relations in Compound Nouns: Perspectives from Inter-Annotator Agreement. <i>Studies in Health Technology and Informatics</i> , 2017, 245, 644-648.	0.2	3
26672	ENPP4 overexpression is associated with no recovery from Barrett's esophagus. <i>International Journal of Clinical and Experimental Pathology</i> , 2020, 13, 2927-2936.	0.5	0
26673	Integrated bioinformatic analysis identifies COL4A3, COL4A4, and KCNJ1 as key biomarkers in Wilms tumor. <i>International Journal of Clinical and Experimental Pathology</i> , 2021, 14, 196-208.	0.5	0
26674	Predicting Tumor Cell Response to Synergistic Drug Combinations Using a Novel Simplified Deep Learning Model. <i>AMIA ... Annual Symposium proceedings</i> , 2020, 2020, 1364-1372.	0.2	3
26675	Laryngeal squamous cell carcinoma cell lines show high tolerance for siRNA-mediated CDK1 knockdown. <i>American Journal of Cancer Research</i> , 2021, 11, 2081-2094.	1.4	1
26676	SERPINH1, Targeted by miR-29b, Modulated Proliferation and Migration of Human Retinal Endothelial Cells Under High Glucose Conditions. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2021, 14, 3471-3483.	1.1	1
26677	Foundations for a Realism-Based Ontology of Protein Aggregates. <i>CEUR Workshop Proceedings</i> , 2020, 2807, K1-K10.	2.3	0
26678	Ovarian Cancer Immunogenicity is Governed by a Narrow Subset of Progenitor Tissue-Resident Memory T-Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
26679	Systems biology and big data analytics. , 2022, , 425-442.		0
26680	RNA-seq for revealing the function of the transcriptome. , 2022, , 105-129.		3

#	ARTICLE	IF	CITATIONS
26681	Transcriptomic profiling of the floral fragrance biosynthesis pathway of <i>Liriodendron</i> and functional characterization of the <i>LtuDXR</i> gene. <i>Plant Science</i> , 2022, 314, 111124.	1.7	6
26682	Gene Ontology: application and importance in functional annotation of the genomic data. , 2022, , 145-157.		0
26683	Systems biomarkers for papillary thyroid cancer prognosis and treatment through multi-omics networks. <i>Archives of Biochemistry and Biophysics</i> , 2022, 715, 109085.	1.4	18
26684	Oleaginous microbes: potential and challenges from waste-to-energy conversion. , 2022, , 221-244.		0
26685	Identification of key genes involved in recovery from spinal cord injury in adult zebrafish. <i>Neural Regeneration Research</i> , 2022, 17, 1334.	1.6	5
26686	Current trends in algal biotechnology for the generation of sustainable biobased products. , 2022, , 213-239.		1
26687	Molecular mechanism of GANT61 combined with doxorubicin in the treatment of gliomas based on network pharmacology. <i>Electronic Journal of Biotechnology</i> , 2022, 55, 18-26.	1.2	0
26688	Genomic characterization and pathogenicity analysis of the <i>Vibrio mimicus</i> Y4 causing red body disease in <i>Macrobrachium nipponense</i> . <i>Aquaculture</i> , 2022, 548, 737701.	1.7	9
26689	Screening of probiotics with efficient α -glucosidase inhibitory ability and study on the structure and function of its extracellular polysaccharide. <i>Food Bioscience</i> , 2022, 45, 101452.	2.0	3
26690	Extracellular vesicles-derived microRNAs expression as biomarkers for neurological radiation injury: Risk assessment for space exploration. <i>Life Sciences in Space Research</i> , 2022, 32, 54-62.	1.2	6
26692	Forecasting Tools in Practical Applications: Selection and Evaluation Methodology. , 2021, , .		0
26693	Bioinformatics analysis of SARS-CoV-2 infection-associated immune injury and therapeutic prediction for COVID-19. <i>Emergency and Critical Care Medicine</i> , 2021, 1, 20-28.	0.1	0
26694	Maternal immune activation downregulates schizophrenia genes in the foetal mouse brain. <i>Brain Communications</i> , 2021, 3, fcab275.	1.5	10
26695	Small RNA sequencing reveals various microRNAs involved in piperine biosynthesis in black pepper (<i>Piper nigrum</i> L.). <i>BMC Genomics</i> , 2021, 22, 838.	1.2	6
26696	Integrated Strategy of UHPLC-Q-TOF-MS and Molecular Networking for Identification of Diterpenoids from <i>Euphorbia fischeriana</i> Steud. and Prediction of the Anti-Breast-Cancer Mechanism by the Network Pharmacological Method. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-19.	0.5	1
26697	Bioinformatic Analysis Identified Hub Genes Associated with Heterocyclic Amines Induced Cytotoxicity of Peripheral Blood Mononuclear Cells. <i>Genes</i> , 2021, 12, 1888.	1.0	4
26698	Quantitative Proteomic Analysis of Mouse Sciatic Nerve Reveals Post-injury Upregulation of ADP-Dependent Glucokinase Promoting Macrophage Phagocytosis. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 777621.	1.4	4
26699	Dynamic Urinary Proteome Changes in Ovalbumin-Induced Asthma Mouse Model Using Data-Independent Acquisition Proteomics. <i>Journal of Asthma and Allergy</i> , 2021, Volume 14, 1355-1366.	1.5	2

#	ARTICLE	IF	CITATIONS
26701	Pathway Enrichment Analysis of Microarray Data From Human Penis of Diabetic and Peyronie's™s Patients, in Comparison with Diabetic Rat Erectile Dysfunction Models. <i>Journal of Sexual Medicine</i> , 2022, 19, 37-53.	0.3	5
26703	Quantitative Analysis of the Cardiac Phosphoproteome in Response to Acute β^2 -Adrenergic Receptor Stimulation In Vivo. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12584.	1.8	4
26704	Dietary palmitic acid promotes a prometastatic memory via Schwann cells. <i>Nature</i> , 2021, 599, 485-490.	13.7	126
26705	A Novel Single-Cell RNA Sequencing Data Feature Extraction Method Based on Gene Function Analysis and Its Applications in Glioma Study. <i>Frontiers in Oncology</i> , 2021, 11, 797057.	1.3	1
26706	BOLD: an ontology-based log debugger for C programs. <i>Automated Software Engineering</i> , 2022, 29, 1.	2.2	1
26707	The importance of automation in genetic diagnosis: Lessons from analyzing an inherited retinal degeneration cohort with the Mendelian Analysis Toolkit (MATK). <i>Genetics in Medicine</i> , 2022, 24, 332-343.	1.1	7
26708	Regeneration of Planarian Auricles and Reestablishment of Chemotactic Ability. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 777951.	1.8	1
26710	Glutathione, carbohydrate and other metabolites of <i>Larix olgensis</i> A. Henry response to polyethylene glycol-simulated drought stress. <i>PLoS ONE</i> , 2021, 16, e0253780.	1.1	6
26711	Asc-Seurat: analytical single-cell Seurat-based web application. <i>BMC Bioinformatics</i> , 2021, 22, 556.	1.2	23
26712	The differentiation state of the Schwann cell progenitor drives phenotypic variation between two contagious cancers. <i>PLoS Pathogens</i> , 2021, 17, e1010033.	2.1	3
26713	Effects of dietary protein levels on growth performance and liver transcriptome changes in juvenile top-mouth culter <i>Erythroculter ilishaeformis</i> . <i>Aquaculture Reports</i> , 2021, 21, 100964.	0.7	5
26715	Gene expression and epigenetic responses of the marine Cladoceran, <i>Evadne nordmanni</i> , and the copepod, <i>Acartia clausi</i> , to elevated CO ₂ . <i>Ecology and Evolution</i> , 2021, 11, 16776-16785.	0.8	6
26716	Categorizing Sequences of Concern by Function To Better Assess Mechanisms of Microbial Pathogenesis. <i>Infection and Immunity</i> , 2022, 90, IAI0033421.	1.0	8
26717	Quantitative high-confidence human mitochondrial proteome and its dynamics in cellular context. <i>Cell Metabolism</i> , 2021, 33, 2464-2483.e18.	7.2	113
26718	A chromosomal level genome sequence for <i>Quasipaa spinosa</i> (Dicroglossidae) reveals chromosomal evolution and population diversity. <i>Molecular Ecology Resources</i> , 2022, 22, 1545-1558.	2.2	3
26720	Landscape genomics of the streamside salamander: Implications for species management in the face of environmental change. <i>Evolutionary Applications</i> , 2022, 15, 220-236.	1.5	4
26721	RNfuzzyApp: an R shiny RNA-seq data analysis app for visualisation, differential expression analysis, time-series clustering and enrichment analysis. <i>F1000Research</i> , 0, 10, 654.	0.8	1
26723	The Prescription of Drug Ontology 2.0 (PDRO): More Than the Sum of Its Parts. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 12025.	1.2	4

#	ARTICLE	IF	CITATIONS
26724	Phosphoproteomic Comparison of Four <i>Eimeria tenella</i> Life Cycle Stages. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12110.	1.8	6
26725	Starvation to Glucose Reprograms Development of Neurovascular Unit in Embryonic Retinal Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 726852.	1.8	3
26726	Construction of a single nucleotide variant score-related gene-based prognostic model in hepatocellular carcinoma: analysis of multi-independent databases and validation in vitro. <i>Cancer Cell International</i> , 2021, 21, 610.	1.8	2
26727	Altered cell and RNA isoform diversity in aging Down syndrome brains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	38
26728	Genome-wide map of N6-methyladenosine circular RNAs identified in mice model of severe acute pancreatitis. <i>World Journal of Gastroenterology</i> , 2021, 27, 7530-7545.	1.4	6
26729	Follicular T cells are clonally and transcriptionally distinct in B cell-driven mouse autoimmune disease. <i>Nature Communications</i> , 2021, 12, 6687.	5.8	12
26730	Identification of Impacted Pathways and Transcriptomic Markers as Potential Mediators of Pulmonary Fibrosis in Transgenic Mice Expressing Human IGFBP5. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12609.	1.8	5
26731	Bone marrow sinusoidal endothelium controls terminal erythroid differentiation and reticulocyte maturation. <i>Nature Communications</i> , 2021, 12, 6963.	5.8	14
26732	Neurogenetics of dynamic connectivity patterns associated with obsessive-compulsive symptoms in healthy children. <i>Biological Psychiatry Global Open Science</i> , 2021, , .	1.0	2
26733	GoVec: Gene Ontology Representation Learning Using Weighted Heterogeneous Graph and Meta-Path. <i>Journal of Computational Biology</i> , 2021, 28, 1196-1207.	0.8	2
26734	Plasma Cell-Free DNA Methylomics of Bipolar Disorder With and Without Rapid Cycling. <i>Frontiers in Neuroscience</i> , 2021, 15, 774037.	1.4	4
26735	Picture word order compound protein interaction: Predicting compound protein interaction using structural images of compounds. <i>Journal of Computational Chemistry</i> , 2021, 43, 255.	1.5	5
26736	Development of an Oxidative Phosphorylation-Related and Immune Microenvironment Prognostic Signature in Uterine Corpus Endometrial Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 753004.	1.8	11
26737	Hepatectomy-Induced Alterations in Hepatic Perfusion and Function - Toward Multi-Scale Computational Modeling for a Better Prediction of Post-hepatectomy Liver Function. <i>Frontiers in Physiology</i> , 2021, 12, 733868.	1.3	21
26739	Integration of transcriptomics and network analysis reveals co-expressed genes in <i>Frankliniella occidentalis</i> larval guts that respond to tomato spotted wilt virus infection. <i>BMC Genomics</i> , 2021, 22, 810.	1.2	9
26740	Cross-validation of SARS-CoV-2 responses in kidney organoids and clinical populations. <i>JCI Insight</i> , 2021, 6, .	2.3	21
26741	Expression Signatures of Long Noncoding RNAs in Left Ventricular Noncompaction. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 763858.	1.1	0
26742	Comparative Transcriptomics and Gene Knockout Reveal Virulence Factors of <i>Arthrinium phaeospermum</i> in <i>Bambusa pervariabilis</i> — <i>Dendrocalamopsis grandis</i> . <i>Journal of Fungi (Basel)</i> , Tj ETQq1 1 0.784314 rgBT /@verlock		

#	ARTICLE	IF	CITATIONS
26743	The <i>Tetragnatha kauaiensis</i> Genome Sheds Light on the Origins of Genomic Novelty in Spiders. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	16
26745	Time-Resolved Extracellular Matrix Atlas of the Developing Human Skin Dermis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 783456.	1.8	8
26746	Exploring Pathway-Based Group Lasso for Cancer Survival Analysis: A Special Case of Multi-Task Learning. <i>Frontiers in Genetics</i> , 2021, 12, 771301.	1.1	1
26747	The protein-protein interaction ontology: for better representing and capturing the biological context of protein interaction. <i>BMC Genomics</i> , 2021, 22, 544.	1.2	4
26748	Identification of intrinsically disordered regions in hub genes of acute myeloid leukemia: A bioinformatics approach. <i>Biotechnology and Applied Biochemistry</i> , 2022, 69, 2304-2322.	1.4	2
26749	Titanium with nanotopography attenuates the osteoclast-induced disruption of osteoblast differentiation by regulating histone methylation. <i>Materials Science and Engineering C</i> , 2022, 134, 112548.	3.8	10
26750	Inhibition of the renin-angiotensin system causes concentric hypertrophy of renal arterioles in mice and humans. <i>JCI Insight</i> , 2021, 6, .	2.3	16
26751	Chromosome-Scale Reference Genome of <i>Amphicarpaea edgeworthii</i> : A New Resource for Amphicarpic Plants Research and Complex Flowering Pattern. <i>Frontiers in Plant Science</i> , 2021, 12, 770660.	1.7	3
26752	Transcriptome and metabolome analysis to reveal major genes of saikosaponin biosynthesis in <i>Bupleurum chinense</i> . <i>BMC Genomics</i> , 2021, 22, 839.	1.2	9
26753	Nucleolar GTPase Bms1 displaces Ttf1 from RFB-sites to balance progression of rDNA transcription and replication. <i>Journal of Molecular Cell Biology</i> , 2022, 13, 902-917.	1.5	4
26754	Identification of Key Deregulated RNA-Binding Proteins in Pancreatic Cancer by Meta-Analysis and Prediction of Their Role as Modulators of Oncogenesis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 713852.	1.8	8
26755	The disease-associated proteins <i>Drosophila</i> Nab2 and Ataxin-2 interact with shared RNAs and coregulate neuronal morphology. <i>Genetics</i> , 2022, 220, .	1.2	4
26757	Identification of KIF4A as a prognostic biomarker for esophageal squamous cell carcinoma. <i>Aging</i> , 2021, 13, 24050-24070.	1.4	5
26758	Identification of Hub Gene GRIN1 Correlated with Histological Grade and Prognosis of Glioma by Weighted Gene Coexpression Network Analysis. <i>BioMed Research International</i> , 2021, 2021, 1-22.	0.9	1
26760	Genetic Evidence for Congenital Vascular Disorders in Patients with VACTERL Association. <i>European Journal of Pediatric Surgery</i> , 2022, 32, 061-066.	0.7	0
26761	Genome-Wide Identification of Long Non-Coding RNAs and Their Potential Functions in Poplar Growth and Phenylalanine Biosynthesis. <i>Frontiers in Genetics</i> , 2021, 12, 762678.	1.1	5
26764	TargetTox: A Feature Selection Pipeline for Identifying Predictive Targets Associated with Drug Toxicity. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 5386-5394.	2.5	7
26765	Inheritance of gene expression throughout fruit development in chili pepper. <i>Scientific Reports</i> , 2021, 11, 22647.	1.6	4

#	ARTICLE	IF	CITATIONS
26766	A Standardized Brain Molecular Atlas: A Resource for Systems Modeling and Simulation. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 604559.	1.4	3
26767	Prediction of Hormone-Binding Proteins Based on K-mer Feature Representation and Naive Bayes. <i>Frontiers in Genetics</i> , 2021, 12, 797641.	1.1	6
26768	Transcription Factors Active in the Anterior Blastema of <i>Schmidtea mediterranea</i> . <i>Biomolecules</i> , 2021, 11, 1782.	1.8	4
26769	A data-driven framework for mapping domains of human neurobiology. <i>Nature Neuroscience</i> , 2021, 24, 1733-1744.	7.1	29
26770	Identification of miRNA-mRNA network and immune-related gene signatures in IgA nephropathy by integrated bioinformatics analysis. <i>BMC Nephrology</i> , 2021, 22, 392.	0.8	8
26774	Undervalued Pseudo- <i>nifH</i> Sequences in Public Databases Distort Metagenomic Insights into Biological Nitrogen Fixers. <i>MSphere</i> , 2021, 6, e0078521.	1.3	17
26775	Identification, Analysis, and Confirmation of Seed Storability-Related Loci in Dongxiang Wild Rice (<i>Oryza rufipogon</i> Griff.). <i>Genes</i> , 2021, 12, 1831.	1.0	5
26776	Comprehensive Transcriptomic Profiling of Murine Osteoclast Differentiation Reveals Novel Differentially Expressed Genes and LncRNAs. <i>Frontiers in Genetics</i> , 2021, 12, 781272.	1.1	8
26777	Early Treatment With a Single Dose of Mesenchymal Stem Cell Derived Extracellular Vesicles Modulates the Brain Transcriptome to Create Neuroprotective Changes in a Porcine Model of Traumatic Brain Injury and Hemorrhagic Shock. <i>Shock</i> , 2022, 57, 281-290.	1.0	7
26778	Inferred expression regulator activities suggest genes mediating cardiometabolic genetic signals. <i>PLoS Computational Biology</i> , 2021, 17, e1009563.	1.5	3
26779	Toll-Like Receptor (TLR) Signaling Enables Cyclic GMP-AMP Synthase (cGAS) Sensing of HIV-1 Infection in Macrophages. <i>MBio</i> , 2021, 12, e0281721.	1.8	13
26780	APOBEC Mutagenesis Inhibits Breast Cancer Growth through Induction of T cell-Mediated Antitumor Immune Responses. <i>Cancer Immunology Research</i> , 2022, 10, 70-86.	1.6	20
26782	LIMD2 is a Prognostic and Predictive Marker in Patients With Esophageal Cancer Based on a ceRNA Network Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 774432.	1.1	5
26783	The Alimant to Bodily Condition knowledgebase (ABCKb): a database connecting plants and human health. <i>BMC Research Notes</i> , 2021, 14, 433.	0.6	1
26784	Comprehensive Analysis of the Transcriptome-Wide m6A Methylation Modification Difference in Liver Fibrosis Mice by High-Throughput m6A Sequencing. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 767051.	1.8	22
26785	Insights into the molecular basis of a yellow leaf color mutant (ym) in tomato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgBT _{1.7} /Overlock 10 Tf 501	1.7	9
26786	Transcriptomic responses to drought stress in <i>Polygonatum kingianum</i> tuber. <i>BMC Plant Biology</i> , 2021, 21, 537.	1.6	7
26788	Hundreds of LncRNAs Display Circadian Rhythmicity in Zebrafish Larvae. <i>Cells</i> , 2021, 10, 3173.	1.8	1

#	ARTICLE	IF	CITATIONS
26789	Development and Validation of a Prognostic N6-Methyladenosine-Related Immune Gene Signature for Lung Adenocarcinoma. <i>Pharmacogenomics and Personalized Medicine</i> , 2021, Volume 14, 1549-1563.	0.4	5
26790	Circ-Usp10 promotes microglial activation and induces neuronal death by targeting miRNA-152-5p/CD84. <i>Bioengineered</i> , 2021, 12, 10812-10822.	1.4	14
26791	A proximity proteomics screen in three-dimensional spheroid cultures identifies novel regulators of lumen formation. <i>Scientific Reports</i> , 2021, 11, 22807.	1.6	5
26792	Key Markers Involved in the Anticancer Response of CD8+ T Cells through the Regulation of Cholesterol Metabolism. <i>Journal of Oncology</i> , 2021, 2021, 1-11.	0.6	6
26793	MicroRNA Sequencing Analysis in Obstructive Sleep Apnea and Depression: Anti-Oxidant and MAOA-Inhibiting Effects of miR-15b-5p and miR-92b-3p through Targeting PTGS1-NF- κ B-SP1 Signaling. <i>Antioxidants</i> , 2021, 10, 1854.	2.2	10
26795	PQN-59 antagonizes microRNA-mediated repression during post-embryonic temporal patterning and modulates translation and stress granule formation in <i>C. elegans</i> . <i>PLoS Genetics</i> , 2021, 17, e1009599.	1.5	5
26797	Chronic pathophysiological changes in the normal brain parenchyma caused by radiotherapy accelerate glioma progression. <i>Scientific Reports</i> , 2021, 11, 22110.	1.6	4
26798	Web-based transcriptome analysis determines a sixteen-gene signature and associated drugs on hearing loss patients: A bioinformatics approach. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e24065.	0.9	6
26800	Heterogeneous recruitment abilities to RNA polymerases generate nonlinear scaling of gene expression with cell volume. <i>Nature Communications</i> , 2021, 12, 6852.	5.8	16
26801	The Pharmacological Mechanism of Guchangzhixie Capsule Against Experimental Colitis. <i>Frontiers in Pharmacology</i> , 2021, 12, 762603.	1.6	5
26802	Grundlagen und Anwendungen von KI. <i>Wissenschaftsethik Und Technikfolgenbeurteilung</i> , 2022, , 13-42.	0.8	1
26803	Proteome-Scale Drug-Target Interaction Predictions: Approaches and Applications. <i>Current Protocols</i> , 2021, 1, e302.	1.3	7
26804	Development of a chemogenomics library for phenotypic screening. <i>Journal of Cheminformatics</i> , 2021, 13, 91.	2.8	5
26805	Identification of transcriptomics biomarkers for the early prediction of the prognosis of septic shock from pneumopathies. <i>BMC Infectious Diseases</i> , 2021, 21, 1190.	1.3	4
26806	Gene expression profiles and pathway enrichment analysis to identification of differentially expressed gene and signaling pathways in epithelial ovarian cancer based on high-throughput RNA-seq data. <i>Genomics</i> , 2022, 114, 161-170.	1.3	13
26807	Potential Regulatory Role of lncRNA-miRNA-mRNA in Coronary Artery Disease (CAD). <i>International Heart Journal</i> , 2021, 62, 1369-1378.	0.5	3
26808	Pan-genome Analyses of 3 Strains of <i>Inonotus obliquus</i> and Prediction of Polysaccharide and Terpenoid Genes. <i>Natural Product Communications</i> , 2021, 16, 1934578X2110609.	0.2	0
26811	Quantitative dissection of multilocus pathogenic variation in an Egyptian infant with severe neurodevelopmental disorder resulting from multiple molecular diagnoses. <i>American Journal of Medical Genetics, Part A</i> , 2022, 188, 735-750.	0.7	14

#	ARTICLE	IF	CITATIONS
26812	Analysis of Serum Biochemical Indexes, Egg Quality, and Liver Transcriptome in Laying Hens Fed Diets Supplemented with <i>Gynostemma pentaphyllum</i> Powder. <i>Genes</i> , 2021, 12, 1942.	1.0	2
26813	Chloroxylenol at environmental concentrations can promote conjugative transfer of antibiotic resistance genes by multiple mechanisms. <i>Science of the Total Environment</i> , 2022, 816, 151599.	3.9	19
26814	Pyroptosis-related gene mediated modification patterns and immune cell infiltration landscapes in cutaneous melanoma to aid immunotherapy. <i>Aging</i> , 2021, 13, 24379-24401.	1.4	12
26815	T2-DAG: a powerful test for differentially expressed gene pathways via graph-informed structural equation modeling. <i>Bioinformatics</i> , 2022, 38, 1005-1014.	1.8	1
26816	p300 or CBP is required for insulin-stimulated glucose uptake in skeletal muscle and adipocytes. <i>JCI Insight</i> , 2022, 7, .	2.3	3
26818	The first high-quality chromosomal genome assembly of a medicinal and edible plant <i>Arctium lappa</i> . <i>Molecular Ecology Resources</i> , 2021, , .	2.2	11
26819	Extensive mitochondrial proteome disturbance occurs during the early stages of acute myocardial ischemia. <i>Experimental and Therapeutic Medicine</i> , 2021, 23, 85.	0.8	5
26822	Avian ceca are indispensable for hindgut enteric nervous system development. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	6
26824	A Superefficient Ochratoxin A Hydrolase with Promising Potential for Industrial Applications. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0196421.	1.4	19
26825	Hub microRNAs and genes in the development of atrial fibrillation identified by weighted gene co-expression network analysis. <i>BMC Medical Genomics</i> , 2021, 14, 271.	0.7	3
26826	Linking Diabetes Mellitus with Alzheimer's Disease: Bioinformatics Analysis for the Potential Pathways and Characteristic Genes. <i>Biochemical Genetics</i> , 2022, 60, 1049-1075.	0.8	10
26827	Severe types of fetopathy are associated with changes in the serological proteome of diabetic mothers. <i>Medicine (United States)</i> , 2021, 100, e27829.	0.4	3
26828	Exosomes produced by melanoma cells significantly influence the biological properties of normal and cancer-associated fibroblasts. <i>Histochemistry and Cell Biology</i> , 2022, 157, 153-172.	0.8	17
26830	A multitask transfer learning framework for the prediction of virus-human protein-protein interactions. <i>BMC Bioinformatics</i> , 2021, 22, 572.	1.2	16
26831	Development of SSR Markers for <i>Psammochloa villosa</i> (Trin.) Bor (Poaceae), a Dominant Species in the Inner Mongolian Plateau. <i>Cytology and Genetics</i> , 2021, 55, 576-582.	0.2	0
26832	Splice-Variant Knock-Out of TGF β 2 Receptors Perturbates the Proteome of Ovarian Carcinoma Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12647.	1.8	1
26833	Circular RNA Expression and Regulation Profiling in Testicular Tissues of Immature and Mature Wandong Cattle (<i>Bos taurus</i>). <i>Frontiers in Genetics</i> , 2021, 12, 685541.	1.1	4
26835	MicroRNA Analysis of Human Stroke Brain Tissue Resected during Decompressive Craniectomy/Stroke-Ectomy Surgery. <i>Genes</i> , 2021, 12, 1860.	1.0	9

#	ARTICLE	IF	CITATIONS
26836	Improvement of Astragaloside on Spermatogenesis in Oligoasthenozoospermia Mouse Induced by Cyclophosphamide. <i>Reproductive Sciences</i> , 2022, 29, 1738-1748.	1.1	8
26837	Statistical testing in transcriptomic neuroimaging studies: A how-to and evaluation of methods assessing spatial and gene specificity. <i>Human Brain Mapping</i> , 2022, 43, 885-901.	1.9	24
26838	Automatic consistency assurance for literature-based gene ontology annotation. <i>BMC Bioinformatics</i> , 2021, 22, 565.	1.2	2
26839	Integrative genome, transcriptome, microRNA, and degradome analysis of water dropwort (<i>Oenanthe</i>) Tj ETQq1 1 0.784314 ggBT /Ov	2.9	39
26840	Development of a custom next-generation sequencing panel for the determination of bladder cancer risk in a Tunisian cohort. <i>Molecular Biology Reports</i> , 2022, 49, 1233-1258.	1.0	4
26841	RNA-seq dataset of subcutaneous adipose tissue: Transcriptional differences between obesity and healthy women. <i>Data in Brief</i> , 2021, 39, 107647.	0.5	2
26842	Identification of genes related to tipburn resistance in Chinese cabbage and preliminary exploration of its molecular mechanism. <i>BMC Plant Biology</i> , 2021, 21, 567.	1.6	4
26843	Decreased miR-940 expression can predict a negative prognosis in early-stage nonsmoking female lung adenocarcinoma. <i>Translational Lung Cancer Research</i> , 2021, 10, 4293-4302.	1.3	3
26845	AD-linked R47H- <i>TREM2</i> mutation induces disease-enhancing microglial states via AKT hyperactivation. <i>Science Translational Medicine</i> , 2021, 13, eabe3947.	5.8	55
26846	Identification of discriminative gene-level and protein-level features associated with pathogenic gain-of-function and loss-of-function variants. <i>American Journal of Human Genetics</i> , 2021, 108, 2301-2318.	2.6	21
26847	Exploring cell-specific miRNA regulation with single-cell miRNA-mRNA co-sequencing data. <i>BMC Bioinformatics</i> , 2021, 22, 578.	1.2	7
26848	Transcriptional Analysis of Maize Leaf Tissue Treated With Seaweed Extract Under Drought Stress. <i>Frontiers in Sustainable Food Systems</i> , 2021, 5, .	1.8	15
26849	Identification of copy number variation-driven molecular subtypes informative for prognosis and treatment in pancreatic adenocarcinoma of a Chinese cohort. <i>EBioMedicine</i> , 2021, 74, 103716.	2.7	14
26850	Antiviral RNA interference in disease vector (Asian longhorned) ticks. <i>PLoS Pathogens</i> , 2021, 17, e1010119.	2.1	6
26851	VectorBase.org updates: bioinformatic resources for invertebrate vectors of human pathogens and related organisms. <i>Current Opinion in Insect Science</i> , 2022, 50, 100860.	2.2	23
26852	The cold adaption profiles of <i>Pseudoalteromonas shioyasakiensis</i> D1497 from Yap trench to cope with cold. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2021, 32, e00689.	2.1	2
26853	Bronchopulmonary dysplasia and wnt pathway-associated single nucleotide polymorphisms. <i>Pediatric Research</i> , 2022, 92, 888-898.	1.1	3
26856	A genome-wide search for determinants of survival in 1926 patients with advanced colorectal cancer with follow-up in over 22,000 patients. <i>European Journal of Cancer</i> , 2021, 159, 247-258.	1.3	6

#	ARTICLE	IF	CITATIONS
26857	Macrophage-Targeted Therapy Unlocks Antitumoral Cross-talk between IFN γ -Secreting Lymphocytes and IL12-Producing Dendritic Cells. <i>Cancer Immunology Research</i> , 2022, 10, 40-55.	1.6	18
26858	Multiscale interactome analysis coupled with off-target drug predictions reveals drug repurposing candidates for human coronavirus disease. <i>Scientific Reports</i> , 2021, 11, 23315.	1.6	10
26859	Genomic and Metabolic Features of an Unexpectedly Predominant, Thermophilic, Assistant Starter Microorganism, <i>Thermus thermophilus</i> , in Chinese Inner Mongolian Cheese. <i>Foods</i> , 2021, 10, 2962.	1.9	4
26860	Integrated genome and tissue engineering enables screening of cancer vulnerabilities in physiologically relevant perfusable ex vivo cultures. <i>Biomaterials</i> , 2022, 280, 121276.	5.7	5
26861	SMAD4 target genes are part of a transcriptional network that integrates the response to BMP and SHH signaling during early limb bud patterning. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	4
26863	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
26864	Dual RNA-Seq Analysis of the Interaction Between Edible Fungus <i>Morchella sextelata</i> and Its Pathogenic Fungus <i>Paecilomyces penicillatus</i> Uncovers the Candidate Defense and Pathogenic Factors. <i>Frontiers in Microbiology</i> , 2021, 12, 760444.	1.5	6
26865	Robust deep learning model for prognostic stratification of pancreatic ductal adenocarcinoma patients. <i>IScience</i> , 2021, 24, 103415.	1.9	6
26866	Multifaceted pathomolecular mechanism of a <i>VWF</i> large deletion involved in the pathogenesis of severe VWD. <i>Blood Advances</i> , 2022, 6, 1038-1053.	2.5	4
26867	The chromosome-level genome provides insight into the molecular mechanism underlying the tortuous branch phenotype of <i>Prunus mume</i> . <i>New Phytologist</i> , 2022, 235, 141-156.	3.5	15
26868	Investigation of hub gene associated with the infection of <i>Staphylococcus aureus</i> via weighted gene co-expression network analysis. <i>BMC Microbiology</i> , 2021, 21, 329.	1.3	0
26869	Physiological and transcriptional evaluation of sweet sorghum seedlings in response to single and combined drought and salinity stress. <i>South African Journal of Botany</i> , 2022, 146, 459-471.	1.2	10
26870	A Survey on Event Extraction for Natural Language Understanding: Riding the Biomedical Literature Wave. <i>IEEE Access</i> , 2021, 9, 160721-160757.	2.6	17
26871	Bacterial membrane vesicles and phages in blood after consumption of <i>Lactisphaera</i> rhamnosus JB-1. <i>Gut Microbes</i> , 2021, 13, 1993583.	4.3	15
26873	Screening and bioinformatics analysis of key biomarkers in acute myocardial infarction. <i>Pteridines</i> , 2021, 32, 79-92.	0.5	3
26874	Construction of a miRNA-mRNA-TFs Network Related to Diabetic Nephropathy. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
26876	Interferon- γ Resistance and Immune Evasion in Glioma Develop via Notch-Regulated Co-Evolution of Malignant and Immune Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
26877	Towards Robust Knowledge Graph Embedding via Multi-Task Reinforcement Learning. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2023, 35, 4321-4334.	4.0	3

#	ARTICLE	IF	CITATIONS
26878	A Sub-Sequence Based Approach to Protein Function Prediction via Multi-Attention Based Multi-Aspect Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	8
26879	Federating Scholarly Infrastructures with GraphQL. <i>Lecture Notes in Computer Science</i> , 2021, , 308-324.	1.0	4
26880	Circulating Monocytes Associated with Anti-PD-1 Resistance in Human Biliary Cancer Induce T Cell Paralysis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
26881	Analysis of a circRNA-, miRNA-, and mRNA-associated ceRNA network reveals potential biomarkers in preeclampsia a ceRNA network in preeclampsia. <i>Annals of Medicine</i> , 2021, 53, 2354-2364.	1.5	5
26882	A Conceptual Model-Based Approach to Improve the Representation and Management of Omics Data in Precision Medicine. <i>IEEE Access</i> , 2021, 9, 154071-154085.	2.6	10
26883	RNA profiles reveal signatures of future health and disease in pregnancy. <i>Nature</i> , 2022, 601, 422-427.	13.7	90
26884	Catalytic Cycling of Human Mitochondrial Lon Protease. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
26885	Binding Pattern Reconstructions of FGF-FGFR Budding-Inducing Signaling in Reef-Building Corals. <i>Frontiers in Physiology</i> , 2021, 12, 759370.	1.3	4
26886	Scenes From Tick Physiology: Proteins of Sialome Talk About Their Biological Processes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 767845.	1.8	3
26887	Screening and analysis of RNAs associated with activated memory CD4 and CD8 T cells in liver cancer. <i>World Journal of Surgical Oncology</i> , 2022, 20, 2.	0.8	7
26888	Comparative Secretome Analyses of Trichoderma/Arabidopsis Co-cultures Identify Proteins for Salt Stress, Plant Growth Promotion, and Root Colonization. <i>Frontiers in Ecology and Evolution</i> , 2022, 9, .	1.1	4
26889	Guanxin V Acts as an Antioxidant in Ventricular Remodeling. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 778005.	1.1	6
26890	Structure-function relationships of the disease-linked A218T oxytocin receptor variant. <i>Molecular Psychiatry</i> , 2022, 27, 907-917.	4.1	17
26891	An Integrative Sialomic Analysis Reveals Molecules From <i>Triatoma sordida</i> (Hemiptera: Reduviidae). <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 798924.	1.8	3
26892	Bioinformatic Analysis of Coexpressed Differentially Expressed Genes and Potential Targets for Intracerebral and Subarachnoid Hemorrhage. <i>World Neurosurgery</i> , 2022, 159, e442-e452.	0.7	2
26893	De novo Transcriptome Assembly of <i>Senna occidentalis</i> Sheds Light on the Anthraquinone Biosynthesis Pathway. <i>Frontiers in Plant Science</i> , 2021, 12, 773553.	1.7	4
26894	Screening and Identification of Key Biomarkers in Lower Grade Glioma via Bioinformatical Analysis. <i>Applied Bionics and Biomechanics</i> , 2022, 2022, 1-12.	0.5	4
26895	Thirteen Independent Genetic Loci Associated with Preserved Processing Speed in a Study of Cognitive Resilience in 330,097 Individuals in the UK Biobank. <i>Genes</i> , 2022, 13, 122.	1.0	3

#	ARTICLE	IF	CITATIONS
26896	Transcriptomic analysis of <i>Pseudomonas ogarae</i> F113 reveals the antagonistic roles of AmrZ and FleQ during rhizosphere adaption. <i>Microbial Genomics</i> , 2022, 8, .	1.0	6
26898	Breaking the ageing paradigm in endometrium: endometrial gene expression related to cilia and ageing hallmarks in women over 35 years. <i>Human Reproduction</i> , 2022, 37, 762-776.	0.4	23
26899	Identification of the pivotal role of SPP1 in kidney stone disease based on multiple bioinformatics analysis. <i>BMC Medical Genomics</i> , 2022, 15, 7.	0.7	7
26901	A simple guide to <i>de novo</i> transcriptome assembly and annotation. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	42
26902	IL-17 Pathway Members as Potential Biomarkers of Effective Systemic Treatment and Cardiovascular Disease in Patients with Moderate-to-Severe Psoriasis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 555.	1.8	13
26903	Antigen presentation and interferon signatures in B cells driven by localized ablative cancer immunotherapy correlate with extended survival. <i>Theranostics</i> , 2022, 12, 639-656.	4.6	8
26904	Revisiting the grammar of Tau aggregation and pathology formation: how new insights from brain pathology are shaping how we study and target Tauopathies. <i>Chemical Society Reviews</i> , 2022, 51, 513-565.	18.7	68
26905	oCEM: Automatic detection and analysis of overlapping co-expressed gene modules. <i>BMC Genomics</i> , 2022, 23, 39.	1.2	3
26906	Robust normalization and transformation techniques for constructing gene coexpression networks from RNA-seq data. <i>Genome Biology</i> , 2022, 23, 1.	3.8	69
26907	The Chromosome-Level Genome of Miracle Fruit (<i>Synsepalum dulcificum</i>) Provides New Insights Into the Evolution and Function of Miraculin. <i>Frontiers in Plant Science</i> , 2021, 12, 804662.	1.7	4
26908	Combined Histo-endoscopic Remission but not Endoscopic Healing Alone in Ulcerative Colitis is Associated with a Mucosal Transcriptional Profile Resembling Healthy Mucosa. <i>Journal of Crohn's and Colitis</i> , 2022, 16, 1020-1029.	0.6	5
26909	Key genes associated with prognosis and metastasis of clear cell renal cell carcinoma. <i>PeerJ</i> , 2022, 10, e12493.	0.9	5
26910	Systems Approaches to Unravel Molecular Function: High-content siRNA Screen Identifies TMEM16A Traffic Regulators as Potential Drug Targets for Cystic Fibrosis. <i>Journal of Molecular Biology</i> , 2022, 434, 167436.	2.0	3
26911	ProteinBERT: a universal deep-learning model of protein sequence and function. <i>Bioinformatics</i> , 2022, 38, 2102-2110.	1.8	193
26912	The genome of oil-Camellia and population genomics analysis provide insights into seed oil domestication. <i>Genome Biology</i> , 2022, 23, 14.	3.8	68
26913	Gene Ontology GAN (GOGAN): a novel architecture for protein function prediction. <i>Soft Computing</i> , 2022, 26, 7653-7667.	2.1	7
26914	RNAseq reveals extensive metabolic disruptions in the sensitive SF-295 cell line treated with schweinfurthins. <i>Scientific Reports</i> , 2022, 12, 359.	1.6	1
26915	A high-quality chromosome-level genome of the endangered roughskin sculpin provides insights into its evolution and adaptation. <i>Molecular Ecology Resources</i> , 2022, 22, 1892-1905.	2.2	1

#	ARTICLE	IF	CITATIONS
26916	Mimic microgravity effect on muscle transcriptome under ionizing radiation. <i>Life Sciences in Space Research</i> , 2022, 32, 96-104.	1.2	2
26917	Quantitative proteomics reveals differential immunoglobulin-associated proteome (IgAP) in patients of acute myocardial infarction and chronic coronary syndromes. <i>Journal of Proteomics</i> , 2022, 252, 104449.	1.2	2
26918	Transcriptomic profiling of watermelon () provides insights into male flowers development. <i>Journal of Integrative Agriculture</i> , 2022, 21, 407-421.	1.7	4
26919	Identification of NLRP3 as a covalent target of 1,6-O,O-diacetylbritanilactone against neuroinflammation by quantitative thiol reactivity profiling (QTRP). <i>Bioorganic Chemistry</i> , 2022, 119, 105536.	2.0	4
26920	Membrane polarization in non-neuronal cells as a potential mechanism of metabolic disruption by depolarizing insecticides. <i>Food and Chemical Toxicology</i> , 2022, 160, 112804.	1.8	3
26921	Global transcriptome profiling in peripheral blood mononuclear cells identifies dysregulation of immune processes in individuals with radiologically isolated syndrome. <i>Multiple Sclerosis and Related Disorders</i> , 2022, 58, 103469.	0.9	3
26922	The potential role of eyestalk in the immunity of <i>Litopenaeus vannamei</i> to <i>Vibrio</i> infection. <i>Fish and Shellfish Immunology</i> , 2022, 121, 62-73.	1.6	5
26923	Fungal pathogens of cereal crops: Proteomic insights into fungal pathogenesis, host defense, and resistance. <i>Journal of Plant Physiology</i> , 2022, 269, 153593.	1.6	14
26924	Complete genome sequence of <i>Pseudoalteromonas</i> sp. Xi13 capable of degrading $\hat{\text{I}}^{\text{e}}$ -selenocarrageenan isolated from the floating ice of Southern Ocean. <i>Marine Genomics</i> , 2022, 61, 100917.	0.4	3
26925	Comparative proteomics and transcriptomics illustrate the allograft-induced stress response in the pearl oyster (<i>Pinctada fucata martensii</i>). <i>Fish and Shellfish Immunology</i> , 2022, 121, 74-85.	1.6	12
26926	Metabolism response of fasting in <i>Octopus sinensis</i> paralarvae revealed by RNA-seq. <i>Aquaculture</i> , 2022, 550, 737859.	1.7	3
26927	Transcriptomics and machine learning to advance schizophrenia genetics: A case-control study using post-mortem brain data. <i>Computer Methods and Programs in Biomedicine</i> , 2022, 214, 106590.	2.6	1
26928	A role for BET proteins in regulating basal, dopamine-induced and cAMP/PKA-dependent transcription in rat striatal neurons. <i>Cellular Signalling</i> , 2022, 91, 110226.	1.7	7
26929	Non-additive gene interactions underpin molecular and phenotypic responses in honey bee larvae exposed to imidacloprid and thymol. <i>Science of the Total Environment</i> , 2022, 814, 152614.	3.9	3
26930	The Screening and Identification of Key Biomarkers in Adrenocortical Carcinoma: Evidence from a Bioinformatics Analysis. <i>Journal of Biomaterials and Tissue Engineering</i> , 2022, 12, 523-532.	0.0	0
26931	Genetic insights unraveling quorum quenching potential of indigenous isolates from an anaerobic membrane bioreactor. <i>Science of the Total Environment</i> , 2022, 811, 152349.	3.9	10
26932	A simplified protocol for performing MAGMA/H-MAGMA gene set analysis utilizing high-performance computing environments. <i>STAR Protocols</i> , 2022, 3, 101083.	0.5	3
26933	Integrated proteomics and transcriptome analysis reveal a decreased catechins metabolism in variegated tea leaves. <i>Scientia Horticulturae</i> , 2022, 295, 110824.	1.7	9

#	ARTICLE	IF	CITATIONS
26934	Neuronal networks: Analysis of brain pathology in Mucopolysaccharidoses – A systems biology approach. <i>Neuroscience Informatics</i> , 2022, 2, 100036.	2.8	1
26935	Transcriptome analysis of the early stage ifnlr1-mutant zebrafish indicates the immune response to auditory dysfunction. <i>Gene Expression Patterns</i> , 2022, 43, 119229.	0.3	0
26936	Exploring an enhanced rhizospheric phenomenon for pluricontaminated soil remediation: Insights from tripartite metatranscriptome analyses. <i>Journal of Hazardous Materials</i> , 2022, 428, 128246.	6.5	10
26937	Integrated Bioinformatics Analysis of Hub Genes and Pathways Associated with a Compression Model of Spinal Cord Injury in Rats. <i>Medical Science Monitor</i> , 2020, 26, e927107.	0.5	6
26938	Using mRNA deep sequencing to analyze differentially expressed genes during Panax notoginseng saponin treatment of ischemic stroke. <i>Molecular Medicine Reports</i> , 2020, 22, 4743-4753.	1.1	1
26939	Identification of key biomarkers and potential signaling pathway associated with poor progression of gastric cancer. <i>Translational Cancer Research</i> , 2020, 9, 5459-5472.	0.4	1
26941	Integrated microarray analysis of key genes and a miRNA-mRNA regulatory network of early-onset preeclampsia. <i>Molecular Medicine Reports</i> , 2020, 22, 4772-4782.	1.1	4
26942	Short hairpin RNA attenuates liver fibrosis by regulating the PPAR α and NF κ B pathways in HBV-induced liver fibrosis in mice. <i>International Journal of Oncology</i> , 2020, 57, 1116-1128.	1.4	4
26943	Association of tricellulin expression with poor colorectal cancer prognosis and metastasis. <i>Oncology Reports</i> , 2020, 44, 2174-2184.	1.2	1
26945	[Corrigendum] Cellular expression profiles of Epstein-Barr virus-transformed B-lymphoblastoid cell lines. <i>Biomedical Reports</i> , 2020, 14, 1-1.	0.9	0
26946	Free Wanderer Powder regulates AMPA receptor homeostasis in chronic restraint stress-induced rat model of depression with liver-depression and spleen-deficiency syndrome. <i>Aging</i> , 2020, 12, 19563-19584.	1.4	9
26947	Upregulated lncRNA HRC2:1 prompts nucleus pulposus cell senescence in intervertebral disc degeneration. <i>Molecular Medicine Reports</i> , 2020, 22, 5251-5261.	1.1	4
26948	Study on the miRNA-mediated regulatory network in the heart adjacent tissues of patients with tetralogy of Fallot. , 2020, , .		0
26949	Exploring biomarkers and therapeutic targets for pressure overload induced heart failure based on microarray data. <i>Cardiovascular Diagnosis and Therapy</i> , 2020, 10, 1226-1237.	0.7	2
26950	Discovered differentially expressed lncRNA AC010973.2 can act as a diagnostic and prognostic biomarker for colon adenocarcinoma. <i>Translational Cancer Research</i> , 2020, 9, 6275-6286.	0.4	1
26951	Joint Bayesian Variable Selection and Graph Estimation for Non-linear SVM with Application to Genomics Data. , 2020, , .		0
26952	The efficacy of chemotherapeutic drug combinations may be predicted by concordance of gene response to the single agents. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	1
26954	Visualizing and Annotating Protein Sequences using A Deep Neural Network. , 2020, , .		3

#	ARTICLE	IF	CITATIONS
26955	Characterization of Analytic and Experimental Uncertainty of RNA-seq Co-expression Network Determination: Application to SCA2. , 2020, , .		0
26957	Transcriptome Analysis Identifies Genes Involved in Rice Panicle Enclosure. <i>Botanical Research</i> , 2021, 10, 770-780.	0.0	0
26958	Integration of transcriptomics and metabolomics to identify key coumarin biosynthetic genes in <i>Bupleurum chinense</i> . <i>Biotechnology and Biotechnological Equipment</i> , 2021, 35, 1858-1868.	0.5	2
26960	Genomic analysis of a pure culture of magnetotactic bacterium <i>Terasakiella</i> sp. SH-1. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 2097-2106.	0.6	3
26961	Answering regular path queries through exemplars. <i>Proceedings of the VLDB Endowment</i> , 2021, 15, 299-311.	2.1	1
26962	Transcriptome changes in maternal peripheral blood during term parturition mimic perturbations preceding spontaneous preterm birth. <i>Biology of Reproduction</i> , 2022, 106, 185-199.	1.2	14
26965	Network pharmacology-based strategy to investigate the active ingredients and molecular mechanisms of <i>Scutellaria Barbata</i> D. Don against radiation pneumonitis. <i>Medicine (United States)</i> , 2021, 100, e27957.	0.4	5
26966	Identifying the temporal electrophysiological and molecular changes that contribute to TSC-associated epileptogenesis. <i>JCI Insight</i> , 2021, 6, .	2.3	7
26967	Physiological, Biochemical and Transcriptomic Analysis of the Aerial Parts (Leaf-Blade and Petiole) of <i>Asarum sieboldii</i> Responding to Drought Stress. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13402.	1.8	1
26968	Draft Genome Sequence of <i>Bacillus pacificus</i> KVCMST-8A-12, Isolated from a Marine Sediment Sample from the Kanyakumari Coast, India. <i>Microbiology Resource Announcements</i> , 2021, 10, e0101121.	0.3	1
26969	The effect and mechanism of Jiao-tai-wan in the treatment of diabetes mellitus with depression based on network pharmacology and experimental analysis. <i>Molecular Medicine</i> , 2021, 27, 154.	1.9	11
26970	Mining the Genome of <i>Bacillus velezensis</i> VB7 (CP047587) for MAMP Genes and Non-Ribosomal Peptide Synthetase Gene Clusters Conferring Antiviral and Antifungal Activity. <i>Microorganisms</i> , 2021, 9, 2511.	1.6	22
26971	Chromosomal-level genome and multi-omics dataset of <i>Pueraria lobata</i> var. <i>thomsonii</i> provide new insights into legume family and the isoflavone and puerarin biosynthesis pathways. <i>Horticulture Research</i> , 2022, 9, .	2.9	10
26972	Targeted gene silencing in the nervous system with CRISPR-Cas13. <i>Science Advances</i> , 2022, 8, eabk2485.	4.7	45
26973	Endothelial and systemic upregulation of miR-34a-5p fine-tunes senescence in progeria. <i>Aging</i> , 2022, 14, 195-224.	1.4	9
26974	The Mouse Gastrointestinal Bacteria Catalogue enables translation between the mouse and human gut microbiotas via functional mapping. <i>Cell Host and Microbe</i> , 2022, 30, 124-138.e8.	5.1	59
26975	Analysis of miRNAs Involved in Mouse Heart Injury Upon Coxsackievirus A2 Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 765445.	1.8	1
26976	Deciphering the etiology and role in oncogenic transformation of the CpG island methylator phenotype: a pan-cancer analysis. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	9

#	ARTICLE	IF	CITATIONS
26977	Identification of Molecular Biomarkers and Key Pathways for Esophageal Carcinoma (EsC): A Bioinformatics Approach. <i>BioMed Research International</i> , 2022, 2022, 1-14.	0.9	4
26978	DisEnrich: database of enriched regions in human dark proteome. <i>Bioinformatics</i> , 2022, 38, 1870-1876.	1.8	1
26979	Molecular Details of Actinomycin D-Treated MRSA Revealed via High-Dimensional Data. <i>Marine Drugs</i> , 2022, 20, 114.	2.2	2
26980	Quantitative Proteome and Transcriptome Dynamics Analysis Reveals Iron Deficiency Response Networks and Signature in Neuronal Cells. <i>Molecules</i> , 2022, 27, 484.	1.7	2
26981	TANGO: A GO-term Embedding Based Method for Protein Semantic Similarity Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, PP, 1-1.	1.9	1
26982	AgroLD: A Knowledge Graph Database for Plant Functional Genomics. <i>Methods in Molecular Biology</i> , 2022, 2443, 527-540.	0.4	2
26983	Inflammatory activation and immune cell infiltration are main biological characteristics of SARS-CoV-2 infected myocardium. <i>Bioengineered</i> , 2022, 13, 2486-2497.	1.4	5
26986	Interaction of Periplasmic Fab Production and Intracellular Redox Balance in <i>Escherichia coli</i> Affects Product Yield. <i>ACS Synthetic Biology</i> , 2022, 11, 820-834.	1.9	4
26987	A functional cellular framework for sex and estrous cycle-dependent gene expression and behavior. <i>Cell</i> , 2022, 185, 654-671.e22.	13.5	52
26988	The cell cycle arrested results in the premature advent of apical leaflets development cessation in <i>Zygophyllum xanthoxylon</i> . <i>Trees - Structure and Function</i> , 2023, 37, 223-237.	0.9	1
26989	Molecular mechanism of inhibitory effects of melatonin on prostate cancer cell proliferation, migration and invasion. <i>PLoS ONE</i> , 2022, 17, e0261341.	1.1	7
26990	Data Integration Challenges for Machine Learning in Precision Medicine. <i>Frontiers in Medicine</i> , 2021, 8, 784455.	1.2	18
26992	Haploidy in somatic cells is induced by mature oocytes in mice. <i>Communications Biology</i> , 2022, 5, 95.	2.0	7
26994	Proteome alterations in the aqueous humor reflect structural and functional phenotypes in patients with advanced normal-tension glaucoma. <i>Scientific Reports</i> , 2022, 12, 1221.	1.6	5
26995	Dynamic Functional Connectivity Alterations and Their Associated Gene Expression Pattern in Autism Spectrum Disorders. <i>Frontiers in Neuroscience</i> , 2021, 15, 794151.	1.4	13
26996	miRNA and lncRNA Expression Networks Modulate Cell Cycle and DNA Repair Inhibition in Senescent Prostate Cells. <i>Genes</i> , 2022, 13, 208.	1.0	7
26997	Central Role of C2H2-Type Zinc Finger-Containing Genes in Pediatric Brain Tumors. <i>Dna</i> , 2022, 2, 1-21.	0.4	0
26998	Comprehensive analysis of expression profile and prognostic significance of interferon regulatory factors in pancreatic cancer. <i>BMC Genomic Data</i> , 2022, 23, 5.	0.7	2

#	ARTICLE	IF	CITATIONS
26999	Identification of potential genes correlated with breast cancer metastasis and prognosis. <i>International Journal of Transgender Health</i> , 2022, 15, 126-133.	1.1	1
27000	A High-Density Genetic Map Enables Genome Synteny and QTL Mapping of Vegetative Growth and Leaf Traits in <i>Gardenia</i> . <i>Frontiers in Genetics</i> , 2021, 12, 802738.	1.1	2
27001	Identification of the Association Between Toll-Like Receptors and T-Cell Activation in Takayasu's Arteritis. <i>Frontiers in Immunology</i> , 2021, 12, 792901.	2.2	3
27002	BATF promotes group 2 innate lymphoid cell-mediated lung tissue protection during acute respiratory virus infection. <i>Science Immunology</i> , 2022, 7, eabc9934.	5.6	20
27003	Comparative transcriptome analysis of the cold resistance of the sterile rice line 33S. <i>PLoS ONE</i> , 2022, 17, e0261822.	1.1	3
27004	Integrative Analysis of the Metabolome and Transcriptome of a Cultivated Pepper and Its Wild Progenitor Chiltepin (<i>Capsicum annuum</i> L. var. <i>glabriusculum</i>) Revealed the Loss of Pungency During <i>Capsicum</i> Domestication. <i>Frontiers in Plant Science</i> , 2021, 12, 783496.	1.7	4
27005	Altered White Matter and microRNA Expression in a Murine Model Related to Williams Syndrome Suggests That miR-34b/c Affects Brain Development via Ptpu and Dcx Modulation. <i>Cells</i> , 2022, 11, 158.	1.8	8
27006	Identification of Core Genes and Pathways in Melanoma Metastasis via Bioinformatics Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 794.	1.8	24
27007	Identification of an at-risk subpopulation with high immune infiltration based on the peroxisome pathway and TIM3 in colorectal cancer. <i>BMC Cancer</i> , 2022, 22, 44.	1.1	8
27008	Comprehensive Detoxification Mechanism Assessment of Red Imported Fire Ant (<i>Solenopsis invicta</i>) against Indoxacarb. <i>Molecules</i> , 2022, 27, 870.	1.7	21
27009	Early-life viral infections are associated with disadvantageous immune and microbiota profiles and recurrent respiratory infections. <i>Nature Microbiology</i> , 2022, 7, 224-237.	5.9	25
27010	PREGO: A Literature and Data-Mining Resource to Associate Microorganisms, Biological Processes, and Environment Types. <i>Microorganisms</i> , 2022, 10, 293.	1.6	15
27011	Developing Biliary Atresia-like Model by Treating Human Liver Organoids with Polyinosinic:Polycytidylic Acid (Poly (I:C)). <i>Current Issues in Molecular Biology</i> , 2022, 44, 644-653.	1.0	3
27012	The Identification and Validation of Hub Genes Associated with Acute Myocardial Infarction Using Weighted Gene Co-Expression Network Analysis. <i>Journal of Cardiovascular Development and Disease</i> , 2022, 9, 30.	0.8	5
27013	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
27015	Interventional and amputation-stage muscle proteomes in the chronically threatened ischemic limb. <i>Clinical and Translational Medicine</i> , 2022, 12, e658.	1.7	7
27016	Epigenome-wide three-way interaction study identifies a complex pattern between <i>TRIM27</i> , <i>KIAA0226</i> , and smoking associated with overall survival of early-stage NSCLC. <i>Molecular Oncology</i> , 2022, 16, 717-731.	2.1	4
27017	Spatial proteogenomics reveals distinct and evolutionarily conserved hepatic macrophage niches. <i>Cell</i> , 2022, 185, 379-396.e38.	13.5	343

#	ARTICLE	IF	CITATIONS
27018	An in silico analysis identifies drugs potentially modulating the cytokine storm triggered by SARS-CoV-2 infection. <i>Scientific Reports</i> , 2022, 12, 1626.	1.6	4
27019	Universal prediction of cell-cycle position using transfer learning. <i>Genome Biology</i> , 2022, 23, 41.	3.8	30
27020	Differential gene expression analysis related to sperm storage in spermathecas of <i>Amphioctopus fangsiao</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 42, 100966.	0.4	0
27021	Mapping the invisible chromatin transactions of prophase chromosome remodeling. <i>Molecular Cell</i> , 2022, 82, 696-708.e4.	4.5	10
27022	Endothelial Cell RNA-Seq Data: Differential Expression and Functional Enrichment Analyses to Study Phenotypic Switching. <i>Methods in Molecular Biology</i> , 2022, 2441, 369-426.	0.4	1
27023	Making sense of the linear genome, gene function and TADs. <i>Epigenetics and Chromatin</i> , 2022, 15, 4.	1.8	15
27024	Genome-wide association studies for growth traits in broilers. <i>BMC Genomic Data</i> , 2022, 23, 1.	0.7	16
27026	Establishing a competing endogenous RNA (ceRNA)-immunoregulatory network associated with the progression of Alzheimer's disease. <i>Annals of Translational Medicine</i> , 2022, 10, 65-65.	0.7	5
27028	Response of Poplar Leaf Transcriptome to Changed Management and Environmental Conditions in Pure and Mixed with Black Locust Stands. <i>Forests</i> , 2022, 13, 147.	0.9	1
27029	Understanding of Waggle Dance in the Honey Bee (<i>Apis mellifera</i>) from the Perspective of Long Non-Coding RNA. <i>Insects</i> , 2022, 13, 111.	1.0	4
27030	Transcriptome analysis of <i>Auricularia fibrillifera</i> fruit-body responses to drought stress and rehydration. <i>BMC Genomics</i> , 2022, 23, 58.	1.2	9
27032	Towards an Ideal In Cell Hybridization-Based Strategy to Discover Protein Interactomes of Selected RNA Molecules. <i>International Journal of Molecular Sciences</i> , 2022, 23, 942.	1.8	0
27033	HERV-W Envelope Triggers Abnormal Dopaminergic Neuron Process through DRD2/PP2A/AKT1/GSK3 for Schizophrenia Risk. <i>Viruses</i> , 2022, 14, 145.	1.5	11
27034	Identification of Phosphorus Stress Related Proteins in the Seedlings of Dongxiang Wild Rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overlo 1.0	1.0	7
27035	HESML: a real-time semantic measures library for the biomedical domain with a reproducible survey. <i>BMC Bioinformatics</i> , 2022, 23, 23.	1.2	3
27036	Exploration of the Role of Serine Proteinase Inhibitor A3 in Alcohol Dependence Using Gene Expression Omnibus Database. <i>Frontiers in Psychiatry</i> , 2021, 12, 779143.	1.3	0
27037	Systematic identification of ACE2 expression modulators reveals cardiomyopathy as a risk factor for mortality in COVID-19 patients. <i>Genome Biology</i> , 2022, 23, 15.	3.8	7
27038	A Pilot Study of Gene Expression Analysis in Peripheral Blood Mononuclear Cells in Response to a Hypocaloric Mediterranean Diet. <i>Disease Markers</i> , 2022, 2022, 1-8.	0.6	1

#	ARTICLE	IF	CITATIONS
27039	Multi-omics differential gene regulatory network inference for lung adenocarcinoma tumor progression biomarker discovery. <i>AICHE Journal</i> , 0, , .	1.8	2
27040	Age-dependent pathogenic characteristics of SARS-CoV-2 infection in ferrets. <i>Nature Communications</i> , 2022, 13, 21.	5.8	31
27041	InterCellar enables interactive analysis and exploration of cell-cell communication in single-cell transcriptomic data. <i>Communications Biology</i> , 2022, 5, 21.	2.0	10
27042	Use of Transposon Directed Insertion-Site Sequencing to Probe the Antibacterial Mechanism of a Model Honey on <i>E. coli</i> K-12. <i>Frontiers in Microbiology</i> , 2021, 12, 803307.	1.5	1
27043	Differences in peripheral immune system gene expression in frontotemporal degeneration. <i>Medicine (United States)</i> , 2022, 101, e28645.	0.4	5
27044	<i>Aggregatimonas sangjinii</i> gen. nov., sp. nov., a novel silver nanoparticle synthesizing bacterium belonging to the family Flavobacteriaceae. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 325-335.	0.7	1
27045	Transcriptomic profiling suggests candidate molecular responses to waterlogging in cassava. <i>PLoS ONE</i> , 2022, 17, e0261086.	1.1	11
27046	Assigning protein function from domain-function associations using DomFun. <i>BMC Bioinformatics</i> , 2022, 23, 43.	1.2	8
27047	Subcellular proteomics of dopamine neurons in the mouse brain. <i>ELife</i> , 2022, 11, .	2.8	30
27048	Genome Sequencing of <i>Herichium coralloides</i> by a Combination of PacBio RS II and Next-Generation Sequencing Platforms. <i>International Journal of Genomics</i> , 2022, 2022, 1-12.	0.8	0
27049	The role of SPI1-TYROBP-FCER1G network in oncogenesis and prognosis of osteosarcoma, and its association with immune infiltration. <i>BMC Cancer</i> , 2022, 22, 108.	1.1	8
27050	Targeting Refractory Mantle Cell Lymphoma for Imaging and Therapy Using C-X-C Chemokine Receptor Type 4 Radioligands. <i>Clinical Cancer Research</i> , 2022, 28, 1628-1639.	3.2	6
27052	Genes Involved in Immune Reinduction May Constitute Biomarkers of Response for Metastatic Melanoma Patients Treated with Targeted Therapy. <i>Biomedicines</i> , 2022, 10, 284.	1.4	2
27053	Hierarchical regulation of autophagy during adipocyte differentiation. <i>PLoS ONE</i> , 2022, 17, e0250865.	1.1	3
27054	Limb development genes underlie variation in human fingerprint patterns. <i>Cell</i> , 2022, 185, 95-112.e18.	13.5	30
27055	GRAND: An Integrated Genome, Transcriptome Resources, and Gene Network Database for <i>Gossypium</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 773107.	1.7	9
27056	The amniotic fluid proteome changes with gestational age in normal pregnancy: a cross-sectional study. <i>Scientific Reports</i> , 2022, 12, 601.	1.6	12
27057	Integration of <i>Aspergillus niger</i> transcriptomic profile with metabolic model identifies potential targets to optimise citric acid production from lignocellulosic hydrolysate. , 2022, 15, 4.		3

#	ARTICLE	IF	CITATIONS
27058	Recombinant HNP-1 Produced by Escherichia coli Triggers Bacterial Apoptosis and Exhibits Antibacterial Activity against Drug-Resistant Bacteria. <i>Microbiology Spectrum</i> , 2022, , e0086021.	1.2	2
27059	Subcellular and regional localization of mRNA translation in midbrain dopamine neurons. <i>Cell Reports</i> , 2022, 38, 110208.	2.9	24
27060	The impact of methodology on the reproducibility and rigor of DNA methylation data. <i>Scientific Reports</i> , 2022, 12, 380.	1.6	3
27061	Prediction of the Mechanisms by Which Quercetin Enhances Cisplatin Action in Cervical Cancer: A Network Pharmacology Study and Experimental Validation. <i>Frontiers in Oncology</i> , 2021, 11, 780387.	1.3	9
27063	Biallelic Variants in PYROXD2 Cause a Severe Infantile Metabolic Disorder Affecting Mitochondrial Function. <i>International Journal of Molecular Sciences</i> , 2022, 23, 986.	1.8	5
27064	Screening of Important Markers in Peripheral Blood Mononuclear Cells to Predict Female Osteoporosis Risk Using LASSO Regression Algorithm and SVM Method. <i>Evolutionary Bioinformatics</i> , 2022, 18, 117693432210750.	0.6	1
27065	Pleiotropic, Unique and Shared Responses Elicited by IL-6 Family Cytokines in Human Vascular Endothelial Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1448.	1.8	8
27066	Identification of potential biomarkers in hepatocellular carcinoma: A network-based approach. <i>Informatics in Medicine Unlocked</i> , 2022, 28, 100864.	1.9	4
27067	Identification of the genome-wide distribution of cyanobacterial group σ factor $\langle scp \rangle$ SigE, accountable for its regulon. <i>Plant Journal</i> , 2022, 110, 548-561.	2.8	3
27068	Differential Transcriptome Analysis Reveals Genes Related to Low- and High-Temperature Stress in the Fall Armyworm, <i>Spodoptera frugiperda</i> . <i>Frontiers in Physiology</i> , 2021, 12, 827077.	1.3	11
27070	Chromosome-level genome assembly of <i>Bactrocera dorsalis</i> reveals its adaptation and invasion mechanisms. <i>Communications Biology</i> , 2022, 5, 25.	2.0	17
27071	Identification of Inflammation-Related Biomarker Pro-ADM for Male Patients With Gout by Comprehensive Analysis. <i>Frontiers in Immunology</i> , 2021, 12, 798719.	2.2	10
27073	The Diesel Tree <i>Sindora glabra</i> Genome Provides Insights Into the Evolution of Oleoresin Biosynthesis. <i>Frontiers in Plant Science</i> , 2021, 12, 794830.	1.7	0
27074	Analysis of Global Gene Expression in Maize (<i>Zea mays</i>) Vegetative and Reproductive Tissues That Differ in Accumulation of Starch and Sucrose. <i>Plants</i> , 2022, 11, 238.	1.6	2
27075	The differential activity of biological processes in tissues and cell subsets can illuminate disease-related processes and cell-type identities. <i>Bioinformatics</i> , 2022, 38, 1584-1592.	1.8	7
27077	Shared Genetic Architecture and Causal Relationship Between Asthma and Cardiovascular Diseases: A Large-Scale Cross-Trait Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 775591.	1.1	9
27078	PBK/TOPK Inhibitor Suppresses the Progression of Prolactinomas. <i>Frontiers in Endocrinology</i> , 2021, 12, 706909.	1.5	1
27079	Effect of Different Initial Fermentation pH on Exopolysaccharides Produced by <i>Pseudoalteromonas agarivorans</i> Hao 2018 and Identification of Key Genes Involved in Exopolysaccharide Synthesis via Transcriptome Analysis. <i>Marine Drugs</i> , 2022, 20, 89.	2.2	12

#	ARTICLE	IF	CITATIONS
27080	Genome-Wide Association Study Identifies Two Common Loci Associated with Pigment Dispersion Syndrome/Pigmentary Glaucoma and Implicates Myopia in its Development. <i>Ophthalmology</i> , 2022, 129, 626-636.	2.5	10
27081	Draft Genome Sequence of <i>Oceanobacillus jordanicus</i> Strain GSFE11, a Halotolerant Plant Growth-Promoting Bacterial Endophyte Isolated From the Jordan Valley. <i>Evolutionary Bioinformatics</i> , 2022, 18, 117693432110711.	0.6	2
27082	Pan-cancer analysis of GALNTs expression identifies a prognostic of GALNTs feature in low grade glioma. <i>Journal of Leukocyte Biology</i> , 2022, 112, 887-899.	1.5	8
27083	Classification and Association Analysis of Gerbera (<i>Gerbera hybrida</i>) Flower Color Traits. <i>Frontiers in Plant Science</i> , 2021, 12, 779288.	1.7	10
27084	Human Astrocytes Exhibit Tumor Microenvironment-, Age-, and Sex-Related Transcriptomic Signatures. <i>Journal of Neuroscience</i> , 2022, 42, 1587-1603.	1.7	24
27085	LRRK2 correlates with macrophage infiltration in pan-cancer. <i>Genomics</i> , 2022, 114, 316-327.	1.3	10
27086	A Photosensitized Singlet Oxygen (1O ₂) Toolbox for Bio-Organic Applications: Tailoring 1O ₂ Generation for DNA and Protein Labelling, Targeting and Biosensing. <i>Molecules</i> , 2022, 27, 778.	1.7	17
27087	Gene and metabolite expression dependence on body mass index in human myocardium. <i>Scientific Reports</i> , 2022, 12, 1425.	1.6	3
27088	From communities to protein complexes: A local community detection algorithm on PPI networks. <i>PLoS ONE</i> , 2022, 17, e0260484.	1.1	8
27089	Enhancing CDK4/6 inhibitor therapy for medulloblastoma using nanoparticle delivery and scRNA-seq-guided combination with sapanisertib. <i>Science Advances</i> , 2022, 8, eabl5838.	4.7	16
27090	Deep models of integrated multiscale molecular data decipher the endothelial cell response to ionizing radiation. <i>IScience</i> , 2022, 25, 103685.	1.9	7
27091	Differential roles for DNAJ isoforms in HTT-polyQ and FUS aggregation modulation revealed by chaperone screens. <i>Nature Communications</i> , 2022, 13, 516.	5.8	17
27092	Single-Cell Sequencing Reveals an Intrinsic Heterogeneity of the Preovulatory Follicular Microenvironment. <i>Biomolecules</i> , 2022, 12, 231.	1.8	8
27093	Characterization of the Genomic Landscape in Cervical Cancer by Next Generation Sequencing. <i>Genes</i> , 2022, 13, 287.	1.0	8
27094	Interactome of <i>Arabidopsis Thaliana</i> . <i>Plants</i> , 2022, 11, 350.	1.6	4
27096	Expression profiles and functions of ferroptosis-related genes in the placental tissue samples of early- and late-onset preeclampsia patients. <i>BMC Pregnancy and Childbirth</i> , 2022, 22, 87.	0.9	12
27097	Genome-wide RNAi screen identifies novel players in human 60S subunit biogenesis including key enzymes of polyamine metabolism. <i>Nucleic Acids Research</i> , 2022, 50, 2872-2888.	6.5	11
27098	Pathogen resistance in <i>Sphagneticola trilobata</i> (Singapore daisy): molecular associations and differentially expressed genes in response to disease from a widespread fungus. <i>Genetica</i> , 2022, 150, 13.	0.5	2

#	ARTICLE	IF	CITATIONS
27099	Comparison of Epidermal Gene Expression Profiles in Mice Aged 1 to 20 Months. <i>Clinical, Cosmetic and Investigational Dermatology</i> , 2022, Volume 15, 69-76.	0.8	0
27100	InterTADs: integration of multi-omics data on topologically associated domains, application to chronic lymphocytic leukemia. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqab121.	1.5	2
27101	Core promoter mutation contributes to abnormal gene expression in bladder cancer. <i>BMC Cancer</i> , 2022, 22, 68.	1.1	3
27102	Interaction with mammalian enteric viruses alters outer membrane vesicle production and content by commensal bacteria. <i>Journal of Extracellular Vesicles</i> , 2022, 11, e12172.	5.5	16
27103	Evaluation of deep convolutional neural networks for in situ hybridization gene expression image representation. <i>PLoS ONE</i> , 2022, 17, e0262717.	1.1	1
27104	Construction and Analysis of the lncRNA-miRNA-mRNA Network Based on Competing Endogenous RNA in Atrial Fibrillation. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 791156.	1.1	7
27105	Identification of <i>Pueraria</i> spp. through DNA barcoding and comparative transcriptomics. <i>BMC Plant Biology</i> , 2022, 22, 10.	1.6	7
27106	Inferring the genetic responses to acute drought stress across an ecological gradient. <i>BMC Genomics</i> , 2022, 23, 3.	1.2	2
27107	PANDA2: protein function prediction using graph neural networks. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac004.	1.5	8
27108	Transcriptome Analysis of Different Sections of Rhizome in <i>Polygonatum sibiricum</i> Red. and Mining Putative Genes Participate in Polysaccharide Biosynthesis. <i>Biochemical Genetics</i> , 2022, 60, 1547-1566.	0.8	8
27109	The genome of the Paleogene relic tree <i>Bretschneidera sinensis</i> : insights into trade-offs in gene family evolution, demographic history, and adaptive SNPs. <i>DNA Research</i> , 2022, 29, .	1.5	5
27110	Catalase (CAT) Gene Family in Wheat (<i>Triticum aestivum</i> L.): Evolution, Expression Pattern and Function Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 542.	1.8	24
27111	RNA-seq-based transcriptomic analysis of AHL-induced biofilm and pyocyanin inhibition in <i>Pseudomonas aeruginosa</i> by <i>Lactobacillus brevis</i> . <i>International Microbiology</i> , 2022, 25, 447-456.	1.1	5
27112	Chromatin profiling reveals heterogeneity in clinical isolates of the human pathogen <i>Aspergillus fumigatus</i> . <i>PLoS Genetics</i> , 2022, 18, e1010001.	1.5	11
27113	Tissue-specific multi-omics analysis of atrial fibrillation. <i>Nature Communications</i> , 2022, 13, 441.	5.8	17
27116	Identification of Differentially Expressed Genes and Pathways in Human Atrial Fibrillation by Bioinformatics Analysis. <i>International Journal of General Medicine</i> , 2022, Volume 15, 103-114.	0.8	3
27117	Engineering an enthesis-like graft for rotator cuff repair: An approach to fabricate highly biomimetic scaffold capable of zone-specifically releasing stem cell differentiation inducers. <i>Bioactive Materials</i> , 2022, 16, 451-471.	8.6	18
27118	Graphlet eigencentralities capture novel central roles of genes in pathways. <i>PLoS ONE</i> , 2022, 17, e0261676.	1.1	2

#	ARTICLE	IF	CITATIONS
27119	Deep neural learning based protein function prediction. <i>Mathematical Biosciences and Engineering</i> , 2022, 19, 2471-2488.	1.0	2
27120	Simple But Efficacious Enrichment of Integral Membrane Proteins and Their Interactions for In-Depth Membrane Proteomics. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100206.	2.5	20
27121	Proteomic screen reveals diverse protein transport between connected neurons in the visual system. <i>Cell Reports</i> , 2022, 38, 110287.	2.9	10
27122	Kinensoside Alleviates Alcoholic Liver Injury by Reducing Oxidative Stress, Inhibiting Endoplasmic Reticulum Stress, and Regulating AMPK-Dependent Autophagy. <i>Frontiers in Pharmacology</i> , 2021, 12, 747325.	1.6	10
27123	Theabrownin isolated from <i>Puerh</i> tea regulates <i>Bacteroidetes</i> to improve metabolic syndrome of rats induced by high-fat, high-sugar and high-salt diet. <i>Journal of the Science of Food and Agriculture</i> , 2022, 102, 4250-4265.	1.7	12
27124	Theabrownin-targeted regulation of intestinal microorganisms to improve glucose and lipid metabolism in Goto-Kakizaki rats. <i>Food and Function</i> , 2022, 13, 1921-1940.	2.1	19
27125	GAAP: A GUI-based Genome Assembly and Annotation Package. <i>Current Genomics</i> , 2022, 23, 77-82.	0.7	3
27126	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
27127	Myeloid-Biased HSC Require Semaphorin 4A From the Bone Marrow Niche for Self-Renewal Under Stress and Life-Long Persistence. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
27128	Risk stratification of gastrointestinal stromal tumors by Nanostring gene expression profiling. <i>Journal of Cancer Research and Clinical Oncology</i> , 2022, 148, 1325-1336.	1.2	1
27129	Sperm acquire epididymis-derived proteins through epididymosomes. <i>Human Reproduction</i> , 2022, 37, 651-668.	0.4	34
27130	Endotype reversal as a novel strategy for screening drugs targeting familial Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2022, 18, 2117-2130.	0.4	9
27131	GWAS and ExWAS of blood mitochondrial DNA copy number identifies 71 loci and highlights a potential causal role in dementia. <i>ELife</i> , 2022, 11, .	2.8	42
27132	Quantitative Metaproteomics and Activity-based Protein Profiling of Patient Fecal Microbiome Identifies Host and Microbial Serine-type Endopeptidase Activity Associated With Ulcerative Colitis. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100197.	2.5	17
27133	Violations of proportional hazard assumption in Cox regression model of transcriptomic data in TCGA pan-cancer cohorts. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 496-507.	1.9	8
27135	Deep learning program to predict protein functions based on sequence information. <i>MethodsX</i> , 2022, 9, 101622.	0.7	4
27136	<i>Pseudarthrobacter albicanus</i> sp. nov., isolated from Antarctic soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5
27137	The initial expression alterations occurring to transcription factors during the formation of breast cancer: Evidence from bioinformatics. <i>Cancer Medicine</i> , 2022, 11, 1371-1395.	1.3	6

#	ARTICLE	IF	CITATIONS
27138	Identification of prognostic biomarkers in papillary renal cell carcinoma and PTTG1 may serve as a biomarker for predicting immunotherapy response. <i>Annals of Medicine</i> , 2022, 54, 211-226.	1.5	10
27139	Characterization of the COPD alveolar niche using single-cell RNA sequencing. <i>Nature Communications</i> , 2022, 13, 494.	5.8	74
27140	Benzaldehyde Attenuates the Fifth Stage Larval Excretoryâ€“Secretory Product of <i>Angiostrongylus cantonensis</i> -Induced Injury in Mouse Astrocytes via Regulation of Endoplasmic Reticulum Stress and Oxidative Stress. <i>Biomolecules</i> , 2022, 12, 177.	1.8	3
27141	An Augmented High-Dimensional Graphical Lasso Method to Incorporate Prior Biological Knowledge for Global Network Learning. <i>Frontiers in Genetics</i> , 2021, 12, 760299.	1.1	3
27142	miR-183-5p promotes proliferation, invasion, and glycolysis of thyroid carcinoma cells by targeting FOXO1. <i>Molecular and Cellular Biochemistry</i> , 2022, 477, 1195-1206.	1.4	8
27143	Increased trunk fat is associated with altered gene expression in breast tissue of normal weight women. <i>Npj Breast Cancer</i> , 2022, 8, 15.	2.3	1
27144	The Landscape of Aminoacyl-tRNA Synthetases Involved in Severe Acute Respiratory Syndrome Coronavirus 2 Infection. <i>Frontiers in Physiology</i> , 2021, 12, 818297.	1.3	10
27145	MEK Inhibition Enhances Presentation of Targetable MHC-I Tumor Antigens in Mutant Melanomas. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
27146	Integrated transcriptomic and metabolomic analyses of Caucasian clover (<i>Trifolium ambiguum</i> Bieb.) in response to freezing stress. <i>Revista Brasileira De Botanica</i> , 2022, 45, 573-585.	0.5	2
27147	Transcriptomic and Chemical Analyses Reveal the Hub Regulators of Flower Color Variation from <i>Camellia japonica</i> Bud Sport. <i>Horticulturae</i> , 2022, 8, 129.	1.2	7
27149	De novo and comparative transcriptomic analysis explain morphological differences in <i>Panax notoginseng</i> taproots. <i>BMC Genomics</i> , 2022, 23, 86.	1.2	3
27152	Inter-tissue convergence of gene expression during ageing suggests age-related loss of tissue and cellular identity. <i>ELife</i> , 2022, 11, .	2.8	26
27154	Analysis of Biosynthetic Gene Clusters, Secretory, and Antimicrobial Peptides Reveals Environmental Suitability of <i>Exiguobacterium profundum</i> PHM11. <i>Frontiers in Microbiology</i> , 2021, 12, 785458.	1.5	6
27155	Precise gene models using long-read sequencing reveal a unique poly(A) signal in <i>Giardia lamblia</i> . <i>Rna</i> , 2022, 28, 668-682.	1.6	2
27156	Gene duplication to the Y chromosome in Trinidadian Guppies. <i>Molecular Ecology</i> , 2022, 31, 1853-1863.	2.0	11
27157	Neuropeptidergic regulation of compulsive ethanol seeking in <i>C. elegans</i> . <i>Scientific Reports</i> , 2022, 12, 1804.	1.6	3
27158	Student biocuration projects as a learning environment. <i>F1000Research</i> , 0, 10, 1023.	0.8	0
27159	Dichotomous Responses to Chronic Fetal Hypoxia Lead to a Predetermined Aging Phenotype. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100190.	2.5	4

#	ARTICLE	IF	CITATIONS
27160	Transcriptome Sequencing and Screening of Anthocyanin-Related Genes in the Leaves of <i>Acer truncatum</i> Bunge. <i>Biochemical Genetics</i> , 2022, 60, 1845-1864.	0.8	4
27161	A practical guide to interpreting and generating bottom-up proteomics data visualizations. <i>Proteomics</i> , 2022, 22, e2100103.	1.3	16
27162	Chronic Marijuana Use Is Associated with Gene Expression Changes in BAL. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2022, 66, 238-239.	1.4	0
27163	Application of Whole Exome Sequencing and Functional Annotations to Identify Genetic Variants Associated with Marfan Syndrome. <i>Journal of Personalized Medicine</i> , 2022, 12, 198.	1.1	2
27164	DDX10 promotes the proliferation and metastasis of colorectal cancer cells via splicing RPL35. <i>Cancer Cell International</i> , 2022, 22, 58.	1.8	9
27165	Genome Sequences of Two Strains of <i>Prototheca wickerhamii</i> Provide Insight Into the Protothecosis Evolution. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 797017.	1.8	2
27166	Upregulation of CD14 in mesenchymal stromal cells accelerates lipopolysaccharide-induced response and enhances antibacterial properties. <i>IScience</i> , 2022, 25, 103759.	1.9	5
27167	β -catenin perturbations control differentiation programs in mouse embryonic stem cells. <i>IScience</i> , 2022, 25, 103756.	1.9	2
27168	Two heads are better than one: current landscape of integrating QSP and machine learning. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2022, 49, 5-18.	0.8	26
27169	Genome-wide identification of C2H2-type zinc finger gene family members and their expression during abiotic stress responses in orchardgrass (<i>Dactylis glomerata</i>). <i>Genome</i> , 2022, 65, 189-203.	0.9	3
27170	Integration of Small RNA and Transcriptome Sequencing Reveal the Roles of miR395 and ATP Sulfurylase in Developing Seeds of Chinese Kale. <i>Frontiers in Plant Science</i> , 2021, 12, 778848.	1.7	4
27171	5 α -reductase inhibitors induce a prostate luminal to club cell transition in human benign prostatic hyperplasia. <i>Journal of Pathology</i> , 2022, 256, 427-441.	2.1	28
27172	Field cancerization profile-based prognosis signatures lead to more robust risk evaluation in hepatocellular carcinoma. <i>IScience</i> , 2022, 25, 103747.	1.9	4
27173	Androgen receptor-mediated transcriptional repression targets cell plasticity in prostate cancer. <i>Molecular Oncology</i> , 2022, 16, 2518-2536.	2.1	2
27174	Creating and maintaining a high-confidence microRNA repository for crop research: A brief review and re-examination of the current crop microRNA registries. <i>Journal of Plant Physiology</i> , 2022, 270, 153636.	1.6	1
27175	Identification of potential immunotherapy biomarkers for breast cancer by bioinformatics analysis. <i>Bioscience Reports</i> , 2022, 42, .	1.1	7
27176	Homogentisic acid induces autophagy alterations leading to chondroptosis in human chondrocytes: Implications in Alkaptonuria. <i>Archives of Biochemistry and Biophysics</i> , 2022, 717, 109137.	1.4	3
27177	Recent advances in T-cell receptor repertoire analysis: Bridging the gap with multimodal single-cell RNA sequencing. <i>Immuninformatics</i> , 2022, 5, 100009.	1.2	27

#	ARTICLE	IF	CITATIONS
27178	Triplication is the main evolutionary driving force of NLP transcription factor family in Chinese cabbage and related species. <i>International Journal of Biological Macromolecules</i> , 2022, 201, 492-506.	3.6	4
27179	Global DNA methylation changes in treated and untreated MS patients measured over time. <i>Journal of Neuroimmunology</i> , 2022, 364, 577808.	1.1	2
27180	Transcriptome profiling reveals major structural genes, transcription factors and biosynthetic pathways involved in leaf senescence and nitrogen remobilization in rainfed spring wheat under different nitrogen fertilization rates. <i>Genomics</i> , 2022, 114, 110271.	1.3	13
27181	Whole genome re-sequencing and transcriptome reveal an alteration in hormone signal transduction in a more-branching mutant of apple. <i>Gene</i> , 2022, 818, 146214.	1.0	2
27182	Pharmacological mechanism of Shenlingbaizhu formula against experimental colitis. <i>Phytomedicine</i> , 2022, 98, 153961.	2.3	14
27183	The complete genome sequence of <i>Shewanella inventionis</i> D1489 reveals its potential for the production of eicosapentaenoic acid. <i>Marine Genomics</i> , 2022, 62, 100932.	0.4	1
27184	The effect of phosphate mining activities on rhizosphere bacterial communities of surrounding vegetables and crops. <i>Science of the Total Environment</i> , 2022, 821, 153479.	3.9	30
27185	Systems pharmacology-based drug discovery and active mechanism of natural products for coronavirus pneumonia (COVID-19): An example using flavonoids. <i>Computers in Biology and Medicine</i> , 2022, 143, 105241.	3.9	15
27186	Cellular response of lung fibroblasts and epithelial cells to particulate matter ₁₀ treatment examined via comparative transcriptome analysis. <i>Molecular Medicine Reports</i> , 2022, 25, .	1.1	0
27187	Schisandrin ^Å suppresses osteosarcoma lung metastasis<i>in vivo</i> by inhibiting the activation of the Wnt/ β -catenin and PI3K/Akt signaling pathways. <i>Oncology Reports</i> , 2022, 47, .	1.2	9
27188	Identification of inflammatory response and alternative splicing in acute kidney injury and experimental verification of the involvement of RNA-binding protein RBFOX1 in this disease. <i>International Journal of Molecular Medicine</i> , 2022, 49, .	1.8	10
27189	Factors That Affect the Rates of Adaptive and Nonadaptive Evolution at the Gene Level in Humans and Chimpanzees. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	0
27190	Leaf color formation mechanisms in <i>Alternanthera bettzickiana</i> elucidated by metabolite and transcriptome analyses. <i>Planta</i> , 2022, 255, 59.	1.6	5
27191	Maladaptive functional changes in alveolar fibroblasts due to perinatal hyperoxia impair epithelial differentiation. <i>JCI Insight</i> , 2022, 7, .	2.3	10
27192	Genomic basis for skin phenotype and cold adaptation in the extinct <i>Steller's</i> sea cow. <i>Science Advances</i> , 2022, 8, eabl6496.	4.7	9
27193	Identification of Olfactory Genes in <i>Monochamus saltuarius</i> and Effects of <i>Bursaphelenchus xylophilus</i> Infestation on Their Expression. <i>Forests</i> , 2022, 13, 258.	0.9	5
27194	Metabolic labeling of secreted matrix to investigate cell-material interactions in tissue engineering and mechanobiology. <i>Nature Protocols</i> , 2022, 17, 618-648.	5.5	14
27195	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

#	ARTICLE	IF	CITATIONS
27196	Neuropeptide signaling and SKN-1 orchestrate differential responses of the proteostasis network to dissimilar proteotoxic insults. <i>Cell Reports</i> , 2022, 38, 110350.	2.9	8
27197	The BMS-LM ontology for biomedical data reporting throughout the lifecycle of a research study: From data model to ontology. <i>Journal of Biomedical Informatics</i> , 2022, 127, 104007.	2.5	1
27198	Immunomodulatory potential of in vivo natural killer T (NKT) activation by NKTT320 in Mauritian-origin cynomolgus macaques. <i>IScience</i> , 2022, 25, 103889.	1.9	2
27199	Deficiency of ribosomal proteins reshapes the transcriptional and translational landscape in human cells. <i>Nucleic Acids Research</i> , 2022, 50, 6601-6617.	6.5	18
27200	Phosphoproteomic Analysis of Breast Cancer-Derived Small Extracellular Vesicles Reveals Disease-Specific Phosphorylated Enzymes. <i>Biomedicines</i> , 2022, 10, 408.	1.4	10
27201	Extensive age-dependent loss of antibody diversity in naturally short-lived turquoise killifish. <i>ELife</i> , 2022, 11, .	2.8	11
27202	Protein phase separation hotspots at the presynapse. <i>Open Biology</i> , 2022, 12, 210334.	1.5	6
27203	Full-Length Transcriptome of the Whale Shark (<i>Rhincodon typus</i>) Facilitates the Genome Information. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	2
27204	Network inference with Granger causality ensembles on single-cell transcriptomics. <i>Cell Reports</i> , 2022, 38, 110333.	2.9	53
27205	Zebrafish models of <i>Alx</i> -linked frontonasal dysplasia reveal a role for <i>Alx1</i> and <i>Alx3</i> in the anterior segment and vasculature of the developing eye. <i>Biology Open</i> , 2022, 11, .	0.6	5
27206	Single-Cell RNA Sequencing Identifies Intra-Graft Population Heterogeneity in Acute Heart Allograft Rejection in Mouse. <i>Frontiers in Immunology</i> , 2022, 13, 832573.	2.2	7
27207	Cold Exposure Drives Weight Gain and Adiposity following Chronic Suppression of Brown Adipose Tissue. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1869.	1.8	3
27208	Single-Cell RNA Sequencing Characterizes the Molecular Heterogeneity of the Larval Zebrafish Optic Tectum. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, 818007.	1.4	8
27209	Dynamic effects of chronic unpredictable mild stress on the hippocampal transcriptome in rats. <i>Molecular Medicine Reports</i> , 2022, 25, .	1.1	2
27210	Polymerase II-Associated Factor 1 Complex-Regulated FLOWERING LOCUS C-Clade Genes Repress Flowering in Response to Chilling. <i>Frontiers in Plant Science</i> , 2022, 13, 817356.	1.7	10
27211	Computational image features of immune architecture is associated with clinical benefit and survival in gynecological cancers across treatment modalities. , 2022, 10, e003833.		10
27212	Protein-DNA/RNA interactions: Machine intelligence tools and approaches in the era of artificial intelligence and big data. <i>Proteomics</i> , 2022, 22, e2100197.	1.3	20
27214	Identification of genes associated with kernel size in almond [<i>Prunus dulcis</i> (Mill.) D.A. Webb] using RNA-Seq. <i>Plant Growth Regulation</i> , 2022, 97, 357-373.	1.8	4

#	ARTICLE	IF	CITATIONS
27215	Necrotizing Enterocolitis: Clinical Features, Histopathological Characteristics, and Genetic Associations. <i>Current Pediatric Reviews</i> , 2022, 18, 210-225.	0.4	2
27216	An overview of bioinformatics, genomics, and transcriptomics resources for bryophytes. <i>Journal of Experimental Botany</i> , 2022, 73, 4291-4305.	2.4	11
27217	Multi-Omics Profiling Specifies Involvement of Alternative Ribosomal Proteins in Response to Zinc Limitation in <i>Mycobacterium smegmatis</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 811774.	1.5	3
27218	Characterization of a small molecule inhibitor of disulfide reductases that induces oxidative stress and lethality in lung cancer cells. <i>Cell Reports</i> , 2022, 38, 110343.	2.9	14
27219	Dynamic Gene Expression and Alternative Splicing Events Demonstrate Co-Regulation of Testicular Differentiation and Maturation by the Brain and Gonad in Common Carp. <i>Frontiers in Endocrinology</i> , 2021, 12, 820463.	1.5	1
27220	A top-down supervised learning approach to hierarchical multi-label classification in networks. <i>Applied Network Science</i> , 2022, 7, .	0.8	8
27222	Adipose-derived stem cell spheroids are superior to single-cell suspensions to improve fat autograft long-term survival. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 1421-1433.	1.6	6
27223	A Neural Network-Based Multi-Label Classifier for Protein Function Prediction. <i>Engineering, Technology & Applied Science Research</i> , 2022, 12, 7974-7981.	0.8	8
27224	Gene-Interaction-Sensitive enrichment analysis in congenital heart disease. <i>BioData Mining</i> , 2022, 15, 4.	2.2	2
27225	Chemical-induced gene expression ranking and its application to pancreatic cancer drug repurposing. <i>Patterns</i> , 2022, 3, 100441.	3.1	9
27226	Macrophages are primed to transdifferentiate into fibroblasts in malignant ascites and pleural effusions. <i>Cancer Letters</i> , 2022, 532, 215597.	3.2	5
27228	First genome-wide association study investigating blood pressure and renal traits in domestic cats. <i>Scientific Reports</i> , 2022, 12, 1899.	1.6	0
27229	A systematically derived overview of the non-ubiquitous pathways and genes that define the molecular and genetic signature of the healthy trabecular meshwork. <i>Genomics</i> , 2022, , 110280.	1.3	1
27230	Exploring the total flavones of <i>Abelmoschus manihot</i> against IAV-induced lung inflammation by network pharmacology. <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, 36.	1.2	2
27231	Integrative RNA-seq and ATAC-seq analyses of phosphodiesterase 6 mutation-induced retinitis pigmentosa. <i>International Ophthalmology</i> , 2022, 42, 2385-2395.	0.6	1
27232	<i>Aequorivita iocasae</i> sp. nov., a halophilic bacterium isolated from sediment collected at a cold seep field in the South China Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	8
27234	Proteomic Analysis of the Antibacterial Effect of Improved Dian Dao San against <i>Propionibacterium acnes</i> . <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-9.	0.5	1
27235	Haplotype-Resolved Genome Analyses Reveal Genetically Distinct Nuclei within a Commercial Cultivar of <i>Lentinula edodes</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 167.	1.5	5

#	ARTICLE	IF	CITATIONS
27236	Dual G9A/EZH2 Inhibition Stimulates Antitumor Immune Response in Ovarian High-Grade Serous Carcinoma. <i>Molecular Cancer Therapeutics</i> , 2022, 21, 522-534.	1.9	20
27237	Proteome analysis of the circadian clock protein PERIOD2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1315-1330.	1.5	6
27238	Unlocking the Memory Component of Alzheimer's Disease: Biological Processes and Pathways across Brain Regions. <i>Biomolecules</i> , 2022, 12, 263.	1.8	2
27241	Investigating the Mechanism of Unilateral Cross Incompatibility in Longan (<i>Dimocarpus longan</i> Lour.) Cultivars (Yiduo A— Shixia). <i>Frontiers in Plant Science</i> , 2021, 12, 821147.	1.7	4
27242	Identifying the candidate genes using co-expression, GO, and machine learning techniques for Alzheimer's disease. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2022, 11, 1.	1.2	1
27243	Insights into the Steps of Breast Cancer's Brain Metastases Development: Tumor Cell Interactions with the Blood's Brain Barrier. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1900.	1.8	8
27246	Genome-Wide Identification of Direct Targets of ZjVND7 Reveals the Putative Roles of Whole-Genome Duplication in Sour Jujube in Regulating Xylem Vessel Differentiation and Drought Tolerance. <i>Frontiers in Plant Science</i> , 2022, 13, 829765.	1.7	1
27247	Systems-based approaches to study immunometabolism. <i>Cellular and Molecular Immunology</i> , 2022, 19, 409-420.	4.8	25
27248	Comparative population genomics in <i>Tabebuia</i> alliance shows evidence of adaptation in Neotropical tree species. <i>Heredity</i> , 2022, 128, 141-153.	1.2	1
27249	The Highly Contiguous Genome Resource of <i>Trichoderma semiorbis</i> FJ059, a Biological Control Agent for Litchi Downy Blight. <i>Phytopathology</i> , 2022, 112, 1391-1395.	1.1	1
27250	Common DNA methylation changes in biliary tract cancers identify subtypes with different immune characteristics and clinical outcomes. <i>BMC Medicine</i> , 2022, 20, 64.	2.3	6
27251	Comparative transcriptomics and multiple phytohormone profiling reveals the molecular immune response of <i>Arabidopsis thaliana</i> to the pathogen <i>Ralstonia solanacearum</i> type III effector RipN. <i>Journal of Plant Pathology</i> , 2022, 104, 591-603.	0.6	1
27252	PRDM paralogs antagonistically balance Wnt/ β -catenin activity during craniofacial chondrocyte differentiation. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	13
27253	Micronutrient supplementation affects DNA methylation in male gonads with potential intergenerational epigenetic inheritance involving the embryonic development through glutamate receptor-associated genes. <i>BMC Genomics</i> , 2022, 23, 115.	1.2	5
27254	BMP4 preserves the developmental potential of mESCs through Ube2s- and Chmp4b-mediated chromosomal stability safeguarding. <i>Protein and Cell</i> , 2022, 13, 580-601.	4.8	3
27255	Identification of recurrent genetic patterns from targeted sequencing panels with advanced data science: a case-study on sporadic and genetic neurodegenerative diseases. <i>BMC Medical Genomics</i> , 2022, 15, 26.	0.7	4
27257	The mining and construction of a knowledge base for gene-disease association in mitochondrial diseases. <i>Scientific Reports</i> , 2021, 11, 23909.	1.6	3
27259	A novel strategy to uncover specific GO terms/phosphorylation pathways in phosphoproteomic data in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2021, 21, 592.	1.6	1

#	ARTICLE	IF	CITATIONS
27260	Meta-Analysis of Transcriptome-Wide Association Studies across 13 Brain Tissues Identified Novel Clusters of Genes Associated with Nicotine Addiction. <i>Genes</i> , 2022, 13, 37.	1.0	1
27261	Genome-Wide Variation Analysis of Four Vegetable Soybean Cultivars Based on Re-Sequencing. <i>Plants</i> , 2022, 11, 28.	1.6	3
27262	Bacteriostatic effects of high-intensity ultrasonic treatment on <i>Bacillus subtilis</i> vegetative cells. <i>Ultrasonics Sonochemistry</i> , 2021, 81, 105862.	3.8	10
27263	Metabolic drug survey highlights cancer cell dependencies and vulnerabilities. <i>Nature Communications</i> , 2021, 12, 7190.	5.8	7
27264	Genome-wide association study identifies variants of <i>GhSAD1</i> conferring cold tolerance in cotton. <i>Journal of Experimental Botany</i> , 2022, 73, 2222-2237.	2.4	9
27266	Profiles of immune cell infiltration and immune-related genes in the tumor microenvironment of osteosarcoma cancer. <i>BMC Cancer</i> , 2021, 21, 1345.	1.1	12
27267	Integrative analysis of lung molecular signatures reveals key drivers of idiopathic pulmonary fibrosis. <i>BMC Pulmonary Medicine</i> , 2021, 21, 404.	0.8	11
27269	Single-Cell Analysis of Aneurysmal Aortic Tissue in Patients with Marfan Syndrome Reveals Dysfunctional TGF- β Signaling. <i>Genes</i> , 2022, 13, 95.	1.0	19
27272	Surviving in a sea of data: a survey of plant genome data resources and issues in building data management systems. <i>Plant Molecular Biology</i> , 2002, 48, 59-74.	2.0	2
27273	DAVID: Database for Annotation, Visualization, and Integrated Discovery. <i>Genome Biology</i> , 2003, 4, P3.	3.8	4,682
27274	Identification and comparison of microRNAs in pituitary gland during prenatal and postnatal stages of sheep by deep sequencing. <i>Journal of Genetics</i> , 2018, 97, 965-975.	0.4	5
27276	Screening of differentially expressed miRNAs during osteogenic/odontogenic differentiation of human dental pulp stem cells exposed to mechanical stress. <i>American Journal of Translational Research (discontinued)</i> , 2021, 13, 11126-11143.	0.0	0
27277	Identification of key pathways and RNAs associated with skeletal muscle atrophy after spinal cord injury. <i>Journal of Musculoskeletal Neuronal Interactions</i> , 2021, 21, 550-559.	0.1	0
27278	Identification of genes and pathways leading to poor prognosis of non-small cell lung cancer using integrated bioinformatics analysis. <i>Translational Cancer Research</i> , 2022, 11, 710-724.	0.4	1
27279	Modern Approaches for Transcriptome Analyses in Plants. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1346, 11-50.	0.8	0
27280	Probabilistic Graphical Models Applied to Biological Networks. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1346, 119-130.	0.8	0
27281	The Gene Signatures of Human Alpha Cells in Types 1 and 2 Diabetes Indicate Disease-Specific Pathways of Alpha Cell Dysfunction. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
27282	Transcriptogram analysis reveals relationship between viral titer and gene sets responses during Corona-virus infection. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, Iqac020.	1.5	2

#	ARTICLE	IF	CITATIONS
27284	Analyzing Effect of Multi-modality in Predicting Protein-Protein Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, PP, 1-1.	1.9	2
27285	Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle <i>Pollicipes pollicipes</i> . GigaScience, 2022, 11, .	3.3	8
27286	Construction of Eriocheir sinensis Protein-protein Interaction Network and Extraction of Molting Sub-network. , 2022, , .		0
27287	An engineered nano-liposome-human ACE2 decoy neutralizes SARS-CoV-2 Spike protein-induced inflammation in both murine and human macrophages. Theranostics, 2022, 12, 2639-2657.	4.6	19
27288	A high-quality assembled genome and its comparative analysis decode the adaptive molecular mechanism of the number one Chinese cotton variety CRI-12. GigaScience, 2022, 11, .	3.3	6
27289	Toxicogenomics for the prediction of carcinogenicity of xenobiotic substances. , 2022, , 283-306.		0
27291	A Semantic Framework Supporting Multilayer Networks Analysis for Rare Diseases. International Journal on Semantic Web and Information Systems, 2022, 18, 1-22.	2.2	6
27292	A high-quality assembly reveals genomic characteristics, phylogenetic status, and causal genes for leucism plumage of Indian peafowl. GigaScience, 2022, 11, .	3.3	10
27293	Investigation of miR-21-5p Key Target Genes and Pathways in Head and Neck Squamous Cell Carcinoma Based on TCGA Database and Bioinformatics Analysis. Technology in Cancer Research and Treatment, 2022, 21, 153303382210812.	0.8	1
27294	Nextcast: A software suite to analyse and model toxicogenomics data. Computational and Structural Biotechnology Journal, 2022, 20, 1413-1426.	1.9	5
27295	Novel split quality measures for stratified multilabel cross validation with application to large and sparse gene ontology datasets. , 2022, 2, 49-62.		2
27296	High Expression of HERV-K (HML-2) Might Stimulate Interferon in COVID-19 Patients. SSRN Electronic Journal, 0, , .	0.4	4
27297	Analysis of Liver Responses to Non-alcoholic Steatohepatitis by mRNA-Sequencing. Methods in Molecular Biology, 2022, 2455, 163-179.	0.4	1
27299	Topological Simplifications of Hypergraphs. IEEE Transactions on Visualization and Computer Graphics, 2023, 29, 3209-3225.	2.9	5
27300	Nutrigenomics in livestock: potential role in physiological regulation and practical applications. Animal Production Science, 2022, 62, 901-912.	0.6	4
27302	An RNA-Based Precision Oncology Platform for Patient-Therapy Alignment in a Diverse Set of Treatment Resistant Malignancies. SSRN Electronic Journal, 0, , .	0.4	0
27303	Genomic Variant Annotation: A Comprehensive Review of Tools and Techniques. Lecture Notes in Networks and Systems, 2022, , 1057-1067.	0.5	1
27304	A multi-network integration approach for measuring disease similarity based on ncRNA regulation and heterogeneous information. BMC Bioinformatics, 2022, 23, 89.	1.2	0

#	ARTICLE	IF	CITATIONS
27305	Integrative Analysis of Spatial Transcriptome with Single-Cell Transcriptome and Single-Cell Epigenome in Mouse Lungs after Immunization. SSRN Electronic Journal, 0, , .	0.4	0
27307	Chromosome-scale assembly and population diversity analyses provide insights into the evolution of <i>Sapindus mukorossi</i> . Horticulture Research, 2022, 9, .	2.9	4
27308	Altered Expression of Specific MicroRNAs in Plasma of Aneurysmal Subarachnoid Hemorrhage Patients. Frontiers in Neurology, 2022, 13, 842888.	1.1	4
27309	Smoking Status and Type 2 Diabetes, and Cardiovascular Disease: A Comprehensive Analysis of Shared Genetic Etiology and Causal Relationship. Frontiers in Endocrinology, 2022, 13, 809445.	1.5	11
27312	The m6A(m)-independent role of FTO in regulating WNT signaling pathways. Life Science Alliance, 2022, 5, e202101250.	1.3	9
27313	Identification of Potential Immune Checkpoint Inhibitor Targets in Gliomas via Bioinformatic Analyses. BioMed Research International, 2022, 2022, 1-16.	0.9	4
27314	Pan-Cancer Analysis and Validation Reveals that D-Dimer-Related Genes are Prognostic and Downregulate CD8+ T Cells via TGF-Beta Signaling in Gastric Cancer. Frontiers in Molecular Biosciences, 2022, 9, 790706.	1.6	2
27315	Comparative Analysis of Gene Expression Profiles in the Adipose Tissue of Obese Adult Mice With Rapid Infantile Growth After Undernourishment In Utero. Frontiers in Endocrinology, 2022, 13, 818064.	1.5	0
27316	Inhibition of miR-128 Enhances Vocal Sequence Organization in Juvenile Songbirds. Frontiers in Behavioral Neuroscience, 2022, 16, 833383.	1.0	0
27317	Etiological roles of core promoter variation in triple-negative breast cancer. Genes and Diseases, 2023, 10, 228-238.	1.5	1
27318	Cold Exposure Induces Depot-Specific Alterations in Fatty Acid Composition and Transcriptional Profile in Adipose Tissues of Pigs. Frontiers in Endocrinology, 2022, 13, 827523.	1.5	4
27319	Decoding the Role of Astrocytes in the Entorhinal Cortex in Alzheimer's Disease Using High-Dimensional Single-Nucleus RNA Sequencing Data and Next-Generation Knowledge Discovery Methodologies: Focus on Drugs and Natural Product Remedies for Dementia. Frontiers in Pharmacology, 2021, 12, 720170.	1.6	12
27320	Missing Links Between Gene Function and Physiology in Genomics. Frontiers in Physiology, 2022, 13, 815874.	1.3	1
27322	Transcriptomic Analysis Reveal the Molecular Mechanisms of Seed Coat Development in Cucurbita pepo L.. Frontiers in Plant Science, 2022, 13, 772685.	1.7	3
27323	iTRAQ Proteomic Analysis of Interactions Between 20E and Phospholipase C in <i>Apolygus lucorum</i> (Meyer-Dall'ara). Frontiers in Physiology, 2022, 13, 845087.	1.3	0
27324	Modeling oxidative injury response in human kidney organoids. Stem Cell Research and Therapy, 2022, 13, 76.	2.4	14
27325	Diverse injury responses of human oligodendrocyte to mediators implicated in multiple sclerosis. Brain, 2022, 145, 4320-4333.	3.7	9
27326	<i>Haloterrigena gelatinilytica</i> sp. nov., a new extremely halophilic archaeon isolated from salt-lake. Archives of Microbiology, 2022, 204, 176.	1.0	1

#	ARTICLE	IF	CITATIONS
27327	A Novel Full-Length Transcriptome Resource for Sea Cucumber <i>Apostichopus japonicus</i> Using Pacbio SMRT Sequencing. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	1
27329	Insights Into the Impact of Small RNA SprC on the Metabolism and Virulence of <i>Staphylococcus aureus</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 746746.	1.8	1
27330	Single-cell dissection of the human brain vasculature. <i>Nature</i> , 2022, 603, 893-899.	13.7	135
27331	Hypertrophic chondrocytes serve as a reservoir for marrow-associated skeletal stem and progenitor cells, osteoblasts, and adipocytes during skeletal development. <i>ELife</i> , 2022, 11, .	2.8	28
27332	PreRBP-TL: prediction of species-specific RNA-binding proteins based on transfer learning. <i>Bioinformatics</i> , 2022, 38, 2135-2143.	1.8	17
27333	Whole Blood Metabolite Profiles Reflect Changes in Energy Metabolism in Heart Failure. <i>Metabolites</i> , 2022, 12, 216.	1.3	5
27335	DVPred: a disease-specific prediction tool for variant pathogenicity classification for hearing loss. <i>Human Genetics</i> , 2022, 141, 401-411.	1.8	6
27336	Identification of Important Genes Involved in the Sex-Differentiation Mechanism of Oriental River Prawn, <i>Macrobrachium nipponense</i> , During the Gonad Differentiation and Development Period. <i>Frontiers in Genetics</i> , 2022, 13, 797796.	1.1	3
27337	Comparative transcriptome analysis provides insights into grain filling commonalities and differences between foxtail millet [<i>Setaria italica</i> (L.) P. Beauv.] varieties with different panicle types. <i>PeerJ</i> , 2022, 10, e12968.	0.9	3
27338	TransformerGO: predicting protein-protein interactions by modelling the attention between sets of gene ontology terms. <i>Bioinformatics</i> , 2022, 38, 2269-2277.	1.8	25
27339	Efficient link prediction in the protein-protein interaction network using topological information in a generative adversarial network machine learning model. <i>BMC Bioinformatics</i> , 2022, 23, 78.	1.2	12
27340	Identification of differentially expressed and methylated genes and construction of a co-expression network in age-related macular degeneration. <i>Annals of Translational Medicine</i> , 2022, 10, 223-223.	0.7	5
27341	Evaluating the detection ability of a range of epistasis detection methods on simulated data for pure and impure epistatic models. <i>PLoS ONE</i> , 2022, 17, e0263390.	1.1	7
27343	Wei2GO: weighted sequence similarity-based protein function prediction. <i>PeerJ</i> , 2022, 10, e12931.	0.9	5
27344	Impact of Pals1 on Expression and Localization of Transporters Belonging to the Solute Carrier Family. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 792829.	1.6	2
27345	Identification of clusterin as a serum biomarker candidate contributed to the lung fibroblasts activation in chronic obstructive pulmonary disease. <i>Chinese Medical Journal</i> , 2022, Publish Ahead of Print, .	0.9	3
27346	Genomic characterization of the world's longest selection experiment in mouse reveals the complexity of polygenic traits. <i>BMC Biology</i> , 2022, 20, 52.	1.7	4
27347	Network Analysis Reveals Different Cellulose Degradation Strategies Across <i>Trichoderma harzianum</i> Strains Associated With XYR1 and CRE1. <i>Frontiers in Genetics</i> , 2022, 13, 807243.	1.1	8

#	ARTICLE	IF	CITATIONS
27348	Quantitative multiplexed proteomics analysis reveals reshaping of the lysine 2-hydroxyisobutyrylome in <i>Fusarium graminearum</i> by tebuconazole. <i>BMC Genomics</i> , 2022, 23, 145.	1.2	7
27349	Deciphering the Interactions of SARS-CoV-2 Proteins with Human Ion Channels Using Machine-Learning-Based Methods. <i>Pathogens</i> , 2022, 11, 259.	1.2	3
27350	Mechanism of action of <i>Tripterygium wilfordii</i> for treatment of idiopathic membranous nephropathy based on network pharmacology. <i>Renal Failure</i> , 2022, 44, 116-125.	0.8	4
27351	Discovery of the Xenon-Protein Interactome Using Large-Scale Measurements of Protein Folding and Stability. <i>Journal of the American Chemical Society</i> , 2022, 144, 3925-3938.	6.6	7
27352	Time-course RNA-seq analysis reveals stage-specific and melatonin-triggered gene expression patterns during the hair follicle growth cycle in <i>Capra hircus</i> . <i>BMC Genomics</i> , 2022, 23, 140.	1.2	10
27353	Comparative transcriptome and weighted correlation network analyses reveal candidate genes involved in chlorogenic acid biosynthesis in sweet potato. <i>Scientific Reports</i> , 2022, 12, 2770.	1.6	8
27354	Comparative proteome analysis reveals the role of negative floral regulators and defense-related genes in phytoplasma infected sesame. <i>Protoplasma</i> , 2022, 259, 1441-1453.	1.0	4
27355	Conserved Regulatory Pathways for Stock-Scion Healing Revealed by Comparative Analysis of Arabidopsis and Tomato Grafting Transcriptomes. <i>Frontiers in Plant Science</i> , 2021, 12, 810465.	1.7	5
27356	Operational tolerance after hematopoietic stem cell transplantation is characterized by distinct transcriptional, phenotypic, and metabolic signatures. <i>Science Translational Medicine</i> , 2022, 14, eabg3083.	5.8	5
27357	Chemerin Impact on Alternative mRNA Transcription in the Porcine Luteal Cells. <i>Cells</i> , 2022, 11, 715.	1.8	7
27358	A High-Quality, Chromosome-Level Genome Provides Insights Into Determinate Flowering Time and Color of Cotton Rose (<i>Hibiscus mutabilis</i>). <i>Frontiers in Plant Science</i> , 2022, 13, 818206.	1.7	3
27359	<i>Halobaculum rubrum</i> sp. nov., an extremely halophilic archaeon isolated from a salt lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	7
27360	Genome-Wide Association Study Reveals Genetic Architecture and Candidate Genes for Yield and Related Traits under Terminal Drought, Combined Heat and Drought in Tropical Maize Germplasm. <i>Genes</i> , 2022, 13, 349.	1.0	7
27361	Physiological and transcriptome analysis reveals the differences in nitrate content between lamina and midrib of flue-cured tobacco. <i>Scientific Reports</i> , 2022, 12, 2932.	1.6	1
27362	Comprehensive Analysis of the Effect of 20(R)-Ginsenoside Rg3 on Stroke Recovery in Rats via the Integrative miRNA-mRNA Regulatory Network. <i>Molecules</i> , 2022, 27, 1573.	1.7	6
27363	MYH10 Governs Adipocyte Function and Adipogenesis through Its Interaction with GLUT4. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2367.	1.8	7
27364	Proteome-defined changes in cellular pathways for decidua and trophoblast tissues associated with location and viability of early-stage pregnancy. <i>Reproductive Biology and Endocrinology</i> , 2022, 20, 36.	1.4	2
27365	Comparative Transcriptome Analysis of Bt Resistant and Susceptible Strains in <i>Ostrinia furnacalis</i> (Guenée) (Lepidoptera: Crambidae). <i>Agriculture (Switzerland)</i> , 2022, 12, 298.	1.4	1

#	ARTICLE	IF	CITATIONS
27367	Identification and Comprehensive Analysis of <i>FREM2</i> Mutation as a Potential Prognostic Biomarker in Colorectal Cancer. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 839617.	1.6	6
27368	Zebrafish information network, the knowledgebase for <i>Danio rerio</i> research. <i>Genetics</i> , 2022, 220, .	1.2	89
27369	Comparative transcriptomes of three different skin sites for the Asiatic toad (<i>Bufo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 Td (gar	0.9	1
27370	SMRT sequencing of full-length transcriptome and gene expression analysis in two chemical types of <i>Pogostemon cablin</i> (Blanco) Benth.. <i>PeerJ</i> , 2022, 10, e12940.	0.9	4
27372	Dynamic Control Balancing Cell Proliferation and Inflammation is Crucial for an Effective Immune Response to Malaria. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 800721.	1.6	8
27373	Stage-differentiated ensemble modeling of DNA methylation landscapes uncovers salient biomarkers and prognostic signatures in colorectal cancer progression. <i>PLoS ONE</i> , 2022, 17, e0249151.	1.1	9
27374	Homozygous variants in <i>AKAP3</i> induce asthenoteratozoospermia and male infertility. <i>Journal of Medical Genetics</i> , 2023, 60, 137-143.	1.5	9
27375	Molecular phylogeography and species distribution modelling evidence of "oceanic" adaptation for <i>Actinidia eriantha</i> with a refugium along the oceanic-continental gradient in a biodiversity hotspot. <i>BMC Plant Biology</i> , 2022, 22, 89.	1.6	6
27376	Multi-Approach Analysis Reveals Pathways of Cold Tolerance Divergence in <i>Camellia japonica</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 811791.	1.7	4
27377	Characterization of Mitochondrial Proteome and Function in Luminal A and Basal-like Breast Cancer Subtypes Reveals Alteration in Mitochondrial Dynamics and Bioenergetics Relevant to Their Diagnosis. <i>Biomolecules</i> , 2022, 12, 379.	1.8	2
27378	Identification of Potential Key Biomarkers and Immune Infiltration in Oral Lichen Planus. <i>Disease Markers</i> , 2022, 2022, 1-20.	0.6	4
27379	Transient Agarose Spot (TAS) Assay: A New Method to Investigate Cell Migration. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2119.	1.8	4
27380	MonaGO: a novel gene ontology enrichment analysis visualisation system. <i>BMC Bioinformatics</i> , 2022, 23, 69.	1.2	12
27382	Proteome Analysis of Urinary Biomarkers in a Bovine IRBP-Induced Uveitis Rat Model via Data-Independent Acquisition and Parallel Reaction Monitoring Proteomics. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 831632.	1.6	1
27383	Harmonizing model organism data in the Alliance of Genome Resources. <i>Genetics</i> , 2022, 220, .	1.2	52
27384	Genome assembly of the JD17 soybean provides a new reference genome for comparative genomics. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
27385	Protective immune trajectories in early viral containment of non-pneumonic SARS-CoV-2 infection. <i>Nature Communications</i> , 2022, 13, 1018.	5.8	16
27386	Zika virus disrupts gene expression in human myoblasts and myotubes: Relationship with susceptibility to infection. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010166.	1.3	3

#	ARTICLE	IF	CITATIONS
27388	Immune Defense Mechanism of <i>Reticulitermes chinensis</i> Snyder (Blattodea: Isoptera) against <i>Serratia marcescens</i> Bizio. <i>Insects</i> , 2022, 13, 226.	1.0	2
27389	Sugarcane Transcriptomics in Response to Abiotic and Biotic Stresses: A Review. <i>Sugar Tech</i> , 2022, 24, 1295-1318.	0.9	5
27390	Genomic Analyses of the Fungus <i>Paraconiothyrium</i> sp. Isolated from the Chinese White Wax Scale Insect Reveals Its Symbiotic Character. <i>Genes</i> , 2022, 13, 338.	1.0	4
27391	Functional buffering via cell-specific gene expression promotes tissue homeostasis and cancer robustness. <i>Scientific Reports</i> , 2022, 12, 2974.	1.6	2
27392	Genome and Comparative Transcriptome Dissection Provide Insights Into Molecular Mechanisms of Sclerotium Formation in Culinary-Medicinal Mushroom <i>Pleurotus tuber-regium</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 815954.	1.5	1
27393	Indolethylamine-N-Methyltransferase Inhibits Proliferation and Promotes Apoptosis of Human Prostate Cancer Cells: A Mechanistic Exploration. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 805402.	1.8	5
27394	Integrative Analyses of Genes Associated With Otologic Disorders in Turner Syndrome. <i>Frontiers in Genetics</i> , 2022, 13, 799783.	1.1	0
27395	Combined Transcriptomic and Proteomic Profiling of <i>E. coli</i> under Microaerobic versus Aerobic Conditions: The Multifaceted Roles of Noncoding Small RNAs and Oxygen-Dependent Sensing in Global Gene Expression Control. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2570.	1.8	5
27396	Cultivating <i>Lentinula edodes</i> on Substrate Containing Composted Sawdust Affects the Expression of Carbohydrate and Aromatic Amino Acid Metabolism-Related Genes. <i>MSystems</i> , 2022, 7, e0082721.	1.7	5
27397	Hyaluronidase-1-mediated glycoalyx impairment underlies endothelial abnormalities in polypoidal choroidal vasculopathy. <i>BMC Biology</i> , 2022, 20, 47.	1.7	3
27398	A Pathway-Specific Polygenic Risk Score Is Associated with Tau Pathology and Cognitive Decline. <i>Journal of Alzheimer's Disease</i> , 2022, 85, 1745-1754.	1.2	4
27400	Combined use of Oxford Nanopore and Illumina sequencing yields insights into soybean structural variation biology. <i>BMC Biology</i> , 2022, 20, 53.	1.7	10
27401	DrGA: cancer driver gene analysis in a simpler manner. <i>BMC Bioinformatics</i> , 2022, 23, 86.	1.2	1
27402	HSPB8 is a Potential Prognostic Biomarker that Correlates With Immune Cell Infiltration in Bladder Cancer. <i>Frontiers in Genetics</i> , 2022, 13, 804858.	1.1	2
27403	High-Quality Genome Sequence Data of <i>Trichoderma gracile</i> HK011-1, a Fungal Antagonistic Agent Against Plant Pathogens. <i>Plant Disease</i> , 2022, 106, 1035-1038.	0.7	2
27404	Environmental Phenol and Paraben Exposure Risks and Their Potential Influence on the Gene Expression Involved in the Prognosis of Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3679.	1.8	9
27405	Whole-Genome and Transcriptome Sequencing-Based Characterization of <i>Bacillus Cereus</i> NR1 From Subtropical Marine Mangrove and Its Potential Role in Sulfur Metabolism. <i>Frontiers in Microbiology</i> , 2022, 13, 856092.	1.5	8
27406	Evaluation of Early Biomarkers of Atherosclerosis Associated with Polychlorinated Biphenyl Exposure: An <i>in Vitro</i> and <i>in Vivo</i> Study. <i>Environmental Health Perspectives</i> , 2022, 130, 37011.	2.8	11

#	ARTICLE	IF	CITATIONS
27407	Integrative Analyses of Circulating mRNA and lncRNA Expression Profile in Plasma of Lung Cancer Patients. <i>Frontiers in Oncology</i> , 2022, 12, 843054.	1.3	2
27408	ADH1C inhibits progression of colorectal cancer through the ADH1C/PHGDH /PSAT1/serine metabolic pathway. <i>Acta Pharmacologica Sinica</i> , 2022, 43, 2709-2722.	2.8	14
27409	A collaborative semantic-based provenance management platform for reproducibility. <i>PeerJ Computer Science</i> , 2022, 8, e921.	2.7	2
27410	Targeting SOX10-deficient cells to reduce the dormant-invasive phenotype state in melanoma. <i>Nature Communications</i> , 2022, 13, 1381.	5.8	31
27411	Comprehensive Analysis of the Transcriptome-Wide m6A Methylation in Mouse Pachytene Spermatocytes and Round Spermatids. <i>Frontiers in Genetics</i> , 2022, 13, 832677.	1.1	3
27412	The NADPARK study: A randomized phase I trial of nicotinamide riboside supplementation in Parkinson's disease. <i>Cell Metabolism</i> , 2022, 34, 396-407.e6.	7.2	111
27414	Comparative Transcriptome Analysis Provides Insight into Spatio-Temporal Expression Characteristics and Genetic Regulatory Network in Postnatal Developing Subcutaneous and Visceral Fat of Bama Pig. <i>Frontiers in Genetics</i> , 2022, 13, 844833.	1.1	4
27415	A multidimensional coding architecture of the vagal interoceptive system. <i>Nature</i> , 2022, 603, 878-884.	13.7	71
27416	Tissue extracellular matrix hydrogels as alternatives to Matrigel for culturing gastrointestinal organoids. <i>Nature Communications</i> , 2022, 13, 1692.	5.8	101
27418	Providing Adverse Outcome Pathways from the AOP-Wiki in a Semantic Web Format to Increase Usability and Accessibility of the Content. <i>Applied in Vitro Toxicology</i> , 2022, 8, 2-13.	0.6	10
27419	Deep Single-Cell-Type Proteome Profiling of Mouse Brain by Nonsurgical AAV-Mediated Proximity Labeling. <i>Analytical Chemistry</i> , 2022, 94, 5325-5334.	3.2	17
27421	The Glycolytic Gatekeeper PDK1 defines different metabolic states between genetically distinct subtypes of human acute myeloid leukemia. <i>Nature Communications</i> , 2022, 13, 1105.	5.8	14
27422	Network Crosstalk as a Basis for Drug Repurposing. <i>Frontiers in Genetics</i> , 2022, 13, 792090.	1.1	0
27423	Early-Life Pb Exposure Might Exert Synapse-Toxic Effects Via Inhibiting Synapse-Associated Membrane Protein 2 (VAMP2) Mediated by Upregulation of miR-34b. <i>Journal of Alzheimer's Disease</i> , 2022, 87, 619-633.	1.2	3
27424	Pituitary Gonadotropin Gene Expression During Induced Onset of Postsmolt Maturation in Male Atlantic Salmon: In Vivo and Tissue Culture Studies. <i>Frontiers in Endocrinology</i> , 2022, 13, 826920.	1.5	4
27425	De novo assembly of a fruit transcriptome set identifies AmMYB10 as a key regulator of anthocyanin biosynthesis in <i>Aronia melanocarpa</i> . <i>BMC Plant Biology</i> , 2022, 22, 143.	1.6	3
27427	Exogenous calcium application enhances salt tolerance of sweet sorghum seedlings. <i>Journal of Agronomy and Crop Science</i> , 2022, 208, 441-453.	1.7	12
27428	Comprehensive Transcriptome Analysis of Stem-Differentiating Xylem Upon Compression Stress in <i>Cunninghamia lanceolata</i> . <i>Frontiers in Genetics</i> , 2022, 13, 843269.	1.1	4

#	ARTICLE	IF	CITATIONS
27429	Mass Spectrometric Behavior and Molecular Mechanisms of Fermented Deoxyanthocyanidins to Alleviate Ulcerative Colitis Based on Network Pharmacology. <i>International Journal of Analytical Chemistry</i> , 2022, 2022, 1-12.	0.4	1
27430	The genome of <i>Hibiscus hamabo</i> reveals its adaptation to saline and waterlogged habitat. <i>Horticulture Research</i> , 2022, 9, uhac067.	2.9	12
27431	Single nucleotide polymorphism discovery and functional annotation analysis of blackberry fruit. <i>Trees - Structure and Function</i> , 0, , 1.	0.9	1
27432	RNA-seq and integrated network analysis reveals the hub genes and key pathway of paclitaxel inhibition on Adriamycin resistant diffuse large B cell lymphoma cells. <i>Bioengineered</i> , 2022, 13, 7607-7621.	1.4	3
27434	Transcriptional analysis of peripheral memory T cells reveals Parkinson's disease-specific gene signatures. <i>Npj Parkinson's Disease</i> , 2022, 8, 30.	2.5	20
27435	Screening of key methylation-driven genes CDO1 in breast cancer based on WGCNA. <i>Cancer Biomarkers</i> , 2022, 34, 571-582.	0.8	1
27436	Gene and Metabolite Co-Analysis through Transcriptome and Metabolome Provide New Insight into Drought Stress Tolerance in <i>Tillandsia</i> (Bromeliaceae). <i>Russian Journal of Plant Physiology</i> , 2022, 69, 1.	0.5	1
27437	Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro. <i>Nature Biotechnology</i> , 2022, 40, 1220-1230.	9.4	46
27438	Pan-Genomic and Transcriptomic Analyses of Marine Pseudoalteromonas agarivorans Hao 2018 Revealed Its Genomic and Metabolic Features. <i>Marine Drugs</i> , 2022, 20, 248.	2.2	0
27439	Integrative Analysis of Biomarkers and Mechanisms in Adamantinomatous Craniopharyngioma. <i>Frontiers in Genetics</i> , 2022, 13, 830793.	1.1	6
27440	<i>CiKN1</i> and <i>CiKN6</i> are involved in leaf development in citrus by regulating <i>CimiR164</i> . <i>Plant Journal</i> , 2022, 110, 828-848.	2.8	10
27441	Bioinformatics Analysis and Identification of Potential Genes Associated with Pathogenesis and Prognosis of Gastric Cancer. <i>Current Medical Science</i> , 2022, 42, 357-372.	0.7	1
27443	RNA-Seq reveals miRNA role in thermogenic regulation in brown adipose tissues of goats. <i>BMC Genomics</i> , 2022, 23, 186.	1.2	7
27444	Pangenome Analysis of the Soilborne Fungal Phytopathogen <i>Rhizoctonia solani</i> and Development of a Comprehensive Web Resource: RsolaniDB. <i>Frontiers in Microbiology</i> , 2022, 13, 839524.	1.5	14
27445	WhiB4 Is Required for the Reactivation of Persistent Infection of <i>Mycobacterium marinum</i> in Zebrafish. <i>Microbiology Spectrum</i> , 2022, 10, e0044321.	1.2	2
27446	Human biliary epithelial cells from discarded donor livers rescue bile duct structure and function in a mouse model of biliary disease. <i>Cell Stem Cell</i> , 2022, 29, 355-371.e10.	5.2	19
27447	Identification and Verification of Potential Hub Genes in Amphetamine-Type Stimulant (ATS) and Opioid Dependence by Bioinformatic Analysis. <i>Frontiers in Genetics</i> , 2022, 13, 837123.	1.1	0
27448	Genome-wide association analysis for susceptibility to infection by <i>Mycobacterium avium</i> ssp. <i>paratuberculosis</i> in US Holsteins. <i>Journal of Dairy Science</i> , 2022, 105, 4301-4313.	1.4	9

#	ARTICLE	IF	CITATIONS
27450	Chondroitin Sulfate Proteoglycans Are De Facto Cellular Receptors for Human Papillomavirus 16 under High Serum Conditions. <i>Journal of Virology</i> , 2022, 96, e0185721.	1.5	7
27451	Acetate Degradation at Low pH by the Moderately Acidophilic Sulfate Reducer <i>Acididesulfobacillus acetoxydans</i> gen. nov. sp. nov.. <i>Frontiers in Microbiology</i> , 2022, 13, 816605.	1.5	6
27452	Transcriptome Analysis Revealed a Cold Stress-Responsive Transcription Factor, PaDREB1A, in <i>Plumbago auriculata</i> That Can Confer Cold Tolerance in Transgenic <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 760460.	1.7	3
27454	In silico Analysis of Publicly Available Transcriptomics Data Identifies Putative Prognostic and Therapeutic Molecular Targets for Papillary Thyroid Carcinoma. <i>International Journal of General Medicine</i> , 2022, Volume 15, 3097-3120.	0.8	1
27455	A chromosome-level genome assembly of <i>Paracymoriza distinctalis</i> (Lepidoptera: Crambidae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	0.6	0
27456	CircOAS3 Regulates Keratinocyte Proliferation and Psoriatic Inflammation by Interacting with Hsc70 via the JNK/STAT3/NF- κ B Signaling Pathway. <i>Inflammation</i> , 2022, 45, 1924-1935.	1.7	7
27457	Tig1 regulates proximo-distal identity during salamander limb regeneration. <i>Nature Communications</i> , 2022, 13, 1141.	5.8	7
27459	Integrative analysis of key microRNA-mRNA complexes and pathways in aortic aneurysm. <i>Annals of Translational Medicine</i> , 2022, 10, 358-358.	0.7	1
27460	Incorporating regulatory interactions into gene-set analyses for GWAS data: A controlled analysis with the MAGMA tool. <i>PLoS Computational Biology</i> , 2022, 18, e1009908.	1.5	3
27461	Generation and Gene Expression Profiles of Grevy's Zebra Induced Pluripotent Stem Cells. <i>Stem Cells and Development</i> , 2022, 31, 250-257.	1.1	3
27464	Learning Ability and Hippocampal Transcriptome Responses to Early and Later Life Environmental Complexities in Dual-Purpose Chicks. <i>Animals</i> , 2022, 12, 668.	1.0	0
27465	Creating ontological definitions for use in science. <i>Qeios</i> , 0, , .	0.0	4
27466	Computing microRNA-gene interaction networks in pan-cancer using miRDriver. <i>Scientific Reports</i> , 2022, 12, 3717.	1.6	3
27467	Differential expression of ginsenoside biosynthesis-related genes at an early developmental stage of <i>Panax vietnamensis</i> . <i>Plant Biotechnology Reports</i> , 2022, 16, 215-228.	0.9	1
27468	GOing Forward With the Cardiac Conduction System Using Gene Ontology. <i>Frontiers in Genetics</i> , 2022, 13, 802393.	1.1	7
27469	High Resistance to Quinclorac in Multiple-Resistant <i>Echinochloa colona</i> Associated with Elevated Stress Tolerance Gene Expression and Enriched Xenobiotic Detoxification Pathway. <i>Genes</i> , 2022, 13, 515.	1.0	9
27470	GATA4/5/6 family transcription factors are conserved determinants of cardiac versus pharyngeal mesoderm fate. <i>Science Advances</i> , 2022, 8, eabg0834.	4.7	14
27471	FlyBase: a guided tour of highlighted features. <i>Genetics</i> , 2022, 220, .	1.2	281

#	ARTICLE	IF	CITATIONS
27472	Analysis of the role and mechanism of EGCG in septic cardiomyopathy based on network pharmacology. <i>PeerJ</i> , 2022, 10, e12994.	0.9	5
27473	Species Persistence with Hybridization in Toad-Headed Lizards Driven by Divergent Selection and Low Recombination. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
27474	A Secondary Metabolism Pathway Involved in the Production of a Putative Toxin Is Expressed at Early Stage of <i>Monilinia laxa</i> Infection. <i>Frontiers in Plant Science</i> , 2022, 13, 818483.	1.7	1
27476	<i>Drosophila</i> functional screening of de novo variants in autism uncovers damaging variants and facilitates discovery of rare neurodevelopmental diseases. <i>Cell Reports</i> , 2022, 38, 110517.	2.9	24
27477	Whole-Genome Sequence Resource of <i>Fusarium oxysporum</i> Strain TH15, a Plant Growth Promoting Endophytic Fungus Isolated from <i>Tetrastigma hemsleyanum</i> . <i>PhytoFrontiers</i> , 2022, 2, 314-319.	0.8	4
27478	Yin Yang 1 regulates ITGAV and ITGB1, contributing to improved prognosis of colorectal cancer. <i>Oncology Reports</i> , 2022, 47, .	1.2	6
27479	Transcriptome Analysis of <i>Plasmodium falciparum</i> Isolates From Benin Reveals Specific Gene Expression Associated With Cerebral Malaria. <i>Journal of Infectious Diseases</i> , 2022, 225, 2187-2196.	1.9	11
27480	Context mining and graph queries on giant biomedical knowledge graphs. <i>Knowledge and Information Systems</i> , 2022, 64, 1239-1262.	2.1	5
27481	Circulating Vitreous microRNA as Possible Biomarker in High Myopic Eyes with Macular Hole. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3647.	1.8	6
27484	Patterns of genomic divergence in sympatric and allopatric speciation of three <i>Mihoutao</i> (<i>Actinidia</i>) species. <i>Horticulture Research</i> , 2022, 9, uhac054.	2.9	5
27485	A phase 2a randomized vehicle-controlled multi-center study of the safety and efficacy of delgocitinib in subjects with moderate-to-severe alopecia areata. <i>Archives of Dermatological Research</i> , 2022, , .	1.1	15
27486	Annotating regulatory elements by heterogeneous network embedding. <i>Bioinformatics</i> , 2022, 38, 2899-2911.	1.8	2
27487	Iron promotes Slc7a11-deficient valvular interstitial cell osteogenic differentiation: A possible mechanism by which ferroptosis participates in intraleaflet hemorrhage-induced calcification. <i>Free Radical Biology and Medicine</i> , 2022, 184, 158-169.	1.3	5
27488	Identification of Down-Regulated ADH1C is Associated With Poor Prognosis in Colorectal Cancer Using Bioinformatics Analysis. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 791249.	1.6	8
27490	CRISPR/Cas9-Mediated Insertion of HIV Long Terminal Repeat within <i>BACH2</i> Promotes Expansion of T Regulatory-like Cells. <i>Journal of Immunology</i> , 2022, 208, 1700-1710.	0.4	4
27491	Tsp-1 is involved in DNA stability through Tgf- β 1 activation domain in cone photoreceptor 661W cells. <i>Cell and Tissue Research</i> , 2022, , 1.	1.5	1
27492	Outstanding prognostic value of novel ferroptosis-related genes in chemoresistance osteosarcoma patients. <i>Scientific Reports</i> , 2022, 12, 5029.	1.6	11
27493	<i>NS</i> encodes an auxin transporter that regulates the "numerous spines" trait in cucumber (<i>Cucumis sativus</i>) fruit. <i>Plant Journal</i> , 2022, 110, 325-336.	2.8	10

#	ARTICLE	IF	CITATIONS
27494	The LINC00452/miR-204/CHST4 Axis Regulating Thymic Tregs Might Be Involved in the Progression of Thymoma-Associated Myasthenia Gravis. <i>Frontiers in Neurology</i> , 2022, 13, 828970.	1.1	3
27495	Identification and New Indication of Melanin-Concentrating Hormone Receptor 1 (MCHR1) Antagonist Derived from Machine Learning and Transcriptome-Based Drug Repositioning Approaches. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3807.	1.8	4
27498	GXP: Analyze and Plot Plant Omics Data in Web Browsers. <i>Plants</i> , 2022, 11, 745.	1.6	1
27499	Uncovering the Pharmacological Mechanisms of Gexia-Zhuyu Formula (GXZY) in Treating Liver Cirrhosis by an Integrative Pharmacology Strategy. <i>Frontiers in Pharmacology</i> , 2022, 13, 793888.	1.6	4
27500	Chemerin Effect on the Endometrial Proteome of the Domestic Pig during Implantation Obtained by LC-MS/MS Analysis. <i>Cells</i> , 2022, 11, 1161.	1.8	3
27501	Screening of Potential Key Biomarkers for Ewing Sarcoma: Evidence from Gene Array Analysis. <i>International Journal of General Medicine</i> , 2022, Volume 15, 2575-2588.	0.8	1
27502	Hormone and carbohydrate metabolism associated genes play important roles in rhizome bud full-year germination of <i>Cephalostachyum pingbianense</i> . <i>Physiologia Plantarum</i> , 2022, 174, e13674.	2.6	6
27503	Comparative Transcriptome Profiling Analysis Reveals the Adaptive Molecular Mechanism of Yellow-Green Leaf in <i>Rosa beggeriana</i> "Aurea". <i>Frontiers in Plant Science</i> , 2022, 13, 845662.	1.7	5
27504	Machine-Learning Analysis of Serum Proteomics in Neuropathic Pain after Nerve Injury in Breast Cancer Surgery Points at Chemokine Signaling via SIRT2 Regulation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3488.	1.8	4
27505	Small genetic variation affecting mRNA isoforms associated with marbling and meat color in beef cattle. <i>Functional and Integrative Genomics</i> , 2022, , 1.	1.4	0
27506	Identification of the TF-miRNA-mRNA co-regulatory networks involved in sepsis. <i>Functional and Integrative Genomics</i> , 2022, 22, 481-489.	1.4	1
27507	Functional Enrichment Analysis of Regulatory Elements. <i>Biomedicines</i> , 2022, 10, 590.	1.4	53
27508	Co-Expression Network Modeling Identifies Specific Inflammation and Neurological Disease-Related Genes mRNA Modules in Mood Disorder. <i>Frontiers in Genetics</i> , 2022, 13, 865015.	1.1	2
27510	Screening Repurposed Antiviral Small Molecules as Antimycobacterial Compounds by a Lux-Based phoP Promoter-Reporter Platform. <i>Antibiotics</i> , 2022, 11, 369.	1.5	3
27511	Whole-genome sequencing reveals host factors underlying critical COVID-19. <i>Nature</i> , 2022, 607, 97-103.	13.7	174
27512	Stripenn detects architectural stripes from chromatin conformation data using computer vision. <i>Nature Communications</i> , 2022, 13, 1602.	5.8	23
27513	Identifying robust functional modules using three-body correlations in <i>Escherichia coli</i> . <i>Journal of Physics Complexity</i> , 2022, 3, 015013.	0.9	0
27514	Enhancement Mechanism of Stibnite Dissolution Mediated by <i>Acidithiobacillus ferrooxidans</i> under Extremely Acidic Condition. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3580.	1.8	4

#	ARTICLE	IF	CITATIONS
27516	A nonredundant role for T _H 17 cell-derived interleukin 22 in antibacterial defense of colonic crypts. <i>Immunity</i> , 2022, 55, 494-511.e11.	6.6	15
27517	Spatial transcriptomic reconstruction of the mouse olfactory glomerular map suggests principles of odor processing. <i>Nature Neuroscience</i> , 2022, 25, 484-492.	7.1	27
27518	Ontologies4Chem: the landscape of ontologies in chemistry. <i>Pure and Applied Chemistry</i> , 2022, 94, 605-622.	0.9	13
27519	Methylation and homologous recombination deficiency-related mutant genes predict the prognosis of lung adenocarcinoma. <i>Journal of Clinical Laboratory Analysis</i> , 2022, 36, e24277.	0.9	3
27520	An analysis of skin thickness in the Dezhou donkey population and identification of candidate genes by RNA-seq. <i>Animal Genetics</i> , 2022, 53, 368-379.	0.6	5
27521	Revealing the contribution of somatic gene mutations to shaping tumor immune microenvironment. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	6
27523	The Key Genes Underlying Pathophysiology Correlation Between the Acute Myocardial Infarction and COVID-19. <i>International Journal of General Medicine</i> , 2022, Volume 15, 2479-2490.	0.8	6
27525	Functional Similarities of Protein-Coding Genes in Topologically Associating Domains and Spatially-Proximate Genomic Regions. <i>Genes</i> , 2022, 13, 480.	1.0	0
27526	Impact of 6 month conjugated equine estrogen versus estradiol-treatment on biomarkers and enriched gene sets in healthy mammary tissue of non-human primates. <i>PLoS ONE</i> , 2022, 17, e0264057.	1.1	0
27527	Transcriptional CDK Inhibitors as Potential Treatment Option for Testicular Germ Cell Tumors. <i>Cancers</i> , 2022, 14, 1690.	1.7	3
27528	Osteogenic Commitment of Human Periodontal Ligament Cells Is Predetermined by Methylation, Chromatin Accessibility and Expression of Key Transcription Factors. <i>Cells</i> , 2022, 11, 1126.	1.8	7
27529	Novel genetic basis of resistance to Bt toxin Cry1Ac in <i>Helicoverpa zea</i> . <i>Genetics</i> , 2022, 221, .	1.2	14
27530	Promoter/enhancer-based controllability of regulatory networks. <i>Scientific Reports</i> , 2022, 12, 3528.	1.6	2
27531	Up-to-Date Pathologic Classification and Molecular Characteristics of Intrahepatic Cholangiocarcinoma. <i>Frontiers in Medicine</i> , 2022, 9, 857140.	1.2	23
27532	Polyopes affinis Suppressed IFN- γ - and TNF- α -Induced Inflammation in Human Keratinocytes via Down-Regulation of the NF- κ B and STAT1 Pathways. <i>Molecules</i> , 2022, 27, 1836.	1.7	5
27533	Genome Sequence and Description of <i>Paracoccus denitrificans</i> Strain R-1, Isolated from Activated Sludge. <i>Microbiology Resource Announcements</i> , 2022, 11, e0123621.	0.3	2
27534	Protoplast Dissociation and Transcriptome Analysis Provides Insights to Salt Stress Response in Cotton. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2845.	1.8	13
27535	The proteogenomic subtypes of acute myeloid leukemia. <i>Cancer Cell</i> , 2022, 40, 301-317.e12.	7.7	43

#	ARTICLE	IF	CITATIONS
27536	Chromosome-Scale Assembly of the <i>Dendrobium nobile</i> Genome Provides Insights Into the Molecular Mechanism of the Biosynthesis of the Medicinal Active Ingredient of <i>Dendrobium</i> . <i>Frontiers in Genetics</i> , 2022, 13, 844622.	1.1	21
27539	Genome-wide transcript and protein analysis highlights the role of protein homeostasis in the aging mouse heart. <i>Genome Research</i> , 2022, , .	2.4	12
27540	Bacterial Homologs of Progesterone and AdipoQ Receptors (PAQRs) Affect Membrane Energetics Homeostasis but Not Fluidity. <i>Journal of Bacteriology</i> , 2022, 204, e0058321.	1.0	2
27541	Cerebrospinal fluid tau levels are associated with abnormal neuronal plasticity markers in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2022, 17, 27.	4.4	30
27542	ImmuneData: an integrated data discovery system for immunology data repositories. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	2
27543	Genome Sequence Resources of <i>Klebsiella michiganensis</i> AKKL-001, Which Causes Bacterial Blight of Mulberry. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 349-351.	1.4	1
27545	Epha1 is a cell-surface marker for the neuromesodermal competent population. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	3
27546	Single-Cell Profiling Reveals Heterogeneity of Primary and Lymph Node Metastatic Tumors and Immune Cell Populations and Discovers Important Prognostic Significance of CCDC43 in Oral Squamous Cell Carcinoma. <i>Frontiers in Immunology</i> , 2022, 13, 843322.	2.2	10
27547	Differentially expressed genes in <i>Mythimna separata</i> under chlorantraniliprole exposure and functional identification. <i>International Journal of Pest Management</i> , 0, , 1-11.	0.9	1
27548	Stimulation of the hepatoportal nerve plexus with focused ultrasound restores glucose homeostasis in diabetic mice, rats and swine. <i>Nature Biomedical Engineering</i> , 2022, 6, 683-705.	11.6	28
27549	Is the proteomic composition of the salivary pellicle dependent on the substrate material?. <i>Proteomics - Clinical Applications</i> , 2022, 16, e2100109.	0.8	8
27550	UV-B and UV-C radiation trigger both common and distinctive signal perceptions and transmissions in <i>Pinus tabulaeformis</i> Carr.. <i>Tree Physiology</i> , 2022, 42, 1587-1600.	1.4	4
27551	The cotton mitochondrial chimeric gene orf610a causes male sterility by disturbing the dynamic balance of ATP synthesis and ROS burst. <i>Crop Journal</i> , 2022, , .	2.3	11
27552	Identification of differentially expressed genes and signaling pathways with <i>Candida</i> infection by bioinformatics analysis. <i>European Journal of Medical Research</i> , 2022, 27, 43.	0.9	3
27553	Iron-Induced Respiration Promotes Antibiotic Resistance in Actinomycete Bacteria. <i>MBio</i> , 2022, 13, e0042522.	1.8	3
27554	Isolation of Anaerobic Bromate-Reducing Bacteria Using Different Carbon Sources and Transcriptomic Insights From <i>Klebsiella variicola</i> Glu3. <i>Frontiers in Microbiology</i> , 2022, 13, 851844.	1.5	2
27555	Circ_0001174 facilitates osteosarcoma cell proliferation, migration, and invasion by targeting the miR-186-5p/MACC1 axis. <i>Journal of Orthopaedic Surgery and Research</i> , 2022, 17, 159.	0.9	5
27556	Transcriptome characterization of <i>Larrea tridentata</i> and identification of genes associated with phenylpropanoid metabolic pathways. <i>PLoS ONE</i> , 2022, 17, e0265231.	1.1	1

#	ARTICLE	IF	CITATIONS
27557	Genomic heterogeneity underlies multidrug resistance in <i>Pseudomonas aeruginosa</i> : A population-level analysis beyond susceptibility testing. <i>PLoS ONE</i> , 2022, 17, e0265129.	1.1	13
27558	Identification and Characterization of the Roles of circCASP9 in Gastric Cancer Based on a circRNA-miRNA-mRNA Regulatory Network. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-16.	1.9	3
27559	Benchmarking the proteomic profile of animal models of mesial temporal epilepsy. <i>Annals of Clinical and Translational Neurology</i> , 2022, 9, 454-467.	1.7	6
27560	Comparative analysis of the <i>Mercenaria mercenaria</i> genome provides insights into the diversity of transposable elements and immune molecules in bivalve mollusks. <i>BMC Genomics</i> , 2022, 23, 192.	1.2	18
27561	Sphingolipid Metabolism as a New Predictive Target Correlated with Aging and AD: A Transcriptomic Analysis. <i>Medicina (Lithuania)</i> , 2022, 58, 493.	0.8	4
27562	Global DNA methylation profiles of Buffalo (<i>Bubalus bubalis</i>) preimplantation embryos produced by handmade cloning and in vitro fertilization. <i>Scientific Reports</i> , 2022, 12, 5161.	1.6	4
27563	Transcriptome profiling of the nonlactating mammary glands of dairy goats reveals the molecular genetic mechanism of mammary cell remodeling. <i>Journal of Dairy Science</i> , 2022, 105, 5238-5260.	1.4	6
27564	Landscape of Molecular Crosstalk Perturbation between Lung Cancer and COVID-19. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 3454.	1.2	2
27565	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. <i>Nature Communications</i> , 2022, 13, 1644.	5.8	63
27571	Beyond AOPs: A Mechanistic Evaluation of NAMs in DART Testing. <i>Frontiers in Toxicology</i> , 2022, 4, 838466.	1.6	16
27572	<i>Parvimonas micra</i> is associated with tumour immune profiles in molecular subtypes of colorectal cancer. <i>Cancer Immunology, Immunotherapy</i> , 2022, 71, 2565-2575.	2.0	10
27573	Ovarian Transcriptomic Analysis of Ninghai Indigenous Chickens at Different Egg-Laying Periods. <i>Genes</i> , 2022, 13, 595.	1.0	5
27574	Hippocampus RNA Sequencing of Pentylentetrazole-Kindled Rats and Upon Treatment of Novel Chemical Q808. <i>Frontiers in Pharmacology</i> , 2022, 13, 820508.	1.6	2
27575	Protocol for isolation and functional validation of label-retaining quiescent colorectal cancer stem cells from patient-derived organoids for RNA-seq. <i>STAR Protocols</i> , 2022, 3, 101225.	0.5	2
27576	Biomimetic radiosensitizers unlock radiogenetics for local interstitial radiotherapy to activate systematic immune responses and resist tumor metastasis. <i>Journal of Nanobiotechnology</i> , 2022, 20, 103.	4.2	25
27577	<i>Jiella sonneratae</i> sp. nov., a novel endophytic bacterium isolated from bark of <i>Sonneratia apetala</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	8
27579	Coronavirus Host Genetics South Africa (COHG-SA) database—a variant database for gene regions associated with SARS-CoV-2 outcomes. <i>European Journal of Human Genetics</i> , 2022, 30, 880-888.	1.4	6
27580	Integrative analyses of biomarkers and pathways for heart failure. <i>BMC Medical Genomics</i> , 2022, 15, 72.	0.7	18

#	ARTICLE	IF	CITATIONS
27581	Association of Circulating Cathepsin B Levels With Blood Pressure and Aortic Dilation. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 762468.	1.1	7
27582	EnsembleFam: towards more accurate protein family prediction in the twilight zone. <i>BMC Bioinformatics</i> , 2022, 23, 90.	1.2	3
27583	Endophytic Bacterium <i>Serratia plymuthica</i> From Chinese Leek Suppressed Apple Ring Rot on Postharvest Apple Fruit. <i>Frontiers in Microbiology</i> , 2021, 12, 802887.	1.5	9
27584	Modeling multi-scale data via a network of networks. <i>Bioinformatics</i> , 2022, 38, 2544-2553.	1.8	30
27585	Gene expression study in monocytes: evidence of inflammatory dysregulation in early-onset obsessive-compulsive disorder. <i>Translational Psychiatry</i> , 2022, 12, 134.	2.4	1
27587	A non-canonical tricarboxylic acid cycle underlies cellular identity. <i>Nature</i> , 2022, 603, 477-481.	13.7	108
27588	Uncovering the genetic profiles underlying the intrinsic organization of the human cerebellum. <i>Molecular Psychiatry</i> , 2022, 27, 2619-2634.	4.1	3
27589	Transcriptional Regulation of Reproductive Diapause in the Convergent Lady Beetle, <i>Hippodamia convergens</i> . <i>Insects</i> , 2022, 13, 343.	1.0	4
27590	Whole-genome sequencing and gene sharing network analysis powered by machine learning identifies antibiotic resistance sharing between animals, humans and environment in livestock farming. <i>PLoS Computational Biology</i> , 2022, 18, e1010018.	1.5	19
27592	<i>Nocardioides mangrovi</i> sp. nov., a novel endophytic actinobacterium isolated from root of <i>Kandelia candel</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5
27593	Assessing Bayesian Phylogenetic Information Content of Morphological Data Using Knowledge From Anatomy Ontologies. <i>Systematic Biology</i> , 2022, 71, 1290-1306.	2.7	6
27594	Chemerin effect on transcriptome of the porcine endometrium during implantation determined by RNA-sequencing. <i>Biology of Reproduction</i> , 2022, 107, 557-573.	1.2	7
27596	Urgent need for consistent standards in functional enrichment analysis. <i>PLoS Computational Biology</i> , 2022, 18, e1009935.	1.5	46
27597	Metabolic incorporation of electron-rich ribonucleosides enhances APEX-seq for profiling spatially restricted nascent transcriptome. <i>Cell Chemical Biology</i> , 2022, 29, 1218-1231.e8.	2.5	7
27598	Whole genome sequencing delineates regulatory, copy number, and cryptic splice variants in early onset cardiomyopathy. <i>Npj Genomic Medicine</i> , 2022, 7, 18.	1.7	14
27599	Characterization of Vegetative Incompatibility in <i>Morchella importuna</i> and Location of the Related-Genes by Bulk Segregant Analysis. <i>Frontiers in Microbiology</i> , 2022, 13, 828514.	1.5	2
27600	Antigen-Presenting B Cells Program the Efferent Lymph T Helper Cell Response. <i>Frontiers in Immunology</i> , 2022, 13, 813203.	2.2	1
27601	MAG2 and MAL Regulate Vesicle Trafficking and Auxin Homeostasis With Functional Redundancy. <i>Frontiers in Plant Science</i> , 2022, 13, 849532.	1.7	0

#	ARTICLE	IF	CITATIONS
27603	Centrosomal protein 290 is a novel prognostic indicator that modulates liver cancer cell ferroptosis via the Nrf2 pathway. <i>Aging</i> , 2022, 14, 2367-2382.	1.4	4
27604	Preclinical Studies on Convalescent Human Immune Plasma-Derived Exosome: Omics and Antiviral Properties to SARS-CoV-2. <i>Frontiers in Immunology</i> , 2022, 13, 824378.	2.2	9
27605	LRP1B is a Potential Biomarker for Tumor Immunogenicity and Prognosis of HCC Patients Receiving ICI Treatment. <i>Journal of Hepatocellular Carcinoma</i> , 2022, Volume 9, 203-220.	1.8	8
27606	Proteomic Identification of a Gastric Tumor ECM Signature Associated With Cancer Progression. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 818552.	1.6	7
27607	Upregulated YB-1 protein promotes glioblastoma growth through a YB-1/CCT4/mLST8/mTOR pathway. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	21
27608	Antifungal Effect of Copper Nanoparticles against <i>Fusarium kuroshium</i> , an Obligate Symbiont of <i>Euwallacea kuroshio</i> Ambrosia Beetle. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 347.	1.5	10
27609	NeuroSCORE is a genome-wide omics-based model that identifies candidate disease genes of the central nervous system. <i>Scientific Reports</i> , 2022, 12, 5427.	1.6	1
27610	Plasma proteome changes linked to late phase response after inhaled allergen challenge in asthmatics. <i>Respiratory Research</i> , 2022, 23, 50.	1.4	2
27612	Comparative whole transcriptome analysis of Parkinson's disease focusing on the efficacy of zonisamide. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2022, , jnnp-2021-328742.	0.9	1
27614	Systematic analysis of olfactory protein's protein interactions network of fruitfly, <i>Drosophila melanogaster</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2022, 110, e21882.	0.6	0
27615	Transcriptome Analysis Reveals a Gene Expression Pattern That Contributes to Sugarcane Bud Propagation Induced by Indole-3-Butyric Acid. <i>Frontiers in Plant Science</i> , 2022, 13, 852886.	1.7	5
27616	Networks and Graphs Discovery in Metabolomics Data Analysis and Interpretation. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 841373.	1.6	35
27617	A recent burst of gene duplications in Triticeae. <i>Plant Communications</i> , 2022, 3, 100268.	3.6	18
27619	Potential Biomarkers and the Molecular Mechanism Associated With DLL4 During Renal Cell Carcinoma Progression. <i>American Journal of the Medical Sciences</i> , 2022, , .	0.4	1
27620	Whole genome sequence of pan drug-resistant clinical isolate of <i>Acinetobacter baumannii</i> ST1890. <i>PLoS ONE</i> , 2022, 17, e0264374.	1.1	4
27621	Selective requirement for polycomb repressor complex 2 in the generation of specific hypothalamic neuronal subtypes. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	4
27622	Genomic signatures of high-altitude adaptation and chromosomal polymorphism in geladas. <i>Nature Ecology and Evolution</i> , 2022, 6, 630-643.	3.4	13
27623	Epithelial cell responses to rhinovirus identify an early-life onset asthma phenotype in adults. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 604-611.	1.5	2

#	ARTICLE	IF	CITATIONS
27624	Identification and Validation of Immune Cells and Hub Genes in Gastric Cancer Microenvironment. <i>Disease Markers</i> , 2022, 2022, 1-18.	0.6	5
27625	FindIT2: an R/Bioconductor package to identify influential transcription factor and targets based on multi-omics data. <i>BMC Genomics</i> , 2022, 23, 272.	1.2	0
27626	Predicted mouse interactome and network-based interpretation of differentially expressed genes. <i>PLoS ONE</i> , 2022, 17, e0264174.	1.1	0
27628	Proteomic Response Revealed Signaling Pathways Involving in the Mechanism of Polymyxin B-Induced Melanogenesis. <i>Microbiology Spectrum</i> , 2022, 10, e0273021.	1.2	1
27629	Draft genome sequence of myo-inositol utilizing <i>Aeromonas dhakensis</i> 1P11S3 isolated from striped catfish (<i>Pangasianodon hypophthalmus</i>) in a local fish farm in Malaysia. <i>Data in Brief</i> , 2022, 41, 107974.	0.5	6
27630	Transcriptome Analysis of <i>Otodectes cynotis</i> in Different Developmental Stages. <i>Frontiers in Microbiology</i> , 2022, 13, 687387.	1.5	0
27631	Astrocyte-Like Cells Transcriptome Changes After Exposure to a Low and Non-cytotoxic MeHg Concentration. <i>Biological Trace Element Research</i> , 2022, , 1.	1.9	0
27632	Genome-scale transcriptomic insights into the gene co-expression network of seed abortion in triploid <i>Siraitia grosvenorii</i> . <i>BMC Plant Biology</i> , 2022, 22, 173.	1.6	2
27633	Transcriptome analysis of Pacific white shrimp (<i>Litopenaeus vannamei</i>) hepatopancreas challenged by <i>Vibrio alginolyticus</i> reveals lipid metabolic disturbance. <i>Fish and Shellfish Immunology</i> , 2022, 123, 238-247.	1.6	21
27634	Human pluripotent stem cell-derived myogenic progenitors undergo maturation to quiescent satellite cells upon engraftment. <i>Cell Stem Cell</i> , 2022, 29, 610-619.e5.	5.2	10
27635	Cellular and transcriptional diversity over the course of human lactation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2121720119.	3.3	19
27636	Genetics of osteopontin in patients with chronic kidney disease: The German Chronic Kidney Disease study. <i>PLoS Genetics</i> , 2022, 18, e1010139.	1.5	5
27637	Characterization of differential gene expression of broiler chicken to thermal stress in discrete developmental stages. <i>Animal Cells and Systems</i> , 2022, 26, 62-69.	0.8	2
27638	m6A-mediated modulation coupled with transcriptional regulation shapes long noncoding RNA repertoire of the cGAS-STING signaling. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1785-1797.	1.9	3
27639	Exploring crucial molecular events in pearl oyster after pre-grafting conditioning by genome-wide bisulfite sequencing for DNA methylation analysis. <i>Fish and Shellfish Immunology</i> , 2022, 123, 10-19.	1.6	2
27640	Knowledge graph construction and application in geosciences: A review. <i>Computers and Geosciences</i> , 2022, 161, 105082.	2.0	46
27641	A chromosome-scale genome assembly of the Mongolian oak (<i>Quercus mongolica</i>). <i>Molecular Ecology Resources</i> , 2022, 22, 2396-2410.	2.2	25
27642	Molecular characterization of myotonic dystrophy fibroblast cell lines for use in small molecule screening. <i>IScience</i> , 2022, 25, 104198.	1.9	6

#	ARTICLE	IF	CITATIONS
27643	Combining biomedical knowledge graphs and text to improve predictions for drug-target interactions and drug-indications. <i>PeerJ</i> , 2022, 10, e13061.	0.9	6
27644	Integrative Analyses of Antler Cartilage Transcriptome and Proteome of Gansu Red Deer (<i>Cervus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.0 5	1.0	5
27645	Spatial proteomics reveals subcellular reorganization in human keratinocytes exposed to UVA light. <i>IScience</i> , 2022, 25, 104093.	1.9	4
27648	Global evolution of the tumor microenvironment associated with progression from preinvasive invasive to invasive human lung adenocarcinoma. <i>Cell Reports</i> , 2022, 39, 110639.	2.9	15
27649	Divergent Adaptations in Autonomic Nerve Activity and Neuroimmune Signaling Associated With the Severity of Inflammation in Chronic Colitis. <i>Inflammatory Bowel Diseases</i> , 2022, 28, 1229-1243.	0.9	8
27650	Cell environment shapes TDP-43 function with implications in neuronal and muscle disease. <i>Communications Biology</i> , 2022, 5, 314.	2.0	21
27651	Design and application of a knowledge network for automatic prioritization of drug mechanisms. <i>Bioinformatics</i> , 2022, 38, 2880-2891.	1.8	9
27652	The potential role of eyestalk in the immunity of <i>Litopenaeus vannamei</i> to <i>Vibrio parahaemolyticus</i> infection II. From the perspective of long non-coding RNA. <i>Fish and Shellfish Immunology</i> , 2022, 124, 300-312.	1.6	6
27653	A Chromosome-Level Reference Genome of Chinese Balloon Flower (<i>Platycodon grandiflorus</i>). <i>Frontiers in Genetics</i> , 2022, 13, 869784.	1.1	7
27654	Autophagy Induced by BCL2-Related ceRNA Network Participates in the Occurrence of COPD. <i>International Journal of COPD</i> , 2022, Volume 17, 791-808.	0.9	4
27655	Tetracycline biotransformation by a novel bacterial strain <i>Alcaligenes</i> sp. T17. <i>Science of the Total Environment</i> , 2022, 832, 155130.	3.9	16
27656	Gene expression profiling of placentae from women with obesity and obstructive sleep apnoea. <i>Placenta</i> , 2022, 121, 53-60.	0.7	1
27657	Exploiting plant transcriptomic databases: Resources, tools, and approaches. <i>Plant Communications</i> , 2022, 3, 100323.	3.6	20
27658	Transcriptome-wide association study for postpartum depression implicates altered B-cell activation and insulin resistance. <i>Molecular Psychiatry</i> , 2022, 27, 2858-2867.	4.1	9
27659	Proteome profiling reveals changes in energy metabolism, transport and antioxidation during drought stress in <i>Nostoc flagelliforme</i> . <i>BMC Plant Biology</i> , 2022, 22, 162.	1.6	7
27660	Hierarchical multi-label classification based on LSTM network and Bayesian decision theory for LncRNA function prediction. <i>Scientific Reports</i> , 2022, 12, 5819.	1.6	2
27661	Description and genome analysis of <i>Luteimonas viscosa</i> sp. nov., a novel bacterium isolated from soil of a sunflower field. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 749-760.	0.7	2
27662	Co-expression Mechanism Analysis of Different Tachyplesin Resistant Strains in <i>Pseudomonas aeruginosa</i> Based on Transcriptome Sequencing. <i>Frontiers in Microbiology</i> , 2022, 13, 871290.	1.5	1

#	ARTICLE	IF	CITATIONS
27663	Intermittent prednisone treatment in mice promotes exercise tolerance in obesity through adiponectin. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	7
27664	Non-linear archetypal analysis of single-cell RNA-seq data by deep autoencoders. <i>PLoS Computational Biology</i> , 2022, 18, e1010025.	1.5	7
27666	Origins and Timing of Emerging Lesions in Advanced Renal Cell Carcinoma. <i>Molecular Cancer Research</i> , 2022, 20, 909-922.	1.5	0
27667	Biometal Dyshomeostasis in Olfactory Mucosa of Alzheimer's Disease Patients. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4123.	1.8	3
27668	Placental and plasma early predictive biomarkers for gestational diabetes mellitus. <i>Proteomics - Clinical Applications</i> , 2022, 16, e2200001.	0.8	3
27669	Bioinformatics Analysis Identified the Hub Genes, mRNA-miRNA-lncRNA Axis, and Signaling Pathways Involved in Rheumatoid Arthritis Pathogenesis. <i>International Journal of General Medicine</i> , 2022, Volume 15, 3879-3893.	0.8	5
27670	MTD: a unique pipeline for host and meta-transcriptome joint and integrative analyses of RNA-seq data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	1
27671	Altered BAF occupancy and transcription factor dynamics in PBAF-deficient melanoma. <i>Cell Reports</i> , 2022, 39, 110637.	2.9	12
27672	De novo genome assembly of <i>Bradysia cellarum</i> (Diptera: Sciaridae), a notorious pest in traditional special vegetables in China. <i>Insect Molecular Biology</i> , 2022, 31, 508-518.	1.0	3
27673	Parthenolide leads to proteomic differences in thyroid cancer cells and promotes apoptosis. <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, 99.	1.2	6
27675	Sequence-dependent model of genes with dual TF factor preference. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194812.	0.9	6
27676	Sequential reinforcement active feature learning for gene signature identification in renal cell carcinoma. <i>Journal of Biomedical Informatics</i> , 2022, 128, 104049.	2.5	1
27677	Developing a Genetic Biomarker-based Diagnostic Model for Major Depressive Disorder using Random Forests and Artificial Neural Networks. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, .	0.6	1
27678	Comparative Genomics Assisted Functional Characterization of <i>Rahnella aceris</i> ZF458 as a Novel Plant Growth Promoting Rhizobacterium. <i>Frontiers in Microbiology</i> , 2022, 13, 850084.	1.5	6
27679	Label-Free LC-MS/MS Analysis Reveals Different Proteomic Profiles between Egg Yolks of Silky Fowl and Ordinary Chickens. <i>Foods</i> , 2022, 11, 1035.	1.9	2
27680	TMT labeled comparative proteomic analysis reveals spleen active immune responses during <i>Clostridium perfringens</i> type C infected piglet diarrhea. <i>PeerJ</i> , 2022, 10, e13006.	0.9	1
27681	Differential transcriptomic landscapes of multiple organs from SARS-CoV-2 early infected rhesus macaques. <i>Protein and Cell</i> , 2022, 13, 920-939.	4.8	9
27682	Protein interaction network analysis reveals genetic enrichment of immune system genes in frontotemporal dementia. <i>Neurobiology of Aging</i> , 2022, 116, 67-79.	1.5	2

#	ARTICLE	IF	CITATIONS
27683	Treatment with Ad5-Porcine Interferon- β Attenuates Ebola Virus Disease in Pigs. <i>Pathogens</i> , 2022, 11, 449.	1.2	2
27685	Gene expression studies of plastic and evolutionary responses to global warming. <i>Current Opinion in Insect Science</i> , 2022, 51, 100918.	2.2	1
27686	Transcriptome and miRNA sequencing analyses reveal the regulatory mechanism of γ -linolenic acid biosynthesis in <i>Paeonia rockii</i> . <i>Food Research International</i> , 2022, 155, 111094.	2.9	5
27687	Bioinformatics study of the potential therapeutic effects of ginsenoside Rf in reversing nonalcoholic fatty liver disease. <i>Biomedicine and Pharmacotherapy</i> , 2022, 149, 112879.	2.5	2
27688	Artificial intelligence techniques for prediction of drug synergy in malignant diseases: Past, present, and future. <i>Computers in Biology and Medicine</i> , 2022, 144, 105334.	3.9	6
27689	Exploring the potential mechanism of radix astragali against ischemic stroke based on network pharmacology and molecular docking. <i>Phytomedicine Plus</i> , 2022, 2, 100244.	0.9	1
27690	Decomposition-based multi-objective optimization approach for PPI network alignment. <i>Knowledge-Based Systems</i> , 2022, 243, 108527.	4.0	4
27691	Genetic diversity and signatures of selection in the mito-gynogenetic olive flounder <i>Paralichthys olivaceus</i> revealed by genome-wide SNP markers. <i>Aquaculture</i> , 2022, 553, 738062.	1.7	4
27692	A system biology approach to determine therapeutic targets by identifying molecular mechanisms and key pathways for type 2 diabetes that are linked to the development of tuberculosis and rheumatoid arthritis. <i>Life Sciences</i> , 2022, 297, 120483.	2.0	10
27693	Transcriptome analysis of infected Crandell Rees Feline Kidney (CRFK) cells by canine parvovirus type 2c Laotian isolates. <i>Gene</i> , 2022, 822, 146324.	1.0	2
27694	Combined proteomic strategies for in-depth venom analysis of the beaked sea snake (<i>Hydrophis</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.2	4
27695	Statistical and machine learning methods to study human CD4+ T cell proteome profiles. <i>Immunology Letters</i> , 2022, 245, 8-17.	1.1	3
27696	Transcriptome analysis of <i>Macrobrachium rosenbergii</i> : Identification of precocious puberty and slow-growing information. <i>Journal of Invertebrate Pathology</i> , 2022, 190, 107752.	1.5	7
27697	MicroRNA-dependent regulation of targeted mRNAs for improved muscle texture in crisp grass carp fed with broad bean. <i>Food Research International</i> , 2022, 155, 111071.	2.9	6
27698	SIP: A computational prediction of S-Adenosyl methionine (SAM) interacting proteins and their interaction sites through primary structures. <i>Computational Biology and Chemistry</i> , 2022, 98, 107662.	1.1	0
27699	Connectomic-genetic signatures in the cerebral small vessel disease. <i>Neurobiology of Disease</i> , 2022, 167, 105671.	2.1	1
27700	Pilot study in human healthy volunteers on the mechanisms underlying remote ischemic conditioning (RIC) "Targeting circulating immune cells and immune-related proteins. <i>Journal of Neuroimmunology</i> , 2022, 367, 577847.	1.1	3
27701	Characterization of olfactory receptor repertoires provides insights into the high-altitude adaptation of the yak based on the chromosome-level genome. <i>International Journal of Biological Macromolecules</i> , 2022, 209, 220-230.	3.6	7

#	ARTICLE	IF	CITATIONS
27702	Comparative transcriptomic analyses reveal differences in the responses of diploid and triploid Pacific oysters (<i>Crassostrea gigas</i>) to thermal stress. <i>Aquaculture</i> , 2022, 555, 738219.	1.7	12
27703	A marine fungus <i>Alternaria alternata</i> FB1 efficiently degrades polyethylene. <i>Journal of Hazardous Materials</i> , 2022, 431, 128617.	6.5	56
27704	Identification of microRNA and gene interactions through bioinformatic integrative analysis for revealing candidate signatures in prostate cancer. <i>Gene Reports</i> , 2022, 27, 101607.	0.4	4
27705	Epigenome-wide association analyses of active injection drug use. <i>Drug and Alcohol Dependence</i> , 2022, 235, 109431.	1.6	5
27706	Analysis of the medication rules of traditional Chinese medicines (TCMs) in treating liver cancer and potential TCMs exploration. <i>Pharmacological Research Modern Chinese Medicine</i> , 2022, 3, 100086.	0.5	5
27707	Finding the "switch" in platelet activation: prediction of key mediators involved in reversal of platelet activation using a novel network biology approach. <i>Journal of Proteomics</i> , 2022, 261, 104577.	1.2	3
27708	Transcriptional responses and reduction in carpogenic germination of <i>Sclerotinia sclerotiorum</i> exposed to volatile organic compounds of <i>Trichoderma azevedoi</i> . <i>Biological Control</i> , 2022, 169, 104897.	1.4	7
27709	Metabolome and whole transcriptome analyses reveal the molecular mechanisms underlying terpenoids biosynthesis in <i>Sapindus mukorossi</i> fruits. <i>Industrial Crops and Products</i> , 2022, 181, 114810.	2.5	5
27710	PM2.5 exposure during pregnancy is associated with altered placental expression of lipid metabolic genes in a US birth cohort. <i>Environmental Research</i> , 2022, 211, 113066.	3.7	7
27711	A Bridging Centrality Plugin for GEPHI and a Case Study for <i>Mycobacterium Tuberculosis</i> H37Rv. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2741-2746.	1.9	2
27712	Genomics Characterization of an Engineered <i>Corynebacterium glutamicum</i> in Bioreactor Cultivation Under Ionic Liquid Stress. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 766674.	2.0	6
27713	Bioinformatics study on different gene expression profiles of fibroblasts and vascular endothelial cells in keloids. <i>Medicine (United States)</i> , 2021, 100, e27777.	0.4	2
27714	Testing biological network motif significance with exponential random graph models. <i>Applied Network Science</i> , 2021, 6, 91.	0.8	4
27715	Comparative transcriptome profiling of <i>Termitomyces</i> sp. between monocultures in vitro and link-stipe of fungus-combs in situ. <i>Letters in Applied Microbiology</i> , 2022, 74, 429-443.	1.0	0
27717	High Expression of CEMIP Correlates Poor Prognosis and the Tumor Microenvironment in Breast Cancer as a Promisingly Prognostic Biomarker. <i>Frontiers in Genetics</i> , 2021, 12, 768140.	1.1	12
27718	Pathway Enrichment Analysis of Microarray Data. <i>Methods in Molecular Biology</i> , 2022, 2401, 147-159.	0.4	0
27719	Potential biomarkers of acute myocardial infarction based on co-expression network analysis. <i>Experimental and Therapeutic Medicine</i> , 2021, 23, 162.	0.8	6
27720	CGN-MPred: Cofunctional Gene Network-based Mutation Prediction from Exposure Conditions. , 2021, ,		1

#	ARTICLE	IF	CITATIONS
27721	Effects of the Expression of Random Sequence Clones on Growth and Transcriptome Regulation in <i>Escherichia coli</i> . <i>Genes</i> , 2022, 13, 53.	1.0	9
27723	Machine Learning Methods for Protein Function Prediction. <i>Algorithms for Intelligent Systems</i> , 2022, , 85-98.	0.5	1
27724	Comparative transcriptomics of the Djungarian hamster hypothalamus during short photoperiod acclimation and spontaneous torpor. <i>FEBS Open Bio</i> , 2022, 12, 443-459.	1.0	8
27725	Comparative transcriptome and DNA methylation analysis in temperature-sensitive genic male sterile wheat BS366. <i>BMC Genomics</i> , 2021, 22, 911.	1.2	11
27726	Graph-guided Bayesian SVM with Adaptive Structured Shrinkage Prior for High-dimensional Data. , 2021, 2021, 4472-4479.		0
27728	Whole-Genome Sequencing of <i>Acer catalpifolium</i> Reveals Evolutionary History of Endangered Species. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
27729	CottonGen: The Community Database for Cotton Genomics, Genetics, and Breeding Research. <i>Plants</i> , 2021, 10, 2805.	1.6	42
27730	Preconditioning With Intermittent Hypobaric Hypoxia Attenuates Stroke Damage and Modulates Endocytosis in Residual Neurons. <i>Frontiers in Neurology</i> , 2021, 12, 750908.	1.1	5
27731	Gene prediction of aging-related diseases based on DNN and Mashup. <i>BMC Bioinformatics</i> , 2021, 22, 597.	1.2	3
27732	Longitudinal DNA methylation dynamics as a practical indicator in clinical epigenetics. <i>Clinical Epigenetics</i> , 2021, 13, 219.	1.8	10
27733	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
27734	ENSAIO SOBRE ONTOLOGIA APLICADA NA RECUPERAÇÃO DA INFORMAÇÃO PARA A CIÊNCIA DA INFORMAÇÃO. <i>PontodeAcesso</i> , 2021, 15, .	0.1	0
27735	Human TRMT112-Methyltransferase Network Consists of Seven Partners Interacting with a Common Co-Factor. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13593.	1.8	8
27736	Barcoded reciprocal hemizyosity analysis via sequencing illuminates the complex genetic basis of yeast thermotolerance. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
27737	Fatty Acyl Sulfonyl Fluoride as an Activity-Based Probe for Profiling Fatty Acid-Associated Proteins in Living Cells. <i>ChemBioChem</i> , 2022, 23, e202100628.	1.3	3
27738	Combined Network Pharmacology and Cytology Experiments to Identify Potential Anti-Breast Cancer Targets and Mechanisms of Delphinidin. <i>Nutrition and Cancer</i> , 2021, , 1-16.	0.9	2
27739	Genome-wide association of single nucleotide polymorphism loci and candidate genes for frog-eye leaf spot (<i>Cercospora soja</i>) resistance in soybean. <i>BMC Plant Biology</i> , 2021, 21, 588.	1.6	6
27740	Transcriptomic Responses of <i>Cordyceps militaris</i> to Salt Treatment During Cordyceps Production. <i>Frontiers in Nutrition</i> , 2021, 8, 793795.	1.6	7

#	ARTICLE	IF	CITATIONS
27741	Identification of key genes associated with esophageal adenocarcinoma based on bioinformatics analysis. <i>Annals of Translational Medicine</i> , 2021, 9, 1711-1711.	0.7	4
27742	Effects of Serum Metabolites on the Pancreatic Transcriptome in Acute Acalculous Cholecystitis. <i>Gastroenterology Research and Practice</i> , 2021, 2021, 1-15.	0.7	1
27743	Potential Novel Modules and Hub Genes as Prognostic Candidates of Thyroid Cancer by Weighted Gene Co-Expression Network Analysis. <i>International Journal of General Medicine</i> , 2021, Volume 14, 9433-9444.	0.8	4
27744	protti: an R package for comprehensive data analysis of peptide- and protein-centric bottom-up proteomics data. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	24
27745	Genome analysis provides insight into hyper-virulence of <i>Streptococcus suis</i> LSM178, a human strain with a novel sequence type 1005. <i>Scientific Reports</i> , 2021, 11, 23919.	1.6	2
27746	<i>Bacillus amyloliquefaciens</i> SN16-1-Induced Resistance System of the Tomato against <i>Rhizoctonia solani</i> . <i>Pathogens</i> , 2022, 11, 35.	1.2	2
27747	The N-Acetylglucosamine Kinase from <i>Yarrowia lipolytica</i> Is a Moonlighting Protein. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13109.	1.8	1
27748	Identification of Keratinocyte Differentiation-Involved Genes for Metastatic Melanoma by Gene Expression Profiles. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-9.	0.7	3
27750	Capturing SNP Association across the NK Receptor and HLA Gene Regions in Multiple Sclerosis by Targeted Penalised Regression Models. <i>Genes</i> , 2022, 13, 87.	1.0	1
27751	Multi-view Clustering for the Integration Analysis of Gene Expression and Methylation Data. , 2021, , .		1
27752	De novo transcriptome assembly and annotation of parthenogenetic lizard <i>Darevskia unisexualis</i> and its parental ancestors <i>Darevskia valentini</i> and <i>Darevskia raddei nairensis</i> . <i>Data in Brief</i> , 2021, 39, 107685.	0.5	1
27753	A Novel Model of Tumor-Infiltrating B Lymphocyte Specific RNA-Binding Protein-Related Genes With Potential Prognostic Value and Therapeutic Targets in Multiple Myeloma. <i>Frontiers in Genetics</i> , 2021, 12, 778715.	1.1	0
27754	Identification of key genes involved in tamoxifen-resistant breast cancer using bioinformatics analysis. <i>Translational Cancer Research</i> , 2021, 10, 5246-5257.	0.4	7
27755	GeneTonic: an R/Bioconductor package for streamlining the interpretation of RNA-seq data. <i>BMC Bioinformatics</i> , 2021, 22, 610.	1.2	21
27756	The Stroma Liquid Biopsy Panel Contains a Stromal-Epithelial Gene Signature Ratio That Is Associated with the Histologic Tumor-Stroma Ratio and Predicts Survival in Colon Cancer. <i>Cancers</i> , 2022, 14, 163.	1.7	4
27757	TriGORank: A Gene Ontology Enriched Learning-to-Rank Framework for Trigenic Fitness Prediction. , 2021, , .		0
27760	Identification of a Lipid Metabolism-Associated Gene Signature Predicting Survival in Breast Cancer. <i>International Journal of General Medicine</i> , 2021, Volume 14, 9503-9513.	0.8	8
27761	JaponicusDB: rapid deployment of a model organism database for an emerging model species. <i>Genetics</i> , 2022, 220, .	1.2	21

#	ARTICLE	IF	CITATIONS
27762	Identification and Characterization of Circular RNAs in Association With the Deposition of Intramuscular Fat in Aohan Fine-Wool Sheep. <i>Frontiers in Genetics</i> , 2021, 12, 759747.	1.1	8
27763	In Silico Investigation of the Biological Implications of Complex DNA Damage with Emphasis in Cancer Radiotherapy through a Systems Biology Approach. <i>Molecules</i> , 2021, 26, 7602.	1.7	2
27765	Ontology-Enriched Specifications Enabling Findable, Accessible, Interoperable, and Reusable Marine Metagenomic Datasets in Cyberinfrastructure Systems. <i>Frontiers in Microbiology</i> , 2021, 12, 765268.	1.5	3
27767	Coexpression of gene transcripts with monoamine oxidase a quantified by human in vivo positron emission tomography. <i>Cerebral Cortex</i> , 2022, 32, 3516-3524.	1.6	5
27768	Transcriptomic analysis provides insights into the immune responses and nutrition in <i>Ostrinia furnacalis</i> larvae parasitized by <i>Macrocentrus cingulum</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2022, 109, e21863.	0.6	6
27769	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
27770	Longitudinal Changes in Cortical Thickness in Adolescents with Autism Spectrum Disorder and Their Association with Restricted and Repetitive Behaviors. <i>Genes</i> , 2021, 12, 2024.	1.0	10
27771	Biosafety and Proteome Profiles of Different Heat Inactivation Methods for <i>Mycobacterium tuberculosis</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0071621.	1.2	1
27772	Recurring exposure to low humidity induces transcriptional and protein level changes in the vocal folds of rabbits. <i>Scientific Reports</i> , 2021, 11, 24180.	1.6	5
27773	Fission stories: using PomBase to understand <i>Schizosaccharomyces pombe</i> biology. <i>Genetics</i> , 2022, 220, .	1.2	60
27774	Dynamic immune response characteristics of piglets infected with <i>Actinobacillus pleuropneumoniae</i> through omic. <i>AMB Express</i> , 2021, 11, 175.	1.4	1
27775	Potential biomarkers and signaling pathways associated with the pathogenesis of primary salivary gland carcinoma: a bioinformatics study. <i>Genomics and Informatics</i> , 2021, 19, e42.	0.4	8
27777	Ultradian rhythms of AKT phosphorylation and gene expression emerge in the absence of the circadian clock components Per1 and Per2. <i>PLoS Biology</i> , 2021, 19, e3001492.	2.6	17
27778	Establishment of Human Pluripotent Stem Cell-Derived Skin Organoids Enabled Pathophysiological Model of SARS-CoV-2 Infection. <i>Advanced Science</i> , 2022, 9, e2104192.	5.6	18
27780	Constructing local cell-specific networks from single-cell data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	18
27781	The antioxidant protein ZmPrx5 contributes resistance to maize stalk rot. <i>Crop Journal</i> , 2021, , .	2.3	0
27782	Transcriptome comparative analysis of ovarian follicles reveals the key genes and signaling pathways implicated in hen egg production. <i>BMC Genomics</i> , 2021, 22, 899.	1.2	16
27784	Competitive endogenous RNA network and pathway-based analysis of LncRNA single-nucleotide polymorphism in myasthenia gravis. <i>Scientific Reports</i> , 2021, 11, 23920.	1.6	3

#	ARTICLE	IF	CITATIONS
27785	Co-existing TP53 and ARID1A mutations promote aggressive endometrial tumorigenesis. PLoS Genetics, 2021, 17, e1009986.	1.5	24
27787	GraphIsoFun: a graph neural network based approach for splice isoform function prediction. , 2021, , .		0
27788	Genomic analysis of <i>Elsinoë</i> arachidis reveals its potential pathogenic mechanism and the biosynthesis pathway of elsinochrome toxin. PLoS ONE, 2021, 16, e0261487.	1.1	3
27789	Toward a Unified Description of Battery Data. Advanced Energy Materials, 2022, 12, .	10.2	33
27790	The In Vivo Transcriptomic Blueprint of Mycobacterium tuberculosis in the Lung. Frontiers in Immunology, 2021, 12, 763364.	2.2	4
27791	Discovering microbe functionality in human disease with a gene-ontology-aware model. , 2021, , .		0
27792	Circular RNA circCCNT2 is upregulated in the anterior cingulate cortex of individuals with bipolar disorder. Translational Psychiatry, 2021, 11, 629.	2.4	3
27793	Systems Biologyâ€œDerived Genetic Signatures of Mastitis in Dairy Cattle: A New Avenue for Drug Repurposing. Animals, 2022, 12, 29.	1.0	3
27794	An Information-Theoretic Framework for Identifying Age-Related Genes Using Human Dermal Fibroblast Transcriptome Data. , 2021, , .		1
27795	The Edible Plant Microbiome represents a diverse genetic reservoir with functional potential in the human host. Scientific Reports, 2021, 11, 24017.	1.6	14
27796	Computational modeling of human-nCoV protein-protein interaction network. Methods, 2022, 203, 488-497.	1.9	5
27797	Recent Advances of Integrative Bio-Omics Technologies to Improve Type 1 Diabetes (T1D) Care. Applied Sciences (Switzerland), 2021, 11, 11602.	1.3	0
27799	Effects of abolishing Whi2 on the proteome and nitrogen catabolite repression-sensitive protein production. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	0
27800	Mechanisms underlying <i>Clostridium pasteurianum</i> â€™s metabolic shift when grown with <i>Geobacter sulfurreducens</i> . Applied Microbiology and Biotechnology, 2022, 106, 865-876.	1.7	3
27802	Investigating changes of proteome in the bovine milk serum after retort processing using proteomics techniques. Food Science and Nutrition, 2022, 10, 307-316.	1.5	1
27803	Transcriptome Analysis of Arbuscular Mycorrhizal <i>Casuarina glauca</i> in Damage Mitigation of Roots on NaCl Stress. Microorganisms, 2022, 10, 15.	1.6	15
27804	Genome-wide identification of enhancers and transcription factors regulating the myogenic differentiation of bovine satellite cells. BMC Genomics, 2021, 22, 901.	1.2	6
27805	Genomic profiling and expression analysis of the diacylglycerol kinase gene family in heterologous hexaploid wheat. PeerJ, 2021, 9, e12480.	0.9	1

#	ARTICLE	IF	CITATIONS
27807	DNA methylation of ARHGAP30 is negatively associated with ARHGAP30 expression in lung adenocarcinoma, which reduces tumor immunity and is detrimental to patient survival. <i>Aging</i> , 2021, 13, 25799-25845.	1.4	4
27808	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021, 12, 7173.	5.8	8
27809	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
27810	Norway spruce deploys tissue-specific responses during acclimation to cold. <i>Plant, Cell and Environment</i> , 2022, 45, 427-445.	2.8	7
27811	Insight Into the Multiple Branches Traits of a Mutant in <i>Larix olgensis</i> by Morphological, Cytological, and Transcriptional Analyses. <i>Frontiers in Plant Science</i> , 2021, 12, 787661.	1.7	3
27812	Explainable Artificial Intelligence (XAI) in Biomedicine: Making AI Decisions Trustworthy for Physicians and Patients. <i>BioMedInformatics</i> , 2022, 2, 1-17.	1.0	42
27814	reString: an open-source Python software to perform automatic functional enrichment retrieval, results aggregation and data visualization. <i>Scientific Reports</i> , 2021, 11, 23458.	1.6	6
27815	Metabolite and Transcriptome Profiling Analysis Revealed That Melatonin Positively Regulates Floral Scent Production in <i>Hedychium coronarium</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 808899.	1.7	16
27816	Profiling senescent cells in human brains reveals neurons with CDKN2D/p19 and tau neuropathology. <i>Nature Aging</i> , 2021, 1, 1107-1116.	5.3	45
27817	Identification of starch candidate genes using SLAF-seq and BSA strategies and development of related SNP-CAPS markers in tetraploid potato. <i>PLoS ONE</i> , 2021, 16, e0261403.	1.1	2
27818	Identification of novel biomarkers in breast cancer via integrated bioinformatics analysis and experimental validation. <i>Bioengineered</i> , 2021, 12, 12431-12446.	1.4	15
27819	Full-Length Transcriptome Sequencing of the Scleractinian Coral <i>Montipora foliosa</i> Reveals the Gene Expression Profile of Coral-Zooxanthellae Holobiont. <i>Biology</i> , 2021, 10, 1274.	1.3	3
27820	Combined Metabolome and Transcriptome Analyses of Young, Mature, and Old Rhizome Tissues of <i>Zingiber officinale</i> Roscoe. <i>Frontiers in Genetics</i> , 2021, 12, 795201.	1.1	4
27821	Identification of hub mRNA, miRNAs and LncRNAs of uveal melanoma with weighted gene correlation network analysis. , 2021, , .		0
27822	The Fungus <i>Metarhizium</i> sp. BCC 4849 Is an Effective and Safe Mycoinsecticide for the Management of Spider Mites and Other Insect Pests. <i>Insects</i> , 2022, 13, 42.	1.0	5
27824	Gene expression associated with individual variability in intrinsic functional connectivity. <i>NeuroImage</i> , 2021, 245, 118743.	2.1	8
27825	OmicsOne: associate omics data with phenotypes in one-click. <i>Clinical Proteomics</i> , 2021, 18, 29.	1.1	2
27826	Targeted Therapy Modulates the Secretome of Cancer-Associated Fibroblasts to Induce Resistance in HER2-Positive Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13297.	1.8	8

#	ARTICLE	IF	CITATIONS
27827	Long noncoding RNA GSEC promotes neutrophil inflammatory activation by supporting PFKFB3-involved glycolytic metabolism in sepsis. <i>Cell Death and Disease</i> , 2021, 12, 1157.	2.7	13
27828	Integral Analyses of Competing Endogenous RNA Mechanisms and DNA Methylation Reveal Regulatory Mechanisms in Osteosarcoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 763347.	1.8	3
27829	A Novel Four-Gene Signature as a Potential Prognostic Biomarker for Hepatocellular Carcinoma. <i>Journal of Oncology</i> , 2021, 2021, 1-12.	0.6	0
27831	Transcriptomic, proteomic, and phosphoproteomic analyses reveal dynamic signaling networks influencing long-grain rice development. <i>Crop Journal</i> , 2021, , .	2.3	1
27833	Genome Characteristics Reveal the Biocontrol Potential of Actinobacteria Isolated From Sugarcane Rhizosphere. <i>Frontiers in Microbiology</i> , 2021, 12, 797889.	1.5	16
27834	Unraveling Admixture, Inbreeding, and Recent Selection Signatures in West African Indigenous Cattle Populations in Benin. <i>Frontiers in Genetics</i> , 2021, 12, 657282.	1.1	5
27835	Integration of embryo–endosperm interaction into a holistic and dynamic picture of seed development using a rice mutant with notched-belly kernels. <i>Crop Journal</i> , 2022, 10, 729-742.	2.3	5
27836	Searching beyond the streetlight: Neonicotinoid exposure alters the neurogenomic state of worker honey bees. <i>Ecology and Evolution</i> , 2021, 11, 18733-18742.	0.8	6
27837	Protein Function Prediction Based on PPI Networks: Network Reconstruction vs Edge Enrichment. <i>Frontiers in Genetics</i> , 2021, 12, 758131.	1.1	20
27839	A Beginner’s Guide on Integrating *Omics Approaches to Study Marine Microbial Communities: Details and Discussions From Sample Collection to Bioinformatics Analysis. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	2
27840	Parallel sequence tagging for concept recognition. <i>BMC Bioinformatics</i> , 2021, 22, 623.	1.2	3
27841	Protein function prediction for newly sequenced organisms. <i>Nature Machine Intelligence</i> , 2021, 3, 1050-1060.	8.3	13
27842	IgA-Dominated Humoral Immune Responses Govern Patients' Outcome in Endometrial Cancer. <i>Cancer Research</i> , 2022, 82, 859-871.	0.4	21
27843	Interferon inducible pseudouridine modification in human mRNA by quantitative nanopore profiling. <i>Genome Biology</i> , 2021, 22, 330.	3.8	44
27844	<i>Mongoliitalea daihaiensis</i> sp. nov., isolated from Daihai Lake in Inner Mongolia. <i>Archives of Microbiology</i> , 2022, 204, 92.	1.0	6
27845	Integrated Gene Expression Profiling Analysis Reveals Potential Molecular Mechanisms and Candidate Biomarkers for Early Risk Stratification and Prediction of STEMI and Post-STEMI Heart Failure Patients. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 736497.	1.1	9
27846	Relation Extraction of Protein Complexes from Dynamic Protein-Protein Interaction Network. <i>Journal of Biomedical Physics and Engineering</i> , 2021, 11, 675-684.	0.5	0
27847	TMT Quantitative Proteomics Analysis Reveals the Effects of Transport Stress on Iron Metabolism in the Liver of Chicken. <i>Animals</i> , 2022, 12, 52.	1.0	14

#	ARTICLE	IF	CITATIONS
27848	Artificial intelligence, molecular subtyping, biomarkers, and precision oncology. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 747-756.	1.1	1
27849	Computational modelling of chromosomally clustering protein domains in bacteria. <i>BMC Bioinformatics</i> , 2021, 22, 593.	1.2	1
27850	Relationship Between KCNQ1 Polymorphism and Type 2 Diabetes Risk in Northwestern China. <i>Pharmacogenomics and Personalized Medicine</i> , 2021, Volume 14, 1731-1751.	0.4	1
27851	Comparative Transcriptomic Analysis of Regenerated Skins Provides Insights into Cutaneous Air-Breathing Formation in Fish. <i>Biology</i> , 2021, 10, 1294.	1.3	4
27852	COSMONET: An R Package for Survival Analysis Using Screening-Network Methods. <i>Mathematics</i> , 2021, 9, 3262.	1.1	4
27853	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	5.8	30
27854	Study on differential gene expression profile of serum exosomes in patients with acute cerebral infarction. <i>Digital Chinese Medicine</i> , 2021, 4, 305-315.	0.5	0
27855	ADAMTS8 Expression is a Potential Prognostic Biomarker for Postoperative Metastasis in Lymph Node-Negative Early-Stage Invasive Breast Carcinoma Patients. <i>Pharmacogenomics and Personalized Medicine</i> , 2021, Volume 14, 1701-1713.	0.4	0
27856	A comprehensive characterization of the transcriptome in enzalutamide resistance prostate cancer. <i>Annals of Translational Medicine</i> , 2021, 9, 1782-1782.	0.7	0
27857	Limited allele-specific gene expression in highly polyploid sugarcane. <i>Genome Research</i> , 2022, 32, 297-308.	2.4	8
27858	Incremental & Semi-Supervised Learning for Functional Analysis of Protein Sequences. , 2021, , .		1
27859	Bioinformatics analysis of candidate genes and potential therapeutic drugs targeting adipose tissue in obesity. <i>Adipocyte</i> , 2022, 11, 1-10.	1.3	5
27861	Identifying Diagnostic and Prognostic Targets for Papillary Thyroid Carcinoma Through Mining Gene Expression BIG Datasets Using Adaptive Filtering and Advanced Bioinformatics Algorithms. , 2021, , .		0
27862	Inhibitory Effect and Potential Mechanism of <i>Lactobacillus plantarum</i> YE4 against Dipeptidyl Peptidase-4. <i>Foods</i> , 2022, 11, 80.	1.9	6
27863	Dental EHR-infused Persona Ontologies to Enrich Dental Dialogue Interaction of Agents. , 2021, 2021, 1818-1825.		0
27864	Complete genome sequence of <i>Bacillus velezensis</i> YYC, a bacterium isolated from the tomato rhizosphere. <i>Archives of Microbiology</i> , 2022, 204, 44.	1.0	7
27865	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2022, , .	3.2	0
27867	Exploring automatic inconsistency detection for literature-based gene ontology annotation. <i>Bioinformatics</i> , 2022, 38, i273-i281.	1.8	0

#	ARTICLE	IF	CITATIONS
27868	Coexpression reveals conserved gene programs that co-vary with cell type across kingdoms. <i>Nucleic Acids Research</i> , 2022, 50, 4302-4314.	6.5	16
27869	Beneficial roles of the AhR ligand FICZ on the regenerative potentials of BMSCs and primed cartilage templates. <i>RSC Advances</i> , 2022, 12, 11505-11516.	1.7	5
27870	DeepGOZero: improving protein function prediction from sequence and zero-shot learning based on ontology axioms. <i>Bioinformatics</i> , 2022, 38, i238-i245.	1.8	23
27871	Development and Applications of Interoperable Biomedical Ontologies for Integrative Data and Knowledge Representation and Multiscale Modeling in Systems Medicine. <i>Methods in Molecular Biology</i> , 2022, 2486, 233-244.	0.4	2
27872	Standardized genome-wide function prediction enables comparative functional genomics: a new application area for Gene Ontologies in plants. <i>GigaScience</i> , 2022, 11, .	3.3	2
27873	Proteomics profiling reveals a distinct high-risk molecular subtype of hypertrophic cardiomyopathy. <i>Heart</i> , 2022, 108, 1807-1814.	1.2	4
27874	High-Content Screening and Computational Prediction Reveal Viral Genes That Suppress the Innate Immune Response. <i>MSystems</i> , 2022, 7, e0146621.	1.7	5
27875	Effects of Luteinizing Hormone Releasing Hormone A2 on Gonad Development in Juvenile Amur Sturgeon, <i>Acipenser schrenckii</i> , Revealed by Transcriptome Profiling Analysis. <i>Frontiers in Genetics</i> , 2022, 13, 859965.	1.1	1
27876	m6A Regulator-Mediated RNA Methylation Modification Patterns are Involved in the Pathogenesis and Immune Microenvironment of Depression. <i>Frontiers in Genetics</i> , 2022, 13, 865695.	1.1	1
27877	Ontologies and Knowledge Graphs in Oncology Research. <i>Cancers</i> , 2022, 14, 1906.	1.7	6
27878	A single-cell liver atlas of <i>Plasmodium vivax</i> infection. <i>Cell Host and Microbe</i> , 2022, 30, 1048-1060.e5.	5.1	29
27879	Identification and characterization of circular RNAs in <i>Longissimus dorsi</i> muscle tissue from two goat breeds using RNA-Seq. <i>Molecular Genetics and Genomics</i> , 2022, 297, 817-831.	1.0	7
27880	Mosaic and non-mosaic protocadherin 19 mutation leads to neuronal hyperexcitability in zebrafish. <i>Neurobiology of Disease</i> , 2022, 169, 105738.	2.1	6
27881	Testicular "Inherited Metabolic Memory" of Ancestral High-Fat Diet Is Associated with Sperm sncRNA Content. <i>Biomedicines</i> , 2022, 10, 909.	1.4	8
27883	Integrative analysis of mutated genes and mutational processes reveals novel mutational biomarkers in colorectal cancer. <i>BMC Bioinformatics</i> , 2022, 23, 138.	1.2	9
27884	The gut environment regulates bacterial gene expression which modulates susceptibility to bacteriophage infection. <i>Cell Host and Microbe</i> , 2022, 30, 556-569.e5.	5.1	24
27885	Genomics, convergent neuroscience and progress in understanding autism spectrum disorder. <i>Nature Reviews Neuroscience</i> , 2022, 23, 323-341.	4.9	81
27886	A systematic review and functional bioinformatics analysis of genes associated with Crohn's disease identify more than 120 related genes. <i>BMC Genomics</i> , 2022, 23, 302.	1.2	7

#	ARTICLE	IF	CITATIONS
27887	Identification of a combined apoptosis and hypoxia gene signature for predicting prognosis and immune infiltration in breast cancer. <i>Cancer Medicine</i> , 2022, 11, 3886-3901.	1.3	9
27888	Transcriptomic analysis to elucidate the response of <i>Apis mellifera</i> ligustica brain tissue to fluvialinate exposure. <i>Animal Biotechnology</i> , 2023, 34, 4175-4186.	0.7	1
27889	A Perspective on Digital Knowledge Representation in Materials Science and Engineering. <i>Advanced Engineering Materials</i> , 2022, 24, .	1.6	10
27890	Mitochondrial 1555 G>A variant as a potential risk factor for childhood glioblastoma. <i>Neuro-Oncology Advances</i> , 2022, 4, vda045.	0.4	1
27891	Comparative transcriptomic analysis of two <i>Cucumis melo</i> var. <i>saccharinus</i> germplasms differing in fruit physical and chemical characteristics. <i>BMC Plant Biology</i> , 2022, 22, 193.	1.6	4
27892	An alternative UPF1 isoform drives conditional remodeling of nonsense-mediated mRNA decay. <i>EMBO Journal</i> , 2022, 41, e108898.	3.5	15
27894	Lipid metabolism regulated by superoxide scavenger trypsin in <i>Hylocereus undatus</i> through multi-omics analyses. <i>Journal of Food Biochemistry</i> , 2022, 46, e14144.	1.2	4
27895	Differential gene expression in nasal airway epithelium from overweight or obese youth with asthma. <i>Pediatric Allergy and Immunology</i> , 2022, 33, e13776.	1.1	5
27896	Ovarian cancer immunogenicity is governed by a narrow subset of progenitor tissue-resident memory T cells. <i>Cancer Cell</i> , 2022, 40, 545-557.e13.	7.7	53
27897	Unveiling the effect of <i>Withania somnifera</i> on neuronal cytoarchitecture and synaptogenesis: A combined <i>in vitro</i> and network pharmacology approach. <i>Phytotherapy Research</i> , 2022, 36, 2524-2541.	2.8	3
27898	Flower color mutation, pink to orange, through CmGATA4 - CCD4a-5 module regulates carotenoids degradation in <i>chrysanthemum</i> . <i>Plant Science</i> , 2022, 322, 111290.	1.7	8
27899	Analysis of human brain tissue derived from DBS surgery. <i>Translational Neurodegeneration</i> , 2022, 11, 22.	3.6	3
27902	Fluvialinate-Induced Changes in MicroRNA Expression Profile of <i>Apis mellifera</i> ligustica Brain Tissue. <i>Frontiers in Genetics</i> , 2022, 13, 855987.	1.1	1
27903	Identification of Intrinsically Disordered Proteins and Regions in a Non-Model Insect Species <i>Ostrinia nubilalis</i> (Hbn.). <i>Biomolecules</i> , 2022, 12, 592.	1.8	3
27904	Progenitor potential of lung epithelial organoid cells in a transplantation model. <i>Cell Reports</i> , 2022, 39, 110662.	2.9	26
27905	Response of aerobic granular sludge to loading shock: Performance and proteomic study. <i>Chemical Engineering Journal</i> , 2022, 444, 136458.	6.6	14
27906	Construction of a circRNA-Mediated ceRNA Network Reveals Novel Biomarkers for Aortic Dissection. <i>International Journal of General Medicine</i> , 2022, Volume 15, 3951-3964.	0.8	3
27907	Identification of NFASC and CHL1 as Two Novel Hub Genes in Endometriosis Using Integrated Bioinformatic Analysis and Experimental Verification. <i>Pharmacogenomics and Personalized Medicine</i> , 2022, Volume 15, 377-392.	0.4	2

#	ARTICLE	IF	CITATIONS
27908	Faster Growth Enhances Low Carbon Fuel and Chemical Production Through Gas Fermentation. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 879578.	2.0	11
27909	Loss of vascular endothelial notch signaling promotes spontaneous formation of tertiary lymphoid structures. <i>Nature Communications</i> , 2022, 13, 2022.	5.8	16
27910	Predicting causal genes from psychiatric genome-wide association studies using high-level etiological knowledge. <i>Molecular Psychiatry</i> , 2022, 27, 3095-3106.	4.1	4
27911	Identification of HMOX1 as a Critical Ferroptosis-Related Gene in Atherosclerosis. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 833642.	1.1	17
27912	Identification and Validation of Hub Genes with Poor Prognosis in Hepatocellular Carcinoma by Integrated Bioinformatical Analysis. <i>International Journal of General Medicine</i> , 2022, Volume 15, 3933-3941.	0.8	2
27913	Inhibition of the succinyl dehydrogenase complex in acute myeloid leukemia leads to a lactate-fuelled respiratory metabolic vulnerability. <i>Nature Communications</i> , 2022, 13, 2013.	5.8	22
27914	Vero cells gain renal tubule markers in low-calcium and magnesium chemically defined media. <i>Scientific Reports</i> , 2022, 12, 6180.	1.6	2
27915	Investigating the disordered regions (MoRFs, SLiMs and LCRs) and functions of mimicry proteins/peptides in silico. <i>PLoS ONE</i> , 2022, 17, e0265657.	1.1	3
27916	PTH2R is related to cell proliferation and migration in ovarian cancer: a multi-omics analysis of bioinformatics and experiments. <i>Cancer Cell International</i> , 2022, 22, 148.	1.8	5
27917	Single-Cell RNA Sequencing of Metastatic Testicular Seminoma Reveals the Cellular and Molecular Characteristics of Metastatic Cell Lineage. <i>Frontiers in Oncology</i> , 2022, 12, 871489.	1.3	6
27919	Transcriptomics Integrated with Metabolomics Reveals 2-Methoxy-1, 4-Naphthoquinone-Based Carbon Dots Induced Molecular Shifts in <i>Penicillium italicum</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 420.	1.5	3
27920	Proteomic Response of <i>Bacillus subtilis</i> Spores under High Pressure Combined with Moderate Temperature and Random Peptide Mixture LK Treatment. <i>Foods</i> , 2022, 11, 1123.	1.9	3
27922	Selection Signature Analyses Revealed Genes Associated With Adaptation, Production, and Reproduction in Selected Goat Breeds in Kenya. <i>Frontiers in Genetics</i> , 2022, 13, 858923.	1.1	4
27923	Full-Length Transcriptome Sequencing Reveals Tissue-Specific Gene Expression Profile of Mangrove Clam <i>Geloina erosa</i> . <i>Frontiers in Physiology</i> , 2022, 13, 851957.	1.3	4
27924	Overlap of vitamin A and vitamin D target genes with CAKUT-related processes. <i>F1000Research</i> , 0, 10, 395.	0.8	1
27925	A new ChEMBL dataset for the similarity-based target fishing engine FastTargetPred: Annotation of an exhaustive list of linear tetrapeptides. <i>Data in Brief</i> , 2022, 42, 108159.	0.5	2
27926	Bioinformatics analysis for identifying micro-RNAs, long noncoding RNAs, transcription factors, and immune genes regulatory networks in diabetic cardiomyopathy using an integrated bioinformatics analysis. <i>Inflammation Research</i> , 2022, 71, 847-858.	1.6	2
27927	Genome-scale phylogeography resolves the native population structure of the Asian longhorned beetle, <i>Anoplophora glabripennis</i> (Motschulsky). <i>Evolutionary Applications</i> , 2022, 15, 934-953.	1.5	7

#	ARTICLE	IF	CITATIONS
27928	Chlamydia pneumoniae Interferes with Macrophage Differentiation and Cell Cycle Regulation to Promote Its Replication. Cellular Microbiology, 2022, 2022, 1-19.	1.1	0
27929	Global post-translational modification profiling of HIV-1-infected cells reveals mechanisms of host cellular pathway remodeling. Cell Reports, 2022, 39, 110690.	2.9	12
27932	Methamphetamine Disturbs Gut Homeostasis and Reshapes Serum Metabolome, Inducing Neurotoxicity and Abnormal Behaviors in Mice. Frontiers in Microbiology, 2022, 13, 755189.	1.5	10
27933	Improving ovarian cancer treatment decision using a novel risk predictive tool. Aging, 2022, 14, 3464-3483.	1.4	4
27934	Identification of Genes Related to Squab Muscle Growth and Lipid Metabolism from Transcriptome Profiles of Breast Muscle and Liver in Domestic Pigeon (Columba livia). Animals, 2022, 12, 1061.	1.0	2
27936	Semantic clustering analysis of E3-ubiquitin ligases in gastrointestinal tract defines genes ontology clusters with tissue expression patterns. BMC Gastroenterology, 2022, 22, 186.	0.8	0
27938	Biodegradation of chlortetracycline by Bacillus cereus LZ01: Performance, degradative pathway and possible genes involved. Journal of Hazardous Materials, 2022, 434, 128941.	6.5	24
27939	Cancer pharmacogenomics: challenges, promises, and its application to cancer drug discovery. , 0, , 499-517.		0
27941	Chemical signalling between plants: mechanistic similarities between phytotoxic allelopathy and host recognition by parasitic plants. , 0, , 55-69.		0
27961	Clique Selection and its Effect on Paraclique Enrichment: An Experimental Study. , 0, , .		0
29171	Dealing with Duplicated Genomes of Teleosts. , 0, , 511-524.		0
29173	Genomics Technologies as Tools in Drug Discovery. , 0, , 25-103.		0
29176	Daily running enhances molecular and physiological circadian rhythms in skeletal muscle. Molecular Metabolism, 2022, 61, 101504.	3.0	14
29177	Deletion and tandem duplications of biosynthetic genes drive the diversity of triterpenoids in Aralia elata. Nature Communications, 2022, 13, 2224.	5.8	34
29178	An extraction from Trametes robiniophila Murr. (<i>Huaier</i>) inhibits non-small cell lung cancer proliferation via targeting to epidermal growth factor receptor. Bioengineered, 2022, 13, 10931-10943.	1.4	3
29179	Multiomics Data Integration Identifies New Molecular Signatures for Abdominal Aortic Aneurysm and Aortic Occlusive Disease: Implications for Early Diagnosis, Prognosis, and Therapeutic Targets. OMICS A Journal of Integrative Biology, 2022, 26, 290-304.	1.0	3
29180	A Semi-Supervised Autoencoder-Based Approach for Protein Function Prediction. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 4957-4965.	3.9	5
29181	Muscle mitochondrial remodeling by intermittent glucocorticoid drugs requires an intact circadian clock and muscle PGC1 β . Science Advances, 2022, 8, eabm1189.	4.7	16

#	ARTICLE	IF	CITATIONS
29182	<i>Pseudomonas aeruginosa</i> Initiates a Rapid and Specific Transcriptional Response during Surface Attachment. <i>Journal of Bacteriology</i> , 2022, 204, e0008622.	1.0	8
29183	Multiple metastatic clones assessed by an integrative multiomics strategy in clear cell renal carcinoma: a case study. <i>Journal of Clinical Pathology</i> , 2022, 75, 426-430.	1.0	2
29184	A Bayesian framework to integrate multi-level genome-scale data for Autism risk gene prioritization. <i>BMC Bioinformatics</i> , 2022, 23, 146.	1.2	0
29185	Trans-cinnamaldehyde protects against phenylephrine-induced cardiomyocyte hypertrophy through the CaMKII/ERK pathway. <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, 115.	1.2	2
29186	Impact of medication on blood transcriptome reveals off-target regulations of beta-blockers. <i>PLoS ONE</i> , 2022, 17, e0266897.	1.1	1
29187	Advances in molecular classification of renal neoplasms. <i>Histology and Histopathology</i> , 2006, 21, 325-39.	0.5	20
29188	Establishing a competing endogenous RNA (ceRNA)-immunoregulatory network associated with the progression of Alzheimer's disease.. <i>Annals of Translational Medicine</i> , 2022, 10, 65.	0.7	0
29190	A Bayes random field approach for integrative large-scale regulatory network analysis. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.0	0
29191	Global sequence properties for superfamily prediction: a machine learning approach. <i>Journal of Integrative Bioinformatics</i> , 2009, 6, 109.	1.0	1
29192	Quality controls in integrative approaches to detect errors and inconsistencies in biological databases. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	5
29193	Complementarity of network and sequence information in homologous proteins. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	17
29194	CASSys: an integrated software-system for the interactive analysis of ChIP-seq data. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 155.	1.0	1
29195	A semi-automated approach for anatomical ontology mapping. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 221.	1.0	1
29196	Probabilistic latent semantic analysis applied to whole bacterial genomes identifies common genomic features. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 243.	1.0	2
29197	Web-based hybrid-dimensional Visualization and Exploration of Cytological Localization Scenarios. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 298.	1.0	3
29198	miRNAs expression pattern and machine learning models elucidate risk for gastric GIST. <i>Cancer Biomarkers</i> , 2022, 33, 237-247.	0.8	1
29199	MDN1 Mutation Is Associated With High Tumor Mutation Burden and Unfavorable Prognosis in Breast Cancer. <i>Frontiers in Genetics</i> , 2022, 13, 857836.	1.1	2
29200	Integrated Metabolomic and Transcriptomic Analysis and Identification of Dammarenediol-II Synthase Involved in Saponin Biosynthesis in <i>Gynostemma longipes</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 852377.	1.7	4

#	ARTICLE	IF	CITATIONS
29206	Identification of hub genes and pathways in bladder cancer using bioinformatics analysis.. American Journal of Clinical and Experimental Urology, 2022, 10, 13-24.	0.4	0
29207	IMEx Databases: Displaying Molecular Interactions into a Single, Standards-Compliant Dataset. Methods in Molecular Biology, 2022, 2449, 27-42.	0.4	4
29208	ProTranslator: Zero-Shot Protein Function Prediction Using Textual Description. Lecture Notes in Computer Science, 2022, , 279-294.	1.0	6
29210	Genetic mechanisms underlying gray matter volume changes in patients with drug-naive first-episode schizophrenia. Cerebral Cortex, 2023, 33, 2328-2341.	1.6	10
29211	GenePlexus: a web-server for gene discovery using network-based machine learning. Nucleic Acids Research, 2022, 50, W358-W366.	6.5	3
29212	A Deep Learning Framework for Predicting Protein Functions With Co-Occurrence of GO Terms. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 833-842.	1.9	4
29214	MCWS-Transformers: Towards an Efficient Modeling of Protein Sequences via Multi Context-Window Based Scaled Self-Attention. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 1188-1199.	1.9	3
29215	From Beginning to End: Expanding the SERINC3 Interactome Through an <i>in silico</i> Analysis. Bioinformatics and Biology Insights, 2022, 16, 117793222210929.	1.0	1
29216	Organization of gene programs revealed by unsupervised analysis of diverse gene-trait associations. Nucleic Acids Research, 2022, 50, e87-e87.	6.5	5
29217	Functional genomics tools for studying microbe-mediated stress tolerance in plants. , 2022, , 175-204.		1
29219	Exome sequencing of hepatocellular carcinoma in lemurs identifies potential cancer drivers. Evolution, Medicine and Public Health, 2022, 10, 221-230.	1.1	0
29222	Characterization and Phylogenetic Analyses of the Complete Mitochondrial Genome of Sugarcane (Saccharum spp. Hybrids) Line A1. Diversity, 2022, 14, 333.	0.7	3
29223	Genome-Wide Identification and Expression Profiling of KCS Gene Family in Passion Fruit (Passiflora) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 13, 872263.	1.7	12
29224	Inheritance of social dominance is associated with global sperm DNA methylation in inbred male mice. Environmental Epigenetics, 0, , .	0.9	0
29225	Transcriptome and biochemical analyses of glutathione-dependent regulation of tomato fruit ripening. Journal of Plant Interactions, 2022, 17, 537-547.	1.0	6
29226	An organ-specific transcriptomic atlas of the medicinal plant <i>Bletilla striata</i> : Protein-coding genes, microRNAs, and regulatory networks. Plant Genome, 2022, 15, e20210.	1.6	5
29227	Transcriptome and metabolome analyses reveal new insights into chlorophyll, photosynthesis, metal ion and phenylpropanoids related pathways during sugarcane ratoon chlorosis. BMC Plant Biology, 2022, 22, 222.	1.6	5
29228	An Improved Genome Sequence Resource of <i>Bipolaris maydis</i> , Causal Agent of Southern Corn Leaf Blight. Phytopathology, 2022, , PHYTO11210490A.	1.1	3

#	ARTICLE	IF	CITATIONS
29229	Proteomic networks associated with tumor-educated macrophage polarization and cytotoxicity potentiated by heat-killed tuberculosis. <i>Scientific Reports</i> , 2022, 12, 6881.	1.6	0
29230	Integrative analysis of TCGA data identifies miRNAs as drug-specific survival biomarkers. <i>Scientific Reports</i> , 2022, 12, 6785.	1.6	1
29231	LM-GVP: an extensible sequence and structure informed deep learning framework for protein property prediction. <i>Scientific Reports</i> , 2022, 12, 6832.	1.6	21
29232	CsbZIP2-miR9748-CsNPF4.4 Module Mediates High Temperature Tolerance of Cucumber Through Jasmonic Acid Pathway. <i>Frontiers in Plant Science</i> , 2022, 13, 883876.	1.7	4
29233	An Arabidopsis mutant deficient in phosphatidylinositol-4-phosphate kinases $\text{Å}1$ and $\text{Å}2$ displays altered auxin-related responses in roots. <i>Scientific Reports</i> , 2022, 12, 6947.	1.6	4
29234	Cancer Metabolic Subtypes and Their Association with Molecular and Clinical Features. <i>Cancers</i> , 2022, 14, 2145.	1.7	3
29235	A Community-Driven, Openly Accessible Molecular Pathway Integrating Knowledge on Malignant Pleural Mesothelioma. <i>Frontiers in Oncology</i> , 2022, 12, 849640.	1.3	4
29236	Targeting Cell Death Mechanism Specifically in Triple Negative Breast Cancer Cell Lines. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4784.	1.8	1
29238	Bone Progenitors Pull the Strings on the Early Metabolic Rewiring Occurring in Prostate Cancer Cells. <i>Cancers</i> , 2022, 14, 2083.	1.7	5
29239	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans. <i>Microbiome</i> , 2022, 10, 67.	4.9	17
29240	Recognition of Gonadal Development in <i>Eriocheir sinensis</i> Based on the Impulse of Love at First Sight. <i>Frontiers in Physiology</i> , 2022, 13, 793699.	1.3	0
29241	The interferon-inducible GTPase MxB promotes capsid disassembly and genome release of herpesviruses. <i>ELife</i> , 2022, 11, .	2.8	16
29242	Inferring Potential Cancer Driving Synonymous Variants. <i>Genes</i> , 2022, 13, 778.	1.0	1
29243	A Prognostic Gene Signature for Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2022, 12, 841530.	1.3	9
29244	Chemical Diversity and Potential Target Network of Woody Peony Flower Essential Oil from Eleven Representative Cultivars (<i>Paeonia Å suffruticosa</i> Andr.). <i>Molecules</i> , 2022, 27, 2829.	1.7	5
29245	Genome annotation of <i>Caenorhabditis briggsae</i> by TEC-RED identifies new exons, paralogs, and conserved and novel operons. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
29246	Intense Innate Immune Responses and Severe Metabolic Disorders in Chicken Embryonic Visceral Tissues Caused by Infection with Highly Virulent Newcastle Disease Virus Compared to the Avirulent Virus: A Bioinformatics Analysis. <i>Viruses</i> , 2022, 14, 911.	1.5	3
29247	Inheritance and Genetic Mapping of Late-Bolting to Early-Bolting Gene, BrEb-1, in Chinese Cabbage (<i>Brassica rapa</i> L.). <i>Agronomy</i> , 2022, 12, 1048.	1.3	0

#	ARTICLE	IF	CITATIONS
29248	The clinical value of miRNA-21 in cervical cancer: A comprehensive investigation based on microarray datasets. <i>PLoS ONE</i> , 2022, 17, e0267108.	1.1	5
29249	Insights into the Molecular Regulation of Lignin Content in Triploid Poplar Leaves. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4603.	1.8	15
29250	Identification of replication fork-associated proteins in <i>Drosophila</i> embryos and cultured cells using iPOND coupled to quantitative mass spectrometry. <i>Scientific Reports</i> , 2022, 12, 6903.	1.6	5
29251	Transcriptome Analysis of the Cf-13-Mediated Hypersensitive Response of Tomato to <i>Cladosporium fulvum</i> Infection. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4844.	1.8	6
29252	Comprehensive Analysis of the Differentially Expressed Transcriptome with ceRNA Networks in a Mouse Model of Liver Cirrhosis. <i>Current Bioinformatics</i> , 2022, 17, 510-520.	0.7	2
29253	Human iPSC-derived-keratinocytes, a useful model to identify and explore pathological phenotype of Epidermolysis Bullosa Simplex.. <i>Journal of Investigative Dermatology</i> , 2022, , .	0.3	2
29254	Bi-allelic variants in <i>SHOC1</i> cause non-obstructive azoospermia with meiosis arrest in humans and mice. <i>Molecular Human Reproduction</i> , 2022, 28, .	1.3	7
29255	Systematic molecular analysis of the human secretome and membrane proteome in gastrointestinal adenocarcinomas. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 3329-3342.	1.6	4
29256	Genome-Wide Association Study and Genomic Selection for Proteinogenic Methionine in Soybean Seeds. <i>Frontiers in Plant Science</i> , 2022, 13, 859109.	1.7	8
29257	Genome-Wide Identification of Associations of Circulating Molecules With Spontaneous Coronary Artery Dissection and Aortic Aneurysm and Dissection. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 874912.	1.1	4
29258	Integrated analysis of transcriptomic data reveals the platelet response in COVID-19 disease. <i>Scientific Reports</i> , 2022, 12, 6851.	1.6	7
29259	Overexpression of lncRNA-Gm2044 in spermatogonia impairs spermatogenesis in partial seminiferous tubules. <i>Poultry Science</i> , 2022, 101, 101930.	1.5	4
29260	An integrated network representation of multiple cancer-specific data for graph-based machine learning. <i>Npj Systems Biology and Applications</i> , 2022, 8, 14.	1.4	4
29262	Identification of Potential Diagnoses Based on Immune Infiltration and Autophagy Characteristics in Major Depressive Disorder. <i>Frontiers in Genetics</i> , 2022, 13, 702366.	1.1	3
29263	Comprehensive enhancer-target gene assignments improve gene set level interpretation of genome-wide regulatory data. <i>Genome Biology</i> , 2022, 23, 105.	3.8	6
29264	Mechanism of Ba Zhen Tang Delaying Skin Photoaging Based on Network Pharmacology and Molecular Docking. <i>Clinical, Cosmetic and Investigational Dermatology</i> , 2022, Volume 15, 763-781.	0.8	3
29265	Network Pharmacology Integrated with Molecular Docking Elucidates the Mechanism of Wuwei Yuganzi San for the Treatment of Coronary Heart Disease. <i>Natural Product Communications</i> , 2022, 17, 1934578X2210939.	0.2	2
29266	A targeted approach to investigating immune genes of an iconic Australian marsupial. <i>Molecular Ecology</i> , 2022, 31, 3286-3303.	2.0	9

#	ARTICLE	IF	CITATIONS
29267	Effects of Chang-Kang-Fang Formula on the Microbiota-Gut-Brain Axis in Rats With Irritable Bowel Syndrome. <i>Frontiers in Pharmacology</i> , 2022, 13, .	1.6	3
29268	High MICAL-L2 expression and its role in the prognosis of colon adenocarcinoma. <i>BMC Cancer</i> , 2022, 22, 487.	1.1	6
29269	Mapping the epithelial-immune cell interactome upon infection in the gut and the upper airways. <i>Npj Systems Biology and Applications</i> , 2022, 8, 15.	1.4	3
29270	Expression profile analysis in cells overexpressing <sc>DRPLA cDNA</sc> to explore the roles of <sc>DRPLA</sc> as a transcriptional coregulator. <i>Neurology and Clinical Neuroscience</i> , 0, , .	0.2	0
29271	Statin therapy inhibits fatty acid synthase via dynamic protein modifications. <i>Nature Communications</i> , 2022, 13, 2542.	5.8	7
29272	Integrative analysis of clinical and epigenetic biomarkers of mortality. <i>Aging Cell</i> , 2022, 21, e13608.	3.0	8
29273	Feature extraction with spectral clustering for gene function prediction using hierarchical multi-label classification. <i>Applied Network Science</i> , 2022, 7, .	0.8	1
29274	Multi-omics signatures of alcohol use disorder in the dorsal and ventral striatum. <i>Translational Psychiatry</i> , 2022, 12, 190.	2.4	11
29276	CrowdGO: Machine learning and semantic similarity guided consensus Gene Ontology annotation. <i>PLoS Computational Biology</i> , 2022, 18, e1010075.	1.5	4
29277	Impact of Environmentally Relevant Concentrations of Bisphenol A (BPA) on the Gene Expression Profile in an In Vitro Model of the Normal Human Ovary. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5334.	1.8	9
29278	Exploration of the Potential Mechanism of the Common Differentially Expressed Genes in Psoriasis and Atopic Dermatitis. <i>BioMed Research International</i> , 2022, 2022, 1-16.	0.9	1
29279	RNA-seq and Network Analysis Reveal Unique Chemokine Activity Signatures in the Synovial Tissue of Patients With Rheumatoid Arthritis. <i>Frontiers in Medicine</i> , 2022, 9, .	1.2	3
29280	Sex-relevant genes in the embryo stage of Chinese soft-shelled turtles as revealed by RNA-Seq analysis. <i>Animal Biology</i> , 2022, -1, 1-19.	0.6	0
29281	Inositol polyphosphate multikinase physically binds to the SWI/SNF complex and modulates BRG1 occupancy in mouse embryonic stem cells. <i>ELife</i> , 2022, 11, .	2.8	5
29282	A Protocol for the Cryopreservation of Human Intestinal Mucosal Biopsies Compatible With Single-Cell Transcriptomics and Ex Vivo Studies. <i>Frontiers in Physiology</i> , 2022, 13, .	1.3	2
29283	Enhancing Data Integration, Interoperability, and Reuse to Address Complex and Emerging Environmental Health Problems. <i>Environmental Science & Technology</i> , 2022, 56, 7544-7552.	4.6	10
29284	High Expression of HERV-K (HML-2) Might Stimulate Interferon in COVID-19 Patients. <i>Viruses</i> , 2022, 14, 996.	1.5	9
29285	Reactive Astrocytes Derived From Human Induced Pluripotent Stem Cells Suppress Oligodendrocyte Precursor Cell Differentiation. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, .	1.4	6

#	ARTICLE	IF	CITATIONS
29286	Biotechnological Combination for Co-contaminated Soil Remediation: Focus on Tripartite α -Meta-Enzymatic Activity. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	5
29287	PRD-Class Homeobox Genes in Bovine Early Embryos: Function, Evolution, and Overlapping Roles. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
29288	Time-series expression profiles of mRNAs and lncRNAs during mammalian palatogenesis. <i>Oral Diseases</i> , 2023, 29, 2163-2176.	1.5	4
29289	Signatures of selection in core and accessory genomes indicate different ecological drivers of diversification among <i>Bacillus cereus</i> clades. <i>Molecular Ecology</i> , 2022, 31, 3584-3597.	2.0	4
29290	deepSimDEF: deep neural embeddings of gene products and gene ontology terms for functional analysis of genes. <i>Bioinformatics</i> , 2022, 38, 3051-3061.	1.8	4
29291	Dataset of De Novo hybrid berry transcriptome profiling and characterization of Piper species (Piper) Tj ETQq1 1 0.784314 rgBT /Over 0.5 80	0.5	0
29292	The Immunometabolic Atlas: A tool for design and interpretation of metabolomics studies in immunology. <i>PLoS ONE</i> , 2022, 17, e0268408.	1.1	1
29293	Pollock: Fishing for Cell States. <i>Bioinformatics Advances</i> , 0, , .	0.9	0
29294	Investigation of two ferroptosis-related molecular subtypes and biomarkers in the progression of gastric adenocarcinoma. <i>International Journal of Transgender Health</i> , 2022, 15, 537-546.	1.1	0
29295	SubcellulaRVis: a web-based tool to simplify and visualise subcellular compartment enrichment. <i>Nucleic Acids Research</i> , 2022, 50, W718-W725.	6.5	7
29296	Wnt11 acts on dermomyotome cells to guide epaxial myotome morphogenesis. <i>ELife</i> , 2022, 11, .	2.8	7
29299	A Four-Gene Prognostic Signature Based on the TEAD4 Differential Expression Predicts Overall Survival and Immune Microenvironment Estimation in Lung Adenocarcinoma. <i>Frontiers in Pharmacology</i> , 2022, 13, .	1.6	1
29301	Two conserved amino acids differentiate the biology of high-risk and low-risk HPV E5 proteins.. <i>Journal of Medical Virology</i> , 2022, , .	2.5	5
29302	The ceRNA Crosstalk between mRNAs and lncRNAs in Diabetes Myocardial Infarction. <i>Disease Markers</i> , 2022, 2022, 1-12.	0.6	0
29303	Whole genome sequencing and analysis of fenvalerate degrading bacteria <i>Citrobacter freundii</i> CD-9. <i>AMB Express</i> , 2022, 12, 51.	1.4	11
29304	Identification of a Cancer Stem Cells Signature of Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	3
29305	Identifying genetic variants and pathways influencing daughter averages for twinning in North American Holstein cattle and evaluating the potential for genomic selection. <i>Journal of Dairy Science</i> , 2022, , .	1.4	1
29306	Text mining for identification of biological entities related to antibiotic resistant organisms. <i>PeerJ</i> , 2022, 10, e13351.	0.9	0

#	ARTICLE	IF	CITATIONS
29307	H3K27 methylation regulates the fate of two cell lineages in male gametophytes. <i>Plant Cell</i> , 2022, 34, 2989-3005.	3.1	7
29308	Use of viral motif mimicry improves the proteome-wide discovery of human linear motifs. <i>Cell Reports</i> , 2022, 39, 110764.	2.9	10
29309	Transcriptomic analysis and discovery of genes involving in enhanced immune protection of Pacific abalone (<i>Haliotis discus hannai</i>) in response to the re-infection of <i>Vibrio parahaemolyticus</i> . <i>Fish and Shellfish Immunology</i> , 2022, 125, 128-140.	1.6	10
29310	Risk Cost Measurement of Value for Money Evaluation Based on Case-Based Reasoning and Ontology: A Case Study of the Urban Rail Transit Public-Private Partnership Projects in China. <i>Sustainability</i> , 2022, 14, 5547.	1.6	4
29311	Development of a Bile Acid-Related Gene Signature for Predicting Survival in Patients with Hepatocellular Carcinoma. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-14.	0.7	1
29312	Pan-cancer analysis of the DNA methylation patterns of long non-coding RNA. <i>Genomics</i> , 2022, 114, 110377.	1.3	5
29313	lncRNAâ€™mRNA Expression Patterns in Invasive Pituitary Adenomas: A Microarray Analysis. <i>BioMed Research International</i> , 2022, 2022, 1-12.	0.9	7
29314	Distinct Injury Responsive Regulatory T Cells Identified by Multi-Dimensional Phenotyping. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	2
29316	Gaur genome reveals expansion of sperm odorant receptors in domesticated cattle. <i>BMC Genomics</i> , 2022, 23, 344.	1.2	3
29317	Lymph node colonization induces tumor-immune tolerance to promote distant metastasis. <i>Cell</i> , 2022, 185, 1924-1942.e23.	13.5	111
29318	Shared genetic loci between depression and cardiometabolic traits. <i>PLoS Genetics</i> , 2022, 18, e1010161.	1.5	18
29319	Small RNA Sequencing in the Tg4â€™42 Mouse Model Suggests the Involvement of snoRNAs in the Etiology of Alzheimerâ€™s Disease. <i>Journal of Alzheimer's Disease</i> , 2022, 87, 1671-1681.	1.2	2
29320	Systematic characterization of gene function in the photosynthetic alga <i>Chlamydomonas reinhardtii</i> . <i>Nature Genetics</i> , 2022, 54, 705-714.	9.4	42
29321	<i>Roseococcus pinisoli</i> sp. nov., lacking pufL and pufM bacteriochlorophyll a: synthesizing genes. <i>Archives of Microbiology</i> , 2022, 204, 293.	1.0	5
29322	Flavivirus Capsid Proteins Inhibit the Interferon Response. <i>Viruses</i> , 2022, 14, 968.	1.5	6
29323	The Mantle Transcriptome of <i>Chamelea gallina</i> (Mollusca: Bivalvia) and Shell Biomineralization. <i>Animals</i> , 2022, 12, 1196.	1.0	1
29325	Identification of Differential Genes of DNA Methylation Associated With Alzheimerâ€™s Disease Based on Integrated Bioinformatics and Its Diagnostic Significance. <i>Frontiers in Aging Neuroscience</i> , 2022, 14, .	1.7	5
29326	Transcriptomic and metabolomic landscape of quinoa during seed germination. <i>BMC Plant Biology</i> , 2022, 22, 237.	1.6	10

#	ARTICLE	IF	CITATIONS
29327	DEPCOD: a tool to detect and visualize co-evolution of protein domains. <i>Nucleic Acids Research</i> , 2022, , .	6.5	0
29328	Evidence of multiple genome duplication events in <i>Mytilus</i> evolution. <i>BMC Genomics</i> , 2022, 23, 340.	1.2	12
29329	Screening of Key Part in IFN Pathway for Herpes Zoster: Evidence from Bioinformatics Analysis. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, .	0.6	0
29330	Exploring the Mechanism of Yi-Jing Decoction in Treating Polycystic Ovary Syndrome by Using Network Pharmacology. <i>Current Medicinal Chemistry</i> , 2022, 29, .	1.2	3
29331	TripletGO: Integrating Transcript Expression Profiles with Protein Homology Inferences for Gene Function Prediction. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1013-1027.	3.0	4
29332	A natural mutator allele shapes mutation spectrum variation in mice. <i>Nature</i> , 2022, 605, 497-502.	13.7	38
29335	Physiological Effects and Transcriptomic Analysis of sbGnRH on the Liver in Pompano (<i>Trachinotus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.5	4
29336	Differentially expressed <i>EREG</i> and <i>SPP1</i> are independent prognostic markers in cervical squamous cell carcinoma. <i>Journal of Obstetrics and Gynaecology Research</i> , 2022, 48, 1848-1858.	0.6	4
29337	Genetic regulation of male sexual development in the oriental river prawn <i>Macrobrachium nipponense</i> during reproductive vs. non-reproductive season. <i>Aquaculture International</i> , 2022, 30, 2059-2079.	1.1	7
29338	Dynamic Transcriptome Profiling Reveals LncRNA-Centred Regulatory Networks in the Modulation of Pluripotency. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	1
29339	LncMIR181A1HG is a novel chromatin-bound epigenetic suppressor of early stage osteogenic lineage commitment. <i>Scientific Reports</i> , 2022, 12, 7770.	1.6	4
29340	Single-Cell RNA Sequencing Profiles Identify Important Pathophysiologic Factors in the Progression of Diabetic Nephropathy. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	5
29341	A Bayesian network structure learning approach to identify genes associated with stress in spleens of chickens. <i>Scientific Reports</i> , 2022, 12, 7482.	1.6	0
29342	Genomic integration to identify molecular biomarkers associated with indicator traits of gastrointestinal nematode resistance in sheep. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 502-516.	0.8	5
29343	Acetylome analysis of acetylation providing new insight into sclerotial generation in medicinal fungus <i>Polyporus umbellatus</i> . <i>Scientific Reports</i> , 2022, 12, 7629.	1.6	2
29344	Acute inflammatory response via neutrophil activation protects against the development of chronic pain. <i>Science Translational Medicine</i> , 2022, 14, eabj9954.	5.8	115
29345	Degron masking outlines degronons, co-degrading functional modules in the proteome. <i>Communications Biology</i> , 2022, 5, 445.	2.0	7
29346	Genomic analysis of <i>Thalassospira</i> sp. SW-3-3 reveals its genetic potential for phthalate pollution remediation. <i>Marine Genomics</i> , 2022, 63, 100953.	0.4	0

#	ARTICLE	IF	CITATIONS
29347	Association of a Novel DOCK2 Mutation-Related Gene Signature With Immune in Hepatocellular Carcinoma. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	4
29348	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. <i>Cancer Genetics</i> , 2022, 264-265, 90-99.	0.2	3
29349	Chicory polysaccharides alleviate high-fat diet-induced non-alcoholic fatty liver disease via alteration of lipid metabolism- and inflammation-related gene expression. <i>Food Science and Human Wellness</i> , 2022, 11, 954-964.	2.2	9
29350	Comparative transcriptomic analysis reveals the potential mechanism of hot water treatment alleviated-chilling injury in banana fruit. <i>Food Research International</i> , 2022, 157, 111296.	2.9	16
29351	Full length transcriptomes analysis of cold-resistance of <i>Apis cerana</i> in Changbai Mountain during overwintering period. <i>Gene</i> , 2022, 830, 146503.	1.0	3
29352	Enrichment analysis on regulatory subspaces: A novel direction for the superior description of cellular responses to SARS-CoV-2. <i>Computers in Biology and Medicine</i> , 2022, 146, 105443.	3.9	0
29353	Integrated systems pharmacology and transcriptomics to dissect the mechanisms of Loki Zupa decoction in the treatment of murine allergic asthma. <i>Journal of Ethnopharmacology</i> , 2022, 294, 115351.	2.0	6
29354	Three-dimensional Structure Databases of Biological Macromolecules. <i>Methods in Molecular Biology</i> , 2022, 2449, 43-91.	0.4	2
29355	Survival-related genes are diversified across cancers but generally enriched in cancer hallmark pathways. <i>BMC Genomics</i> , 2021, 22, 918.	1.2	1
29356	Protein N-glycosylation aberrations and glycoproteomic network alterations in osteoarthritis and osteoarthritis with type 2 diabetes. <i>Scientific Reports</i> , 2022, 12, 6977.	1.6	6
29357	Natural selenium stress influences the changes of antibiotic resistome in seleniferous forest soils. <i>Environmental Microbiomes</i> , 2022, 17, 26.	2.2	8
29358	Reclassification of Hepatocellular Cancer With Neural-Related Genes. <i>Frontiers in Oncology</i> , 2022, 12, .	1.3	4
29359	Diagnosis of pulmonary tuberculosis via identification of core genes and pathways utilizing blood transcriptional signatures: a multicohort analysis. <i>Respiratory Research</i> , 2022, 23, 125.	1.4	3
29360	Lymph node stromal cells support the maturation of pre-DCs into cDC-like cells via colony-stimulating factor 1. <i>Immunology</i> , 2022, 166, 475-491.	2.0	3
29361	Identification and Transcriptome Analysis of Genes Related to Membrane Lipid Regulation in Sweet Sorghum under Salt Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5465.	1.8	5
29362	Identification of Context-Specific Fitness Genes Associated With Metabolic Rearrangements for Prognosis and Potential Treatment Targets for Liver Cancer. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	1
29363	Pan-Cancer Single-Cell Analysis Reveals the Core Factors and Pathway in Specific Cancer Stem Cells of Upper Gastrointestinal Cancer. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, .	2.0	2
29364	CAPTURE of the Human U2 snRNA Genes Expands the Repertoire of Associated Factors. <i>Biomolecules</i> , 2022, 12, 704.	1.8	1

#	ARTICLE	IF	CITATIONS
29365	Nuclear oligo hashing improves differential analysis of single-cell RNA-seq. <i>Nature Communications</i> , 2022, 13, 2666.	5.8	0
29366	Proteome-wide prediction and analysis of the <i>Cryptosporidium parvum</i> protein-protein interaction network through integrative methods. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2322-2331.	1.9	2
29367	Proteogenomic characterization of 2002 human cancers reveals pan-cancer molecular subtypes and associated pathways. <i>Nature Communications</i> , 2022, 13, 2669.	5.8	78
29368	Low Dose Gamma Irradiation of <i>Trypanosoma evansi</i> Parasites Identifies Molecular Changes That Occur to Repair Radiation Damage and Gene Transcripts That May Be Involved in Establishing Disease in Mice Post-Irradiation. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	0
29369	De novo transcriptome analysis of industrially important agarophyte <i>Gracilaria dura</i> (Rhodophyta: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Algal Research, 2022, 65, 102712.	2.4	1
29370	Modular Multi-Source Prediction of Drug Side-Effects With DruGNN. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1211-1220.	1.9	8
29371	Machine learning: its challenges and opportunities in plant system biology. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 3507-3530.	1.7	26
29372	Immune-Related Biomarkers Associated with Lung Metastasis from the Colorectal Cancer Microenvironment. <i>Journal of Interferon and Cytokine Research</i> , 2022, 42, 220-234.	0.5	0
29373	ASC-J9 Blocks Cell Proliferation and Extracellular Matrix Production of Keloid Fibroblasts through Inhibiting STAT3 Signaling. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5549.	1.8	7
29374	Investigating the Molecular Mechanism of Quercetin Protecting against Podocyte Injury to Attenuate Diabetic Nephropathy through Network Pharmacology, MicroarrayData Analysis, and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-13.	0.5	4
29375	Spatial Mapping of Plant N-Glycosylation Cellular Heterogeneity Inside Soybean Root Nodules Provided Insights Into Legume-Rhizobia Symbiosis. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	7
29376	A molecular view of amyotrophic lateral sclerosis through the lens of interaction network modules. <i>PLoS ONE</i> , 2022, 17, e0268159.	1.1	2
29377	Transcription elongation is finely tuned by dozens of regulatory factors. <i>ELife</i> , 2022, 11, .	2.8	8
29378	Characterization of m ⁶ A modifications in the contemporary Zika virus genome and host cellular transcripts. <i>Journal of Medical Virology</i> , 2022, 94, 4309-4318.	2.5	1
29379	<i>Oceanisphaera pacifica</i> sp. nov., isolated from the intestine of <i>Trichiurus japonicus</i> . <i>Archives of Microbiology</i> , 2022, 204, 338.	1.0	1
29380	Construction and comprehensive analysis of a lncRNA-mRNA interactive network to reveal a potential lncRNA for hepatic encephalopathy development. <i>Human Cell</i> , 2022, , .	1.2	3
29381	A Molecular Analysis of Neural Olfactory Placode Differentiation in Human Pluripotent Stem Cells. <i>Stem Cells and Development</i> , 2022, 31, 507-520.	1.1	2
29382	The Cooperation Databank: Machine-Readable Science Accelerates Research Synthesis. <i>Perspectives on Psychological Science</i> , 2022, 17, 1472-1489.	5.2	15

#	ARTICLE	IF	CITATIONS
29383	Genome mining reveals polysaccharide-degrading potential and new antimicrobial gene clusters of novel intestinal bacterium <i>Paenibacillus jilinensis</i> sp. nov.. <i>BMC Genomics</i> , 2022, 23, 380.	1.2	2
29384	Complete genome sequence of <i>Pseudomonas stutzeri</i> S116 owning bifunctional catalysis provides insights into affecting performance of microbial fuel cells. <i>BMC Microbiology</i> , 2022, 22, 137.	1.3	7
29385	Identification of LINE retrotransposons and long non-coding RNAs expressed in the octopus brain. <i>BMC Biology</i> , 2022, 20, 116.	1.7	6
29386	Identifying Alzheimer's genes via brain transcriptome mapping. <i>BMC Medical Genomics</i> , 2022, 15, 116.	0.7	1
29387	CBEA: Competitive balances for taxonomic enrichment analysis. <i>PLoS Computational Biology</i> , 2022, 18, e1010091.	1.5	3
29388	Human phospho-signaling networks of SARS-CoV-2 infection are rewired by population genetic variants. <i>Molecular Systems Biology</i> , 2022, 18, e10823.	3.2	8
29389	Identification of combined biomarkers for predicting the risk of osteoporosis using machine learning. <i>Aging</i> , 2022, 14, 4270-4280.	1.4	4
29390	An Herbal Product Alleviates Bleomycin-Induced Pulmonary Fibrosis in Mice via Regulating NF- κ B/TNF- α Signaling in Macrophages. <i>Frontiers in Pharmacology</i> , 2022, 13, 805432.	1.6	6
29391	Lupus Susceptibility Loci Predispose Mice to Clonal Lymphocytic Responses and Myeloid Expansion. <i>Journal of Immunology</i> , 2022, 208, 2403-2424.	0.4	5
29393	Blood transcriptomics identifies immune signatures indicative of infectious complications in childhood cancer patients with febrile neutropenia. <i>Clinical and Translational Immunology</i> , 2022, 11, .	1.7	5
29394	The interplay between lncRNAs, RNA-binding proteins and viral genome during SARS-CoV-2 infection reveals strong connections with regulatory events involved in RNA metabolism and immune response. <i>Theranostics</i> , 2022, 12, 3946-3962.	4.6	14
29395	Layer-Specific Modules Detection in Cancer Multi-Layer Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1170-1179.	1.9	12
29396	Big Data in healthcare from a sex and gender perspective. , 2022, , 77-93.		0
29402	Novel reusable animal model for comparative evaluation of in vivo growth and protein-expression of <i>Escherichia coli</i> O157 strains in the bovine rumen. <i>PLoS ONE</i> , 2022, 17, e0268645.	1.1	1
29403	An Myh11 single lysine deletion causes aortic dissection by reducing aortic structural integrity and contractility. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
29404	Screening the Potential Biomarkers of COVID-19-Related Thrombosis Through Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	0
29405	Identification of Hub Genes in Colorectal Adenocarcinoma by Integrated Bioinformatics. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	2
29407	Combined use of specific length amplified fragment sequencing (SLAF-seq) and bulked segregant analysis (BSA) for rapid identification of genes influencing fiber content of hemp (<i>Cannabis sativa</i> L.). <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2

#	ARTICLE	IF	CITATIONS
29408	Chromosome-Scale, Haplotype-Resolved Genome Assembly of Non-Sex-Reversal Females of Swamp Eel Using High-Fidelity Long Reads and Hi-C Data. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	2
29409	Full-Length Transcriptional Analysis of the Same Soybean Genotype With Compatible and Incompatible Reactions to <i>Heterodera glycines</i> Reveals Nematode Infection Activating Plant Defense Response. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	4
29410	Whole-genome sequencing and functional analysis of a novel chitin-degrading strain <i>Rhodococcus</i> sp. 11-3. <i>Journal of Bioscience and Bioengineering</i> , 2022, , .	1.1	0
29411	Transcriptome Analysis of Traditional Chinese Medicine “Kechuaning Plaster”™ in the Treatment of Asthma. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2023, 26, 778-788.	0.6	1
29412	Characterization of a small <i>tRNA</i> binding protein that interacts with the archaeal proteasome complex. <i>Molecular Microbiology</i> , 0, , .	1.2	1
29413	Daprodustat prevents cyclosporine-A-mediated anemia and peritubular capillary loss. <i>Kidney International</i> , 2022, 102, 750-765.	2.6	4
29415	Discovery of bioactive microbial gene products in inflammatory bowel disease. <i>Nature</i> , 2022, 606, 754-760.	13.7	38
29416	Putative Biomarkers in Tears for Diabetic Retinopathy Diagnosis. <i>Frontiers in Medicine</i> , 2022, 9, .	1.2	15
29417	Identification of Potential Biomarkers for Ryanodine Receptor 1 (RYR1) Mutation-Associated Myopathies Using Bioinformatics Approach. <i>Disease Markers</i> , 2022, 2022, 1-11.	0.6	0
29418	The Translational Landscape of SARS-CoV-2-infected Cells Reveals Suppression of Innate Immune Genes. <i>MBio</i> , 2022, 13, .	1.8	21
29419	Identification of Four Novel Prognostic Biomarkers and Construction of Two Nomograms in Adrenocortical Carcinoma: A Multi-Omics Data Study via Bioinformatics and Machine Learning Methods. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	1.6	1
29420	Tissue-specific gene expression in obese hyperglycemic mice. <i>International Journal of Transgender Health</i> , 2022, 15, 555-561.	1.1	2
29421	Serum miRNA Profile in Diabetic Patients With Ischemic Heart Disease as a Promising Non-Invasive Biomarker. <i>Frontiers in Endocrinology</i> , 2022, 13, .	1.5	6
29422	Dynamic Changes in Ascorbic Acid Content during Fruit Development and Ripening of <i>Actinidia latifolia</i> (an Ascorbate-Rich Fruit Crop) and the Associated Molecular Mechanisms. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5808.	1.8	7
29423	Epigenetic Silencing of PTEN and Epi-Transcriptional Silencing of MDM2 Underlied Progression to Secondary Acute Myeloid Leukemia in Myelodysplastic Syndrome Treated with Hypomethylating Agents. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5670.	1.8	1
29424	Digital Cell Atlas of Mouse Uterus: From Regenerative Stage to Maturational Stage. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	1
29427	Single-molecule long-read sequencing analysis improves genome annotation and sheds new light on the transcripts and splice isoforms of <i>Zoysia japonica</i> . <i>BMC Plant Biology</i> , 2022, 22, .	1.6	7
29428	A Quantitative Proteomic Approach Explores the Possible Mechanisms by Which the Small Molecule Stemazole Promotes the Survival of Human Neural Stem Cells. <i>Brain Sciences</i> , 2022, 12, 690.	1.1	2

#	ARTICLE	IF	CITATIONS
29430	Transcriptomics Integrated with Metabolomics Unveil Carotenoids Accumulation and Correlated Gene Regulation in White and Yellow-Fleshed Turnip (<i>Brassica rapa</i> ssp. <i>rapa</i>). <i>Genes</i> , 2022, 13, 953.	1.0	0
29431	Comparative Proteomic Analysis Reveals the Effect of Selenoprotein W Deficiency on Oligodendrogenesis in Fear Memory. <i>Antioxidants</i> , 2022, 11, 999.	2.2	4
29434	R-loop Mapping and Characterization During <i>Drosophila</i> Embryogenesis Reveals Developmental Plasticity in R-loop Signatures. <i>Journal of Molecular Biology</i> , 2022, 434, 167645.	2.0	3
29435	RNA-seq analysis unveils temperature and nutrient adaptation mechanisms relevant for pathogenicity in <i>Vibrio parahaemolyticus</i> . <i>Aquaculture</i> , 2022, , 738397.	1.7	6
29436	De novo transcriptome analysis reveals the molecular regulatory mechanism underlying the response to excess nitrogen in <i>Azolla</i> spp.. <i>Aquatic Toxicology</i> , 2022, 248, 106202.	1.9	4
29437	The whole transcriptome analysis and the circRNA-lncRNA network construction in arsenic trioxide-treated mice myocardium. <i>Biomedicine and Pharmacotherapy</i> , 2022, 151, 113183.	2.5	9
29438	Comparative genome analysis of the monogonont marine rotifer <i>Brachionus manjavacas</i> Australian strain: Potential application for ecotoxicology and environmental genomics. <i>Marine Pollution Bulletin</i> , 2022, 180, 113752.	2.3	2
29439	Characterization and functional analysis of the MADS-box EgAGL9 transcription factor from the mesocarp of oil palm (<i>Elaeis guineensis</i> Jacq.). <i>Plant Science</i> , 2022, 321, 111317.	1.7	3
29440	Delineating genome-wide alternative splicing landscapes and their functional significance in orchids. <i>South African Journal of Botany</i> , 2022, 148, 552-560.	1.2	4
29441	Transcriptomic analysis of Simpson Golabi Behmel syndrome cells during differentiation exhibit BAT-like function. <i>Tissue and Cell</i> , 2022, 77, 101822.	1.0	1
29442	Analysis of the landscape of human enhancer sequences in biological databases. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2728-2744.	1.9	0
29443	B- and T-Cell-Intrinsic Regulation of Germinal Centers by Thymic Stromal Lymphopoietin Signaling. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
29444	HHFS: A Hybrid Hierarchical Feature Selection Method for Ageing Gene Classification. <i>IEEE Transactions on Cognitive and Developmental Systems</i> , 2023, 15, 690-699.	2.6	6
29445	Proteomic-based evidence for adult neurogenesis in birds and mammals as indicated from cerebrospinal fluid. <i>Neural Regeneration Research</i> , 2022, 17, 2576.	1.6	0
29447	FAM83A antisense RNA 1 (<i>FAM83A-AS1</i>) silencing impairs cell proliferation and induces autophagy via MET-AMPK ϵ signaling in lung adenocarcinoma. <i>Bioengineered</i> , 2022, 13, 13312-13327.	1.4	7
29448	Genotype-phenotype correlation of T-cell subtypes reveals senescent and cytotoxic genes in Alzheimer's disease. <i>Human Molecular Genetics</i> , 2022, 31, 3355-3366.	1.4	2
29449	Challenges in Information-Mining the Materials Literature: A Case Study and Perspective. <i>Chemistry of Materials</i> , 2022, 34, 4821-4827.	3.2	3
29450	Mapping the cardiac vascular niche in heart failure. <i>Nature Communications</i> , 2022, 13, .	5.8	31

#	ARTICLE	IF	CITATIONS
29451	A tensor-based bi-random walks model for protein function prediction. BMC Bioinformatics, 2022, 23, .	1.2	4
29452	Bioinformatics Analysis for Identifying Differentially Expressed MicroRNAs Derived from Plasma Exosomes Associated with Radiotherapy Resistance in Non-Small-Cell Lung Cancer. Applied Bionics and Biomechanics, 2022, 2022, 1-8.	0.5	6
29453	Cryopreservation of Endangered Ornamental Plants and Fruit Crops from Tropical and Subtropical Regions. Biology, 2022, 11, 847.	1.3	13
29454	Single-cell transcriptomics of adult macaque hippocampus reveals neural precursor cell populations. Nature Neuroscience, 2022, 25, 805-817.	7.1	47
29455	Cross-tissue, single-cell stromal atlas identifies shared pathological fibroblast phenotypes in four chronic inflammatory diseases. Med, 2022, 3, 481-518.e14.	2.2	51
29456	Identification of a neural development gene expression signature in colon cancer stem cells reveals a role for EGR2 in tumorigenesis. Science, 2022, 25, 104498.	1.9	9
29457	Pan-Genomes Provide Insights into the Genetic Basis of Auricularia heimuer Domestication. Journal of Fungi (Basel, Switzerland), 2022, 8, 581.	1.5	1
29459	Identification of Core Genes and Screening of Potential Targets in Intervertebral Disc Degeneration Using Integrated Bioinformatics Analysis. Frontiers in Genetics, 0, 13, .	1.1	7
29460	Transcriptomics and Metabolomics Analyses Reveal High Induction of the Phenolamide Pathway in Tomato Plants Attacked by the Leafminer Tuta absoluta. Metabolites, 2022, 12, 484.	1.3	9
29461	CancerOmicsNet: a multi-omics network-based approach to anti-cancer drug profiling. Oncotarget, 2022, 13, 695-706.	0.8	12
29462	miRNA-432 and SLC38A1 as Predictors of Hepatocellular Carcinoma Complicated with Alcoholic Steatohepatitis. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-18.	1.9	2
29463	Identification and Regulatory Network Analysis of Genes Related to Reproductive Performance in the Hypothalamus and Pituitary of Angus Cattle. Genes, 2022, 13, 965.	1.0	1
29466	Interaction Between Cecal Metabolites and Liver Lipid Metabolism Pathways During Induced Molting in Laying Hens. Frontiers in Physiology, 2022, 13, .	1.3	3
29467	The Role of Transposable Elements of the Human Genome in Neuronal Function and Pathology. International Journal of Molecular Sciences, 2022, 23, 5847.	1.8	11
29468	An equivalence test between features lists, based on the Sorensenâ€“Dice index and the joint frequencies of GO term enrichment. BMC Bioinformatics, 2022, 23, .	1.2	0
29470	Shortcuts in Stochastic Systems and Control of Biophysical Processes. Physical Review X, 2022, 12, .	2.8	12
29471	New Views of Old Proteins: Clarifying the Enigmatic Proteome. Molecular and Cellular Proteomics, 2022, 21, 100254.	2.5	16
29473	The Osmoprotectant Switch of Potassium to Compatible Solutes in an Extremely Halophilic Archaea Halorubrum kocurii 2020YC7. Genes, 2022, 13, 939.	1.0	11

#	ARTICLE	IF	CITATIONS
29474	SETDB1 Restrains Endogenous Retrovirus Expression and Antitumor Immunity during Radiotherapy. <i>Cancer Research</i> , 2022, 82, 2748-2760.	0.4	14
29475	Identification of Ferroptosis-Related Hub Genes and Their Association with Immune Infiltration in Chronic Obstructive Pulmonary Disease by Bioinformatics Analysis. <i>International Journal of COPD</i> , 0, Volume 17, 1219-1236.	0.9	9
29476	Connectivity Mapping Using a Novel sv2a Loss-of-Function Zebrafish Epilepsy Model as a Powerful Strategy for Anti-epileptic Drug Discovery. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, .	1.4	2
29478	Complete Genome Analysis of Highly Pathogenic Non-O1/O139 <i>Vibrio cholerae</i> Isolated From <i>Macrobrachium rosenbergii</i> Reveals Pathogenicity and Antibiotic Resistance-Related Genes. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	5
29479	Bacterial Infection Induces Ultrastructural and Transcriptional Changes in the King Oyster Mushroom (<i>Pleurotus eryngii</i>). <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	6
29480	Genome-wide SNP analysis reveals the selection signatures of two indigenous buffalo breeds in Sichuan. <i>Conservation Genetics Resources</i> , 0, , .	0.4	0
29481	Comparative genomic analysis reveals cellulase plays an important role in the pathogenicity of <i>Setosphaeria turcica</i> f. sp. <i>zeae</i> . <i>Fungal Biology</i> , 2022, , .	1.1	0
29482	Full-Length Transcriptome Sequencing Analysis and Characterization of Gene Isoforms Involved in Flavonoid Biosynthesis in the Seedless Kiwifruit Cultivar "Chengxiang" (<i>Actinidia arguta</i>). <i>Diversity</i> , 2022, 14, 424.	0.7	2
29483	Effects of Lightning on Rhizosphere Soil Properties, Bacterial Communities, and Active Components of <i>Camellia sinensis</i> var. <i>assamica</i> . <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	1
29485	Analysis of Huntington's Disease Modifiers Using the Hyperbolic Mapping of the Protein Interaction Network. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5853.	1.8	5
29486	Molecular Signatures of Response to Mecasermin in Children With Rett Syndrome. <i>Frontiers in Neuroscience</i> , 2022, 16, .	1.4	2
29489	Alcohol induced increases in sperm Histone H3 lysine 4 trimethylation correlate with increased placental CTCF occupancy and altered developmental programming. <i>Scientific Reports</i> , 2022, 12, .	1.6	13
29490	The chromosome-level genome of a free-floating aquatic weed <i>Pistia stratiotes</i> provides insights into its rapid invasion. <i>Molecular Ecology Resources</i> , 2022, 22, 2732-2743.	2.2	7
29491	Comparative Transcriptomics of Gonads Reveals the Molecular Mechanisms Underlying Gonadal Development in Giant Freshwater Prawns (<i>Macrobrachium rosenbergii</i>). <i>Journal of Marine Science and Engineering</i> , 2022, 10, 737.	1.2	4
29493	Identification of the Active Compound of Liu Wei Di Huang Wan for Treatment of Gestational Diabetes Mellitus via Network Pharmacology and Molecular Docking. <i>Journal of Diabetes Research</i> , 2022, 2022, 1-13.	1.0	3
29494	Analysis of differential gene expression profiles uncovers mechanisms of Xuesaitong injection against cerebral ischemia-reperfusion injury. <i>Phytomedicine</i> , 2022, , 154224.	2.3	1
29495	An Insight Into Pentatricopeptide-Mediated Chloroplast Necrosis via microRNA395a During <i>Rhizoctonia solani</i> Infection. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
29498	Trained Immunity in Perivascular Adipose Tissue of Abdominal Aortic Aneurysm—A Novel Concept for a Still Elusive Disease. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	7

#	ARTICLE	IF	CITATIONS
29501	Evaluating the Immune Response in Treatment-Naive Hospitalised Patients With Influenza and COVID-19. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	6
29503	Single-cell transcriptomics reveals lineage trajectory of human scalp hair follicle and informs mechanisms of hair graying. <i>Cell Discovery</i> , 2022, 8, .	3.1	11
29504	7-Methoxyisoflavone ameliorates atopic dermatitis symptoms by regulating multiple signaling pathways and reducing chemokine production. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
29505	Chemical reaction network knowledge graphs: the OntoRXN ontology. <i>Journal of Cheminformatics</i> , 2022, 14, .	2.8	3
29506	SLiMan: An Integrative Web Server for Exploring Short Linear Motif-Mediated Interactions in Interactomes. <i>Journal of Proteome Research</i> , 2022, 21, 1654-1663.	1.8	4
29507	Circulating Exosomal miR-144-3p from Crohn's Disease Patients Inhibits Human Umbilical Vein Endothelial Cell Function by Targeting FN1. <i>Disease Markers</i> , 2022, 2022, 1-12.	0.6	1
29508	Aerobic Denitrification of <i>Pseudomonas stutzeri</i> yjy-10 and Genomic Analysis of This Process. <i>Applied Biochemistry and Microbiology</i> , 2022, 58, 294-301.	0.3	2
29509	Incubation of canine dermal fibroblasts with serum from dogs with atopic dermatitis activates extracellular matrix signalling and represses oxidative phosphorylation. <i>Veterinary Research Communications</i> , 0, .	0.6	0
29510	Integrated Analysis of Glutathione Metabolic Pathway in Pancreatic Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	1
29511	Overexpression of ERCC6L correlates with poor prognosis and confers malignant phenotypes of lung adenocarcinoma. <i>Oncology Reports</i> , 2022, 48, .	1.2	2
29512	A Robust Immuno-Prognostic Model of Non-Muscle-Invasive Bladder Cancer Indicates Dynamic Interaction in Tumor Immune Microenvironment Contributes to Cancer Progression. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	2
29513	Computation-Based Discovery of Potential Targets for Rheumatoid Arthritis and Related Molecular Screening and Mechanism Analysis of Traditional Chinese Medicine. <i>Disease Markers</i> , 2022, 2022, 1-19.	0.6	3
29515	Exploration of the Nurse Shark (<i>Ginglymostoma cirratum</i>) Plasma Immunoproteome Using High-Resolution LC-MS/MS. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	4
29516	The chromosome-level genome for <i>Toxicodendron vernicifluum</i> provides crucial insights into Anacardiaceae evolution and urushiol biosynthesis. <i>iScience</i> , 2022, 25, 104512.	1.9	6
29517	Simulating the restoration of normal gene expression from different thyroid cancer stages using deep learning. <i>BMC Cancer</i> , 2022, 22, .	1.1	0
29520	Characterisation of a nucleo-adhesome. <i>Nature Communications</i> , 2022, 13, .	5.8	4
29521	Air pollution induces <i>Staphylococcus aureus</i> USA300 respiratory tract colonization mediated by specific bacterial genetic responses involving the global virulence gene regulators Agr and Sae. <i>Environmental Microbiology</i> , 2022, 24, 4449-4465.	1.8	5
29522	Integrated proteogenomic characterization of urothelial carcinoma of the bladder. <i>Journal of Hematology and Oncology</i> , 2022, 15, .	6.9	26

#	ARTICLE	IF	CITATIONS
29524	Genomic consequences of artificial selection during early domestication of a wood fibre crop. <i>New Phytologist</i> , 2022, 235, 1944-1956.	3.5	1
29525	RSK1 promotes mammalian axon regeneration by inducing the synthesis of regeneration-related proteins. <i>PLoS Biology</i> , 2022, 20, e3001653.	2.6	9
29526	Image analysis reveals molecularly distinct patterns of TILs in NSCLC associated with treatment outcome. <i>Npj Precision Oncology</i> , 2022, 6, .	2.3	20
29528	Brain proteome profiling implicates the complement and coagulation cascade in multiple system atrophy brain pathology. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	6
29529	Parallel metatranscriptome analysis reveals degradation of plant secondary metabolites by beetles and their gut symbionts. <i>Molecular Ecology</i> , 2022, 31, 3999-4016.	2.0	7
29530	De novo reconstruction of cell interaction landscapes from single-cell spatial transcriptome data with DeepLinc. <i>Genome Biology</i> , 2022, 23, .	3.8	10
29532	A consensus view of the proteome of the last universal common ancestor. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	10
29534	InterCellDB: A User-Defined Database for Inferring Intercellular Networks. <i>Advanced Science</i> , 2022, 9, .	5.6	5
29537	Silibinin protects against sepsis and septic myocardial injury in an NR1H3-dependent pathway. <i>Free Radical Biology and Medicine</i> , 2022, 187, 141-157.	1.3	12
29538	Transcriptome meta-analysis of valproic acid exposure in human embryonic stem cells. <i>European Neuropsychopharmacology</i> , 2022, 60, 76-88.	0.3	3
29539	Transcriptomic response of the harmful algae <i>Heterosigma akashiwo</i> to polyphosphate utilization and phosphate stress. <i>Harmful Algae</i> , 2022, 117, 102267.	2.2	5
29540	Kaempferol antagonizes adipogenesis by repressing histone H3K4 methylation at PPAR β target genes. <i>Biochemical and Biophysical Research Communications</i> , 2022, 617, 48-54.	1.0	9
29560	Establishment and verification of a prognostic model of liver cancer by RNA-binding proteins based on the TCGA database. <i>Translational Cancer Research</i> , 2022, 11, 1925-1937.	0.4	1
29561	Network pharmacology-based analysis of the effects of puerarin on sarcopenia. <i>Annals of Translational Medicine</i> , 2022, 10, 671-671.	0.7	1
29562	Detecting Structural Variants and Associated Gene Presence-Absence Variation Phenomena in the Genomes of Marine Organisms. <i>Methods in Molecular Biology</i> , 2022, , 53-76.	0.4	2
29564	MiR-4458-loaded gelatin nanospheres target COL11A1 for DDR2/SRC signaling pathway inactivation to suppress the progression of estrogen receptor-positive breast cancer. <i>Biomaterials Science</i> , 2022, 10, 4596-4611.	2.6	5
29565	Transcriptome Analysis of Artificial Cultivated Mushrooms in Qinba Mountains. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
29567	The Development of Mechanical Allodynia in Diabetic Rats Revealed by Single-Cell RNA-Seq. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	9

#	ARTICLE	IF	CITATIONS
29569	Increased expression of tribbles homolog 3 predicts poor prognosis and correlates with tumor immunity in clear cell renal cell carcinoma: a bioinformatics study. <i>Bioengineered</i> , 2022, 13, 14000-14012.	1.4	6
29570	Expression Analysis of Pre-Harvest Sprouting Tolerant Korean Wheat via Transcriptomic Analysis. <i>Han'guk Yukchong Hakhoe Chi</i> , 2022, 54, 104-118.	0.2	2
29571	The dynamic cellular and molecular features during the development of radiation proctitis revealed by transcriptomic profiling in mice. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
29572	The Parkinson's disease protein alpha-synuclein is a modulator of processing bodies and mRNA stability. <i>Cell</i> , 2022, 185, 2035-2056.e33.	13.5	57
29573	Proteomics Reveals Long-Term Alterations in Signaling and Metabolic Pathways Following Both Myocardial Infarction and Chemically Induced Denervation. <i>Neurochemical Research</i> , 0, , .	1.6	0
29574	Joint analysis of functionally related genes yields further candidates associated with Tetralogy of Fallot. <i>Journal of Human Genetics</i> , 2022, 67, 613-615.	1.1	2
29575	SFARI genes and where to find them; modelling Autism Spectrum Disorder specific gene expression dysregulation with RNA-seq data. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
29576	Deep embeddings to comprehend and visualize microbiome protein space. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
29578	DNA Methylation and RNA-Sequencing Analysis to Identify Genes Related to Spontaneous Leaf Spots in a Wheat Variety "Zhongkenuomai No.1". <i>Agronomy</i> , 2022, 12, 1519.	1.3	0
29579	Regulating Strategies of Transcription and Alternative Splicing for Cold Tolerance Harpadon nehereus Fish. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	3
29580	A chromosome-level genome assembly for the rabbit tapeworm <i>Taenia pisiformis</i> . <i>Gene</i> , 2022, 834, 146650.	1.0	2
29581	<i>Orrella daihaiensis</i> sp. nov., a bacterium isolated from Daihai Lake in Inner Mongolia. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	4
29582	HemI 2.0: an online service for heatmap illustration. <i>Nucleic Acids Research</i> , 2022, 50, W405-W411.	6.5	24
29583	Single-nucleus profiling of human dilated and hypertrophic cardiomyopathy. <i>Nature</i> , 2022, 608, 174-180.	13.7	115
29584	Circulating microRNAs (miR-16, miR-22, miR-122) expression and early diagnosis of hepatocellular carcinoma. <i>Journal of Clinical Laboratory Analysis</i> , 2022, 36, .	0.9	13
29585	Remote ischemic preconditioning causes transient cell cycle arrest and renal protection by a NF-κB dependent Sema5B pathway. <i>JCI Insight</i> , 2022, 7, .	2.3	6
29586	Integrated Transcriptome Profiling Identifies Prognostic Hub Genes as Therapeutic Targets of Glioblastoma: Evidenced by Bioinformatics Analysis. <i>ACS Omega</i> , 2022, 7, 22531-22550.	1.6	5
29587	Neuropilin-1 is present on Foxp3+ T regulatory cell-derived small extracellular vesicles and mediates immunity against skin transplantation. <i>Journal of Extracellular Vesicles</i> , 2022, 11, .	5.5	14

#	ARTICLE	IF	CITATIONS
29588	Longitudinal plasma proteomic profiling of patients with non-small cell lung cancer undergoing immune checkpoint blockade. , 2022, 10, e004582.		16
29589	Identification of potential gene markers in gestational diabetes mellitus. Journal of Clinical Laboratory Analysis, 0, , .	0.9	1
29590	Integration of the <i>Salmonella</i> Typhimurium Methylome and Transcriptome Reveals That DNA Methylation and Transcriptional Regulation Are Largely Decoupled under Virulence-Related Conditions. MBio, 2022, 13, .	1.8	6
29591	Logic of the temporal compartmentalization of the hepatic metabolic cycle. Physiology, 0, , .	1.6	1
29592	Secukinumab for the treatment of adult-onset pityriasis rubra pilaris: a single-arm clinical trial with transcriptomic analysis. British Journal of Dermatology, 2022, 187, 650-658.	1.4	19
29593	Comprehensive RNA Expression Analysis Revealed Biological Functions of Key Gene Sets and Identified Disease-Associated Cell Types Involved in Rat Traumatic Brain Injury. Journal of Clinical Medicine, 2022, 11, 3437.	1.0	2
29594	Dietary Long-Chain n-3 Polyunsaturated Fatty Acid Supplementation Alters Electrophysiological Properties in the Nucleus Accumbens and Emotional Behavior in Na ⁺ -ve and Chronically Stressed Mice. International Journal of Molecular Sciences, 2022, 23, 6650.	1.8	4
29595	Genome-wide translation control analysis of developing human neurons. Molecular Brain, 2022, 15, .	1.3	2
29596	Combined transcriptome and metabolome analysis of Nerium indicum L. elaborates the key pathways that are activated in response to witches [®] broom disease. BMC Plant Biology, 2022, 22, .	1.6	5
29597	Anticancer effects of herbal medicines in pancreatic ductal adenocarcinoma through modulation of steroid hormone response proteins. Scientific Reports, 2022, 12, .	1.6	2
29598	Interleukin-17 governs hypoxic adaptation of injured epithelium. Science, 2022, 377, .	6.0	75
29599	Spatial centrosome proteome of human neural cells uncovers disease-relevant heterogeneity. Science, 2022, 376, .	6.0	25
29600	Translocating proteins compartment-specifically alter the fate of epithelial-mesenchymal transition in a compartmentalized Boolean network model. Npj Systems Biology and Applications, 2022, 8, .	1.4	0
29601	Integrative PheWAS analysis in risk categorization of major depressive disorder and identifying their associations with genetic variants using a latent topic model approach. Translational Psychiatry, 2022, 12, .	2.4	2
29602	A joint optimization framework integrated with biological knowledge for clustering incomplete gene expression data. Soft Computing, 2023, 27, 13639-13656.	2.1	2
29603	A Comprehensive Pan-Cancer Analysis of the Tumorigenic Role of Matrix Metalloproteinase 7 (MMP7) Across Human Cancers. Frontiers in Oncology, 0, 12, .	1.3	6
29605	Whole-Blood and Peripheral Mononuclear Cell Transcriptional Response to Prolonged Altitude Exposure in Well-Trained Runners. Clinical Journal of Sport Medicine, 2022, Publish Ahead of Print, .	0.9	2
29606	CaveCrawler: an interactive analysis suite for cavefish bioinformatics. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	0

#	ARTICLE	IF	CITATIONS
29607	Calculating genetic risk for dysfunction in pleiotropic biological processes using whole exome sequencing data. <i>Journal of Neurodevelopmental Disorders</i> , 2022, 14, .	1.5	0
29608	Transcriptional Profiling of <i>Leishmania infantum</i> Infected Dendritic Cells: Insights into the Role of Immunometabolism in Host-Parasite Interaction. <i>Microorganisms</i> , 2022, 10, 1271.	1.6	6
29609	Predicting prognosis and clinical features of the tumor microenvironment based on ferroptosis score in patients with breast cancer. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
29611	Integrative transcriptome-wide analysis of atopic dermatitis for drug repositioning. <i>Communications Biology</i> , 2022, 5, .	2.0	12
29612	Integrating Network Pharmacology and Experimental Validation to Explore the Key Mechanism of Gubitong Recipe in the Treatment of Osteoarthritis. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-25.	0.7	3
29613	RNA-Seq and Gene Ontology Analysis Reveal Differences Associated With Low R/FR-Induced Shade Responses in Cultivated Lentil and a Wild Relative. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
29614	Identification of Immune-Related Gene Signature in Stanford Type A Aortic Dissection. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
29615	Transcriptome and Metabolome Analysis of Upland Cotton (<i>Gossypium hirsutum</i>) Seed Pretreatment with MgSO ₄ in Response to Salinity Stress. <i>Life</i> , 2022, 12, 921.	1.1	5
29616	Ascorbate peroxidase-mediated in situ labelling of proteins in secreted exosomes. <i>Journal of Extracellular Vesicles</i> , 2022, 11, .	5.5	6
29617	Draft Genome Sequences Resources of Mulberry Dwarf Phytoplasma Strain MDGZ-01 Associated with Mulberry Yellow Dwarf (MYD) Diseases. <i>Plant Disease</i> , 2022, 106, 2239-2242.	0.7	4
29618	Gene network analysis reveals candidate genes related with the hair follicle development in sheep. <i>BMC Genomics</i> , 2022, 23, .	1.2	13
29619	Antennal transcriptome analysis of olfactory genes and tissue expression profiling of odorant binding proteins in <i>Semanotus bifasciatus</i> (cerambycidae: coleoptera). <i>BMC Genomics</i> , 2022, 23, .	1.2	5
29620	Transcriptome Analysis Reveals the Regulatory Networks of Cytokinin in Promoting Floral Feminization in <i>Castanea henryi</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 6389.	1.8	6
29622	Tree House Explorer: A Novel Genome Browser for Phylogenomics. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
29623	Phylotranscriptomic analyses reveal multiple whole-genome duplication events, the history of diversification and adaptations in the Araceae. <i>Annals of Botany</i> , 2023, 131, 199-214.	1.4	7
29624	Spatial profiling of early primate gastrulation in utero. <i>Nature</i> , 2022, 609, 136-143.	13.7	56
29625	Direct genetic effects, maternal genetic effects, and maternal genetic sensitivity on prenatal heat stress for calf diseases and corresponding genomic loci in German Holsteins. <i>Journal of Dairy Science</i> , 2022, 105, 6795-6808.	1.4	8
29626	Quantifying concordant genetic effects of de novo mutations on multiple disorders. <i>ELife</i> , 0, 11, .	2.8	3

#	ARTICLE	IF	CITATIONS
29627	Human Follicular Mites: Ectoparasites Becoming Symbionts. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	6
29628	Computational Analysis of High-Dimensional DNA Methylation Data for Cancer Prognosis. <i>Journal of Computational Biology</i> , 0, .	0.8	1
29629	Dengue Virus-2 Infection Affects Fecundity and Elicits Specific Transcriptional Changes in the Ovaries of <i>Aedes aegypti</i> Mosquitoes. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
29630	Genome sequence of <i>Gossypium anomalum</i> facilitates interspecific introgression breeding. <i>Plant Communications</i> , 2022, 3, 100350.	3.6	14
29631	Pathway importance by graph convolutional network and Shapley additive explanations in gene expression phenotype of diffuse large B-cell lymphoma. <i>PLoS ONE</i> , 2022, 17, e0269570.	1.1	2
29632	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
29633	Omics-based integrated analysis identified IKZF2 as a biomarker associated with lupus nephritis. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
29634	Machine-learning-optimized Cas12a barcoding enables the recovery of single-cell lineages and transcriptional profiles. <i>Molecular Cell</i> , 2022, 82, 3103-3118.e8.	4.5	14
29635	Integrated Multi-Omics Analysis Model to Identify Biomarkers Associated With Prognosis of Breast Cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	12
29636	The onset of PI3K-related vascular malformations occurs during angiogenesis and is prevented by the AKT inhibitor miransertib. <i>EMBO Molecular Medicine</i> , 2022, 14, .	3.3	19
29639	Digital quantification of p16-positive foci in fibrotic interstitial lung disease is associated with a phenotype of idiopathic pulmonary fibrosis with reduced survival. <i>Respiratory Research</i> , 2022, 23, .	1.4	3
29640	Genome Analysis of a Novel Polysaccharide-Degrading Bacterium <i>Paenibacillus algicola</i> and Determination of Alginate Lyases. <i>Marine Drugs</i> , 2022, 20, 388.	2.2	5
29641	Icariside II Restores Vascular Smooth Muscle Cell Contractile Phenotype by Enhancing the Focal Adhesion Signaling Pathway in the Rat Vascular Remodeling Model. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2
29642	Protein Subcellular Localization Prediction Model Based on Graph Convolutional Network. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2022, 14, 937-946.	2.2	5
29643	Global analyses of mRNA expression in human sensory neurons reveal eIF5A as a conserved target for inflammatory pain. <i>FASEB Journal</i> , 2022, 36, .	0.2	6
29644	Amoxicillin-resistant <i>Streptococcus pneumoniae</i> can be resensitized by targeting the mevalonate pathway as indicated by sCRilecs-seq. <i>ELife</i> , 0, 11, .	2.8	11
29645	SAPFIR: A webserver for the identification of alternative protein features. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	0
29647	Using Virtual Choreographies to Identify Office Users' Behaviors to Target Behavior Change Based on Their Potential to Impact Energy Consumption. <i>Energies</i> , 2022, 15, 4354.	1.6	1

#	ARTICLE	IF	CITATIONS
29648	Regional Downregulation of Dopamine Receptor D1 in Bilateral Dorsal Lateral Geniculate Nucleus of Monocular Form-Deprived Amblyopia Models. <i>Frontiers in Neuroscience</i> , 0, 16, .	1.4	0
29649	3-oxo-C12:2-HSL, quorum sensing molecule from human intestinal microbiota, inhibits pro-inflammatory pathways in immune cells via bitter taste receptors. <i>Scientific Reports</i> , 2022, 12, .	1.6	9
29650	A hexa-species transcriptome atlas of mammalian embryogenesis delineates metabolic regulation across three different implantation modes. <i>Nature Communications</i> , 2022, 13, .	5.8	14
29651	Network assisted analysis of de novo variants using protein-protein interaction information identified 46 candidate genes for congenital heart disease. <i>PLoS Genetics</i> , 2022, 18, e1010252.	1.5	3
29652	Functional Heterogeneity of the Young and Old Duplicate Genes in Tung Tree (<i>Vernicia fordii</i>). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
29653	Genomic and transcriptomic analyses of <i>Bacillus methylotrophicus</i> NJ13 reveal a molecular response strategy combating <i>Ilyonectria robusta</i> causing ginseng rusty root rot. <i>Biological Control</i> , 2022, , 104972.	1.4	6
29654	The impact of genetic modifiers on variation in germline mutation rates within and among human populations. <i>Genetics</i> , 2022, 221, .	1.2	6
29655	PD-L1 blockade restores CAR T cell activity through IFN- γ -regulation of CD163+ M2 macrophages. , 2022, 10, e004400.		16
29656	Metatranscriptomics captures dynamic shifts in mycorrhizal coordination in boreal forests. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	12
29657	Genome-wide association study of musical beat synchronization demonstrates high polygenicity. <i>Nature Human Behaviour</i> , 2022, 6, 1292-1309.	6.2	33
29658	Identification of molecular mechanism of the anti-lung cancer effect of Jin Ning Fang using network pharmacology and its experimental verification. <i>International Journal of Transgender Health</i> , 2022, 15, 745-759.	1.1	2
29659	The TIP60-ATM axis regulates replication fork stability in BRCA-deficient cells. <i>Oncogenesis</i> , 2022, 11, .	2.1	3
29660	Enhancers of Host Immune Tolerance to Bacterial Infection Discovered Using Linked Computational and Experimental Approaches. <i>Advanced Science</i> , 2022, 9, .	5.6	3
29661	Genomic, Metabolic, and Immunological Characterization of GMP-Grade <i>Mycobacterium phlei</i> . <i>Microbiology Spectrum</i> , 0, , .	1.2	0
29662	Integrated liver proteomics and metabolomics identify metabolic pathways affected by pantothenic acid deficiency in Pekin ducks. <i>Animal Nutrition</i> , 2022, 11, 1-14.	2.1	4
29663	Single-cell sequencing reveals microglia induced angiogenesis by specific subsets of endothelial cells following spinal cord injury. <i>FASEB Journal</i> , 2022, 36, .	0.2	9
29664	Investigation of the Pharmacological Effect and Mechanism of Jinbei Oral Liquid in the Treatment of Idiopathic Pulmonary Fibrosis Using Network Pharmacology and Experimental Validation. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	1
29665	Temporal Whole-Transcriptomic Analysis of Characterized In Vitro and Ex Vivo Primary Nasal Epithelia. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	1

#	ARTICLE	IF	CITATIONS
29666	Proteomic profiling of the carbon-starved <i>Escherichia coli</i> reveals upregulation of stress-inducible pathways implicated in biological adhesion and methylglyoxal metabolism. <i>Research in Microbiology</i> , 2022, 173, 103968.	1.0	0
29667	Exposure of Keratinocytes to <i>Candida Albicans</i> in the Context of Atopic Milieu Induces Changes in the Surface Glycosylation Pattern of Small Extracellular Vesicles to Enhance Their Propensity to Interact With Inhibitory Siglec Receptors. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	7
29668	Ptpn1 deletion protects oval cells against lipoapoptosis by favoring lipid droplet formation and dynamics. <i>Cell Death and Differentiation</i> , 2022, 29, 2362-2380.	5.0	4
29669	Single-Cell RNA-Seq Reveals Heterogeneity of Cell Communications between Schwann Cells and Fibroblasts within Vestibular Schwannoma Microenvironment. <i>American Journal of Pathology</i> , 2022, 192, 1230-1249.	1.9	9
29670	Integrating Mechanistic Information to Predict Drug-Drug Interactions and Associated Relevance for Decision Support. , 2022, , .		1
29671	Systematic identification of molecular mediators of interspecies sensing in a community of two frequently coinfecting bacterial pathogens. <i>PLoS Biology</i> , 2022, 20, e3001679.	2.6	14
29672	Transcriptome analysis reveals regulation mechanism of methyl jasmonate-induced terpenes biosynthesis in <i>Curcuma wenyujin</i> . <i>PLoS ONE</i> , 2022, 17, e0270309.	1.1	9
29673	Features and Colonization Strategies of <i>Enterococcus faecalis</i> in the Gut of <i>Bombyx mori</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
29674	Functional Analysis of the Cortical Transcriptome and Proteome Reveal Neurogenesis, Inflammation, and Cell Death after Repeated Traumatic Brain Injury <i>in vivo</i> . <i>Neurotrauma Reports</i> , 2022, 3, 224-239.	0.5	1
29677	Empowering the discovery of novel target-disease associations via machine learning approaches in the open targets platform. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	5
29678	Transcriptome analysis of <i>Stipa purpurea</i> interacted with endophytic <i>Bacillus subtilis</i> in response to temperature and ultraviolet stress. <i>Plant Growth Regulation</i> , 0, , .	1.8	2
29679	Identification and Validation of Candidate Gene Module Along With Immune Cells Infiltration Patterns in Atherosclerosis Progression to Plaque Rupture via Transcriptome Analysis. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	8
29680	The Bioinformatic Study Uncovers Probable Critical Genes Involved in the Pathophysiology of Biliary Atresia. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-11.	0.7	1
29681	Bioinformatics Approach Predicts Candidate Targets for SARS-CoV-2 Infections to COPD Patients. <i>BioMed Research International</i> , 2022, 2022, 1-12.	0.9	1
29682	A Transcriptomic Atlas Underlying Developmental Plasticity of Seasonal Forms of <i>Bicyclus anynana</i> Butterflies. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
29683	New Mutations in <i>cls</i> Lead to Daptomycin Resistance in a Clinical Vancomycin- and Daptomycin-Resistant <i>Enterococcus faecium</i> Strain. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
29685	Integrated Metabolomics and Transcriptome Analyses Unveil Pathways Involved in Sugar Content and Rind Color of Two Sugarcane Varieties. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	11
29686	Analysis and pharmacological modulation of senescence in human epithelial stem cells. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 3977-3994.	1.6	2

#	ARTICLE	IF	CITATIONS
29687	Proteome analysis of urinary biomarkers in a cigarette smoke-induced COPD rat model. <i>Respiratory Research</i> , 2022, 23, .	1.4	5
29688	A Current Encyclopedia of Bioinformatics Tools, Data Formats and Resources for Mass Spectrometry Lipidomics. <i>Metabolites</i> , 2022, 12, 584.	1.3	10
29689	Phospho-proteomics identifies a critical role of ATF2 in pseudorabies virus replication. <i>Virologica Sinica</i> , 2022, 37, 591-600.	1.2	1
29690	The Transcriptome Profile of Retinal Pigment Epithelium and M μ ller Cell Lines Protected by Risuteganib Against Hydrogen Peroxide Stress. <i>Journal of Ocular Pharmacology and Therapeutics</i> , 2022, 38, 513-526.	0.6	2
29691	Full-Length Transcriptome Construction of the Blue Crab <i>Callinectes sapidus</i> . <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
29692	Comprehensive analysis of lncRNA-miRNA-mRNA networks during osteogenic differentiation of bone marrow mesenchymal stem cells. <i>BMC Genomics</i> , 2022, 23, .	1.2	7
29694	Comparative genomics reveals low levels of inter- and intraspecies diversity in the causal agents of dwarf and common bunt of wheat and hint at conspecificity of <i>Tilletia caries</i> and <i>T. laevis</i> . <i>IMA Fungus</i> , 2022, 13, .	1.7	5
29695	Comparative transcriptome analysis reveals a rapid response to phosphorus deficiency in a phosphorus-efficient rice genotype. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
29696	The chromosome-scale assembly of endive (<i>Cichorium endivia</i>) genome provides insights into the sesquiterpenoid biosynthesis. <i>Genomics</i> , 2022, 114, 110400.	1.3	6
29697	Gene Expression Profiling in Abdominal Aortic Aneurysms. <i>Journal of Clinical Medicine</i> , 2022, 11, 3260.	1.0	3
29698	Impact of circadian time of dosing on cardiomyocyte-autonomous effects of glucocorticoids. <i>Molecular Metabolism</i> , 2022, 62, 101528.	3.0	3
29699	Comparative proteomic analyses of resistant and susceptible crucian carp to <i>Gyrodactylus kobayashii</i> infection. <i>Aquaculture Reports</i> , 2022, 25, 101221.	0.7	0
29700	Breaking boundaries: Pan BETi disrupt 3D chromatin structure, BD2-selective BETi are strictly epigenetic transcriptional regulators. <i>Biomedicine and Pharmacotherapy</i> , 2022, 152, 113230.	2.5	8
29701	Traditional herbal formula Jiao-tai-wan improves chronic restrain stress-induced depression-like behaviors in mice. <i>Biomedicine and Pharmacotherapy</i> , 2022, 153, 113284.	2.5	7
29702	Multi-stage transcriptome profiling of the neglected food-borne echinostome <i>Artyfechinostomum sufrartyfex</i> reveal potential diagnostic and drug targets. <i>Acta Tropica</i> , 2022, 233, 106564.	0.9	1
29703	The effects of salinities stress on histopathological changes, serum biochemical index, non-specific immune and transcriptome analysis in red swamp crayfish <i>Procambarus clarkii</i> . <i>Science of the Total Environment</i> , 2022, 840, 156502.	3.9	20
29704	Transcriptome profiles of genes related to growth and virulence potential in <i>Vibrio alginolyticus</i> treated with modified clay. <i>Microbiological Research</i> , 2022, 262, 127095.	2.5	6
29705	Distinct gene expression patterns in a tamoxifen-sensitive human mammary carcinoma xenograft and its tamoxifen-resistant subline MaCa 3366/TAM. <i>Molecular Cancer Therapeutics</i> , 2005, 4, 151-170.	1.9	67

#	ARTICLE	IF	CITATIONS
29706	Knowledge Graph Embedding by Translating on Hyperplanes. Proceedings of the AAAI Conference on Artificial Intelligence, 2014, 28, .	3.6	1,640
29707	Early Prediction and Longitudinal Modeling of Preeclampsia from Multiomics. SSRN Electronic Journal, 0, , .	0.4	0
29708	EGFL7 Promotes Osteoblast Differentiation of Human Bone Mesenchymal Stem Cells Partly Via Downregulation of Notch Signaling. SSRN Electronic Journal, 0, , .	0.4	0
29709	BioModels Database: A Public Repository for Sharing Models of Biological Processes. , 2022, , 463-467.		0
29710	Bioinformatics Analyses of Regulatory Network of Biomarkers in Chondrocytes from Patients with Osteoarthritis. Brazilian Archives of Biology and Technology, 0, 65, .	0.5	1
29711	Optogenetic Control of the Integrated Stress Response Reveals Proportional Encoding and the Stress Memory Landscape. SSRN Electronic Journal, 0, , .	0.4	0
29712	Effects of long-term administration of Q808 on hippocampal transcriptome in healthy rats. Chemical and Pharmaceutical Bulletin, 2022, , .	0.6	0
29713	Histidine-specific bioconjugation<i>via</i>visible-light-promoted thioacetal activation. Chemical Science, 2022, 13, 8289-8296.	3.7	9
29714	GinkgoDB: an ecological genome database for the living fossil, Ginkgo biloba. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	9
29715	PRODUCTION OF MANNOSYLERYTHRITOL LIPIDS: BIOSYNTHESIS, MULTI-OMICS APPROACHES AND COMMERCIAL EXPLOITATION. Molecular Omics, 0, , .	1.4	0
29716	An accurate prediction model of digenic interaction for estimating pathogenic gene pairs of human diseases. Computational and Structural Biotechnology Journal, 2022, 20, 3639-3652.	1.9	4
29717	groupCox-a doubly regularized Cox model for survival analysis. , 2022, , .		0
29718	A versatile new tool derived from a bacterial deubiquitylase to detect and purify ubiquitylated substrates and their interacting proteins. PLoS Biology, 2022, 20, e3001501.	2.6	2
29719	Antioxidant Mechanism of Lactiplantibacillus plantarum KM1 Under H2O2 Stress by Proteomics Analysis. Frontiers in Microbiology, 0, 13, .	1.5	6
29720	Full-Length Transcriptomics Reveals Complex Molecular Mechanism of Salt Tolerance in Bromus inermis L.. Frontiers in Plant Science, 0, 13, .	1.7	5
29721	DIP2 is a unique regulator of diacylglycerol lipid homeostasis in eukaryotes. ELife, 0, 11, .	2.8	5
29724	N(6)-methyladenosine methylation-regulated polo-like kinase 1 cell cycle homeostasis as a potential target of radiotherapy in pancreatic adenocarcinoma. Scientific Reports, 2022, 12, .	1.6	13
29725	GREM1 is required to maintain cellular heterogeneity in pancreatic cancer. Nature, 2022, 607, 163-168.	13.7	31

#	ARTICLE	IF	CITATIONS
29726	ConSIG: consistent discovery of molecular signature from OMIC data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	37
29728	From Transcriptomics, Metabolomics to Functional Studies: Extracellular ATP Induces TGF- β -Like Epithelial Mesenchymal Transition in Lung Cancer Cells. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
29729	Diagnostic and Predictive Values of Ferroptosis-Related Genes in Child Sepsis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	13
29730	Genetic structure and genome-wide association study of a genomic panel of two-row, spring barley (<i>Hordeum vulgare</i> L.) with differential reaction to <i>Fusarium</i> head blight (<i>Fusarium</i>) Tj ETQq1 1 0.784314 0.8 BT /Overlock 10 0.8 2022, 44, 874-891.	0.8	10
29731	Contribution of model organism phenotypes to the computational identification of human disease genes. <i>DMM Disease Models and Mechanisms</i> , 2022, 15, .	1.2	5
29732	Whole Transcriptome Sequencing Reveals Drought Resistance-Related Genes in Upland Cotton. <i>Genes</i> , 2022, 13, 1159.	1.0	4
29734	EGFAFS: A Novel Feature Selection Algorithm Based on Explosion Gravitation Field Algorithm. <i>Entropy</i> , 2022, 24, 873.	1.1	1
29735	Semantics of Dairy Fermented Foods: A Microbiologist's Perspective. <i>Foods</i> , 2022, 11, 1939.	1.9	2
29738	Systematic Functional Annotation Workflow for Insects. <i>Insects</i> , 2022, 13, 586.	1.0	12
29739	Vascular Regulation by Super Enhancer-Derived LINC00607. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	4
29740	A TP53 Related Immune Prognostic Model for the Prediction of Clinical Outcomes and Therapeutic Responses in Lung Adenocarcinoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
29741	Genome-Wide Dissection of the Genetic Basis for Drought Tolerance in <i>Gossypium hirsutum</i> L. Races. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
29742	DEVEA: an interactive shiny application for Differential Expression analysis, data Visualization and Enrichment Analysis of transcriptomics data. <i>F1000Research</i> , 0, 11, 711.	0.8	0
29743	A Computational Framework to Characterize the Cancer Drug Induced Effect on Aging Using Transcriptomic Data. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	0
29744	Inferring functional communities from partially observed biological networks exploiting geometric topology and side information. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
29745	Dysregulation of Neuropeptide and Tau Peptide Signatures in Human Alzheimer's Disease Brain. <i>ACS Chemical Neuroscience</i> , 2022, 13, 1992-2005.	1.7	13
29746	The regulatory role of <i>HOX</i> interacting lncRNA in oral cancer: An <i>in silico</i> analysis. <i>Journal of Oral Pathology and Medicine</i> , 2022, 51, 684-693.	1.4	2
29747	A chromosome-level genome assembly of the orange wheat blossom midge, <i>Sitodiplosis mosellana</i> (Diptera: Cecidomyiidae) provides insights into the evolution of a detoxification system. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	1

#	ARTICLE	IF	CITATIONS
29748	Genome-Wide Evolutionary Analysis of Putative Non-Specific Herbicide Resistance Genes and Compilation of Core Promoters between Monocots and Dicots. <i>Genes</i> , 2022, 13, 1171.	1.0	5
29749	Genome Assembly and Analysis of the Flavonoid and Phenylpropanoid Biosynthetic Pathways in Fingerroot Ginger (<i>Boesenbergia rotunda</i>). <i>International Journal of Molecular Sciences</i> , 2022, 23, 7269.	1.8	1
29750	Single-Cell RNA Sequencing Unravels Upregulation of Immune Cell Crosstalk in Relapsed Pediatric Ependymoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
29751	Monitoring Protein Import into the Endoplasmic Reticulum in Living Cells with Proximity Labeling. <i>ACS Chemical Biology</i> , 2022, 17, 1963-1977.	1.6	4
29752	Online <i>in silico</i> validation of disease and gene sets, clusterings or subnetworks with DIGEST. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
29753	Integrated Bioinformatics Analysis for Identifying the Significant Genes as Poor Prognostic Markers in Gastric Adenocarcinoma. <i>Journal of Oncology</i> , 2022, 2022, 1-12.	0.6	0
29754	Exploration of the Mechanisms of Differential Indole Alkaloid Biosynthesis in Dedifferentiated and Cambial Meristematic Cells of <i>Catharanthus roseus</i> Using Transcriptome Sequencing. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
29755	Harnessing the Full Potential of Multi-Omic Analyses to Advance the Study and Treatment of Chronic Kidney Disease. , 0, 2, .		1
29756	De novo Transcriptome Analysis of Drought-Adapted Cluster Bean (Cultivar RGC-1025) Reveals the Wax Regulatory Genes Involved in Drought Resistance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
29758	Identification of Potential miRNA-mRNA Regulatory Network in Denervated Muscular Atrophy by Bioinformatic Analysis. <i>BioMed Research International</i> , 2022, 2022, 1-12.	0.9	0
29759	Comparative Transcriptome Profiling Reveals the Genes Involved in Storage Root Expansion in Sweetpotato (<i>Ipomoea batatas</i> (L.) Lam.). <i>Genes</i> , 2022, 13, 1156.	1.0	3
29760	Defective VWF secretion due to expression of <i>MYH9</i> -RD E1841K mutant in endothelial cells disrupts hemostasis. <i>Blood Advances</i> , 2022, 6, 4537-4552.	2.5	1
29761	Ferroptosis and Autophagy-Related Genes in the Pathogenesis of Ischemic Cardiomyopathy. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	9
29762	Quality-controlled R-loop meta-analysis reveals the characteristics of R-loop consensus regions. <i>Nucleic Acids Research</i> , 2022, 50, 7260-7286.	6.5	7
29763	Anti-hepatic carcinoma mechanisms of calycosin through targeting of ferroptosis. <i>Intelligent Medicine</i> , 2022, , .	1.6	0
29764	Genome sequence and pathogenicity of <i>Vibrio vulnificus</i> strain MCCC 1A08743 isolated from contaminated prawns. <i>Biology Open</i> , 2022, 11, .	0.6	2
29765	Identification of stress-related genes by co-expression network analysis based on the improved turbot genome. <i>Scientific Data</i> , 2022, 9, .	2.4	6
29767	Reduction of Cardiac Fibrosis by Interference With YAP-Dependent Transactivation. <i>Circulation Research</i> , 2022, 131, 239-257.	2.0	26

#	ARTICLE	IF	CITATIONS
29768	Isolation, Identification, and Investigation of Pathogenic Bacteria From Common Carp (Cyprinus) Tj ETQq0 0 0 rgBT, /Overlock, 2022, 10 Tf 50 7	2.2	2
29769	TSNAPred: predicting type-specific nucleic acid binding residues via an ensemble approach. Briefings in Bioinformatics, 2022, 23, .	3.2	2
29770	Dissecting the Genetic Structure of Maize Leaf Sheaths at Seedling Stage by Image-Based High-Throughput Phenotypic Acquisition and Characterization. Frontiers in Plant Science, 0, 13, .	1.7	1
29771	Identification of a Prognostic Model Based on Fatty Acid Metabolism-Related Genes of Head and Neck Squamous Cell Carcinoma. Frontiers in Genetics, 0, 13, .	1.1	9
29772	Estrogen hormone is an essential sex factor inhibiting inflammation and immune response in COVID-19. Scientific Reports, 2022, 12, .	1.6	25
29773	Comprehensive Genome-Wide Identification and Expression Profiling of Eceriferum (CER) Gene Family in Passion Fruit (Passiflora edulis) Under Fusarium kyushuense and Drought Stress Conditions. Frontiers in Plant Science, 0, 13, .	1.7	12
29774	Novel App knock-in mouse model shows key features of amyloid pathology and reveals profound metabolic dysregulation of microglia. Molecular Neurodegeneration, 2022, 17, .	4.4	26
29775	Identification of hub genes and regulatory networks in histologically unstable carotid atherosclerotic plaque by bioinformatics analysis. BMC Medical Genomics, 2022, 15, .	0.7	6
29777	New insights into cypermethrin insecticide resistance mechanisms of <i>Culex pipiens pallens</i> by proteome analysis. Pest Management Science, 2022, 78, 4579-4588.	1.7	2
29778	Diet and feeding pattern modulate diurnal dynamics of the ileal microbiome and transcriptome. Cell Reports, 2022, 40, 111008.	2.9	32
29779	Virofree, an Herbal Medicine-Based Formula, Interrupts the Viral Infection of Delta and Omicron Variants of SARS-CoV-2. Frontiers in Pharmacology, 0, 13, .	1.6	7
29780	The splicing factor RBM17 drives leukemic stem cell maintenance by evading nonsense-mediated decay of pro-leukemic factors. Nature Communications, 2022, 13, .	5.8	3
29781	Chromosome-scale assembly and annotation of the perennial ryegrass genome. BMC Genomics, 2022, 23, .	1.2	17
29782	Mechanisms of Action of Semen Ziziphi spinosae in the Treatment of Tourette Syndrome. Degenerative Neurological and Neuromuscular Disease, 0, Volume 12, 85-96.	0.7	0
29783	Scalable multiplex co-fractionation/mass spectrometry platform for accelerated protein interactome discovery. Nature Communications, 2022, 13, .	5.8	20
29784	Computational Modeling of Macrophage Iron Sequestration during Host Defense against Aspergillus. MSphere, 2022, 7, .	1.3	3
29787	The Construction and Analysis of Infiltrating Immune Cell and ceRNA Networks in Diabetic Foot Ulcer. Frontiers in Endocrinology, 0, 13, .	1.5	3
29788	SLPred: a multi-view subcellular localization prediction tool for multi-location human proteins. Bioinformatics, 2022, 38, 4226-4229.	1.8	3

#	ARTICLE	IF	CITATIONS
29790	Polaramycin B, and not physical interaction, is the signal that rewires fungal metabolism in the Streptomyces-Aspergillus interaction. <i>Environmental Microbiology</i> , 2022, 24, 4899-4914.	1.8	4
29791	Genomic Characterization by Whole-Exome Sequencing of Hypermobility Spectrum Disorder. <i>Genes</i> , 2022, 13, 1269.	1.0	1
29792	Natural variation in root suberization is associated with local environment in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2022, 236, 385-398.	3.5	8
29793	Potential ferroptosis-related diagnostic and prognostic biomarkers in laryngeal cancer. <i>European Archives of Oto-Rhino-Laryngology</i> , 2022, 279, 5277-5288.	0.8	2
29794	Arecoline promotes proliferation and migration of human HepG2 cells through activation of the PI3K/AKT/mTOR pathway. <i>Hereditas</i> , 2022, 159, .	0.5	6
29795	Alternative splicing patterns reveal prognostic indicator in muscle-invasive bladder cancer. <i>World Journal of Surgical Oncology</i> , 2022, 20, .	0.8	2
29796	A campaign targeting a conserved Hsp70 binding site uncovers how subcellular localization is linked to distinct biological activities. <i>Cell Chemical Biology</i> , 2022, 29, 1303-1316.e3.	2.5	7
29797	Single-cell RNA sequencing reveals localized tumour ablation and intratumoural immunostimulant delivery potentiate T cell mediated tumour killing. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	9
29798	Lilac (<i>Syringa oblata</i>) genome provides insights into its evolution and molecular mechanism of petal color change. <i>Communications Biology</i> , 2022, 5, .	2.0	13
29799	Bioinformatics Analysis Identifies Potential Ferroptosis Key Gene in Type 2 Diabetic Islet Dysfunction. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	7
29800	Mouse models of <i>NADK2</i> deficiency analyzed for metabolic and gene expression changes to elucidate pathophysiology. <i>Human Molecular Genetics</i> , 2022, 31, 4055-4074.	1.4	4
29801	New Evidence of Tiger Subspecies Differentiation and Environmental Adaptation: Comparison of the Whole Genomes of the Amur Tiger and the South China Tiger. <i>Animals</i> , 2022, 12, 1817.	1.0	2
29802	p53 Binding Sites in Long Terminal Repeat 5Hs (LTR5Hs) of Human Endogenous Retrovirus K Family (HML-2 Subgroup) Play Important Roles in the Regulation of LTR5Hs Transcriptional Activity. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	11
29803	Cytokine Activation Reveals Tissue-Imprinted Gene Profiles of Mesenchymal Stromal Cells. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
29804	Transcriptomic analysis of starch accumulation patterns in different glutinous sorghum seeds. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
29805	Weighted Gene Correlation Network Analysis (WGCNA) of <i>Arabidopsis</i> Somatic Embryogenesis (SE) and Identification of Key Gene Modules to Uncover SE-Associated Hub Genes. <i>International Journal of Genomics</i> , 2022, 2022, 1-24.	0.8	4
29806	Refining bulk segregant analyses: ontology-mediated discovery of flowering time genes in <i>Brassica oleracea</i> . <i>Plant Methods</i> , 2022, 18, .	1.9	1
29807	The role of toll-like receptors (TLRs) in pan-cancer. <i>Annals of Medicine</i> , 2022, 54, 1918-1937.	1.5	4

#	ARTICLE	IF	CITATIONS
29808	Effect of Environmental Temperatures on Proteome Composition of Salmonella enterica Serovar Typhimurium. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100265.	2.5	5
29809	More phenomenology in psychiatry? Applied ontology as a method towards integration. <i>Lancet Psychiatry</i> , 2022, 9, 751-758.	3.7	10
29810	Increased Development of Th1, Th17, and Th1.17 Cells Under T1 Polarizing Conditions in Juvenile Idiopathic Arthritis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	8
29812	Cell cycle arrest explains the observed bulk 3D genomic alterations in response to long-term heat shock in K562 cells. <i>Genome Research</i> , 0, , .	2.4	0
29813	Genome-wide Association Study Shows That Executive Functioning Is Influenced by GABAergic Processes and Is a Neurocognitive Genetic Correlate of Psychiatric Disorders. <i>Biological Psychiatry</i> , 2023, 93, 59-70.	0.7	21
29815	Transcriptome and Metabolome Analyses Reveal the Involvement of Multiple Pathways in Flowering Intensity in Mango. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8
29816	Differential expression profile and in-silico functional analysis of long noncoding RNA and mRNA in duck embryo fibroblasts infected with duck plague virus. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
29817	Regional gene expression patterns are associated with task-specific brain activation during reward and emotion processing measured with functional <scp>MRI</scp>. <i>Human Brain Mapping</i> , 2022, 43, 5266-5280.	1.9	2
29818	Lim Domain Binding 3 (Ldb3) Identified as a Potential Marker of Cardiac Extracellular Vesicles. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7374.	1.8	2
29819	Network Pharmacology-Based Prediction and Pharmacological Validation of Effects of Astragali Radix on Acetaminophen-Induced Liver Injury. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	3
29820	Interferon- β resistance and immune evasion in glioma develop via Notch-regulated co-evolution of malignant and immune cells. <i>Developmental Cell</i> , 2022, 57, 1847-1865.e9.	3.1	15
29821	Transcriptome Sequencing of <i>Agave angustifolia</i> Reveals Conservation and Diversification in the Expression of Cinnamyl Alcohol Dehydrogenase Genes in Agave Species. <i>Agriculture (Switzerland)</i> , 2022, 12, 1003.	1.4	3
29822	Upper airway gene expression shows a more robust adaptive immune response to SARS-CoV-2 in children. <i>Nature Communications</i> , 2022, 13, .	5.8	7
29823	Shared Genetics and Causality Between Decaffeinated Coffee Consumption and Neuropsychiatric Diseases: A Large-Scale Genome-Wide Cross-Trait Analysis and Mendelian Randomization Analysis. <i>Frontiers in Psychiatry</i> , 0, 13, .	1.3	3
29824	Characterization of <i>Cronobacter sakazakii</i> Strains Originating from Plant-Origin Foods Using Comparative Genomic Analyses and Zebrafish Infectivity Studies. <i>Microorganisms</i> , 2022, 10, 1396.	1.6	6
29826	The heterogeneous pharmacological medical biochemical network PharMeBINet. <i>Scientific Data</i> , 2022, 9, .	2.4	2
29831	Metabolome and transcriptome profiling reveal regulatory network and mechanism of flavonoid biosynthesis during color formation of <i>Dioscorea cirrhosa</i> L. <i>PeerJ</i> , 0, 10, e13659.	0.9	2
29832	Integrated Metabolomic and Transcriptomic Analysis Reveals the Effect of Artificial Shading on Reducing the Bitter Taste of Bamboo Shoots. <i>Horticulturae</i> , 2022, 8, 594.	1.2	2

#	ARTICLE	IF	CITATIONS
29833	TogolID: an exploratory ID converter to bridge biological datasets. <i>Bioinformatics</i> , 2022, 38, 4194-4199.	1.8	6
29834	Chromatin Separation Regulators Predict the Prognosis and Immune Microenvironment Estimation in Lung Adenocarcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
29835	Selective expression of variant surface antigens enables <i>Plasmodium falciparum</i> to evade immune clearance in vivo. <i>Nature Communications</i> , 2022, 13, .	5.8	5
29837	Consensus draft of the native mouse podocyte-ome. <i>American Journal of Physiology - Renal Physiology</i> , 2022, 323, F182-F197.	1.3	6
29838	Gene expression of the white-rot fungus <i>Lenzites gibbosa</i> during wood degradation. <i>Mycologia</i> , 0, , 1-16.	0.8	1
29839	Melon shoot organization 1, encoding an AGRONAUTE7 protein, plays a crucial role in plant development. <i>Theoretical and Applied Genetics</i> , 0, , .	1.8	1
29840	Chromosome-Level Genome Assembly and Transcriptome Comparison Analysis of <i>Cephalopholis sonnerati</i> and Its Related Grouper Species. <i>Biology</i> , 2022, 11, 1053.	1.3	4
29841	Multi-omics profiling of collagen-induced arthritis mouse model reveals early metabolic dysregulation via SIRT1 axis. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
29842	Quantitative proteomics analysis to assess protein expression levels in the ovaries of pubescent goats. <i>BMC Genomics</i> , 2022, 23, .	1.2	0
29844	A human adipose tissue cell-type transcriptome atlas. <i>Cell Reports</i> , 2022, 40, 111046.	2.9	30
29845	Deconstructing cold-induced brown adipocyte neogenesis in mice. <i>ELife</i> , 0, 11, .	2.8	20
29846	Network pharmacology-based strategy for predicting therapy targets of Sanqi and Huangjing in diabetes mellitus. <i>World Journal of Clinical Cases</i> , 2022, 10, 6900-6914.	0.3	2
29847	Genome-wide binding analysis of transcription factor <i>Rice Indeterminate 1</i> reveals a complex network controlling rice floral transition. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 1690-1705.	4.1	2
29848	Identification and Validation of Autophagy-Related Genes in Primary Ovarian Insufficiency by Gene Expression Profile and Bioinformatic Analysis. <i>Analytical Cellular Pathology</i> , 2022, 2022, 1-17.	0.7	1
29849	Catalytic promiscuity of <i>O</i> -methyltransferases from <i>Corydalis yanhusuo</i> leading to the structural diversity of benzylisoquinoline alkaloids. <i>Horticulture Research</i> , 0, , .	2.9	7
29850	Increased CSF-decorin predicts brain pathological changes driven by Alzheimer's amyloidosis. <i>Acta Neuropathologica Communications</i> , 2022, 10, .	2.4	8
29851	Exploring Manually Curated Annotations of Intrinsically Disordered Proteins with DisProt. <i>Current Protocols</i> , 2022, 2, .	1.3	2
29852	CRISPR-Cas9-mediated mutagenesis of kiwifruit <i>BFT</i> genes results in an evergrowing but not early flowering phenotype. <i>Plant Biotechnology Journal</i> , 2022, 20, 2064-2076.	4.1	20

#	ARTICLE	IF	CITATIONS
29853	Differential regulation of mRNAs and lncRNAs related to lipid metabolism in Duolang and Small Tail Han sheep. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
29854	Transcriptomic Insight into Viviparous Growth in Water Lily. <i>BioMed Research International</i> , 2022, 2022, 1-18.	0.9	0
29855	Biomimetic generation of the strongest known biomaterial found in limpet tooth. <i>Nature Communications</i> , 2022, 13, .	5.8	5
29856	MiR-30c-1-3p targets matrix metalloproteinase 9 involved in the rupture of abdominal aortic aneurysms. <i>Journal of Molecular Medicine</i> , 0, , .	1.7	1
29858	Identification of microRNAs and their target genes related to the accumulation of anthocyanin in purple potato tubers (<sc><i>Solanum tuberosum</i></sc>). <i>Plant Direct</i> , 2022, 6, .	0.8	4
29859	Protein expression profiling identifies a prognostic model for ovarian cancer. <i>BMC Women's Health</i> , 2022, 22, .	0.8	1
29860	Single-cell network biology characterizes cell type gene regulation for drug repurposing and phenotype prediction in Alzheimer's disease. <i>PLoS Computational Biology</i> , 2022, 18, e1010287.	1.5	9
29861	Characterizing the extracellular matrix transcriptome of cervical, endometrial, and uterine cancers. <i>Matrix Biology Plus</i> , 2022, 15, 100117.	1.9	6
29862	Optimizing component formula suppresses lung cancer by blocking DTL-mediated PDCD4 ubiquitination to regulate the MAPK/JNK pathway. <i>Journal of Ethnopharmacology</i> , 2022, 299, 115546.	2.0	6
29863	Prospective role and immunotherapeutic targets of sideroflexin protein family in lung adenocarcinoma: evidence from bioinformatics validation. <i>Functional and Integrative Genomics</i> , 2022, 22, 1057-1072.	1.4	30
29864	Revealing the difference of α -amylase and CYP6AE76 gene between polyphagous <i>Conogethes punctiferalis</i> and oligophagous <i>C. pinicolalis</i> by multiple-omics and molecular biological technique. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
29865	Analysis on the desert adaptability of indigenous sheep in the southern edge of Taklimakan Desert. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
29866	Gene Coexpression Connectivity Predicts Gene Targets Underlying High Ionic-Liquid Tolerance in <i>Yarrowia lipolytica</i> . <i>MSystems</i> , 2022, 7, .	1.7	1
29867	Genome-wide identification of drought-responsive microRNAs and their target genes in Chinese jujube by deep sequencing. <i>Genes and Genomics</i> , 2023, 45, 231-245.	0.5	3
29868	Time and phenotype-dependent transcriptome analysis in AAV-TGF β 1 and Bleomycin-induced lung fibrosis models. <i>Scientific Reports</i> , 2022, 12, .	1.6	8
29869	Chromosome-level assembly and analysis of the Thymus genome provide insights into glandular secretory trichome formation and monoterpenoid biosynthesis in thyme. <i>Plant Communications</i> , 2022, 3, 100413.	3.6	20
29870	Transcriptome analysis and phenotyping of walnut seedling roots under nitrogen stresses. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
29873	A Narrative Literature Review of Natural Language Processing Applied to the Occupational Exposome. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 8544.	1.2	5

#	ARTICLE	IF	CITATIONS
29874	Bioinformatic prediction of putative conveyers of O-GlcNAc transferase intellectual disability. <i>Journal of Biological Chemistry</i> , 2022, 298, 102276.	1.6	4
29875	Lipolysis regulates major transcriptional programs in brown adipocytes. <i>Nature Communications</i> , 2022, 13, .	5.8	16
29876	Gene function prediction in five model eukaryotes exclusively based on gene relative location through machine learning. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
29877	Genome-Wide Analysis of microRNAs Identifies the Lipid Metabolism Pathway to Be a Defining Factor in Adipose Tissue From Different Sheep. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	3
29878	Excessive Sodium Intake Leads to Cardiovascular Disease by Promoting Sex-Specific Dysfunction of Murine Heart. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	2
29880	Beneficial Effect of Selenium Doped Carbon Quantum Dots Supplementation on the in vitro Development Competence of Ovine Oocytes. <i>International Journal of Nanomedicine</i> , 0, Volume 17, 2907-2924.	3.3	4
29881	The Protective Effect of Edaravone on TDP-43 Plus Oxidative Stress-Induced Neurotoxicity in Neuronal Cells: Analysis of Its Neuroprotective Mechanisms Using RNA Sequencing. <i>Pharmaceuticals</i> , 2022, 15, 842.	1.7	7
29882	Dynamic Transcriptomic Profiling During Liver Development in Schizothorax Prenanti. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	3
29883	Proteomic characterisation of triple negative breast cancer cells following CDK4/6 inhibition. <i>Scientific Data</i> , 2022, 9, .	2.4	4
29884	The evolutionary history of human spindle genes includes back-and-forth gene flow with Neandertals. <i>ELife</i> , 0, 11, .	2.8	12
29885	REDfly: An Integrated Knowledgebase for Insect Regulatory Genomics. <i>Insects</i> , 2022, 13, 618.	1.0	9
29886	Exploring the Mutational Landscape of Isolated Congenital Heart Defects: An Exome Sequencing Study Using Cardiac DNA. <i>Genes</i> , 2022, 13, 1214.	1.0	4
29887	Spatially resolved proteomic map shows that extracellular matrix regulates epidermal growth. <i>Nature Communications</i> , 2022, 13, .	5.8	26
29888	The Childhood Acute Illness and Nutrition (CHAIN) network nested case-cohort study protocol: a multi-omics approach to understanding mortality among children in sub-Saharan Africa and South Asia. <i>Gates Open Research</i> , 0, 6, 77.	2.0	1
29889	Methylated RNA Immunoprecipitation Sequencing Reveals the m6A Landscape in Oral Squamous Cell Carcinoma. <i>Journal of Immunology Research</i> , 2022, 2022, 1-13.	0.9	1
29890	Single-cell transcriptomes identifies characteristic features of mouse macrophages in liver Mallory-Denk bodies formation. <i>Experimental and Molecular Pathology</i> , 2022, 127, 104811.	0.9	4
29891	Call for Papers: Semantics-enabled Biomedical Literature Analytics. <i>Journal of Biomedical Informatics</i> , 2022, , 104134.	2.5	0
29893	Transcriptome innovations in primates revealed by single-molecule long-read sequencing. <i>Genome Research</i> , 2022, 32, 1448-1462.	2.4	6

#	ARTICLE	IF	CITATIONS
29894	Additive Effect of CD73 Inhibitor in Colorectal Cancer Treatment With CDK4/6 Inhibitor Through Regulation of PD-L1. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 14, 769-788.	2.3	6
29895	Comparative transcriptomics identifies candidate genes involved in the evolutionary transition from dehiscent to indehiscent fruits in <i>Lepidium</i> (Brassicaceae). <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
29896	The Seizure-Associated Genes Across Species (SAGAS) database offers insights into epilepsy genes, pathways and treatments. <i>Epilepsia</i> , 2022, 63, 2403-2412.	2.6	7
29897	Interspecies Isobaric Labeling-Based Quantitative Proteomics Reveals Protein Changes in the Ovary of <i>Aedes aegypti</i> Coinfected With ZIKV and Wolbachia. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
29898	Ddp1 Cooperates with Ppx1 to Counter a Stress Response Initiated by Nonvacuolar Polyphosphate. <i>MBio</i> , 2022, 13, .	1.8	10
29899	Pan-Cancer Analysis Reveals the Prognostic Potential of the THAP9/THAP9-AS1 Sense-Antisense Gene Pair in Human Cancers. <i>Non-coding RNA</i> , 2022, 8, 51.	1.3	0
29900	Role of PsnWRKY70 in Regulatory Network Response to Infection with <i>Alternaria alternata</i> (Fr.) Keissl in <i>Populus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 7537.	1.8	6
29901	Phylogenies of the 16S rRNA gene and its hypervariable regions lack concordance with core genome phylogenies. <i>Microbiome</i> , 2022, 10, .	4.9	43
29902	Prognostic value of metabolic genes in lung adenocarcinoma via integrative analyses. <i>Genomics</i> , 2022, 114, 110425.	1.3	0
29903	Effect of <i>Saccharomyces cerevisiae</i> cell-free supernatant on the physiology, quorum sensing, and protein synthesis of lactic acid bacteria. <i>LWT - Food Science and Technology</i> , 2022, 165, 113732.	2.5	9
29904	KG-Predict: A knowledge graph computational framework for drug repurposing. <i>Journal of Biomedical Informatics</i> , 2022, 132, 104133.	2.5	28
29905	Exosome-mediated transduction of mechanical force regulates prostate cancer migration via microRNA. <i>Biochemistry and Biophysics Reports</i> , 2022, 31, 101299.	0.7	5
29906	Alterations of RNAs in the insula related to cocaine-induced condition place preference in adolescent mice. <i>Biochemical and Biophysical Research Communications</i> , 2022, 621, 109-115.	1.0	1
29907	Molecular response of <i>Anoxybacillus</i> sp. PDR2 under azo dye stress: An integrated analysis of proteomics and metabolomics. <i>Journal of Hazardous Materials</i> , 2022, 438, 129500.	6.5	13
29908	Protocol for establishing a protein-protein interaction network using tandem affinity purification followed by mass spectrometry in mammalian cells. <i>STAR Protocols</i> , 2022, 3, 101569.	0.5	6
29909	The trichloroethylene metabolite S-(1,2-dichlorovinyl)-l-cysteine inhibits lipopolysaccharide-induced inflammation transcriptomic pathways and cytokine secretion in a macrophage cell model. <i>Toxicology in Vitro</i> , 2022, 84, 105429.	1.1	1
29910	Organophosphate flame retardant TDCPP: A risk factor for renal cancer?. <i>Chemosphere</i> , 2022, 305, 135485.	4.2	7
29911	A Stochastic Model for Detecting Heterogeneous Link Communities in Complex Networks. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2015, 29, .	3.6	11

#	ARTICLE	IF	CITATIONS
29912	Marginalized Denoising for Link Prediction and Multi-Label Learning. Proceedings of the AAAI Conference on Artificial Intelligence, 2015, 29, .	3.6	13
29913	Tandem Mass Tag-based proteomics analysis reveals the vital role of inflammation in traumatic brain injury in a mouse model. Neural Regeneration Research, 2023, 18, 155.	1.6	4
29919	Full-length transcriptome sequencing analysis and characterization, development and validation of microsatellite markers in <i>Kengyilia melanthera</i> . Frontiers in Plant Science, 0, 13, .	1.7	2
29920	Copy Number Variation of Circulating Tumor DNA (ctDNA) Detected Using NIPT in Neoadjuvant Chemotherapy-Treated Ovarian Cancer Patients. Frontiers in Genetics, 0, 13, .	1.1	6
29921	Transcriptome and Metabonomic Analysis of <i>Tamarix ramosissima</i> Potassium (K+) Channels and Transporters in Response to NaCl Stress. Genes, 2022, 13, 1313.	1.0	12
29922	Comparative genomic analysis reveals cellulase plays an important role in the pathogenicity of <i>Setosphaeria turcica</i> f. sp. <i>zeae</i> . Frontiers in Microbiology, 0, 13, .	1.5	1
29923	Identification of New Toxicity Mechanisms in Drug-Induced Liver Injury through Systems Pharmacology. Genes, 2022, 13, 1292.	1.0	0
29924	N6-methyladenosine modulates long non-coding RNA in the developing mouse heart. Cell Death Discovery, 2022, 8, .	2.0	4
29925	Full-Length Transcriptome Sequencing and Comparative Transcriptomic Analysis Provide Insights Into the Ovarian Maturation of <i>Exopalaemon carinicauda</i> . Frontiers in Marine Science, 0, 9, .	1.2	3
29926	Kidney Cancer Biomarker Selection Using Regularized Survival Models. Cells, 2022, 11, 2311.	1.8	1
29927	Activation of the integrated stress response is a vulnerability for multidrug-resistant <i>Scp>FBXW7</scp></i> deficient cells. EMBO Molecular Medicine, 2022, 14, .	3.3	12
29928	Transcriptome and Metabolome Analyses of <i>Codonopsis convolvulacea</i> Kurz Tuber, Stem, and Leaf Reveal the Presence of Important Metabolites and Key Pathways Controlling Their Biosynthesis. Frontiers in Genetics, 0, 13, .	1.1	2
29930	Ageing endometrium in young women: molecular classification of endometrial aging-based markers in women younger than 35 years with recurrent implantation failure. Journal of Assisted Reproduction and Genetics, 2022, 39, 2143-2151.	1.2	4
29931	Overcoming selection bias in synthetic lethality prediction. Bioinformatics, 2022, 38, 4360-4368.	1.8	3
29933	Unveiling Co-Infection in Cystic Fibrosis Airways: Transcriptomic Analysis of <i>Pseudomonas aeruginosa</i> and <i>Staphylococcus aureus</i> Dual-Species Biofilms. Frontiers in Genetics, 0, 13, .	1.1	7
29934	Mutant Huntingtin Protein Interaction Map Implicates Dysregulation of Multiple Cellular Pathways in Neurodegeneration of Huntington's Disease. Journal of Huntington's Disease, 2022, 11, 243-267.	0.9	8
29935	Uncovering the Effect and Mechanism of <i>Rhizoma Corydalis</i> on Myocardial Infarction Through an Integrated Network Pharmacology Approach and Experimental Verification. Frontiers in Pharmacology, 0, 13, .	1.6	3
29936	Use of Autoreactive Antibodies in Blood of Patients with Pancreatic Intraductal Papillary Mucinous Neoplasms (IPMN) for Grade Distinction and Detection of Malignancy. Cancers, 2022, 14, 3562.	1.7	1

#	ARTICLE	IF	CITATIONS
29937	Antifungal Activity of Endophytic Bacillus K1 Against Botrytis cinerea. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
29938	Massively parallel pooled screening reveals genomic determinants of nanoparticle delivery. <i>Science</i> , 2022, 377, .	6.0	72
29939	Identified potential biomarkers may predict primary nonresponse to infliximab in patients with ulcerative colitis. <i>Autoimmunity</i> , 2022, 55, 538-548.	1.2	5
29941	The contribution of whole-exome sequencing to intellectual disability diagnosis and knowledge of underlying molecular mechanisms: A systematic review and meta-analysis. <i>Mutation Research - Reviews in Mutation Research</i> , 2022, 790, 108428.	2.4	11
29942	Mapping the single-cell landscape of acral melanoma and analysis of the molecular regulatory network of the tumor microenvironments. <i>ELife</i> , 0, 11, .	2.8	10
29943	Epigenetically silenced apoptosis-associated tyrosine kinase (AATK) facilitates a decreased expression of Cyclin D1 and WEE1, phosphorylates TP53 and reduces cell proliferation in a kinase-dependent manner. <i>Cancer Gene Therapy</i> , 2022, 29, 1975-1987.	2.2	6
29944	A microengineered Brain-Chip to model neuroinflammation in humans. <i>IScience</i> , 2022, 25, 104813.	1.9	20
29946	Genome-Wide Association Analysis and Genetic Parameters for Feed Efficiency and Related Traits in Yorkshire and Duroc Pigs. <i>Animals</i> , 2022, 12, 1902.	1.0	1
29947	High-dimension to high-dimension screening for detecting genome-wide epigenetic and noncoding RNA regulators of gene expression. <i>Bioinformatics</i> , 2022, 38, 4078-4087.	1.8	1
29948	The BASP1 transcriptional corepressor modifies chromatin through lipid-dependent and lipid-independent mechanisms. <i>IScience</i> , 2022, 25, 104796.	1.9	5
29949	Gene expression profiling before and after internode culture for adventitious shoot formation in ipecac. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	1
29950	Intratumoral spatial heterogeneity of tumor-infiltrating lymphocytes is a significant factor for precisely stratifying prognostic immune subgroups of microsatellite instability-high colorectal carcinomas. <i>Modern Pathology</i> , 2022, 35, 2011-2022.	2.9	10
29951	Cold exposure induces lipid dynamics and thermogenesis in brown adipose tissue of goats. <i>BMC Genomics</i> , 2022, 23, .	1.2	13
29952	A supervised protein complex prediction method with network representation learning and gene ontology knowledge. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	2
29953	Genome-wide identification and comparative analysis of MATE gene family in Cucurbitaceae species and their regulatory role in melon (<i>Cucumis melo</i>) under salt stress. <i>Horticulture Environment and Biotechnology</i> , 0, , .	0.7	9
29954	Catalytic cycling of human mitochondrial Lon protease. <i>Structure</i> , 2022, 30, 1254-1268.e7.	1.6	3
29956	Transcriptome Dynamics in the Developing Larynx, Trachea, and Esophagus. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	2
29957	Expansion and functional analysis of the SR-related protein family across the domains of life. <i>Rna</i> , 2022, 28, 1298-1314.	1.6	7

#	ARTICLE	IF	CITATIONS
29958	Comparative analysis of differentially abundant proteins between high and low intramuscular fat content groups in donkeys. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	3
29959	Identification and characterization of four immune-related signatures in keloid. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	9
29960	Heterogeneous nuclear ribonucleoprotein U (HNRNPU) safeguards the developing mouse cortex. <i>Nature Communications</i> , 2022, 13, .	5.8	13
29962	Transcriptome analysis of peach fruit under 1-MCP treatment provides insights into regulation network in melting peach softening. <i>Food Quality and Safety</i> , 2022, 6, .	0.6	6
29963	Ribosomal RNA-Depletion Provides an Efficient Method for Successful Dual RNA-Seq Expression Profiling of a Marine Sponge Holobiont. <i>Marine Biotechnology</i> , 0, , .	1.1	0
29966	Alveolar macrophages in early stage COPD show functional deviations with properties of impaired immune activation. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	12
29967	Identification of Differential Expression Genes between Volume and Pressure Overloaded Hearts Based on Bioinformatics Analysis. <i>Genes</i> , 2022, 13, 1276.	1.0	0
29969	TMT-based proteomic analysis of liquorice root in response to drought stress. <i>BMC Genomics</i> , 2022, 23, .	1.2	7
29970	Transcriptomic and proteomic retinal pigment epithelium signatures of age-related macular degeneration. <i>Nature Communications</i> , 2022, 13, .	5.8	28
29971	Taste 2 Receptor Is Involved in Differentiation of 3T3-L1 Preadipocytes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8120.	1.8	2
29972	Ciliogenesis requires sphingolipid-dependent membrane and axoneme interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	10
29974	The Culture Dish Surface Influences the Phenotype and Dissociation Strategy in Distinct Mouse Macrophage Populations. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
29975	Abduction Framework for Repairing Incomplete EL Ontologies: Complexity Results and Algorithms. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2014, 28, .	3.6	9
29976	A Framework for Supporting Well-being using the Character Computing Ontology - Anxiety and Sleep Quality during COVID-19. <i>Open Psychology</i> , 2022, 4, 205-218.	0.2	0
29977	Using FlyBase: A Database of Drosophila Genes and Genetics. <i>Methods in Molecular Biology</i> , 2022, , 1-34.	0.4	15
29978	Chromosome-Scale Genome Assembly of the African Giant Pouched Rat (<i>Cricetomys Ansoergei</i>) and Evolutionary Analysis Reveals Evidence of Olfactory Specialization. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
29979	Recombinant human chorionic gonadotropin induces signaling pathways towards cancer prevention in the breast of BRCA1/2 mutation carriers. <i>European Journal of Cancer Prevention</i> , 0, Publish Ahead of Print, .	0.6	0
29980	Identification of critical genes associated with radiotherapy resistance in cervical cancer by bioinformatics. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1

#	ARTICLE	IF	CITATIONS
29981	FLASHIda enables intelligent data acquisition for top-down proteomics to boost proteoform identification counts. <i>Nature Communications</i> , 2022, 13, .	5.8	8
29982	Long Non-Coding RNA and mRNA Profiles in the Spinal Cord of Rats with Resiniferatoxin-Induced Neuropathic Pain. <i>Journal of Pain Research</i> , 0, Volume 15, 2149-2160.	0.8	0
29983	Gene Updater: a web tool that autocorrects and updates for Excel misidentified gene names. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
29984	Identify an innovative ferroptosis-related gene in hepatocellular carcinoma. <i>Journal of Clinical Laboratory Analysis</i> , 0, , .	0.9	3
29985	Omics approaches to discover pathophysiological pathways contributing to human pain. <i>Pain</i> , 2022, 163, S69-S78.	2.0	15
29986	CoGO: a contrastive learning framework to predict disease similarity based on gene network and ontology structure. <i>Bioinformatics</i> , 2022, 38, 4380-4386.	1.8	5
29987	DIACYLGLYCEROL KINASE 5 participates in flagellin-induced signaling in Arabidopsis. <i>Plant Physiology</i> , 2022, 190, 1978-1996.	2.3	11
29988	Spotlight on Exosomal Non-Coding RNAs in Breast Cancer: An In Silico Analysis to Identify Potential lncRNA/circRNA-miRNA-Target Axis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8351.	1.8	9
29989	Construction and validation of a cuproptosis-related lncRNA signature as a novel and robust prognostic model for colon adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	32
29990	Molecular Link in Flavonoid and Amino Acid Biosynthesis Contributes to the Flavor of Changqing Tea in Different Seasons. <i>Foods</i> , 2022, 11, 2289.	1.9	5
29991	Complete Genome Sequence Resource for <i>Pseudomonas amygdali</i> pv. <i>loropetali</i> Strain AAC Causing Bacterial Gall of <i>Loropetalum chinense</i> . <i>Plant Disease</i> , 0, , .	0.7	1
29992	Integrative analysis of transcriptome and miRNAome reveals molecular mechanisms regulating pericarp thickness in sweet corn during kernel development. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
29993	Pan-cancer integrative analysis of whole-genome De novo somatic point mutations reveals 17 cancer types. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
29994	Molecular Circuit Discovery for Mechanobiology of Cardiovascular Disease. <i>Regenerative Engineering and Translational Medicine</i> , 0, , .	1.6	0
29995	âŸ•ä°Žâ•ç»†èfžæ°æ@çš,,ç™Œç—†ââŒÉ©±âŠ'æ"jâ•-è†â^«æ-1æ³•. <i>Scientia Sinica Informationis</i> , 2022, , .	0.2	0
29996	The PAICE suite reveals circadian posttranscriptional timing of noncoding RNAs and spliceosome components in <i>Mus musculus</i> macrophages. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	1
29998	Divergent Host-Microbe Interaction and Pathogenesis Proteins Detected in Recently Identified <i>Liberibacter</i> Species. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
30001	Activation of Oncogenic and Immune-Response Pathways Is Linked to Disease-Specific Survival in Merkel Cell Carcinoma. <i>Cancers</i> , 2022, 14, 3591.	1.7	7

#	ARTICLE	IF	CITATIONS
30002	Characterization of methylation patterns associated with lifestyle factors and vitamin D supplementation in a healthy elderly cohort from Southwest Sweden. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
30006	Cancer-associated fibroblast-derived exosomal microRNA-20a suppresses the PTEN/PI3K-AKT pathway to promote the progression and chemoresistance of non-small cell lung cancer. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	42
30007	Evolutionary Genomics of a Subdivided Species. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	8
30008	Transcriptional progressive patterns from mild to severe renal ischemia/reperfusion-induced kidney injury in mice. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
30009	orsum: a Python package for filtering and comparing enrichment analyses using a simple principle. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	8
30011	In silico development and experimental validation of a novel 7-gene signature based on PI3K pathway-related genes in bladder cancer. <i>Functional and Integrative Genomics</i> , 2022, 22, 797-811.	1.4	7
30012	Integration of probabilistic functional networks without an external Gold Standard. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	0
30013	AKT1 Transcriptomic Landscape in Breast Cancer Cells. <i>Cells</i> , 2022, 11, 2290.	1.8	8
30014	Pro-Survival Factor EDEM3 Confers Therapy Resistance in Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8184.	1.8	5
30015	Dynamic changes in O-GlcNAcylation regulate osteoclast differentiation and bone loss via nucleoporin 153. <i>Bone Research</i> , 2022, 10, .	5.4	8
30017	Adaptive Bird-like Genome Miniaturization During the Evolution of Scallop Swimming Lifestyle. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1066-1077.	3.0	1
30018	Identification of aberrantly methylated differentially expressed genes and pro-tumorigenic role of KIF2C in melanoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
30019	Mutations in SORL1 and MTHFDL1 possibly contribute to the development of Alzheimer's disease in a multigenerational Colombian Family. <i>PLoS ONE</i> , 2022, 17, e0269955.	1.1	1
30020	Molecular Framework of Mouse Endothelial Cell Dysfunction during Inflammation: A Proteomics Approach. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8399.	1.8	4
30021	Microgel culture and spatial identity mapping elucidate the signalling requirements for primate epiblast and amnion formation. <i>Development (Cambridge)</i> , 0, , .	1.2	6
30022	Molecular Mechanisms Related to Responses to Oxidative Stress and Antioxidative Therapies in COVID-19: A Systematic Review. <i>Antioxidants</i> , 2022, 11, 1609.	2.2	21
30023	Genomic and Transcriptional Characteristics of Strain <i>Rum-meliibacillus</i> sp. TYF-LIM-RU47 with an Aptitude of Directly Producing Acetoin from Lignocellulose. <i>Fermentation</i> , 2022, 8, 414.	1.4	1
30024	Multi-omics Analyses Provide Insight into the Biosynthesis Pathways of Fucoxanthin in <i>Isochrysis galbana</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1138-1153.	3.0	9

#	ARTICLE	IF	CITATIONS
30025	Pathogenesis and Therapeutic Targets of Focal Cortical Dysplasia Based on Bioinformatics Analysis. <i>Neurochemical Research</i> , 2022, 47, 3506-3521.	1.6	3
30026	Single cell spatial analysis reveals the topology of immunomodulatory purinergic signaling in glioblastoma. <i>Nature Communications</i> , 2022, 13, .	5.8	27
30027	TTN as a candidate gene for distal arthrogryposis type 10 pathogenesis. <i>Journal of Genetic Engineering and Biotechnology</i> , 2022, 20, 119.	1.5	1
30028	A β -Secretase Inhibitor Attenuates Cell Cycle Progression and Invasion in Human Oral Squamous Cell Carcinoma: An In Vitro Study. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8869.	1.8	3
30029	m6A regulator-mediated RNA methylation modification patterns are involved in immune microenvironment regulation of coronary heart disease. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	3
30030	Genetic adaptations to SIV across chimpanzee populations. <i>PLoS Genetics</i> , 2022, 18, e1010337.	1.5	0
30031	Deficiency of the bZIP transcription factors Mafg and Mafk causes misexpression of genes in distinct pathways and results in lens embryonic developmental defects. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	10
30032	Predicting the specific substrate for transmembrane transport proteins using BERT language model. , 2022, , .		1
30033	Genome sequence and comparative analysis of fungal antagonistic strain <i>Bacillus velezensis</i> LJBV19. <i>Folia Microbiologica</i> , 2023, 68, 73-86.	1.1	4
30034	Dissection of the macrophage response towards infection by the <i>Leishmania</i> -viral endosymbiont duo and dynamics of the type I interferon response. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	0
30035	MGEFNP: a multi-view graph embedding method for gene function prediction based on adaptive estimation with GCN. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
30037	A Rule-Based Inference Framework to Explore and Explain the Biological Related Mechanisms of Potential Drug-Drug Interactions. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-9.	0.7	0
30038	Id2 exerts tumor suppressor properties in lung cancer through its effects on cancer cell invasion and migration. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
30040	OsVTC1-1 Gene Silencing Promotes a Defense Response in Rice and Enhances Resistance to <i>Magnaporthe oryzae</i> . <i>Plants</i> , 2022, 11, 2189.	1.6	2
30041	Comparative Transcriptomic and Metabolic Analyses Reveal the Coordinated Mechanisms in <i>Pinus koraiensis</i> under Different Light Stress Conditions. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9556.	1.8	6
30042	Analysis of Amino Acids in the Roots of <i>Tamarix ramosissima</i> by Application of Exogenous Potassium (K ⁺) under NaCl Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9331.	1.8	8
30044	Genome-wide scan for selective sweeps identifies novel loci associated with resistance to mastitis in German Holstein cattle. <i>Journal of Animal Breeding and Genetics</i> , 2023, 140, 92-105.	0.8	4
30045	Integrated multi-omics reveals cellular and molecular interactions governing the invasive niche of basal cell carcinoma. <i>Nature Communications</i> , 2022, 13, .	5.8	19

#	ARTICLE	IF	CITATIONS
30046	SETD2 regulates gene transcription patterns and is associated with radiosensitivity in lung adenocarcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
30048	Tofacitinib blocks IFN-regulated biomarker genes in skin fibroblasts and keratinocytes in a systemic sclerosis trial. <i>JCI Insight</i> , 2022, 7, .	2.3	22
30050	An Extensive Study of Phenol Red Thread as a Novel Non-Invasive Tear Sampling Technique for Proteomics Studies: Comparison with Two Commonly Used Methods. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8647.	1.8	1
30051	Comparative genomics provides insights into the potential biocontrol mechanism of two <i>Lysobacter</i> enzymogenes strains with distinct antagonistic activities. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
30052	Compendium of proteins containing segments that exhibit <scp>zeroâ€tolerance</scp> to amino acid variation in humans. <i>Protein Science</i> , 2022, 31, .	3.1	0
30053	Conceptual framework for the insect metamorphosis from larvae to pupae by transcriptomic profiling, a case study of <i>Helicoverpa armigera</i> (Lepidoptera: Noctuidae). <i>BMC Genomics</i> , 2022, 23, .	1.2	1
30054	Data Incompleteness May form a Hard-to-Overcome Barrier to Decoding Lifeâ€™s Mechanism. <i>Biology</i> , 2022, 11, 1208.	1.3	4
30055	Disturbance of Key Cellular Subproteomes upon Propofol Treatment Is Associated with Increased Permeability of the Blood-Brain Barrier. <i>Proteomes</i> , 2022, 10, 28.	1.7	1
30056	SOX transcription factors direct TCF-independent WNT/ β -catenin responsive transcription to govern cell fate in human pluripotent stem cells. <i>Cell Reports</i> , 2022, 40, 111247.	2.9	21
30057	Effect of a Stannous Fluoride Dentifrice on Biofilm Composition, Gene Expression and Biomechanical Properties. <i>Microorganisms</i> , 2022, 10, 1691.	1.6	6
30058	Comparative Genomics of Mortierellaceae Provides Insights into Lipid Metabolism: Two Novel Types of Fatty Acid Synthase. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 891.	1.5	4
30060	Characterizing isoform switching events in esophageal adenocarcinoma. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 29, 749-768.	2.3	5
30062	Integrated co-expression network analysis uncovers novel tissue-specific genes in major depressive disorder and bipolar disorder. <i>Frontiers in Psychiatry</i> , 0, 13, .	1.3	3
30064	Quantitative proteomic analytic approaches to identify metabolic changes in the medial prefrontal cortex of rats exposed to space radiation. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	3
30065	Temporally divergent regulatory mechanisms govern neuronal diversification and maturation in the mouse and marmoset neocortex. <i>Nature Neuroscience</i> , 2022, 25, 1049-1058.	7.1	16
30066	Genome-Wide Characterization Reveals Variation Potentially Involved in Pathogenicity and Mycotoxins Biosynthesis of <i>Fusarium proliferatum</i> Causing Spikelet Rot Disease in Rice. <i>Toxins</i> , 2022, 14, 568.	1.5	4
30067	High expression of cuproptosis-related SLC31A1 gene in relation to unfavorable outcome and deregulated immune cell infiltration in breast cancer: an analysis based on public databases. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	26
30068	What is a supercoiling-sensitive gene? Insights from topoisomerase I inhibition in the Gram-negative bacterium <i>Dickeya dadantii</i> . <i>Nucleic Acids Research</i> , 2022, 50, 9149-9161.	6.5	4

#	ARTICLE	IF	CITATIONS
30070	Identification of the genetic locus associated with the crinkled leaf phenotype in a soybean (<i>Glycine</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.7	9
30071	Comparative Genomics Insights into a Novel Biocontrol Agent <i>Paenibacillus peoriae</i> Strain ZF390 against Bacterial Soft Rot. <i>Biology</i> , 2022, 11, 1172.	1.3	2
30072	Comparative transcriptome and adaptive evolution analysis on the main liver and attaching liver of <i>Pareuchiloglanis macrotrema</i> . <i>Journal of Applied Genetics</i> , 0, , .	1.0	0
30073	Simultaneous testing of rule- and model-based approaches for runs of homozygosity detection opens up a window into genomic footprints of selection in pigs. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
30074	The chromosome-level holly (<i>Ilex latifolia</i>) genome reveals key enzymes in triterpenoid saponin biosynthesis and fruit color change. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
30075	Molecular Identification of Spatially Distinct Anabolic Responses to Mechanical Loading in Murine Cortical Bone. <i>Journal of Bone and Mineral Research</i> , 2020, 37, 2277-2287.	3.1	4
30076	Motor neuron-derived induced pluripotent stem cells as a drug screening platform for amyotrophic lateral sclerosis. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	1
30077	Embryo model completes gastrulation to neurulation and organogenesis. <i>Nature</i> , 2022, 610, 143-153.	13.7	112
30078	Systematic Review and Meta-analysis of Peripheral Blood DNA Methylation Studies in Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2023, 17, 185-198.	0.6	13
30079	Alteration of DNA supercoiling serves as a trigger of short-term cold shock repressed genes of <i>E. coli</i> . <i>Nucleic Acids Research</i> , 2022, 50, 8512-8528.	6.5	3
30080	Forecasting climate change response in an alpine specialist songbird reveals the importance of considering novel climate. <i>Diversity and Distributions</i> , 2022, 28, 2239-2254.	1.9	4
30081	Does Childhood Obesity Trigger Neuroinflammation?. <i>Biomedicines</i> , 2022, 10, 1953.	1.4	6
30082	Full-length transcriptome analysis of maize root tips reveals the molecular mechanism of cold stress during the seedling stage. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	7
30083	Proinflammatory changes in the maternal circulation, maternal fetal interface, and placental transcriptome in preterm birth. <i>American Journal of Obstetrics and Gynecology</i> , 2023, 228, 332.e1-332.e17.	0.7	10
30085	Fine-mapping and association analysis of candidate genes for papilla number in sea cucumber, <i>Apostichopus japonicus</i> . <i>Marine Life Science and Technology</i> , 2022, 4, 343-355.	1.8	2
30086	Transcriptomic heterogeneity of cultured ADSCs corresponds to embolic risk in the host. <i>IScience</i> , 2022, 25, 104822.	1.9	4
30087	Support vector machine based disease classification model employing hasten eagle Cuculidae search optimization. <i>Concurrency Computation Practice and Experience</i> , 2022, 34, .	1.4	2
30088	Transcriptome profiling in psoriasis: NB-UVB treatment-associated transcriptional changes and modulation of autoinflammation in perilesional skin in early-phase disease. <i>Journal of Dermatological Science</i> , 2022, 107, 123-132.	1.0	8

#	ARTICLE	IF	CITATIONS
30090	Integrative analyses of mRNA and microRNA expression profiles reveal the innate immune mechanism for the resistance to <i>Vibrio parahaemolyticus</i> infection in <i>Epinephelus coioides</i> . <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
30091	Genome-Wide Analysis of the NAC Family Associated with Two Paleohexaploidization Events in the Tomato. <i>Life</i> , 2022, 12, 1236.	1.1	2
30093	A general kernel boosting framework integrating pathways for predictive modeling based on genomic data. , 2022, , .		0
30094	Functional Pathway and Process Enrichment Analysis of Genes Associated With Morphological Abnormalities of the Outer Ear. <i>Journal of Craniofacial Surgery</i> , 0, Publish Ahead of Print, .	0.3	1
30095	Identification of long non-coding RNAs and microRNAs involved in anther development in the tropical <i>Camellia oleifera</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	2
30096	Transcriptome and Metabolome Analyses Revealed the Response Mechanism of Sugar Beet to Salt Stress of Different Durations. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9599.	1.8	8
30099	POPEYE intercellular localization mediates cell-specific iron deficiency responses. <i>Plant Physiology</i> , 2022, 190, 2017-2032.	2.3	4
30101	EMT-Related Gene Signature Predicts the Prognosis in Uveal Melanoma Patients. <i>Journal of Oncology</i> , 2022, 2022, 1-19.	0.6	5
30102	Protein diffusion in <i>Escherichia coli</i> cytoplasm scales with the mass of the complexes and is location dependent. <i>Science Advances</i> , 2022, 8, .	4.7	22
30103	GREAP: a comprehensive enrichment analysis software for human genomic regions. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
30104	Comprehensive analysis of karyopherin alpha family expression in lung adenocarcinoma: Association with prognostic value and immune homeostasis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
30105	Arc Regulates Transcription of Genes for Plasticity, Excitability and Alzheimer's Disease. <i>Biomedicines</i> , 2022, 10, 1946.	1.4	14
30106	Genomic-Analysis-Oriented Drug Repurposing in the Search for Novel Antidepressants. <i>Biomedicines</i> , 2022, 10, 1947.	1.4	6
30107	Transcriptional activation of auxin biosynthesis drives developmental reprogramming of differentiated cells. <i>Plant Cell</i> , 2022, 34, 4348-4365.	3.1	25
30109	Primary cilia and SHH signaling impairments in human and mouse models of Parkinson's disease. <i>Nature Communications</i> , 2022, 13, .	5.8	16
30110	Metacells untangle large and complex single-cell transcriptome networks. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	14
30111	Microarray Analysis Workflow Based on a Genetic Algorithm to Discover Potential Hub Genes. <i>Current Bioinformatics</i> , 2022, 17, 787-792.	0.7	1
30112	Assessment and Optimization of Explainable Machine Learning Models Applied to Transcriptomic Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 899-911.	3.0	7

#	ARTICLE	IF	CITATIONS
30113	Suppression of FOXP3 expression by the AP-1 family transcription factor BATF3 requires partnering with IRF4. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	7
30115	Restructured membrane contacts rewire organelles for human cytomegalovirus infection. <i>Nature Communications</i> , 2022, 13, .	5.8	16
30116	Network pharmacology and molecular docking technology-based predictive study of the active ingredients and potential targets of rhubarb for the treatment of diabetic nephropathy. <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, .	1.2	13
30117	Investigating calcification-related candidates in a non-symbiotic scleractinian coral, <i>Tubastraea</i> spp.. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
30119	Network pharmacology reveals multitarget mechanism of action of drugs to be repurposed for COVID-19. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	8
30120	Identification of missing hierarchical relations in the vaccine ontology using acquired term pairs. <i>Journal of Biomedical Semantics</i> , 2022, 13, .	0.9	1
30121	Ribosomes: The New Role of Ribosomal Proteins as Natural Antimicrobials. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9123.	1.8	17
30124	The VINE complex is an endosomal VPS9-domain GEF and SNX-BAR coat. <i>ELife</i> , 0, 11, .	2.8	1
30125	COYOTE: Sequence Derived Structural Descriptors Based Computational Identification of Glycoproteins. <i>Journal of Bioinformatics and Computational Biology</i> , 0, , .	0.3	0
30126	Energetics, but not development, is impacted in coral embryos exposed to ocean acidification. <i>Journal of Experimental Biology</i> , 2022, 225, .	0.8	1
30129	TALE-cmap: Protein function prediction based on a TALE-based architecture and the structure information from contact map. <i>Computers in Biology and Medicine</i> , 2022, 149, 105938.	3.9	2
30130	Multivariate phenotype analysis enables genome-wide inference of mammalian gene function. <i>PLoS Biology</i> , 2022, 20, e3001723.	2.6	1
30131	Linkage Disequilibrium, Haplotype Block Structures, Effective Population Size and Genome-Wide Signatures of Selection of Two Conservation Herds of the South African Nguni Cattle. <i>Animals</i> , 2022, 12, 2133.	1.0	4
30133	Early Deregulation Of Cholangiocyte NR0B2 During Primary Sclerosing Cholangitis. , 2022, , .		1
30134	Distinct, opposing functions for CFlm59 and CFlm68 in mRNA alternative polyadenylation of <i>Pten</i> and in the PI3K/Akt signalling cascade. <i>Nucleic Acids Research</i> , 2022, 50, 9397-9412.	6.5	3
30135	hCoCena: horizontal integration and analysis of transcriptomics datasets. <i>Bioinformatics</i> , 2022, 38, 4727-4734.	1.8	4
30136	Integrative Analyses of Biomarkers Associated with Endoplasmic Reticulum Stress in Ischemic Stroke. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-21.	0.7	1
30139	Risk Stratification for Breast Cancer Patient by Simultaneous Learning of Molecular Subtype and Survival Outcome Using Genetic Algorithm-Based Gene Set Selection. <i>Cancers</i> , 2022, 14, 4120.	1.7	0

#	ARTICLE	IF	CITATIONS
30140	Biomarkers of Inflammation Increase with Tau and Neurodegeneration but not with Amyloid- β^2 in a Heterogenous Clinical Cohort. <i>Journal of Alzheimer's Disease</i> , 2022, 89, 1303-1314.	1.2	2
30141	Sulfur and methane oxidation by a single microorganism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	19
30142	Comparative Transcriptome Profiling Reveals Potential Candidate Genes, Transcription Factors, and Biosynthetic Pathways for Phosphite Response in Potato (<i>Solanum tuberosum</i> L.). <i>Genes</i> , 2022, 13, 1379.	1.0	1
30143	mvPPT: A Highly Efficient and Sensitive Pathogenicity Prediction Tool for Missense Variants. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 414-426.	3.0	2
30144	Dissecting Molecular Heterogeneity of Circulating Tumor Cells (CTCs) from Metastatic Breast Cancer Patients through Copy Number Aberration (CNA) and Single Nucleotide Variant (SNV) Single Cell Analysis. <i>Cancers</i> , 2022, 14, 3925.	1.7	5
30145	A revised multi-tissue, multi-platform epigenetic clock model for methylation array data. <i>Journal of Mathematical Chemistry</i> , 0, , .	0.7	0
30146	Functional networks of the human bromodomain-containing proteins. <i>Frontiers in Bioinformatics</i> , 0, 2, .	1.0	0
30148	A regulatory network of Sox and Six transcription factors initiate a cell fate transformation during hearing regeneration in adult zebrafish. <i>Cell Genomics</i> , 2022, 2, 100170.	3.0	13
30149	Defect in BrMS1, a PHD-finger transcription factor, induces male sterility in ethyl methane sulfonate-mutagenized Chinese cabbage (<i>Brassica rapa</i> L. ssp. <i>pekinensis</i>). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
30150	Improved genome assembly provides new insights into the environmental adaptation of the American cockroach, <i>Periplaneta americana</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2022, 111, .	0.6	3
30151	The impact of PrsA over-expression on the <i>Bacillus subtilis</i> transcriptome during fed-batch fermentation of alpha-amylase production. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	6
30152	Cyclin-Dependent Kinase Subunit 2 (CKS2) as a Prognostic Marker for Stages III Invasive Non-Mucinous Lung Adenocarcinoma and Its Role in Affecting Drug Sensitivity. <i>Cells</i> , 2022, 11, 2611.	1.8	1
30153	The human blood transcriptome exhibits time-of-day-dependent response to hypoxia: Lessons from the highest city in the world. <i>Cell Reports</i> , 2022, 40, 111213.	2.9	8
30154	Altered gene expression profiles impair the nervous system development in individuals with 15q13.3 microdeletion. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
30155	Comparative Transcriptome Analysis Reveals Genes Associated with the Gossypol Synthesis and Gland Morphogenesis in <i>Gossypium hirsutum</i> . <i>Genes</i> , 2022, 13, 1452.	1.0	0
30156	Predicting recurrence and metastasis risk of endometrial carcinoma via prognostic signatures identified from multi-omics data. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
30157	Brain-specific genes contribute to chronic but not to acute back pain. <i>Pain Reports</i> , 2022, 7, e1018.	1.4	14
30159	Transcriptome profiling of somatic embryogenesis in wheat (<i>Triticum aestivum</i> L.) influenced by auxin, calcium and brassinosteroid. <i>Plant Growth Regulation</i> , 2022, 98, 599-612.	1.8	3

#	ARTICLE	IF	CITATIONS
30160	Lycorine inhibits angiogenesis by docking to PDGFR β . <i>BMC Cancer</i> , 2022, 22, .	1.1	3
30161	De novo transcriptome revealed genes involved in anthocyanin biosynthesis, transport, and regulation in a mutant of <i>Acer pseudosieboldianum</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	2
30162	The chromatin remodeling protein ATRX positively regulates IRF3-dependent type I interferon production and interferon-induced gene expression. <i>PLoS Pathogens</i> , 2022, 18, e1010748.	2.1	4
30165	Schizophrenia Polygenic Risk During Typical Development Reflects Multiscale Cortical Organization. <i>Biological Psychiatry Global Open Science</i> , 2023, 3, 1083-1093.	1.0	4
30166	Development and validation of a prognostic gene expression signature for lower-grade glioma following surgery and adjuvant radiotherapy. <i>Radiotherapy and Oncology</i> , 2022, , .	0.3	0
30167	A microRNA α microRNA crosstalk network inferred from genome-wide single nucleotide polymorphism variants in natural populations of <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
30168	Epigenetic and integrative cross-omics analyses of cerebral white matter hyperintensities on MRI. <i>Brain</i> , 2023, 146, 492-506.	3.7	12
30169	Enhancing Protein Function Prediction Performance by Utilizing AlphaFold-Predicted Protein Structures. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 4008-4017.	2.5	14
30170	miR-150 promotes progressive T cell differentiation via inhibiting FOXP1 and RC3H1. <i>Human Immunology</i> , 2022, 83, 778-788.	1.2	3
30171	Subtype and cell type specific expression of lncRNAs provide insight into breast cancer. <i>Communications Biology</i> , 2022, 5, .	2.0	10
30173	The nearly complete assembly of the <i>Cercis chinensis</i> genome and Fabaceae phylogenomic studies provide insights into new gene evolution. <i>Plant Communications</i> , 2023, 4, 100422.	3.6	4
30174	Chromosome silencing in vitro reveals trisomy 21 causes cell-autonomous deficits in angiogenesis and early dysregulation in Notch signaling. <i>Cell Reports</i> , 2022, 40, 111174.	2.9	5
30175	Identification of growth regulators using cross-species network analysis in plants. <i>Plant Physiology</i> , 2022, 190, 2350-2365.	2.3	8
30176	Decoding regulatory associations of G-quadruplex with epigenetic and transcriptomic functional components. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
30177	Characterization of interactions of dietary cholesterol with the murine and human gut microbiome. <i>Nature Microbiology</i> , 2022, 7, 1390-1403.	5.9	41
30178	Cuproptosis-related gene index: A predictor for pancreatic cancer prognosis, immunotherapy efficacy, and chemosensitivity. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	24
30179	Concentration-response gene expression analysis in zebrafish reveals phenotypically-anchored transcriptional responses to retene. <i>Frontiers in Toxicology</i> , 0, 4, .	1.6	3
30180	Shining light on the transcriptome: Molecular regulatory networks leading to a fast-growth phenotype by continuous light in an environmentally sensitive teleost (<i>Atherinopsidae</i>). <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2022, 235, 112550.	1.7	2

#	ARTICLE	IF	CITATIONS
30181	Isoform function prediction by Gene Ontology embedding. <i>Bioinformatics</i> , 2022, 38, 4581-4588.	1.8	5
30182	Effects of Exogenous Potassium (K ⁺) Application on the Antioxidant Enzymes Activities in Leaves of <i>Tamarix ramosissima</i> under NaCl Stress. <i>Genes</i> , 2022, 13, 1507.	1.0	3
30183	DNA and RNA Binding Proteins: From Motifs to Roles in Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9329.	1.8	0
30184	Transcriptomic Analyses of Grapevine Leafroll-Associated Virus 3 Infection in Leaves and Berries of Cabernet Franc™. <i>Viruses</i> , 2022, 14, 1831.	1.5	5
30185	Effects of Natural Rheum tanguticum on the Cell Wall Integrity of Resistant Phytopathogenic <i>Pectobacterium carotovorum</i> subsp. <i>Carotovorum</i> . <i>Molecules</i> , 2022, 27, 5291.	1.7	1
30186	Transcriptome-Based Identification, Characterization, Evolutionary Analysis, and Expression Pattern Analysis of the WRKY Gene Family and Salt Stress Response in <i>Panax ginseng</i> . <i>Horticulturae</i> , 2022, 8, 756.	1.2	3
30187	Identification of sex-biased and neurodevelopment genes via brain transcriptome in <i>Ostrinia furnacalis</i> . <i>Frontiers in Physiology</i> , 0, 13, .	1.3	0
30188	Glia Maturation Factor-1 ² Supports Liver Regeneration by Remodeling Actin Network to Enhance STAT3 Proliferative Signals. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, , .	2.3	1
30189	Exploring the medicinally important secondary metabolites landscape through the lens of transcriptome data in fenugreek (<i>Trigonella foenum graecum</i> L.). <i>Scientific Reports</i> , 2022, 12, .	1.6	9
30190	Transcriptome and Metabolome Analyses of Salt Stress Response in Cotton (<i>Gossypium hirsutum</i>) Seed Pretreated with NaCl. <i>Agronomy</i> , 2022, 12, 1849.	1.3	2
30191	Integrated analysis of lncRNA-associated ceRNA network in p16-positive and p16-negative head and neck squamous cell carcinoma. <i>Medicine (United States)</i> , 2022, 101, e26120.	0.4	1
30192	Comprehensive genome sequence analysis of the devastating tobacco bacterial phytopathogen <i>Ralstonia solanacearum</i> strain FJ1003. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
30193	Spatial Proteomics Reveals Differences in the Cellular Architecture of Antibody-Producing CHO and Plasma Cell-Derived Cells. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100278.	2.5	1
30194	Fc Fragment of IgE Receptor Ig (FCER1G) acts as a key gene involved in cancer immune infiltration and tumour microenvironment. <i>Immunology</i> , 2023, 168, 302-319.	2.0	7
30195	Genomic and transcriptomic profiling of phoenix colonies. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
30196	Comparative transcriptomic analysis of <i>Rosa sterilis</i> inflorescence branches with different trichome types reveals an R3-MYB transcription factor that negatively regulates trichome formation. <i>Journal of Integrative Agriculture</i> , 2022, 21, 2926-2942.	1.7	2
30198	Identification and whole-genome sequencing analysis of <i>Vibrio vulnificus</i> strains causing pearl gentian grouper disease in China. <i>BMC Microbiology</i> , 2022, 22, .	1.3	4
30199	An Association Study of DNA Methylation and Gene Expression in Angelman Syndrome: A Bioinformatics Approach. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9139.	1.8	0

#	ARTICLE	IF	CITATIONS
30200	Neurotrophin Pathway Receptors NGFR and TrkA Control Perineural Invasion, Metastasis, and Pain in Oral Cancer. <i>Advanced Biology</i> , 2022, 6, .	1.4	5
30202	Transcriptomic data exploration of consensus genes and molecular mechanisms between chronic obstructive pulmonary disease and lung adenocarcinoma. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
30203	Endophytic bacterium <i>Bacillus aryabhattai</i> induces novel transcriptomic changes to stimulate plant growth. <i>PLoS ONE</i> , 2022, 17, e0272500.	1.1	10
30204	Transcriptomic analysis of <i>Sitophilus zeamais</i> in response to limonene fumigation. <i>Pest Management Science</i> , 2022, 78, 4774-4782.	1.7	9
30205	Development of dim-light vision in the nocturnal reef fish family Holocentridae. I: Retinal gene expression. <i>Journal of Experimental Biology</i> , 2022, 225, .	0.8	7
30206	Functional Compensation of Mouse Duplicates by their Paralogs Expressed in the Same Tissues. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	2
30208	Comprehensive analyses of transcriptomes induced by Lyme spirochete infection to CNS model system. <i>Infection, Genetics and Evolution</i> , 2022, 103, 105349.	1.0	0
30209	MicroRNA expression profiles in the granulosa cells of infertile patients undergoing progestin primed ovarian stimulation. <i>European Journal of Obstetrics, Gynecology and Reproductive Biology</i> , 2022, 276, 228-235.	0.5	1
30210	Integrative analysis of spatial transcriptome with single-cell transcriptome and single-cell epigenome in mouse lungs after immunization. <i>IScience</i> , 2022, 25, 104900.	1.9	6
30211	$\langle \text{mml:math xmlns:mml}=\text{"http://www.w3.org/1998/Math/MathML"} \text{ altimg}=\text{"si35.svg"} \rangle \langle \text{mml:mrow} \rangle \langle \text{mml:mi} \rangle \text{b} \langle \text{mml:mi} \rangle \langle \text{mml:mrow} \rangle \langle \text{mml:math} \rangle$ -Scaled-attention: A novel fast attention mechanism for efficient modeling of protein sequences. <i>Information Sciences</i> , 2022, 609, 1098-1112.	4.0	0
30212	lbtLD modulates reactive oxygen species scavenging and DNA protection to confer salinity stress tolerance in tobacco. <i>Plant Science</i> , 2022, 323, 111415.	1.7	5
30213	Prediction of protein mononucleotide binding sites using AlphaFold2 and machine learning. <i>Computational Biology and Chemistry</i> , 2022, 100, 107744.	1.1	3
30214	Adaptive radiation in <i>Orinus</i> , an endemic alpine grass of the Qinghai-Tibet Plateau, based on comparative transcriptomic analysis. <i>Journal of Plant Physiology</i> , 2022, 277, 153786.	1.6	1
30215	Identification of molecular initiating events and key events leading to endocrine disrupting effects of PFOA: Integrated molecular dynamic, transcriptomic, and proteomic analyses. <i>Chemosphere</i> , 2022, 307, 135881.	4.2	2
30218	Comparative genomic analysis of the genus <i>Marinomonas</i> and taxonomic study of <i>Marinomonas algarum</i> sp. nov., isolated from red algae <i>Gelidium amansii</i> . <i>Archives of Microbiology</i> , 2022, 204, .	1.0	4
30219	Decoding competitive endogenous RNA regulatory network in postoperative cognitive dysfunction. <i>Frontiers in Neuroscience</i> , 0, 16, .	1.4	6
30221	c-MAF coordinates enterocyte zonation and nutrient uptake transcriptional programs. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	12
30222	Full-Length Transcriptome Maps of Reef-Building Coral Illuminate the Molecular Basis of Calcification, Symbiosis, and Circadian Genes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11135.	1.8	0

#	ARTICLE	IF	CITATIONS
30223	Translation Comes First: Ancient and Convergent Selection of Codon Usage Bias Across Prokaryotic Genomes. <i>Journal of Molecular Evolution</i> , 0, , .	0.8	0
30226	Single-molecule Real-time (SMRT) Sequencing Facilitates Transcriptome Research and Genome Annotation of the Fish <i>Sillago sinica</i> . <i>Marine Biotechnology</i> , 2022, 24, 1002-1013.	1.1	1
30228	Non-apoptotic activity of the mitochondrial protein SMAC/Diablo in lung cancer: Novel target to disrupt survival, inflammation, and immunosuppression. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
30229	Dynamic miRNA profile of host T cells during early hepatic stages of <i>Schistosoma japonicum</i> infection. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
30230	Influence of <i>Bacillus subtilis</i> strain Z-14 on microbial communities of wheat rhizospheric soil infested with <i>Gaeumannomyces graminis</i> var. <i>tritici</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
30231	Comprehensive analysis of key genes and pathways for biological and clinical implications in thyroid-associated ophthalmopathy. <i>BMC Genomics</i> , 2022, 23, .	1.2	6
30233	Extracellular vesicles derived from <i>Trichinella Spiralis</i> larvae promote the polarization of macrophages to M2b type and inhibit the activation of fibroblasts. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
30234	Candidate chemosensory receptors in the antennae and maxillae of <i>Spodoptera frugiperda</i> (J. E. Smith) larvae. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	3
30235	Time and age dependent regulation of neuroinflammation in a rat model of mesial temporal lobe epilepsy: Correlation with human data. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	2
30236	GJA1/CX43 High Expression Levels in the Cervical Spinal Cord of ALS Patients Correlate to Microglia-Mediated Neuroinflammatory Profile. <i>Biomedicines</i> , 2022, 10, 2246.	1.4	3
30237	Molecular mechanism of <i>Ginkgo biloba</i> in treating type 2 diabetes mellitus combined with non-alcoholic fatty liver disease based on network pharmacology, molecular docking, and experimental evaluations. <i>Journal of Food Biochemistry</i> , 2022, 46, .	1.2	3
30238	Quantitative phosphoproteome analysis of <i>Streptomyces coelicolor</i> by immobilized zirconium (IV) affinity chromatography and mass spectrometry reveals novel regulated protein phosphorylation sites and sequence motifs. <i>Journal of Proteomics</i> , 2022, 269, 104719.	1.2	1
30239	Human alpha cell transcriptomic signatures of types 1 and 2 diabetes highlight disease-specific dysfunction pathways. <i>IScience</i> , 2022, 25, 105056.	1.9	11
30240	Applied ontology for phenomenological psychopathology? A cautionary tale – Authors' reply. <i>Lancet Psychiatry</i> , 2022, 9, 766.	3.7	1
30241	LONP1 downregulation with ageing contributes to osteoarthritis via mitochondrial dysfunction. <i>Free Radical Biology and Medicine</i> , 2022, 191, 176-190.	1.3	8
30242	Systematic elucidation of the pharmacological mechanisms of <i>Hedysarum Multijugum Maxim</i> for treating rhinitis via network. <i>Phytomedicine Plus</i> , 2022, 2, 100341.	0.9	0
30243	Comprehensive identification and expression profiling of immune-related lncRNAs and their target genes in the intestine of turbot (<i>Scophthalmus maximus</i> L.) in response to <i>Vibrio anguillarum</i> infection. <i>Fish and Shellfish Immunology</i> , 2022, 130, 233-243.	1.6	3
30244	<i>Fructus ligustri lucidi</i> suppresses inflammation and restores the microbiome profile in murine colitis models. <i>Phytomedicine</i> , 2022, 106, 154438.	2.3	3

#	ARTICLE	IF	CITATIONS
30245	Proteomic analysis of Morus leaf epidermis indicates the roles of photosystems and ROS in UV-B response. <i>Industrial Crops and Products</i> , 2022, 188, 115683.	2.5	0
30246	A β -glucan from <i>Aureobasidium pullulans</i> enhanced the antitumor effect with rituximab against SU-DHL-8. <i>International Journal of Biological Macromolecules</i> , 2022, 220, 1356-1367.	3.6	0
30247	Butanol production from Thai traditional beverage (Sato) factory wastewater using newly isolated <i>Clostridium beijerinckii</i> CUEA02. <i>Biochemical Engineering Journal</i> , 2022, 187, 108648.	1.8	1
30248	KIF17 maintains the epithelial phenotype of breast cancer cells and curbs tumour metastasis. <i>Cancer Letters</i> , 2022, 548, 215904.	3.2	1
30249	Semi-supervised nonparametric Bayesian modelling of spatial proteomics. <i>Annals of Applied Statistics</i> , 2022, 16, .	0.5	3
30250	Deciphering the role of predicted miRNAs of polyomaviruses in carcinogenesis. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2022, 1868, 166537.	1.8	0
30251	Whole-genome sequence data of cellulase-producing fungi <i>Trichoderma asperellum</i> PK1J2, isolated from palm empty fruit bunch in Riau, Indonesia. <i>Data in Brief</i> , 2022, 45, 108607.	0.5	1
30252	Genomic variants-driven drug repurposing for tuberculosis by utilizing the established bioinformatic-based approach. <i>Biochemistry and Biophysics Reports</i> , 2022, 32, 101334.	0.7	3
30253	Microbiome structure in biofilms from a volcanic island in Maritime Antarctica investigated by genome-centric metagenomics and metatranscriptomics. <i>Microbiological Research</i> , 2022, 265, 127197.	2.5	3
30254	The first transcriptome dataset of roselle (<i>Hibiscus sabdariffa</i> L.) calyces during maturation. <i>Data in Brief</i> , 2022, 45, 108613.	0.5	0
30255	Co-existence of flocs and granules in aerobic granular sludge system: Performance, microbial community and proteomics. <i>Chemical Engineering Journal</i> , 2023, 451, 139011.	6.6	13
30256	Novel split quality measures for stratified multilabel cross validation with application to large and sparse gene ontology datasets. , 2022, 2, 49-62.		0
30257	Integrated Bioinformatics Analysis to Identify the Potential Molecular Biomarkers for Neuropathic Pain Among Patient of Lumbar Disc Prolapse and COVID-19. <i>Lecture Notes in Networks and Systems</i> , 2022, , 789-805.	0.5	0
30258	A Novel Synthetic Lethality Prediction Method Based on Bidirectional Attention Learning. <i>Lecture Notes in Computer Science</i> , 2022, , 356-363.	1.0	0
30259	Integrating multimodal data through interpretable heterogeneous ensembles. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	5
30260	The field of protein function prediction as viewed by different domain scientists. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	4
30261	Mesenchymal stromal cell-derived extracellular vesicles afford neuroprotection by modulating PI3K/AKT pathway and calcium oscillations. <i>International Journal of Biological Sciences</i> , 2022, 18, 5345-5368.	2.6	24
30262	Physiology and Molecular Basis of Thallium Toxicity and Accumulation in <i>Arabidopsis Thaliana</i> . <i>SSRN Electronic Journal</i> , 0, , .	0.4	2

#	ARTICLE	IF	CITATIONS
30263	Bioinformatic analyses of hydroxylated polybrominated diphenyl ethers toxicities on impairment of adrenocortical secretory function. <i>Environmental Health and Preventive Medicine</i> , 2022, 27, 38-38.	1.4	2
30264	Metagenomic Approaches for the Discovery of Pollutant-Remediating Enzymes: Recent Trends and Challenges. , 2022, , 571-604.		0
30265	Draft Genomes Sequences of 11 <i>Geodermatophilaceae</i> Strains Isolated from Building Stones from New England and Indian Stone Ruins found at historic sites in Tamil Nadu, India. <i>Journal of Genomics</i> , 2022, 10, 69-77.	0.6	1
30266	ChemBioPort: an online portal to navigate the structure, function and chemical inhibition of the human proteome. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	2
30267	A roadmap for the functional annotation of protein families: a community perspective. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	14
30268	Identification of differentially expressed genes and their major pathways among the patient with COVID-19, cystic fibrosis, and chronic kidney disease. <i>Informatics in Medicine Unlocked</i> , 2022, 32, 101038.	1.9	4
30269	Bayesian Learning of Graph Substructures. <i>Bayesian Analysis</i> , 2023, 18, .	1.6	2
30270	The potential of a data centred approach & knowledge graph data representation in chemical safety and drug design. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4837-4849.	1.9	3
30271	Horizontal Integration: Disease “ Cancer Systems Biology. , 2022, , .		0
30272	Cryobiomics in tropical and subtropical horticultural crops. , 2022, , 91-118.		0
30273	Venom composition of <i>Trimeresurus albolabris</i> , <i>T. insularis</i> , <i>T. puniceus</i> and <i>T. purpureomaculatus</i> from Indonesia. <i>Journal of Venomous Animals and Toxins Including Tropical Diseases</i> , 0, 28, .	0.8	5
30274	Identification of candidate sex-specific genomic regions in male and female Asian arowana genomes. <i>GigaScience</i> , 2022, 11, .	3.3	0
30275	Prediction and validation of host-pathogen interactions by a versatile inference approach using <i>Aspergillus fumigatus</i> as a case study. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4225-4237.	1.9	1
30276	WGRLR: A Weighted Group Regularized Logistic Regression for Cancer Diagnosis and Gene Selection. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1563-1573.	1.9	6
30277	Comparative proteomic changes in rabbit vocal folds undergoing systemic dehydration and systemic rehydration. <i>Journal of Proteomics</i> , 2023, 270, 104734.	1.2	2
30278	Improving diagnosis accuracy of non-small cell lung carcinoma on noisy data by adaptive group lasso regularized multinomial regression. <i>Biomedical Signal Processing and Control</i> , 2023, 79, 104148.	3.5	2
30279	Endocytosis of the thrombopoietin receptor Mpl regulates megakaryocyte and erythroid maturation in mice. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
30280	Identification of Novel Genes Associated with Partial Resistance to <i>Aphanomyces</i> Root Rot in Field Pea by BSR-Seq Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9744.	1.8	5

#	ARTICLE	IF	CITATIONS
30281	Environment-specificity and universality of the microbial growth law. <i>Communications Biology</i> , 2022, 5, .	2.0	0
30282	WhichTF is functionally important in your open chromatin data?. <i>PLoS Computational Biology</i> , 2022, 18, e1010378.	1.5	33
30283	Optical imaging and spectroscopy for the study of the human brain: status report. <i>Neurophotonics</i> , 2022, 9, .	1.7	45
30284	Determination of a prediction model for therapeutic response and prognosis based on chemokine signaling-related genes in stage III lung squamous cell carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
30285	Gene Expression Landscape of Chronic Myeloid Leukemia K562 Cells Overexpressing the Tumor Suppressor Gene PTPRG. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9899.	1.8	4
30288	Decreased Levels of DNA Methylation in the <i>PCDHA</i> Gene Cluster as a Risk Factor for Early-Onset High Myopia in Young Children. , 2022, 63, 31.		3
30289	Therapeutic Effects of Retinoic Acid in Lipopolysaccharide-Induced Cardiac Dysfunction: Network Pharmacology and Experimental Validation. <i>Journal of Inflammation Research</i> , 0, Volume 15, 4963-4979.	1.6	2
30290	Critical Analysis of Multi-Omic Data from a Strain of <i>Plutella xylostella</i> Resistant to <i>Bacillus thuringiensis</i> Cry1Ac Toxin. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 11419-11428.	2.4	2
30291	Downregulation of S100A9 Reverses Cisplatin-Resistance and Inhibits Proliferation and Migration in Hypopharyngeal Carcinoma. <i>Journal of Oncology</i> , 2022, 2022, 1-12.	0.6	1
30293	Biological control and plant growth promotion properties of <i>Streptomyces albidoflavus</i> St-220 isolated from <i>Salvia miltiorrhiza</i> rhizosphere. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	15
30294	De Novo Prediction of Drug Targets and Candidates by Chemical Similarity-Guided Network-Based Inference. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9666.	1.8	2
30295	Effect of Water Activity on Conidia Germination in <i>Aspergillus flavus</i> . <i>Microorganisms</i> , 2022, 10, 1744.	1.6	0
30296	Transcriptome analysis reveals critical factors for survival after adenovirus serotype 4 infection. <i>Poultry Science</i> , 2023, 102, 102150.	1.5	1
30298	Blue Brain Nexus: An open, secure, scalable system for knowledge graph management and data-driven science. <i>Semantic Web</i> , 2023, 14, 697-727.	1.1	2
30299	The RNA helicase DDX5 cooperates with EHMT2 to sustain alveolar rhabdomyosarcoma growth. <i>Cell Reports</i> , 2022, 40, 111267.	2.9	3
30300	Genome-wide analysis of Chinese keloid patients identifies novel causative genes. <i>Annals of Translational Medicine</i> , 2022, 10, 883-883.	0.7	3
30301	AIMP1 promotes multiple myeloma malignancy through interacting with ANP32A to mediate histone H3 acetylation. <i>Cancer Communications</i> , 2022, 42, 1185-1206.	3.7	3
30302	Dynamic changes in the transcriptome landscape of <i>Arabidopsis thaliana</i> in response to cold stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2

#	ARTICLE	IF	CITATIONS
30303	Primitive genotypic characteristics in umbilical cord neutrophils identified by single-cell transcriptome profiling and functional prediction. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
30304	Cellular transcriptional alterations of peripheral blood in Alzheimer's disease. <i>BMC Medicine</i> , 2022, 20, .	2.3	15
30305	Development of multivariable risk signature based on four immune-related RNA-binding proteins to predict survival and immune status in lung adenocarcinoma. <i>Translational Cancer Research</i> , 2022, 11, 2591-2606.	0.4	1
30306	Rational Approach to Finding Genes Encoding Molecular Biomarkers: Focus on Breast Cancer. <i>Genes</i> , 2022, 13, 1538.	1.0	0
30307	Lactic acid from vaginal microbiota enhances cervicovaginal epithelial barrier integrity by promoting tight junction protein expression. <i>Microbiome</i> , 2022, 10, .	4.9	25
30308	Steroidogenic factor 1 (NR5A1) induces multiple transcriptional changes during differentiation of human gonadal-like cells. <i>Differentiation</i> , 2022, . .	1.0	2
30309	Transcriptomic Analysis of Radish (<i>Raphanus sativus</i> L.) Roots with CLE41 Overexpression. <i>Plants</i> , 2022, 11, 2163.	1.6	4
30310	Sherlock: an open-source data platform to store, analyze and integrate Big Data for computational biologists. <i>F1000Research</i> , 0, 10, 409.	0.8	0
30311	Amino acid transporter gene TaATL1 from <i>Triticum aestivum</i> L. improves growth under nitrogen sufficiency and is down regulated under nitrogen deficiency. <i>Planta</i> , 2022, 256, .	1.6	1
30312	A High-Throughput Search for SFXN1 Physical Partners Led to the Identification of ATAD3, HSD10 and TIM50. <i>Biology</i> , 2022, 11, 1298.	1.3	2
30314	Next generation sequencing reveals miR-431 and miR-1303 as immune-regulating microRNAs for active tuberculosis. <i>Journal of Infection</i> , 2022, 85, 519-533.	1.7	3
30316	TROP2 Represents a Negative Prognostic Factor in Colorectal Adenocarcinoma and Its Expression Is Associated with Features of Epithelial-Mesenchymal Transition and Invasiveness. <i>Cancers</i> , 2022, 14, 4137.	1.7	5
30317	Precision Oncology: An Ensembled Machine Learning Approach to Identify a Candidate mRNA Panel for Stratification of Patients with Breast Cancer. <i>OMICS A Journal of Integrative Biology</i> , 2022, 26, 504-511.	1.0	1
30318	Mutations in <i>BCOR</i> , a co-repressor of <i>CRX/OTX2</i> , are associated with early-onset retinal degeneration. <i>Science Advances</i> , 2022, 8, .	4.7	6
30319	A chromosome-scale genome assembly of <i>Quercus gilva</i> : Insights into the evolution of <i>Quercus</i> section <i>Cyclobalanopsis</i> (Fagaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8
30320	Identification of differentially expressed genes induced by aberrant methylation in acute myeloid leukemia using integrated bioinformatics analyses. <i>Oncology Letters</i> , 2022, 24, .	0.8	1
30321	Loss of <i>Serpina1</i> in Mice Leads to Altered Gene Expression in Inflammatory and Metabolic Pathways. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10425.	1.8	3
30322	Histidine kinase inhibitors impair shoot regeneration in <i>Arabidopsis thaliana</i> via cytokinin signaling and SAM patterning determinants. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3

#	ARTICLE	IF	CITATIONS
30323	Integration of clinical and genomic data to enhance precision medicine: a case of study applied to the retina-macula. <i>Software and Systems Modeling</i> , 2023, 22, 159-174.	2.2	3
30324	Bioinformatics and systems biology approach to identify the pathogenetic link of Long COVID and Myalgic Encephalomyelitis/Chronic Fatigue Syndrome. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	9
30325	Spatiotemporal patterns of gliosis and neuroinflammation in presenilin 1/2 conditional double knockout mice. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	4
30326	Analysis of Tumor-Infiltrating T-Cell Transcriptomes Reveal a Unique Genetic Signature across Different Types of Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11065.	1.8	4
30328	Circulating monocytes associated with anti-PD-1 resistance in human biliary cancer induce T cell paralysis. <i>Cell Reports</i> , 2022, 40, 111384.	2.9	8
30330	Metabolization and sequestration of plant specialized metabolites in insect herbivores: Current and emerging approaches. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	4
30331	Weakly activated core neuroinflammation pathways were identified as a central signaling mechanism contributing to the chronic neurodegeneration in Alzheimer's disease. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	1.7	7
30332	De novo metatranscriptomic exploration of gene function in the millipede holobiont. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
30333	The Molecular Network behind Volatile Aroma Formation in Pear (<i>Pyrus</i> spp. Panguxiang) Revealed by Transcriptome Profiling via Fatty Acid Metabolic Pathways. <i>Life</i> , 2022, 12, 1494.	1.1	1
30334	Transcriptional states of CAR-T infusion relate to neurotoxicity – lessons from high-resolution single-cell SOM expression portraying. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
30335	Detoxification Gene Families at the Genome-Wide Level of Rhus Gall Aphid <i>Schlechtendalia chinensis</i> . <i>Genes</i> , 2022, 13, 1627.	1.0	1
30336	Systematic assessment of pathway databases, based on a diverse collection of user-submitted experiments. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
30337	Genomic Profiling of Non-O157 Shiga Toxigenic <i>Escherichia coli</i> -Infecting Bacteriophages from South Africa. <i>Phage</i> , 2022, 3, 221-230.	0.8	1
30338	Multi-Omics Analysis of GNL3L Expression, Prognosis, and Immune Value in Pan-Cancer. <i>Cancers</i> , 2022, 14, 4595.	1.7	1
30339	Pityriasis Rubra Pilaris Transcriptomics Implicate T Helper 17 Signaling and Correlate with Response to Ixekizumab, with Distinct Gene Expression Profiles in Nonresponders. <i>Journal of Investigative Dermatology</i> , 2023, 143, 501-504.e1.	0.3	2
30340	Transcriptomic and metabolic signatures of diatom plasticity to light fluctuations. <i>Plant Physiology</i> , 2022, 190, 2295-2314.	2.3	5
30341	Comparative genome analysis unravels pathogenicity of <i>Xanthomonas albilineans</i> causing sugarcane leaf scald disease. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
30342	Dopaminergic Gene Dosage Reveals Distinct Biological Partitions between Autism and Developmental Delay as Revealed by Complex Network Analysis and Machine Learning Approaches. <i>Journal of Personalized Medicine</i> , 2022, 12, 1579.	1.1	2

#	ARTICLE	IF	CITATIONS
30343	Complete mitochondrial genome sequencing and identification of candidate genes responsible for C5-type cytoplasmic male sterility in cabbage (<i>B. oleracea</i> var. <i>capitata</i>). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
30344	De novo sphingolipid biosynthesis necessitates detoxification in cancer cells. <i>Cell Reports</i> , 2022, 40, 111415.	2.9	5
30345	Identification of early biomarkers of transcriptomics in alveolar macrophage for the prognosis of intubated ARDS patients. <i>BMC Pulmonary Medicine</i> , 2022, 22, .	0.8	1
30346	Whole-genome assembly and analysis of a medicinal fungus: <i>Inonotus hispidus</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
30347	Comparison of Transcriptomic Signatures between Monkeypox-Infected Monkey and Human Cell Lines. <i>Journal of Immunology Research</i> , 2022, 2022, 1-17.	0.9	23
30348	SILAC-based quantitative proteomics to investigate the eicosanoid associated inflammatory response in activated macrophages. <i>Journal of Inflammation</i> , 2022, 19, .	1.5	0
30349	Time-course RNA-seq analysis provides an improved understanding of genetic regulation in response to cold stress from white clover (<i>Trifolium repens</i> L.). <i>Biotechnology and Biotechnological Equipment</i> , 2022, 36, 745-752.	0.5	6
30351	Niacin inhibits post-acidification of yogurt based on the mining of LDB_RS00370 biomarker gene. <i>Food Research International</i> , 2022, 162, 111929.	2.9	0
30352	Whole-exome sequencing reveals a comprehensive germline mutation landscape and identifies twelve novel predisposition genes in Chinese prostate cancer patients. <i>PLoS Genetics</i> , 2022, 18, e1010373.	1.5	4
30353	Integrated network pharmacology analysis, molecular docking, LC-MS analysis and bioassays revealed the potential active ingredients and underlying mechanism of <i>Scutellariae radix</i> for COVID-19. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
30354	Transcriptomic profiling of cotton leaves in response to cotton aphid damage. <i>Acta Physiologiae Plantarum</i> , 2022, 44, .	1.0	1
30356	Exploration of Hub Genes in Retinopathy of Prematurity Based on Bioinformatics Analysis of the Oxygen-Induced Retinopathy Model. <i>Journal of Ophthalmology</i> , 2022, 2022, 1-12.	0.6	0
30358	Screening of immune-related genes against bacterial infection in <i>Ostrinia furnacalis</i> (Lepidoptera: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.2	0
30360	Early Mid-pregnancy Blood-Based Proteins as Possible Biomarkers of Increased Infant Birth Size in Sex-Stratified Analyses. <i>Reproductive Sciences</i> , 0, , .	1.1	1
30361	Functional role of cyanidin-3-O-glucoside in osteogenesis: A pilot study based on RNA-seq analysis. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	1
30362	Speciation genomics and the role of depth in the divergence of rockfishes (<i>Sebastes</i>) revealed through Pool-seq analysis of enriched sequences. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	2
30364	Involvement of endothelins in neuroprotection of valosin-containing protein modulators against retinal ganglion cell damage. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
30365	Proteome Analysis of Swine Macrophages after Infection with Two Genotype II African Swine Fever Isolates of Different Pathogenicity. <i>Viruses</i> , 2022, 14, 2140.	1.5	2

#	ARTICLE	IF	CITATIONS
30366	Comparative Toxicogenomics Database (CTD): update 2023. <i>Nucleic Acids Research</i> , 2023, 51, D1257-D1262.	6.5	143
30368	Endometrial gene expression differences in women with coronavirus disease 2019. <i>Fertility and Sterility</i> , 2022, 118, 1159-1169.	0.5	10
30369	Genetics, molecular control and clinical relevance of habituation learning. <i>Neuroscience and Biobehavioral Reviews</i> , 2022, 143, 104883.	2.9	3
30371	Genomic analyses of the <i>Linum distyly</i> supergene reveal convergent evolution at the molecular level. <i>Current Biology</i> , 2022, 32, 4360-4371.e6.	1.8	24
30372	Bioinformatics analysis identifies potential biomarkers involved in the metastasis of locoregionally advanced nasopharyngeal carcinoma. <i>Medicine (United States)</i> , 2022, 101, e30126.	0.4	3
30373	Identification of therapeutically potential targets and their ligands for the treatment of OSCC. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	6
30374	Development and verification of an immune-related gene prognostic index for gastric cancer. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
30375	An integrated metabolome and transcriptome approach reveals the fruit flavor and regulatory network during jujube fruit development. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
30377	RNA sequencing-based identification of microRNAs in the antler cartilage of Gansu red deer (<i>Cervus elaphus kansuensis</i>). <i>PeerJ</i> , 0, 10, e13947.	0.9	1
30378	Analysis of the Antennal Transcriptome and Identification of Tissue-specific Expression of Olfactory-related Genes in <i>Micromelalopha troglodyta</i> (Lepidoptera: Notodontidae). <i>Journal of Insect Science</i> , 2022, 22, .	0.6	0
30379	Using Genomes and Evolutionary Analyses to Screen for Host-Specificity and Positive Selection in the Plant Pathogen <i>Xylella fastidiosa</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	6
30380	Comprehensive analysis reveals potential hub genes and therapeutic drugs in an acquired lymphedema model. <i>Gland Surgery</i> , 2022, 11, 1507-1517.	0.5	1
30381	First Report and Comparative Genomic Analysis of a <i>Mycoplasma mycoides</i> Subspecies <i>capri</i> HN-A in Hainan Island. <i>Microorganisms</i> , 2022, 10, 1908.	1.6	0
30382	Brain metastases: It takes two factors for a primary cancer to metastasize to brain. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	1
30383	RTX-KG2: a system for building a semantically standardized knowledge graph for translational biomedicine. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	15
30384	Bioinformatic identification of differentially expressed genes associated with hepatocellular carcinoma prognosis. <i>Medicine (United States)</i> , 2022, 101, e30678.	0.4	0
30385	Surface Layer Protein Pattern of <i>Levilactobacillus brevis</i> Strains Investigated by Proteomics. <i>Nutrients</i> , 2022, 14, 3679.	1.7	2
30386	PFP-GO: Integrating protein sequence, domain and protein-protein interaction information for protein function prediction using ranked GO terms. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2

#	ARTICLE	IF	CITATIONS
30387	Integrated analysis of the expression profiles of the lncRNA-miRNA-mRNA ceRNA network in granulosa and cumulus cells from yak ovaries. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
30389	HTCA: a database with an in-depth characterization of the single-cell human transcriptome. <i>Nucleic Acids Research</i> , 2023, 51, D1019-D1028.	6.5	11
30391	Effect of Autolyzed <i>Yarrowia lipolytica</i> on the Growth Performance, Antioxidant Capacity, Intestinal Histology, Microbiota, and Transcriptome Profile of Juvenile Largemouth Bass (<i>Micropterus</i>) Tj ETQqO 0 0 rgBT /Overl... doi:10.1186/s12916-023-02572-0	1.8	5
30392	Key factors for differential drought tolerance in two contrasting wild materials of <i>Artemisia wellbyi</i> identified using comparative transcriptomics. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	1
30393	Signatures associated with homologous recombination deficiency and immune regulation to improve clinical outcomes in patients with lung adenocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
30394	In-depth proteomic analysis reveals unique subtype-specific signatures in human small-cell lung cancer. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	9
30395	MCU controls melanoma progression through a redox-controlled phenotype switch. <i>EMBO Reports</i> , 2022, 23, .	2.0	10
30396	The general law of plasma proteome alterations occurring in the lifetime of Chinese individuals reveals the importance of immunity. <i>Aging</i> , 2022, 14, 7065-7092.	1.4	0
30397	Bioinformatics identification of miR-145 promotes NSCLC progression and induces PI3K/AKT and p38 pathways by targeting small glutamine-rich tetratricopeptide repeat-containing protein beta. <i>FEBS Journal</i> , 2023, 290, 1134-1150.	2.2	3
30398	Analysis of genome and methylation changes in Chinese indigenous chickens over time provides insight into species conservation. <i>Communications Biology</i> , 2022, 5, .	2.0	5
30400	Differential venom gland gene expression analysis of juvenile and adult scorpions <i>Androctonus crassicauda</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	4
30402	Genome-wide analysis of CNVs in three populations of Tibetan sheep using whole-genome resequencing. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
30403	Multi-omics data integration for hepatocellular carcinoma subtyping with multi-kernel learning. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
30404	Recombinant Actifensin and Defensin-d2 Induce Critical Changes in the Proteomes of Multidrug-Resistant <i>Pseudomonas aeruginosa</i> and <i>Candida albicans</i> . <i>Microbiology Spectrum</i> , 0, , .	1.2	0
30405	Novel clinical, molecular and bioinformatics insights into the genetic background of autism. <i>Human Genomics</i> , 2022, 16, .	1.4	2
30407	Prediction of evolutionary constraint by genomic annotations improves functional prioritization of genomic variants in maize. <i>Genome Biology</i> , 2022, 23, .	3.8	7
30408	Development of de-novo transcriptome assembly and SSRs in allohexaploid Brassica with functional annotations and identification of heat-shock proteins for thermotolerance. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
30410	Cell-type-specific genes associated with cortical structural abnormalities in pediatric bipolar disorder. <i>Psychoradiology</i> , 2022, 2, 56-65.	1.0	2

#	ARTICLE	IF	CITATIONS
30411	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
30412	Causal discovery in high-dimensional, multicollinear datasets. , 0, 2, .		1
30413	Investigate the stemness of adult adipose-derived stromal cells based on single-cell RNA sequencing. <i>Cell Biology International</i> , 2022, 46, 2118-2131.	1.4	2
30414	Group 3 innate lymphoid cells require BATF to regulate gut homeostasis in mice. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	12
30415	Genome-wide meta-analysis for Alzheimer's disease cerebrospinal fluid biomarkers. <i>Acta Neuropathologica</i> , 2022, 144, 821-842.	3.9	38
30416	Systematic analysis competing endogenous RNA coexpression network as a potentially prediction prognostic biomarker for colon adenocarcinoma. <i>Medicine (United States)</i> , 2022, 101, e30681.	0.4	2
30417	A new CCCH-type zinc finger-related lncRNA signature predicts the prognosis of clear cell renal cell carcinoma patients. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
30418	A phased, chromosome-scale genome of 'Honeycrisp' apple (<i>Malus domestica</i>). <i>GigaByte</i> , 0, 2022, 1-15.	0.0	6
30419	Expression of ICOS in the salivary glands of patients with primary Sjogren's syndrome and its molecular mechanism. <i>Molecular Medicine Reports</i> , 2022, 26, .	1.1	0
30420	Calcium homeostasis disruption initiates rapid growth after microfragmentation in the scleractinian coral <i>Porites lobata</i> . <i>Ecology and Evolution</i> , 2022, 12, .	0.8	4
30421	Computational approaches for predicting variant impact: An overview from resources, principles to applications. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	11
30422	Streptomycetes: Derived Active Extract Inhibits <i>Candida albicans</i> Biofilm Formation. <i>Current Microbiology</i> , 2022, 79, .	1.0	0
30423	Tuning heterologous glucan biosynthesis in yeast to understand and exploit plant starch diversity. <i>BMC Biology</i> , 2022, 20, .	1.7	3
30424	Transcriptomic plasticity of the hypothalamic osmoregulatory control centre of the Arabian dromedary camel. <i>Communications Biology</i> , 2022, 5, .	2.0	3
30425	A pyroptosis-related gene signature predicting survival and tumor immune microenvironment in breast cancer and validation. <i>BMC Cancer</i> , 2022, 22, .	1.1	1
30426	Genome-Wide Identification and Expression Analysis of the Zinc Finger Protein Gene Subfamilies under Drought Stress in <i>Triticum aestivum</i> . <i>Plants</i> , 2022, 11, 2511.	1.6	5
30427	Transcriptional regulation mechanism of flavonoids biosynthesis gene during fruit development in <i>Astragalus membranaceus</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
30428	Microarray and Bioinformatics Analysis of Differential Gene and lncRNA Expression during Erythropoietin Treatment of Acute Spinal Cord Injury in Rats. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-13.	0.7	1

#	ARTICLE	IF	CITATIONS
30430	Heterozygous LRP1 deficiency causes developmental dysplasia of the hip by impairing triradiate chondrocytes differentiation due to inhibition of autophagy. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	6
30432	Text-based experiment retrieval in genomic databases. Journal of Information Science, 0, , 016555152211186.	2.0	0
30433	Whole-Genome Analysis of Acinetobacter baumannii Strain AB43 Containing a Type I-Fb CRISPR-Cas System: Insights into the Relationship with Drug Resistance. Molecules, 2022, 27, 5665.	1.7	1
30434	The RNA-Binding Landscape of HAX1 Protein Indicates Its Involvement in Translation and Ribosome Assembly. Cells, 2022, 11, 2943.	1.8	2
30437	Human Plasma Proteome During Normal Pregnancy. Journal of Proteome Research, 2022, 21, 2687-2702.	1.8	7
30438	BioGNN: How Graph Neural Networks Can Solve Biological Problems. Intelligent Systems Reference Library, 2023, , 211-231.	1.0	2
30439	Transcriptomic analysis of mRNA expression in giant congenital melanocytic nevi. Gene, 2023, 850, 146894.	1.0	0
30440	DNA methylation profile in CpG-depleted regions uncovers a high-risk subtype of early-stage colorectal cancer. Journal of the National Cancer Institute, 2023, 115, 52-61.	3.0	6
30442	Integrative Functional Genomic Analysis in Multiplex Autism Families from Kazakhstan. Disease Markers, 2022, 2022, 1-26.	0.6	2
30443	EPM2A acts as a protective factor in prostate cancer, evidence from a real-world patient cohort. Frontiers in Pharmacology, 0, 13, .	1.6	0
30445	Chromosome-level genome assembly and resequencing of camphor tree (<i>Cinnamomum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 T biosynthesis of <i>Cinnamomum</i> . Horticulture Research, 2022, 9, .	2.9	5
30446	Analysis of rare disruptive germline mutations in 2135 enriched BRCA-negative breast cancers excludes additional high-impact susceptibility genes. Annals of Oncology, 2022, 33, 1318-1327.	0.6	6
30447	A chromosome-level genome assembly of the redfin culter (<i>Chanodichthys erythropterus</i>). Scientific Data, 2022, 9, .	2.4	3
30448	Modular derivation of diverse, regionally discrete human posterior CNS neurons enables discovery of transcriptomic patterns. Science Advances, 2022, 8, .	4.7	6
30449	Comprehensive analysis of clinical prognosis and CLIC1 immune invasion in lung adenocarcinoma. Medicine (United States), 2022, 101, e30760.	0.4	1
30451	Decoding the formation of diverse petal colors of <i>Lagerstroemia indica</i> by integrating the data from transcriptome and metabolome. Frontiers in Plant Science, 0, 13, .	1.7	7
30452	Complement membrane attack complex is an immunometabolic regulator of NLRP3 activation and IL-18 secretion in human macrophages. Frontiers in Immunology, 0, 13, .	2.2	2
30453	Complementary CRISPR genome-wide genetic screens in PARP10-knockout and overexpressing cells identify synthetic interactions for PARP10-mediated cellular survival. Oncotarget, 2022, 13, 1078-1091.	0.8	2

#	ARTICLE	IF	CITATIONS
30454	dynDeepDRIM: a dynamic deep learning model to infer direct regulatory interactions using time-course single-cell gene expression data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
30456	Hyperactivation of mTORC1 in a double hit mutant zebrafish model of tuberous sclerosis complex causes increased seizure susceptibility and neurodevelopmental abnormalities. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	3
30457	Overexpression of cotton GhNAC072 gene enhances drought and salt stress tolerance in transgenic Arabidopsis. <i>BMC Genomics</i> , 2022, 23, .	1.2	8
30458	Oncogenic RAS commandeers amino acid sensing machinery to aberrantly activate mTORC1 in multiple myeloma. <i>Nature Communications</i> , 2022, 13, .	5.8	5
30459	Ethylene emitted by viral pathogen-infected pepper (<i>Capsicum annuum</i> L.) plants is a volatile chemical cue that attracts aphid vectors. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
30461	Arms race and fluctuating selection dynamics in <i>Pseudomonas aeruginosa</i> bacteria coevolving with phage <i>OMKO1</i> . <i>Journal of Evolutionary Biology</i> , 2022, 35, 1475-1487.	0.8	11
30462	Dosing Regimen of Aditoprim and Sulfamethoxazole Combination for the <i>Glaesserella parasuis</i> Containing Resistance and Virulence Genes. <i>Pharmaceutics</i> , 2022, 14, 2058.	2.0	1
30463	Reclassification of endometrial cancer and identification of key genes based on neural-related genes. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
30464	Isoform-resolved mRNA profiling of ribosome load defines interplay of HIF and mTOR dysregulation in kidney cancer. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 871-880.	3.6	6
30465	Progeria and Aging Omics Based Comparative Analysis. <i>Biomedicines</i> , 2022, 10, 2440.	1.4	3
30466	Integrative Analysis of Motor Neuron and Microglial Transcriptomes from SOD1G93A Mice Models Uncover Potential Drug Treatments for ALS. <i>Journal of Molecular Neuroscience</i> , 2022, 72, 2360-2376.	1.1	5
30467	Genome-wide post-transcriptional regulation of bovine mammary gland response to <i>Streptococcus uberis</i> . <i>Journal of Applied Genetics</i> , 2022, 63, 771-782.	1.0	5
30468	Case report: Difference in outcomes between two cases of Hailey-Hailey disease treated with apremilast. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
30469	Spatiotemporal NF- κ B dynamics encodes the position, amplitude, and duration of local immune inputs. <i>Science Advances</i> , 2022, 8, .	4.7	18
30470	Protection of zero-valent iron nanoparticles against sepsis and septic heart failure. <i>Journal of Nanobiotechnology</i> , 2022, 20, .	4.2	5
30471	Urbanization drives adaptive evolution in a Neotropical bird. <i>Environmental Epigenetics</i> , 0, , .	0.9	0
30472	Genome-wide analysis of <i>Keratinibaculum paraultunense</i> strain KD-1 \hat{A} T and its key genes and metabolic pathways involved in the anaerobic degradation of feather keratin. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	2
30473	Comparative Transcriptomic Analysis of mRNAs, miRNAs and lncRNAs in the Longissimus dorsi Muscles between Fat-Type and Lean-Type Pigs. <i>Biomolecules</i> , 2022, 12, 1294.	1.8	4

#	ARTICLE	IF	CITATIONS
30474	Identification of Survival-Related Genes in Acute Myeloid Leukemia (AML) Based on Cytogenetically Normal AML Samples Using Weighted Gene Coexpression Network Analysis. <i>Disease Markers</i> , 2022, 2022, 1-19.	0.6	3
30475	Integrative analysis of metabolite GWAS illuminates the molecular basis of pleiotropy and genetic correlation. <i>ELife</i> , 0, 11, .	2.8	14
30476	Î±-Hemihydrate calcium sulfate/n-hydroxyapatite combined with metformin promotes osteogenesis in vitro and in vivo. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	3
30477	Expression profile of long non-coding RNA in inner Mongolian cashmere goat with putative roles in hair follicles development. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
30478	Physiological and Molecular Characteristics of Southern Leaf Blight Resistance in Sweet Corn Inbred Lines. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10236.	1.8	1
30479	Disease- and headache-specific microRNA signatures and their predicted mRNA targets in peripheral blood mononuclear cells in migraineurs: role of inflammatory signalling and oxidative stress. <i>Journal of Headache and Pain</i> , 2022, 23, .	2.5	11
30480	Multifarious Translational Regulation during Replicative Aging in Yeast. <i>Journal of Fungi (Basel)</i> , Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50	1.5	1
30481	Identification of neoplasm-specific signatures of miRNA interactions by employing a systems biology approach. <i>PeerJ</i> , 0, 10, e14149.	0.9	1
30482	From multitude to singularity: An up-to-date overview of scRNA-seq data generation and analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
30483	Inhibition of <i>Staphylococcus aureus</i> biofilm formation by gurmarin, a plant-derived cyclic peptide. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	4
30484	Tissue- and cell-type-specific molecular and functional signatures of 16p11.2 reciprocal genomic disorder across mouse brain and human neuronal models. <i>American Journal of Human Genetics</i> , 2022, 109, 1789-1813.	2.6	13
30486	Comprehensive analysis of key m5C modification-related genes in type 2 diabetes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
30487	Integration of genome and transcriptome reveal molecular regulation mechanism of early flowering trait in <i>Prunus</i> genus (<i>Prunus mume</i> and <i>Prunus persica</i>). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
30488	Self-reactivity of CD8 T-cell clones determines their differentiation status rather than their responsiveness in infections. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
30489	Genomic insight into the nocturnal adaptation of the black-crowned night heron (<i>Nycticorax</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	1.2	2
30490	IMP1/IGF2BP1 in human colorectal cancer extracellular vesicles. <i>American Journal of Physiology - Renal Physiology</i> , 2022, 323, G571-G585.	1.6	5
30491	Species-specific transcriptomic changes upon respiratory syncytial virus infection in cotton rats. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
30492	Signals of adaptation to agricultural stress in the genomes of two European bumblebees. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2

#	ARTICLE	IF	CITATIONS
30493	BIONIC: biological network integration using convolutions. <i>Nature Methods</i> , 2022, 19, 1250-1261.	9.0	17
30494	Accurate prediction of functional states of cis-regulatory modules reveals common epigenetic rules in humans and mice. <i>BMC Biology</i> , 2022, 20, .	1.7	5
30495	Floral organ transcriptome in <i>Camellia sasanqua</i> provided insight into stamen petaloid. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	1
30496	Shikonin Mediates Apoptosis through G Protein-Coupled Estrogen Receptor of Ovarian Cancer Cells. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-18.	0.5	1
30497	Integrative analysis of macrophage ribo-Seq and RNA-Seq data define glucocorticoid receptor regulated inflammatory response genes into distinct regulatory classes. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5622-5638.	1.9	2
30498	Opposing effects of chronic glucagon receptor agonism and antagonism on amino acids, hepatic gene expression, and alpha cells. <i>iScience</i> , 2022, 25, 105296.	1.9	10
30501	A single administration of hIL-7-hyFc induces long-lasting T-cell expansion with maintained effector functions. <i>Blood Advances</i> , 2022, 6, 6093-6107.	2.5	6
30502	Triploid production and performance in hybrid grouper (<i>Epinephelus fuscoguttatus</i> × <i>Epinephelus</i>) Tj ETQq1.1 0.784314 rgBT / Overlock 107	1.7	1
30503	Toward a data infrastructure for the Plant Cell Atlas. <i>Plant Physiology</i> , 2023, 191, 35-46.	2.3	3
30504	Transcriptome and 16S rRNA analysis revealed the response of largemouth bass (<i>Micropterus</i>) Tj ETQq1.1 0.784314 rgBT / Overlock 107	2.2	7
30505	Genome-wide identification and expression of TIFY family in cassava (<i>Manihot esculenta</i> Crantz). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
30506	Function-based classification of hazardous biological sequences: Demonstration of a new paradigm for biohazard assessments. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	3
30507	Transcriptome analysis reveals the roles of phytohormone signaling in tea plant (<i>Camellia sinensis</i> L.) flower development. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2
30508	Comparative genomics of <i>Sarcoptes scabiei</i> provide new insights into adaptation to permanent parasitism and within-host species divergence. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 3468-3484.	1.3	4
30509	RNA-seq profiling reveals different pathways between remodelled vessels and myocardium in Hypertrophic Cardiomyopathy. <i>Microcirculation</i> , 0, , .	1.0	2
30510	Physiological and transcriptomic analysis uncovers salinity stress mechanisms in a facultative crassulacean acid metabolism plant <i>Dendrobium officinale</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
30511	A novel subtype to predict prognosis and treatment response with DNA driver methylation in transcription in ovarian cancer. <i>Epigenomics</i> , 0, , .	1.0	0
30512	The pharmacological evidence of the chang-yan-ning formula in the treatment of colitis. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	5

#	ARTICLE	IF	CITATIONS
30513	A comprehensive study on ultrasonic deactivation of opportunistic pathogen <i>Saccharomyces cerevisiae</i> in food processing: From transcriptome to phenotype. <i>LWT - Food Science and Technology</i> , 2022, 170, 114069.	2.5	3
30514	Description and genomic characterization of <i>Jiella flava</i> sp. nov., isolated from <i>Acrostichum aureum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	2
30515	Prognostic Significance of ANGPTL4 in Lung Adenocarcinoma: A Meta-Analysis Based on Integrated TCGA and GEO Databases. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-16.	0.5	2
30517	Omics profiling identifies the regulatory functions of the MAPK/ERK pathway in nephron progenitor metabolism. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	1
30519	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
30520	Different skeletal protein toolkits achieve similar structure and performance in the tropical coral <i>Stylophora pistillata</i> and the temperate <i>Oculina patagonica</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	2
30521	Learning with cone-based geometric models and orthologics. <i>Annals of Mathematics and Artificial Intelligence</i> , 2022, 90, 1159-1195.	0.9	2
30522	ChemPert: mapping between chemical perturbation and transcriptional response for non-cancer cells. <i>Nucleic Acids Research</i> , 2023, 51, D877-D889.	6.5	7
30523	Transcriptome analysis reveals differential effects of beta-cypermethrin and fipronil insecticides on detoxification mechanisms in <i>Solenopsis invicta</i> . <i>Frontiers in Physiology</i> , 0, 13, .	1.3	9
30524	Expression pattern and clinical value of Key RNA methylation modification regulators in ischemic stroke. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
30525	Integrated single-cell analysis-based classification of vascular mononuclear phagocytes in mouse and human atherosclerosis. <i>Cardiovascular Research</i> , 2023, 119, 1676-1689.	1.8	31
30526	Krüppel-like factor 7 influences translation and pathways involved in ribosomal biogenesis in breast cancer. <i>Breast Cancer Research</i> , 2022, 24, .	2.2	5
30527	Obtaining genetics insights from deep learning via explainable artificial intelligence. <i>Nature Reviews Genetics</i> , 2023, 24, 125-137.	7.7	86
30528	Identification and characterization of lncRNAs and the interaction of lncRNA-mRNA in <i>Epinephelus coioides</i> induced with Singapore grouper iridovirus infection. <i>Fish and Shellfish Immunology</i> , 2022, 131, 441-453.	1.6	3
30529	Short-term transcriptomic changes in the mouse neural tube induced by an acute alcohol exposure. <i>Alcohol</i> , 2023, 106, 1-9.	0.8	1
30530	Alzheimer's disease: insights from a network medicine perspective. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
30531	Comparative transcriptomics analysis pipeline for the meta-analysis of phylogenetically divergent datasets (CoRMAP). <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	2
30533	Proteomic profiling of extracellular vesicles suggests Collectin10 as potential biomarker in relapsing head and neck squamous cell carcinoma. <i>Trillium Extracellular Vesicles</i> , 2022, 4, 9-17.	0.1	0

#	ARTICLE	IF	CITATIONS
30534	Predicted COVID-19 molecular effects on endometrium reveal key dysregulated genes and functions. <i>Molecular Human Reproduction</i> , 2022, 28, .	1.3	5
30535	GlycAP, a glycoproteomic analysis platform for site-specific N-glycosylation research. <i>International Journal of Mass Spectrometry</i> , 2022, 482, 116947.	0.7	1
30538	IMGT-KG: A Knowledge Graph for Immunogenetics. <i>Lecture Notes in Computer Science</i> , 2022, , 628-642.	1.0	0
30539	Evidentea visual analytics tool for data enrichment in SNP-based phylogenetic trees. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	1
30540	Single Cell Transcriptomics. , 2022, , 87-102.		0
30541	Quantitative proteomic analysis provides insight into the survival mechanism of <i>Salmonella typhimurium</i> under high-intensity ultrasound treatment. <i>Current Research in Food Science</i> , 2022, 5, 1740-1749.	2.7	5
30542	Finer resolution analysis of transcriptional programming during the active migration of chicken primordial germ cells. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5911-5924.	1.9	2
30543	T Cell Transcriptome in Chromosome 22q11.2 Deletion Syndrome. <i>Journal of Immunology</i> , 2022, 209, 874-885.	0.4	1
30544	The limits of molecular signatures for pancreatic ductal adenocarcinoma subtyping. <i>NAR Cancer</i> , 2022, 4, .	1.6	2
30545	Identification of DNA methylation-regulated differentially expressed genes in RA by integrated analysis of DNA methylation and RNA-Seq data. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	4
30547	Integrating genome-wide association study with RNA-seq revealed <i>DBI</i> as a good candidate gene for intramuscular fat content in Beijing black pigs. <i>Animal Genetics</i> , 2023, 54, 24-34.	0.6	5
30548	Genomic and phenotypic biology of a novel <i>Dickeya zeae</i> WH1 isolated from rice in China: Insights into pathogenicity and virulence factors. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
30549	Molecular determinants of TRAF6 binding specificity suggest that native interaction partners are not optimized for affinity. <i>Protein Science</i> , 2022, 31, .	3.1	1
30551	Chronic Cadmium Exposure Induces Impaired Olfactory Learning and Altered Brain Gene Expression in Honey Bees (<i>Apis mellifera</i>). <i>Insects</i> , 2022, 13, 988.	1.0	5
30552	GlycoEnzOnto: a GlycoEnzyme pathway and molecular function ontology. <i>Bioinformatics</i> , 2022, 38, 5413-5420.	1.8	4
30553	A brief survey of tools for genomic regions enrichment analysis. <i>Frontiers in Bioinformatics</i> , 0, 2, .	1.0	7
30554	Leaf-transcriptome profiles of <i>phoebe bournei</i> provide insights into temporal drought stress responses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
30555	Statistical and functional convergence of common and rare genetic influences on autism at chromosome 16p. <i>Nature Genetics</i> , 2022, 54, 1630-1639.	9.4	14

#	ARTICLE	IF	CITATIONS
30556	A divide-and-conquer approach for genomic prediction in rubber tree using machine learning. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
30557	PsnWRKY70 Negatively Regulates NaHCO ₃ Tolerance in Populus. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13086.	1.8	1
30561	Integrated Quantitative Targeted Lipidomics and Proteomics Reveal Unique Fingerprints of Multiple Metabolic Conditions. <i>Biomolecules</i> , 2022, 12, 1439.	1.8	2
30562	Bioinformatics Analysis Identifies TNFRSF1A as a Biomarker of Liver Injury in Sepsis TNFRSF1A is a Biomarker for Septic Liver Injury. <i>Genetical Research</i> , 2022, 2022, 1-10.	0.3	0
30563	Transcriptome and metabolome analyses provide insights into the relevance of pericarp thickness variations in <i>Camellia drupifera</i> and <i>Camellia oleifera</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
30564	Genome-wide identification of the rubber tree superoxide dismutase (<i>SOD</i>) gene family and analysis of its expression under abiotic stress. <i>PeerJ</i> , 0, 10, e14251.	0.9	7
30565	E-SNPs&GO: embedding of protein sequence and function improves the annotation of human pathogenic variants. <i>Bioinformatics</i> , 2022, 38, 5168-5174.	1.8	9
30566	Sexual dimorphism of early transcriptional reprogramming in degenerating peripheral nerves. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	1
30567	<i>Rhizobium etli</i> 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
30568	Electroneutral Polymer Nanodiscs Enable Interference-Free Probing of Membrane Proteins in a Lipid-Bilayer Environment. <i>Small</i> , 2022, 18, .	5.2	17
30569	Small extravesicular <sc>microRNA</sc> in head and neck squamous cell carcinoma and its potential as a liquid biopsy for early detection. <i>Head and Neck</i> , 2023, 45, 212-224.	0.9	7
30570	Identification of a 5-Hydroxymethylation Signature in Circulating Cell-Free DNA for the Noninvasive Detection of Colorectal Cancer. <i>Journal of Oncology</i> , 2022, 2022, 1-15.	0.6	0
30571	Genetic identification of SNP markers and candidate genes associated with sugarcane smut resistance using BSR-Seq. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
30572	Comparative and Phylogenetic Analysis of Chloroplast Genomes of Two Medicinal Species of <i>Spatholobus</i>. <i>Journal of AOAC INTERNATIONAL</i> , 0, , .	0.7	0
30574	Learning deep representations of enzyme thermal adaptation. <i>Protein Science</i> , 2022, 31, .	3.1	6
30575	Gene expression profile suggests different mechanisms underlying sporadic and familial mesial temporal lobe epilepsy. <i>Experimental Biology and Medicine</i> , 2022, 247, 2233-2250.	1.1	2
30576	Genome Sequence Resource of <i>Trichothecium roseum</i> (ZM-Tr2021), the Causal Agent of Postharvest Pink Rot. <i>Plant Disease</i> , 2023, 107, 205-209.	0.7	3
30577	Whole-genome sequencing and comparative genomic analysis of a pathogenic Enterocytozoon hepatopenaei strain isolated from <i>Litopenaeus vannamei</i> . <i>Aquaculture International</i> , 2023, 31, 523-546.	1.1	4

#	ARTICLE	IF	CITATIONS
30579	ICSDA: a multi-modal deep learning model to predict breast cancer recurrence and metastasis risk by integrating pathological, clinical and gene expression data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	15
30581	Morphology and gene expression profiling provide complementary information for mapping cell state. <i>Cell Systems</i> , 2022, 13, 911-923.e9.	2.9	35
30582	Identification of Heme Oxygenase-1 as a Putative DNA-Binding Protein. <i>Antioxidants</i> , 2022, 11, 2135.	2.2	2
30583	Transcriptome and Proteome Co-Profiling Offers an Understanding of Pre-Harvest Sprouting (PHS) Molecular Mechanisms in Wheat (<i>Triticum aestivum</i>). <i>Plants</i> , 2022, 11, 2807.	1.6	2
30584	The chromosome-level genome of <i>Akebia trifoliata</i> as an important resource to study plant evolution and environmental adaptation in the Cretaceous. <i>Plant Journal</i> , 2022, 112, 1316-1330.	2.8	14
30585	System Biology Approaches Identified Novel Biomarkers and their Signaling Pathways Involved in Renal Cell Carcinoma (RCC) with Different Human Diseases. <i>Bioscience Reports</i> , 0, , .	1.1	1
30586	Altered microvasculature in pancreatic islets from subjects with type 1 diabetes. <i>PLoS ONE</i> , 2022, 17, e0276942.	1.1	8
30587	Characterization of the interactome profiling of <i>Mycoplasma fermentans</i> DnaK in cancer cells reveals interference with key cellular pathways. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
30588	Subcellular location of source proteins improves prediction of neoantigens for immunotherapy. <i>EMBO Journal</i> , 2022, 41, .	3.5	2
30589	Characterisation of ethnic differences in DNA methylation between UK-resident South Asians and Europeans. <i>Clinical Epigenetics</i> , 2022, 14, .	1.8	11
30591	Tetrabromobisphenol A effects on differentiating mouse embryonic stem cells reveals unexpected impact on immune system. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
30592	The Role of Long Noncoding RNAs on Male Infertility: A Systematic Review and In Silico Analysis. <i>Biology</i> , 2022, 11, 1510.	1.3	6
30593	ESKAPE Act Plus: Pathway Activation Analysis for Bacterial Pathogens. <i>MSystems</i> , 2022, 7, .	1.7	4
30594	Multimomics Profiling of Toxins in the Venom of the Amazonian Spider <i>Acanthoscurria juruenicola</i> . <i>Journal of Proteome Research</i> , 2022, 21, 2783-2797.	1.8	3
30595	DNA methylation loci identification for pan-cancer early-stage diagnosis and prognosis using a new distributed parallel partial least squares method. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
30597	Heterologous expression of the TaPI-PLC1-2B gene enhanced drought and salt tolerance in transgenic rice seedlings. <i>Heredity</i> , 0, , .	1.2	0
30598	Single-cell RNA-seq reveals the communications between extracellular matrix-related components and Schwann cells contributing to the earlobe keloid formation. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	4
30599	Potential common mechanism of four Chinese patent medicines recommended by diagnosis and treatment protocol for COVID-19 in medical observation period. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	0

#	ARTICLE	IF	CITATIONS
30600	Towards a dispositionalist (and unifying) account of addiction. <i>Theoretical Medicine and Bioethics</i> , 0, , .	0.4	0
30602	Pan-cancer analysis supports MAPK12 as a potential prognostic and immunotherapeutic target in multiple tumor types, including in THCA. <i>Oncology Letters</i> , 2022, 24, .	0.8	5
30603	A single cell transcriptional roadmap of human pacemaker cell differentiation. <i>ELife</i> , 0, 11, .	2.8	11
30605	Expression Profiles of Kidney Mitochondrial Proteome during the Progression of the Unilateral Ureteral Obstruction: Focus on Energy Metabolism Adaptions. <i>Metabolites</i> , 2022, 12, 936.	1.3	3
30606	Annexin A1 exerts renoprotective effects in experimental crescentic glomerulonephritis. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	1
30607	Benefits of global mutant huntingtin lowering diminish over time in a Huntington's disease mouse model. <i>JCI Insight</i> , 2022, 7, .	2.3	7
30608	Identification of Differentially Expressed Genes Associated with the Prognosis and Diagnosis of Hepatocellular Carcinoma by Integrated Bioinformatics Analysis. <i>BioMed Research International</i> , 2022, 2022, 1-12.	0.9	4
30610	A Plasma Circular RNA Profile Differentiates Subjects with Alzheimer's Disease and Mild Cognitive Impairment from Healthy Controls. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13232.	1.8	7
30612	Computational pharmacogenomic screen identifies drugs that potentiate the anti-breast cancer activity of statins. <i>Nature Communications</i> , 2022, 13, .	5.8	5
30613	Tissue-specific transcriptome responses to Fusarium head blight and Fusarium root rot. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
30614	Fluopyram activates systemic resistance in soybean. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
30615	Propagation, detection and correction of errors using the sequence database network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	6
30616	Defining the extent of gene function using ROC curvature. <i>Bioinformatics</i> , 0, , .	1.8	1
30617	Nutrient accumulation and transcriptome patterns during grain development in rice. <i>Journal of Experimental Botany</i> , 2023, 74, 909-930.	2.4	10
30618	CD146 is closely associated with the prognosis and molecular features of osteosarcoma: Guidance for personalized clinical treatment. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
30619	Single-cell transcriptomes from turtle livers reveal sensitivity of hepatic immune cells to bacteria-infection. <i>Fish and Shellfish Immunology</i> , 2022, , .	1.6	2
30621	Transcriptomic, cytological, and physiological analyses reveal the potential regulatory mechanism in Tartary buckwheat under cadmium stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
30622	An interactive analysis of the mouse oviductal miRNA profiles. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	0

#	ARTICLE	IF	CITATIONS
30623	Investigating the effects and mechanisms of Erchen Decoction in the treatment of colorectal cancer by network pharmacology and experimental validation. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2
30624	Preliminary study on the molecular features of mutation in multiple primary oral cancer by whole exome sequencing. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
30625	A novel promising diagnostic candidate selected by screening the transcriptome of <i>Babesia gibsoni</i> (Wuhan isolate) asexual stages in infected beagles. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	0
30626	Combining mass spectrometry and machine learning to discover bioactive peptides. <i>Nature Communications</i> , 2022, 13, .	5.8	14
30628	Loss of NECTIN1 triggers melanoma dissemination upon local IGF1 depletion. <i>Nature Genetics</i> , 2022, 54, 1839-1852.	9.4	7
30629	SCRAP: a bioinformatic pipeline for the analysis of small chimeric RNA-seq data. <i>Rna</i> , 0, , rna.079240.122.	1.6	2
30630	Identification of potential hub genes of gastric cancer. <i>Medicine (United States)</i> , 2022, 101, e30741.	0.4	1
30631	The extracellular matrix fibulin 7 maintains epidermal stem cell heterogeneity during skin aging. <i>EMBO Reports</i> , 0, , .	2.0	4
30632	Pathogenicity Variation in Two Genomes of <i>Cercospora</i> Species Causing Gray Leaf Spot in Maize. <i>Molecular Plant-Microbe Interactions</i> , 2023, 36, 14-25.	1.4	4
30633	HIV specific CD8+ TRM-like cells in tonsils express exhaustive signatures in the absence of natural HIV control. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
30634	Genome sequencing reveals evidence of adaptive variation in the genus <i>Zea</i> . <i>Nature Genetics</i> , 2022, 54, 1736-1745.	9.4	29
30636	PubChem 2023 update. <i>Nucleic Acids Research</i> , 2023, 51, D1373-D1380.	6.5	526
30637	Genome-Wide Transcriptional Profiling Reveals PHACTR1 as a Novel Molecular Target of Resveratrol in Endothelial Homeostasis. <i>Nutrients</i> , 2022, 14, 4518.	1.7	0
30639	Clinically relevant treatment of PDX models reveals patterns of neuroblastoma chemoresistance. <i>Science Advances</i> , 2022, 8, .	4.7	8
30640	Exploring Epigenomic Datasets by ChIPseeker. <i>Current Protocols</i> , 2022, 2, .	1.3	75
30641	Exploratory analysis of interleukin-8 in hospitalized COVID-19 patients. <i>Immunity, Inflammation and Disease</i> , 2022, 10, .	1.3	1
30642	Comparative genomics and pangenomics of vancomycin-resistant and susceptible <i>Enterococcus faecium</i> from Irish hospitals. <i>Journal of Medical Microbiology</i> , 2022, 71, .	0.7	4
30643	Eusocial Transition in Blattodea: Transposable Elements and Shifts of Gene Expression. <i>Genes</i> , 2022, 13, 1948.	1.0	2

#	ARTICLE	IF	CITATIONS
30644	In Vitro Anti-Proliferative and Apoptotic Effects of Hydroxytyrosyl Oleate on SH-SY5Y Human Neuroblastoma Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12348.	1.8	13
30645	Core promoter in TNBC is highly mutated with rich ethnic signature. <i>Briefings in Functional Genomics</i> , 0, , .	1.3	0
30646	Neuronal temperature perception induces specific defenses that enable <i>C. elegans</i> to cope with the enhanced reactivity of hydrogen peroxide at high temperature. <i>ELife</i> , 0, 11, .	2.8	5
30647	Identification of miRNA biomarkers for breast cancer by combining ensemble regularized multinomial logistic regression and Cox regression. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	4
30648	Network biology analysis of P23H rhodopsin interactome identifies protein and mRNA quality control mechanisms. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
30649	SNP-based high-density linkage map construction and QTL mapping of black spot disease resistance in Chinese sand pear. <i>Journal of Applied Genetics</i> , 0, , .	1.0	0
30651	Ectopic expression of HIV-1 Tat modifies gene expression in cultured B cells: implications for the development of B-cell lymphomas in HIV-1-infected patients. <i>PeerJ</i> , 0, 10, e13986.	0.9	2
30653	Transcriptomic profiling of sporadic Alzheimer's disease patients. <i>Molecular Brain</i> , 2022, 15, .	1.3	7
30654	A Network Pharmacology Study on the Cervix Prescription for Treatment of Cervical Cancer. <i>Journal of Immunology Research</i> , 2022, 2022, 1-13.	0.9	3
30655	Quantum computing algorithms: getting closer to critical problems in computational biology. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	10
30656	Gene Networks Involved in Plant Heat Stress Response and Tolerance. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11970.	1.8	10
30657	An automatic hypothesis generation for plausible linkage between xanthium and diabetes. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
30658	A comprehensive survey of the approaches for pathway analysis using multi-omics data integration. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	13
30659	Identification of QTLs Controlling Radish Root Shape Using Multiple Populations. <i>Horticulturae</i> , 2022, 8, 931.	1.2	4
30660	Identification and functional analysis of m6A in the mammary gland tissues of dairy goats at the early and peak lactation stages. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	3
30661	Integrated genetic analysis of leaf blast resistance in upland rice: QTL mapping, bulked segregant analysis and transcriptome sequencing. <i>AoB PLANTS</i> , 2022, 14, .	1.2	1
30662	Identification of long non-coding RNA-microRNA-mRNA regulatory modules and their potential roles in drought stress response in wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
30663	Network regression analysis for binary and ordinal categorical phenotypes in transcriptome-wide association studies. <i>Genetics</i> , 0, , .	1.2	1

#	ARTICLE	IF	CITATIONS
30664	In-Depth Characterization of the <i>Clostridioides difficile</i> Phosphoproteome to Identify Ser/Thr Kinase Substrates. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100428.	2.5	5
30665	PGG.SV: a whole-genome-sequencing-based structural variant resource and data analysis platform. <i>Nucleic Acids Research</i> , 2023, 51, D1109-D1116.	6.5	3
30666	Unpacking COVID-19 Systems Biology in Lung and Whole Blood with Transcriptomics and miRNA Regulators. <i>OMICS A Journal of Integrative Biology</i> , 2022, 26, 608-621.	1.0	1
30667	Integrative Bioinformatics Analysis Revealed Mitochondrial Dysfunction-Related Genes Underlying Intervertebral Disc Degeneration. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-35.	1.9	6
30668	Exogenous Nitric Oxide Alleviates the Damage Caused by Tomato Yellow Leaf Curl Virus in Tomato through Regulation of Peptidase Inhibitor Genes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12542.	1.8	3
30670	A chromosome-level genome of <i>Semiothisa cinerearia</i> provides insights into its genome evolution and control. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
30671	Muscle Transcriptomic Circuits Linked to Periarticular Physiology in End-Stage Osteoarthritis. <i>Physiological Genomics</i> , 0, , .	1.0	2
30672	Trans-interaction of risk loci 6p24.1 and 10q11.21 is associated with endothelial damage in coronary artery disease. <i>Atherosclerosis</i> , 2022, , .	0.4	2
30673	Role of EFNA1 SNP (rs12904) in Tumorigenesis and Metastasis of Colorectal Cancer: A Bioinformatic Analysis and HRM SNP Genotyping Verification. <i>Asian Pacific Journal of Cancer Prevention</i> , 2022, 23, 3523-3531.	0.5	0
30675	Integrating Genomic Information with Tumor-Immune Microenvironment in Triple-Negative Breast Cancer. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 13901.	1.2	1
30676	Integrated analysis and exploration of potential shared gene signatures between carotid atherosclerosis and periodontitis. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	4
30678	Role of IAA and Primary Metabolites in Two Rounds of Adventitious Root Formation in Softwood Cuttings of <i>Camellia sinensis</i> (L.). <i>Agronomy</i> , 2022, 12, 2486.	1.3	4
30680	A novel signature model based on mitochondrial-related genes for predicting survival of colon adenocarcinoma. <i>BMC Medical Informatics and Decision Making</i> , 2022, 22, .	1.5	2
30681	Severe testing with high-dimensional omics data for enhancing biomedical scientific discovery. <i>Npj Systems Biology and Applications</i> , 2022, 8, .	1.4	1
30683	Identification of adenylate cyclase 2 methylation in bladder cancer with implications for prognosis and immunosuppressive microenvironment. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
30684	In silico investigations identified Butyl Xanilate to competently target CK2 β (CSNK2A1) for therapy of chronic lymphocytic leukemia. <i>Scientific Reports</i> , 2022, 12, .	1.6	14
30685	Identification of proteomic landscape of drug-binding proteins in live cells by proximity-dependent target ID. <i>Cell Chemical Biology</i> , 2022, 29, 1739-1753.e6.	2.5	8
30687	Formation of toxic oligomers of polyQ-expanded Huntingtin by prion-mediated cross-seeding. <i>Molecular Cell</i> , 2022, 82, 4290-4306.e11.	4.5	7

#	ARTICLE	IF	CITATIONS
30688	Charting plant gene functions in the multi-omics and single-cell era. <i>Trends in Plant Science</i> , 2023, 28, 283-296.	4.3	21
30689	CXCL12 defines lung endothelial heterogeneity and promotes distal vascular growth. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	2
30693	Comparative Genomic Analysis of 31 <i>Phytophthora</i> Genomes Reveals Genome Plasticity and Horizontal Gene Transfer. <i>Molecular Plant-Microbe Interactions</i> , 2023, 36, 26-46.	1.4	6
30695	CellMarker 2.0: an updated database of manually curated cell markers in human/mouse and web tools based on scRNA-seq data. <i>Nucleic Acids Research</i> , 2023, 51, D870-D876.	6.5	141
30697	The landscape of transcriptional and translational changes over 22 years of bacterial adaptation. <i>ELife</i> , 0, 11, .	2.8	18
30698	Screening of key biomarkers in osteoporosis: Evidence from bioinformatic analysis. <i>International Journal of Rheumatic Diseases</i> , 0, , .	0.9	1
30699	Physiological and protein profiling analysis provides insight into the underlying molecular mechanism of potato tuber development regulated by jasmonic acid in vitro. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
30700	Transcriptome Profiling of the Hippocampal Seizure Network Implicates a Role for Wnt Signaling during Epileptogenesis in a Mouse Model of Temporal Lobe Epilepsy. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12030.	1.8	5
30701	Gene set analysis of transcriptomics data identifies new biological processes associated with early markers of atherosclerosis but not with those of osteoporosis: Atherosclerosis-osteoporosis co/multimorbidity study in the Young Finns Study. <i>Atherosclerosis</i> , 2022, 361, 1-9.	0.4	0
30702	CommPath: An R package for inference and analysis of pathway-mediated cell-cell communication chain from single-cell transcriptomics. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5978-5983.	1.9	3
30703	DiffBrainNet: Differential analyses add new insights into the response to glucocorticoids at the level of genes, networks and brain regions. <i>Neurobiology of Stress</i> , 2022, 21, 100496.	1.9	3
30704	Molecular Mechanisms Regulating the Oil Biosynthesis in Olive (<i>Olea europaea</i> L.) Fruits Revealed by Transcriptomic Analysis. <i>Agronomy</i> , 2022, 12, 2718.	1.3	1
30706	Chromosome-level genome assembly of the bar-headed goose (<i>Anser indicus</i>). <i>Scientific Data</i> , 2022, 9, .	2.4	2
30707	MethBank 4.0: an updated database of DNA methylation across a variety of species. <i>Nucleic Acids Research</i> , 2023, 51, D208-D216.	6.5	7
30708	CRdb: a comprehensive resource for deciphering chromatin regulators in human. <i>Nucleic Acids Research</i> , 2023, 51, D88-D100.	6.5	1
30709	Transcriptomic analysis of graft liver provides insight into the immune response of rat liver transplantation. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	0
30710	Transcriptome and metabolome analyses of Shatian pomelo (<i>Citrus grandis</i> var. Shatinyu Hort) leaves provide insights into the overexpression of the gibberellin-induced gene CcGASA4. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
30712	Increased Carbon Dioxide Respiration Prevents the Effects of Acceleration/Deceleration Elicited Mild Traumatic Brain Injury. <i>Neuroscience</i> , 2022, , .	1.1	1

#	ARTICLE	IF	CITATIONS
30713	Identification of MicroRNAs Related to Phytohormone Signal Transduction and Self-incompatibility of Rabbiteye Blueberry Pollen. <i>Journal of the American Society for Horticultural Science</i> , 2022, 147, 300-311.	0.5	1
30714	The Immediate Early Response of Lens Epithelial Cells to Lens Injury. <i>Cells</i> , 2022, 11, 3456.	1.8	4
30715	3D biocomposite culture enhances differentiation of dopamine-like neurons from SH-SY5Y cells: A model for studying Parkinson's disease phenotypes. <i>Biomaterials</i> , 2022, 290, 121858.	5.7	7
30716	Identification of diagnostic genes for both Alzheimer's disease and Metabolic syndrome by the machine learning algorithm. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	17
30718	Titanium nanoparticles activate a transcriptional response in Arabidopsis that enhances tolerance to low phosphate, osmotic stress and pathogen infection. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
30719	Transcription factor MAFB controls type I and II interferon response-mediated host immunity in Mycobacterium tuberculosis-infected macrophages. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
30720	The Childhood Acute Illness and Nutrition (CHAIN) network nested case-cohort study protocol: a multi-omics approach to understanding mortality among children in sub-Saharan Africa and South Asia. <i>Gates Open Research</i> , 0, 6, 77.	2.0	2
30721	A comprehensive set of ER protein disulfide isomerase family members supports the biogenesis of proinflammatory interleukin 12 family cytokines. <i>Journal of Biological Chemistry</i> , 2022, 298, 102677.	1.6	2
30722	Accelerating the adoption of research data management strategies. <i>Matter</i> , 2022, 5, 3614-3642.	5.0	2
30723	RNA-seq identifies differentially expressed genes involved in csal1 overexpression in granulosa cells of prehierarchal follicles in Chinese Dagu hens. <i>Poultry Science</i> , 2023, 102, 102310.	1.5	2
30724	The expression of apoptosis related genes in HK-2 cells overexpressing PPM1K was determined by RNA-seq analysis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
30725	EDomics: a comprehensive and comparative multi-omics database for animal evo-devo. <i>Nucleic Acids Research</i> , 2023, 51, D913-D923.	6.5	5
30727	Characteristic Genes and Immune Infiltration Analysis for Acute Rejection after Kidney Transplantation. <i>Disease Markers</i> , 2022, 2022, 1-22.	0.6	3
30728	Exploring the mechanism of andrographolide in the treatment of gastric cancer through network pharmacology and molecular docking. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
30729	Excessive HSP70/TLR2 activation leads to remodeling of the tumor immune microenvironment to resist chemotherapy sensitivity of mFOLFOX in colorectal cancer. <i>Clinical Immunology</i> , 2022, 245, 109157.	1.4	4
30730	Watermelon responds to organic fertilizer by enhancing root-associated acid phosphatase activity to improve organic phosphorus utilization. <i>Journal of Plant Physiology</i> , 2022, 279, 153838.	1.6	4
30731	Transcriptomic and physiological analyses unravel the effect and mechanism of halosulfuron-methyl on the symbiosis between rhizobium and soybean. <i>Ecotoxicology and Environmental Safety</i> , 2022, 247, 114248.	2.9	3
30732	Single-molecule mechanical studies of chaperones and their clients. <i>Biophysics Reviews</i> , 2022, 3, .	1.0	4

#	ARTICLE	IF	CITATIONS
30733	The chromosome-level <i>Melaleuca alternifolia</i> genome provides insights into the molecular mechanisms underlying terpenoids biosynthesis. <i>Industrial Crops and Products</i> , 2022, 189, 115819.	2.5	4
30734	Time course gene expression experiments. , 2023, , 85-110.		0
30735	Transcriptomics in agricultural sciences: capturing changes in gene regulation during abiotic or biotic stress. , 2023, , 257-283.		0
30736	Transcriptomics and genetic engineering. , 2023, , 43-65.		0
30737	Whole transcriptome sequencing analysis of synergistic combinations of plant-based antimicrobials and zinc oxide nanoparticles against <i>Campylobacter jejuni</i> . <i>Microbiological Research</i> , 2023, 266, 127246.	2.5	0
30738	Transcriptome signatures of wastewater effluent exposure in larval zebrafish vary with seasonal mixture composition in an effluent-dominated stream. <i>Science of the Total Environment</i> , 2023, 856, 159069.	3.9	4
30740	Semantic Breakthrough in Drug Discovery. <i>Synthesis Lectures on Data, Semantics and Knowledge</i> , 2015, , .	3.9	2
30741	MAGCN: A Multiple Attention Graph Convolution Networks for Predicting Synthetic Lethality. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, , 1-10.	1.9	2
30742	PSPGO: Cross-Species Heterogeneous Network Propagation for Protein Function Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1713-1724.	1.9	1
30743	Integrative metabolome and transcriptome analyses reveals the black fruit coloring mechanism of <i>Crataegus maximowiczii</i> C. K. Schneid. <i>Plant Physiology and Biochemistry</i> , 2023, 194, 111-121.	2.8	10
30744	RNA-Seq revealed the effect of adding different proportions of wheat diet on fat metabolism of Tibetan lamb. <i>Gene</i> , 2023, 851, 147031.	1.0	3
30745	Integrating Genome-Wide Association Study with RNA-Sequencing Reveals HDAC9 as a Candidate Gene Influencing Loin Muscle Area in Beijing Black Pigs. <i>Biology</i> , 2022, 11, 1635.	1.3	1
30746	Hackathon in Teaching: Applying Machine Learning to Life Sciences Tasks. <i>Lecture Notes in Networks and Systems</i> , 2023, , 236-246.	0.5	0
30747	The combination of SMRT sequencing and Illumina sequencing highlights organ-specific and age-specific expression patterns of miRNAs in Sika Deer. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	1
30748	Modeling community standards for metadata as templates makes data FAIR. <i>Scientific Data</i> , 2022, 9, .	2.4	8
30749	Chromosome-scale genome assembly of the African giant pouched rat (<i>Cricetomys ansorgei</i>) and evolutionary analysis reveals evidence of olfactory specialization. <i>Genomics</i> , 2022, 114, 110521.	1.3	2
30750	Identification of the miR-423-3p/VLDLR Regulatory Network for Glioma Using Transcriptome Analysis. <i>Neurochemical Research</i> , 2022, 47, 3864-3901.	1.6	1
30751	Genome-wide survey reveals the phylogenomic relationships of <i>Chirolophis japonicus</i> Herzenstein, 1890 (Stichaeidae, Perciformes). <i>ZooKeys</i> , 0, 1129, 55-72.	0.5	2

#	ARTICLE	IF	CITATIONS
30752	Gene set proximity analysis: expanding gene set enrichment analysis through learned geometric embeddings, with drug-repurposing applications in COVID-19. <i>Bioinformatics</i> , 2023, 39, .	1.8	6
30754	Identification of visual cortex cell types and species differences using single-cell RNA sequencing. <i>Nature Communications</i> , 2022, 13, .	5.8	12
30756	A systematic study of HIF1A cofactors in hypoxic cancer cells. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
30757	Understanding the Role of Yeast Yme1 in Mitochondrial Function Using Biochemical and Proteomics Analyses. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13694.	1.8	0
30758	Cytoplasmic pool of U1 spliceosome protein SNRNP70 shapes the axonal transcriptome and regulates motor connectivity. <i>Current Biology</i> , 2022, 32, 5099-5115.e8.	1.8	7
30759	Bioinformatics tools and data resources for assay development of fluid protein biomarkers. <i>Biomarker Research</i> , 2022, 10, .	2.8	8
30760	A lightweight classification of adaptor proteins using transformer networks. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	5
30761	Whole-genome assembly and annotation for the little yellow croaker (<i>Larimichthys polyactis</i>) provide insights into the evolution of hermaphroditism and gonochorism. <i>Molecular Ecology Resources</i> , 2023, 23, 632-658.	2.2	4
30763	A Comprehensive Study of De Novo Mutations on the Protein-Protein Interaction Interfaces Provides New Insights into Developmental Delay. <i>Biomolecules</i> , 2022, 12, 1643.	1.8	0
30764	Genetic changes in F1 hybrids of the genetically divergent <i>Solanum</i> L., <i>Solanum melongena</i> L. – <i>Solanum aethiopicum</i> L. <i>Plant Growth Regulation</i> , 0, , .	1.8	0
30765	Toward Best Practices for Imaging Transcriptomics of the Human Brain. <i>Biological Psychiatry</i> , 2023, 93, 391-404.	0.7	23
30767	Construction of a Prognostic Model Based on Cuproptosis-Related lncRNA Signatures in Pancreatic Cancer. <i>Canadian Journal of Gastroenterology and Hepatology</i> , 2022, 2022, 1-12.	0.8	8
30768	Deep learning in drug discovery: an integrative review and future challenges. <i>Artificial Intelligence Review</i> , 2023, 56, 5975-6037.	9.7	32
30769	Combined Transcriptome and Metabolome Profiling Provide Insights into Cold Responses in Rapeseed (<i>Brassica napus</i> L.) Genotypes with Contrasting Cold-Stress Sensitivity. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13546.	1.8	5
30770	Integrative learning of structured high-dimensional data from multiple datasets. <i>Statistical Analysis and Data Mining</i> , 2023, 16, 120-134.	1.4	0
30771	Chronic constriction injury-induced changes in circular RNA expression profiling of the dorsal root ganglion in a rat model of neuropathic pain. <i>BMC Neuroscience</i> , 2022, 23, .	0.8	2
30774	Transcriptomic responses of females to consumption of nuptial food gifts as a potential mediator of sexual conflict in decorated crickets. <i>Journal of Evolutionary Biology</i> , 2023, 36, 183-194.	0.8	1
30775	Glucagon receptor antagonism impairs and glucagon receptor agonism enhances triglycerides metabolism in mice. <i>Molecular Metabolism</i> , 2022, 66, 101639.	3.0	4

#	ARTICLE	IF	CITATIONS
30777	Single-cell RNA-sequencing and microarray analyses to explore the pathological mechanisms of chronic thromboembolic pulmonary hypertension. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	2
30778	Ubiquitin-based pathway acts inside chloroplasts to regulate photosynthesis. <i>Science Advances</i> , 2022, 8, .	4.7	18
30779	Construction and Comprehensive Analysis of miRNAs and Target mRNAs in Longissimus dorsi Muscle of Queshan Black and Large White Pigs. <i>Life</i> , 2022, 12, 1814.	1.1	0
30781	Lipocalin-2 participates in sepsis-induced myocardial injury by mediating lipid accumulation and mitochondrial dysfunction. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	6
30782	Dopamine-inhibited POMCDrd2+ neurons in the ARC acutely regulate feeding and body temperature. <i>JCI Insight</i> , 2022, 7, .	2.3	2
30783	High conopeptide diversity in <i>Conus striatus</i> : Revealed by integration of two transcriptome sequencing platforms. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
30784	A novel cuproptosis-related gene signature of prognosis and immune microenvironment in head and neck squamous cell carcinoma cancer. <i>Journal of Cancer Research and Clinical Oncology</i> , 2023, 149, 203-218.	1.2	10
30785	Ts66Yah, a mouse model of Down syndrome with improved construct and face validity. <i>DMM Disease Models and Mechanisms</i> , 2022, 15, .	1.2	19
30786	Microenvironmental reprogramming of human dermal papilla cells for hair follicle tissue engineering. <i>Acta Biomaterialia</i> , 2023, 165, 31-49.	4.1	7
30787	Deciphering the impact of genetic variation on human polyadenylation using APARENT2. <i>Genome Biology</i> , 2022, 23, .	3.8	12
30788	Altered Cortical Palmitoylation Induces Widespread Molecular Disturbances in Parkinson's Disease. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14018.	1.8	6
30791	Exploration of the shared gene signatures and molecular mechanisms between atherosclerosis and rheumatoid arthritis via multi-microarray data analyses. <i>Annals of Translational Medicine</i> , 2022, 10, 1164-1164.	0.7	0
30792	Ontology development is consensus creation, not (merely) representation. <i>Applied Ontology</i> , 2022, 17, 495-513.	1.0	3
30794	CORUM: the comprehensive resource of mammalian protein complexesâ€“2022. <i>Nucleic Acids Research</i> , 2023, 51, D539-D545.	6.5	34
30795	Novel insight into anthocyanin metabolism and molecular characterization of its key regulators in <i>Camellia sasanqua</i> . <i>Plant Molecular Biology</i> , 2023, 111, 249-262.	2.0	2
30796	Identification and Characterization of Novel Mutations in Chronic Kidney Disease (CKD) and Autosomal Dominant Polycystic Kidney Disease (ADPKD) in Saudi Subjects by Whole-Exome Sequencing. <i>Medicina (Lithuania)</i> , 2022, 58, 1657.	0.8	3
30797	Proteomic Landscape and Deduced Functions of the Cardiac 14-3-3 Protein Interactome. <i>Cells</i> , 2022, 11, 3496.	1.8	11
30798	Longitudinal Epigenome-Wide Analysis of Kidney Transplant Recipients Pretransplant and Posttransplant. <i>Kidney International Reports</i> , 2023, 8, 330-340.	0.4	3

#	ARTICLE	IF	CITATIONS
30799	Transcription Analysis of Liver and Muscle Tissues from Landrace Finishing Pigs with Different Feed Conversion Ratios. <i>Genes</i> , 2022, 13, 2067.	1.0	5
30800	Complementary evolution of coding and noncoding sequence underlies mammalian hairlessness. <i>ELife</i> , 0, 11, .	2.8	13
30801	The single-cell expression profile of transposable elements and transcription factors in human early biparental and uniparental embryonic development. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	4
30802	Construction of a mitochondrial dysfunction related signature of diagnosed model to obstructive sleep apnea. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
30803	Repression of DERL3 via DNA methylation by Epstein-Barr virus latent membrane protein 1 in nasopharyngeal carcinoma. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2023, 1869, 166598.	1.8	4
30804	Identification of hub genes regulating the cell activity and function of adipose-derived stem cells under oxygen-glucose deprivation. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	1
30806	Circulating miRNA Expression Profiling in Breast Cancer Molecular Subtypes: Applying Machine Learning Analysis in Bioinformatics. <i>Cancer Diagnosis & Prognosis</i> , 2022, 2, 739-749.	0.3	4
30807	COMBATdb: a database for the COVID-19 Multi-Omics Blood Atlas. <i>Nucleic Acids Research</i> , 2023, 51, D896-D905.	6.5	4
30808	CD1d-dependent rewiring of lipid metabolism in macrophages regulates innate immune responses. <i>Nature Communications</i> , 2022, 13, .	5.8	10
30809	KRAB family is involved in network shifts in response to osmotic stress in camels. <i>Animal Cells and Systems</i> , 2022, 26, 348-357.	0.8	0
30810	Comparative proteomic analysis reveals differential protein expression of <i>Hypsizygus marmoratus</i> in response to different light qualities. <i>International Journal of Biological Macromolecules</i> , 2022, 223, 1320-1334.	3.6	5
30811	Architecture of the outbred brown fat proteome defines regulators of metabolic physiology. <i>Cell</i> , 2022, 185, 4654-4673.e28.	13.5	9
30812	Protein disulfide isomerase A3 activity promotes extracellular accumulation of proteins relevant to basal breast cancer outcomes in human MDA-MB-A231 breast cancer cells. <i>American Journal of Physiology - Cell Physiology</i> , 2023, 324, C113-C132.	2.1	2
30813	Ontology-based feature engineering in machine learning workflows for heterogeneous epilepsy patient records. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
30814	Inactivation of <i>Notch4</i> Attenuated Pancreatic Tumorigenesis in Mice. <i>Cancer Research Communications</i> , 2022, 2, 1601-1616.	0.7	1
30815	Machine learning algorithm and deep neural networks identified a novel subtype in hepatocellular carcinoma. <i>Cancer Biomarkers</i> , 2022, 35, 305-320.	0.8	2
30816	M2 macrophage-related gene signature in chronic rhinosinusitis with nasal polyps. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	8
30817	Ascertaining cells' synaptic connections and RNA expression simultaneously with barcoded rabies virus libraries. <i>Nature Communications</i> , 2022, 13, .	5.8	4

#	ARTICLE	IF	CITATIONS
30818	Identification of RNA N6-methyladenosine regulation in epilepsy: Significance of the cell death mode, glycometabolism, and drug reactivity. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
30819	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
30820	Chromosome-level genome assembly reveals potential epigenetic mechanisms of the thermal tolerance in the oriental fruit fly, <i>Bactrocera dorsalis</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 225, 430-441.	3.6	6
30822	Derivation of nociceptive sensory neurons from hiPSCs with early patterning and temporally controlled <i>NEUROG2</i> overexpression. <i>Cell Reports Methods</i> , 2022, 2, 100341.	1.4	2
30823	Genome- and transcriptome-wide association studies of 386,000 Asian and European-ancestry women provide new insights into breast cancer genetics. <i>American Journal of Human Genetics</i> , 2022, 109, 2185-2195.	2.6	10
30824	ID1 and CEBPA coordinate epidermal progenitor cell differentiation. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	2
30825	A comparative analysis of telomere length maintenance circuits in fission and budding yeast. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
30826	Cortical profiles of numerous psychiatric disorders and normal development share a common pattern. <i>Molecular Psychiatry</i> , 0, , .	4.1	2
30827	An extracellular receptor tyrosine kinase motif orchestrating intracellular STAT activation. <i>Nature Communications</i> , 2022, 13, .	5.8	3
30831	A prognostic gene signature for gastric cancer and the immune infiltration-associated mechanism underlying the signature gene, <i>PLG</i> . <i>Clinical and Translational Oncology</i> , 0, , .	1.2	2
30832	Metagenomics revealing molecular profiles of microbial community structure and metabolic capacity in Bamucuo lake, Tibet. <i>Environmental Research</i> , 2023, 217, 114847.	3.7	2
30833	Systematic analysis of membrane contact sites in <i>Saccharomyces cerevisiae</i> uncovers modulators of cellular lipid distribution. <i>ELife</i> , 0, 11, .	2.8	14
30834	SmDXS5, acting as a molecular valve, plays a key regulatory role in the primary and secondary metabolism of tanshinones in <i>Salvia miltiorrhiza</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
30835	A molecular signature of lung-resident CD8+ T cells elicited by subunit vaccination. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
30837	miRNAâ€œmRNAâ€œprotein dysregulated network in COPD in women. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
30839	Transcriptomic profiling analysis to identify genes associated with PA biosynthesis and insolubilization in the late stage of fruit development in C-PCNA persimmon. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
30840	LINC00839 promotes malignancy of liver cancer via binding <i>FMNL2</i> under hypoxia. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
30841	Phenotypic and Differential Gene Expression Analyses of Phase Transition in <i>Oedaleus asiaticus</i> under High-Density Population Stress. <i>Insects</i> , 2022, 13, 1034.	1.0	0

#	ARTICLE	IF	CITATIONS
30842	Complete genome sequence of piezotolerant <i>Stutzerimonas kunmingensis</i> 7850S isolated from the sediment of the Mariana Trench. <i>Marine Genomics</i> , 2022, 66, 100996.	0.4	0
30843	De novo molecular subtyping of salivary gland tissue in the context of Sjögren's syndrome heterogeneity. <i>Clinical Immunology</i> , 2022, 245, 109171.	1.4	1
30844	Genome editing and bioinformatics. <i>Gene and Genome Editing</i> , 2022, 3-4, 100018.	1.3	2
30845	Mapping the mutual transcriptional responses during <i>Candida albicans</i> and human macrophage interactions by dual RNA-sequencing. <i>Microbial Pathogenesis</i> , 2022, 173, 105864.	1.3	0
30846	Neutralization of the adaptor protein PAG by monoclonal antibody limits murine tumor growth. <i>Molecular Therapy - Methods and Clinical Development</i> , 2022, 27, 380-390.	1.8	2
30847	GOProFormer: A Multi-Modal Transformer Method for Gene Ontology Protein Function Prediction. <i>Biomolecules</i> , 2022, 12, 1709.	1.8	7
30848	Protein function annotation based on heterogeneous biological networks. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
30851	A Novel Immune-Related Gene Prognostic Index (IRGPI) in Pancreatic Adenocarcinoma (PAAD) and Its Implications in the Tumor Microenvironment. <i>Cancers</i> , 2022, 14, 5652.	1.7	3
30853	ViLoNâ€”a multi-layer network approach to data integration demonstrated for patient stratification. <i>Nucleic Acids Research</i> , 0, , .	6.5	0
30854	Genome-wide <scp>DNA</scp> methylation profiling in tongue squamous cell carcinoma. <i>Oral Diseases</i> , 2024, 30, 259-271.	1.5	0
30857	Complete genome analysis of <i>Pseudomonas furukawaii</i> ZS1 isolated from grass carp (<i>Ctenopharyngodon idellus</i>) culture water. <i>Genome</i> , 0, , .	0.9	1
30858	On the Feasibility of Using an Ultra-Fast DirectMS1 Method of Proteome-Wide Analysis for Searching Drug Targets in Chemical Proteomics. <i>Biochemistry (Moscow)</i> , 2022, 87, 1342-1353.	0.7	1
30859	Genomic signals of local adaptation and hybridization in Asian white birch. <i>Molecular Ecology</i> , 2023, 32, 595-612.	2.0	4
30860	Parallel evolution of amphioxus and vertebrate small-scale gene duplications. <i>Genome Biology</i> , 2022, 23, .	3.8	14
30862	A Pan-Transcriptome Analysis Indicates Efficient Downregulation of the FIB Genes Plays a Critical Role in the Response of Alfalfa to Cold Stress. <i>Plants</i> , 2022, 11, 3148.	1.6	3
30864	Transcriptome analysis reveals genes expression pattern of <i>Spirodela polyrhiza</i> response to heat stress. <i>International Journal of Biological Macromolecules</i> , 2023, 225, 767-775.	3.6	6
30865	Semantic interoperability: ontological unpacking of a viral conceptual model. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	4
30866	Comprehensive analysis of a red-peel kiwi berry mutant reveals key genes are responsible for anthocyanin biosynthesis in fruit. <i>Scientia Horticulturae</i> , 2023, 309, 111682.	1.7	2

#	ARTICLE	IF	CITATIONS
30867	Potential targets and mechanisms of photobiomodulation for spinal cord injury. <i>Neural Regeneration Research</i> , 2022, .	1.6	0
30868	Biomedical knowledge graph embeddings for personalized medicine: Predicting disease-gene associations. <i>Expert Systems</i> , 2023, 40, .	2.9	5
30869	Peripheral blood mononuclear cell phenotype and function are maintained after overnight shipping of whole blood. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
30874	Evidence of shared transcriptomic dysregulation of HNRNPU-related disorder between human organoids and embryonic mice. <i>IScience</i> , 2023, 26, 105797.	1.9	4
30875	Structural characterization of four <i>Rhododendron</i> spp. chloroplast genomes and comparative analyses with other azaleas. <i>Biocell</i> , 2023, 47, 657-668.	0.4	1
30876	Cis-regulatory Element Frequency Modules and their Phase Transition across Hominidae. <i>Springer Handbooks of Computational Statistics</i> , 2022, , 371-395.	0.2	0
30877	Chemical tools for study and modulation of biomolecular phase transitions. <i>Chemical Science</i> , 2022, 13, 14226-14245.	3.7	4
30878	PlagueKD: a knowledge graph-based plague knowledge database. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	1
30879	Parallel Exchange of Randomized SubGraphs for Optimization of Network Alignment: PERSONA. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, , 1-14.	1.9	0
30880	Multi-View Clustering for Integration of Gene Expression and Methylation Data With Tensor Decomposition and Self-Representation Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 2050-2063.	1.9	4
30881	A Network Pharmacological Approach to Explore the Mechanisms of TongXieYaoFang in Inflammatory Bowel Disease. <i>Brazilian Journal of Pharmaceutical Sciences</i> , 0, 58, .	1.2	0
30882	A Chromosome-level assembly of the Japanese eel genome, insights into gene duplication and chromosomal reorganization. <i>GigaScience</i> , 2022, 11, .	3.3	4
30883	GCompare: An R package to compare functional enrichment analysis between two species. <i>Genomics</i> , 2023, 115, 110528.	1.3	0
30884	Leveraging class hierarchy for detecting missing annotations on hierarchical multi-label classification. <i>Computers in Biology and Medicine</i> , 2023, 152, 106423.	3.9	1
30885	A statistical perspective of gene set analysis with trait-specific QTL in molecular crop breeding. , 2023, , 17-43.		0
30886	The Caribbean-Hispanic Alzheimer's disease brain transcriptome reveals ancestry-specific disease mechanisms. <i>Neurobiology of Disease</i> , 2023, 176, 105938.	2.1	5
30887	Extracellular matrix-based sticky sealants for scar-free corneal tissue reconstruction. <i>Biomaterials</i> , 2023, 292, 121941.	5.7	8
30888	Chromosomal-level genome and multi-omics dataset provides new insights into leaf pigmentation in <i>Acer palmatum</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 227, 93-104.	3.6	4

#	ARTICLE	IF	CITATIONS
30889	Trypanosoma evansi secretome carries potential biomarkers for Surra diagnosis. Journal of Proteomics, 2023, 272, 104789.	1.2	2
30890	Transcriptome analysis revealed mechanisms involved in improved germination and growth of sugarcane by ultrasonic treatment. Industrial Crops and Products, 2023, 192, 116104.	2.5	6
30891	Two faces of TEMPO (2,2,6,6-tetramethylpiperidinyl-1-oxyl) – An antioxidant or a toxin?. Biochimica Et Biophysica Acta - Molecular Cell Research, 2023, 1870, 119412.	1.9	4
30892	The complete genome sequence of Pseudomonas chengduensis BC1815 for genome mining of PET degrading enzymes. Marine Genomics, 2023, 67, 101008.	0.4	3
30893	Genomic analysis of Marinimicrobium sp. C6131 reveals its genetic potential involved in chitin metabolism. Marine Genomics, 2023, 67, 101007.	0.4	0
30894	Genome-wide identification, characterization, and expression profile ofNBS-LRRgene family in sweet orange (Citrus sinensis). Gene, 2023, 854, 147117.	1.0	10
30895	Bioactivity of bacteria associated with Red Sea nudibranchs and whole genome sequence of Nocardiosis dassonvillei RACA-4. Marine Genomics, 2023, 67, 101004.	0.4	2
30896	De novo transcriptome assembly of Coffea liberica reveals phylogeny and expression atlas of phenylalanine ammonia-lyase genes in Coffea species. Industrial Crops and Products, 2023, 192, 116029.	2.5	0
30897	Genome-wide characterization of the common bean kinome: Catalog and insights into expression patterns and genetic organization. Gene, 2023, 855, 147127.	1.0	3
30898	Comprehensive analysis of necroptosis-related long noncoding RNA to predict prognosis, immune status, and immunotherapeutic response in clear cell renal cell carcinoma. Translational Cancer Research, 2021, .	0.4	0
30899	Protein Molecular Function Annotation Based onTransformer Embeddings. Lecture Notes in Computer Science, 2022, , 210-220.	1.0	0
30900	Paralog Explorer: A resource for mining information about paralogs in common research organisms. Computational and Structural Biotechnology Journal, 2022, 20, 6570-6577.	1.9	7
30901	Comparison of functional classification systems. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	1
30903	Analysis of the Antioxidant Mechanism of Tamarix ramosissima Roots under NaCl Stress Based on Physiology, Transcriptomic and Metabolomic. Antioxidants, 2022, 11, 2362.	2.2	2
30904	Single-Cell Sequencing Reveals the Regulatory Role of Maresin1 on Neutrophils during Septic Lung Injury. Cells, 2022, 11, 3733.	1.8	0
30905	Identification of the Inner Cell Mass and the Trophectoderm Responses after an In Vitro Exposure to Glucose and Insulin during the Preimplantation Period in the Rabbit Embryo. Cells, 2022, 11, 3766.	1.8	1
30906	Cancer subtyping with heterogeneous multi-omics data via hierarchical multi-kernel learning. Briefings in Bioinformatics, 2023, 24, .	3.2	2
30907	Draft Genome Sequence of Carrot Alternaria Leaf Blight Pathogen <i>Alternaria dauci</i> . Plant Disease, 2023, 107, 2197-2200.	0.7	1

#	ARTICLE	IF	CITATIONS
30908	Nucleosomes and their complexes in the cryoEM era: Trends and limitations. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	2
30909	Optimal construction of a functional interaction network from pooled library CRISPR fitness screens. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	3
30911	Blood transcriptome comparison between sexes and their function in 4-week Rhode Island red chickens. <i>Animal Cells and Systems</i> , 2022, 26, 358-368.	0.8	1
30912	Regeneration pattern and genome-wide transcription profile of rhizome axillary buds after perennial rice harvest. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
30915	NUSAP1 and PCLAF (KIA0101) Downregulation by Neoadjuvant Therapy is Associated with Better Therapeutic Outcomes and Survival in Breast Cancer. <i>Journal of Oncology</i> , 2022, 2022, 1-14.	0.6	1
30916	Overexpression of a novel gene (Pt2015) endows the commercial diatom <i>Phaeodactylum tricornutum</i> high lipid content and grazing resistance. , 2022, 15, .		2
30919	Genomic basis of the giga-chromosomes and giga-genome of tree peony <i>Paeonia ostii</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	16
30920	Terminal Uridylyltransferases TUT4/7 Regulate microRNA and mRNA Homeostasis. <i>Cells</i> , 2022, 11, 3742.	1.8	2
30922	Transection injury differentially alters the proteome of the human sural nerve. <i>PLoS ONE</i> , 2022, 17, e0260998.	1.1	3
30923	Meta-analysis of genome-wide association studies uncovers shared candidate genes across breeds for pig fatness trait. <i>BMC Genomics</i> , 2022, 23, .	1.2	7
30924	Transcriptome profiling of <i>Paraburkholderia aromaticivorans</i> AR20-38 during ferulic acid bioconversion. <i>AMB Express</i> , 2022, 12, .	1.4	1
30926	Controlled and Synchronised Vascular Regeneration upon the Implantation of Iloprost- and Cationic Amphiphilic Drugs-Conjugated Tissue-Engineered Vascular Grafts into the Ovine Carotid Artery: A Proteomics-Empowered Study. <i>Polymers</i> , 2022, 14, 5149.	2.0	4
30927	African Suid Genomes Provide Insights into the Local Adaptation to Diverse African Environments. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
30928	Comparative transcriptomic and metabolomic analyses reveal the delaying effect of naringin on postharvest decay in citrus fruit. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
30929	Changes of Mutations and Copy Number and Enhanced Cell Migration during Breast Tumorigenesis. <i>Advanced Biology</i> , 0, , 2200072.	1.4	0
30930	A Model-Based Prognostic Predictor for Urothelial Bladder Carcinoma Through the Integrated Bioinformatics Analysis. , 2022, , .		0
30932	Cis-regulatory mutations associate with transcriptional and post-transcriptional deregulation of gene regulatory programs in cancers. <i>Nucleic Acids Research</i> , 2022, 50, 12131-12148.	6.5	2
30933	Unveiling sex-based differences in Parkinson's disease: a comprehensive meta-analysis of transcriptomic studies. <i>Biology of Sex Differences</i> , 2022, 13, .	1.8	20

#	ARTICLE	IF	CITATIONS
30934	1,25(OH)2D3 Promotes Macrophage Efferocytosis Partly by Upregulating ASAP2 Transcription via the VDR-Bound Enhancer Region and ASAP2 May Affect Antiviral Immunity. <i>Nutrients</i> , 2022, 14, 4935.	1.7	3
30936	Calcioprotein Particles Cause Physiologically Significant Pro-Inflammatory Response in Endothelial Cells and Systemic Circulation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14941.	1.8	6
30937	First insight into H3K4me3 modification in the rapid growth of <i>Alexandrium pacificum</i> (dinoflagellates). <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
30938	Multi-omics analysis identifies osteosarcoma subtypes with distinct prognosis indicating stratified treatment. <i>Nature Communications</i> , 2022, 13, .	5.8	20
30939	Comparative transcriptome analysis of wheat in response to corn leaf aphid, <i>Rhopalosiphum maidis</i> F. infestation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
30940	A tumor vasculature-based imaging biomarker for predicting response and survival in patients with lung cancer treated with checkpoint inhibitors. <i>Science Advances</i> , 2022, 8, .	4.7	6
30942	Transcriptomics Profiling of <i>Acer pseudosieboldianum</i> Molecular Mechanism against Freezing Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14676.	1.8	1
30943	Characteristics of the Genome, Transcriptome and Ganoderic Acid of the Medicinal Fungus <i>Ganoderma lingzhi</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1257.	1.5	3
30944	LncRNA-mRNA co-expression analysis revealed 8 core lncRNAs in rheumatoid arthritis of collagen-induced arthritis rats. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	0
30945	Combined transcriptome and metabolome analysis revealed pathways involved in improved salt tolerance of <i>Gossypium hirsutum</i> L. seedlings in response to exogenous melatonin application. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
30947	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
30949	Analysis of the Potential Relationship between Aging and Pulmonary Fibrosis Based on Transcriptome. <i>Life</i> , 2022, 12, 1961.	1.1	0
30950	Salvage Chemotherapy with Cisplatin, Ifosfamide, and Paclitaxel in Aggressive Variant of Metastatic Castration-Resistant Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14948.	1.8	2
30951	MAP4K4/JNK Signaling Pathway Stimulates Proliferation and Suppresses Apoptosis of Human Spermatogonial Stem Cells and Lower Level of MAP4K4 Is Associated with Male Infertility. <i>Cells</i> , 2022, 11, 3807.	1.8	1
30952	UV-B induces the expression of flavonoid biosynthetic pathways in blueberry (<i>Vaccinium corymbosum</i>) calli. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	9
30953	Pharos 2023: an integrated resource for the understudied human proteome. <i>Nucleic Acids Research</i> , 2023, 51, D1405-D1416.	6.5	22
30954	A single N6-methyladenosine site regulates lncRNA HOTAIR function in breast cancer cells. <i>PLoS Biology</i> , 2022, 20, e3001885.	2.6	15
30955	P<i> </i>DBPred: a novel computational model for discovery of DNA binding proteins in plants. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	6

#	ARTICLE	IF	CITATIONS
30956	Host transcriptome and microbiome interactions in Holstein cattle under heat stress condition. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
30957	Genome-Wide Gene-Set Analysis Approaches in Amyotrophic Lateral Sclerosis. <i>Journal of Personalized Medicine</i> , 2022, 12, 1932.	1.1	2
30958	Bone Marrow Macrophages Induce Inflammation by Efferocytosis of Apoptotic Prostate Cancer Cells via HIF-1 α Stabilization. <i>Cells</i> , 2022, 11, 3712.	1.8	3
30959	Inference of epigenetic subnetworks by Bayesian regression with the incorporation of prior information. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
30960	Identification of a novel cell cycle-related risk signature predicting prognosis in patients with pancreatic adenocarcinoma. <i>Medicine (United States)</i> , 2022, 101, e29683.	0.4	2
30961	Genes related to allergen exposure in allergic rhinitis: a gene-chip-based study in a mouse model. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	0
30962	Identification of immune cell function in breast cancer by integrating multiple single-cell data. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
30963	The effect of SNPs in lncRNA as ceRNA on the risk and prognosis of hepatocellular carcinoma. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
30965	A Genome-Wide Association Study Reveals a BDNF-Centered Molecular Network Associated with Alcohol Dependence and Related Clinical Measures. <i>Biomedicines</i> , 2022, 10, 3007.	1.4	1
30966	Proteomic characterization of spontaneously regrowing spinal cord following injury in the teleost fish <i>Apteronotus leptorhynchus</i> , a regeneration-competent vertebrate. <i>Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology</i> , 2022, 208, 671-706.	0.7	1
30967	Limited carbon cycling due to high-pressure effects on the deep-sea microbiome. <i>Nature Geoscience</i> , 2022, 15, 1041-1047.	5.4	12
30968	Whole-genome methylation analysis reveals epigenetic variation between wild-type and nontransgenic cloned, ASMT transgenic cloned dairy goats generated by the somatic cell nuclear transfer. <i>Journal of Animal Science and Biotechnology</i> , 2022, 13, .	2.1	2
30969	Kinase signalling in excitatory neurons regulates sleep quantity and depth. <i>Nature</i> , 2022, 612, 512-518.	18.7	25
30970	Heightened cocaine-seeking in male rats associates with a distinct transcriptomic profile in the medial prefrontal cortex. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	3
30971	Improving automatic GO annotation with semantic similarity. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	3
30972	Characterization and genetic dissection of maize ear leaf midrib acquired by 3D digital technology. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
30973	Impacts of multiple anthropogenic stressors on the transcriptional response of <i>Gammarus fossarum</i> in a mesocosm field experiment. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
30974	Drug Side Effect Prediction with Deep Learning Molecular Embedding in a Graph-of-Graphs Domain. <i>Mathematics</i> , 2022, 10, 4550.	1.1	1

#	ARTICLE	IF	CITATIONS
30975	Scrutiny of NolA and NodD1 Regulatory Roles in Symbiotic Compatibility Unveils New Insights into Bradyrhizobium guangxiense CCBAU53363 Interacting with Peanut (Arachis hypogaea) and Mung Bean (Vigna radiata). Microbiology Spectrum, 2023, 11, .	1.2	2
30976	Analysis of protein expression changes in patients with prediabetes using proteomics approaches. Rapid Communications in Mass Spectrometry, 2023, 37, .	0.7	1
30977	Inhibition of cholesterol transport impairs Cavâ€ trafficking and small extracellular vesicles secretion, promoting amphisome formation in melanoma cells. Traffic, 2023, 24, 76-94.	1.3	5
30978	Identification of key programmed cell death-related genes and immune infiltration in extracorporeal membrane oxygenation treatment for acute myocardial infarction based on bioinformatics analysis. Frontiers in Cardiovascular Medicine, 0, 9, .	1.1	0
30979	Genomic and metabolic features of Bacillus cereus, inhibiting the growth of Sclerotinia sclerotiorum by synthesizing secondary metabolites. Archives of Microbiology, 2023, 205, .	1.0	6
30980	Integrated transcriptome-proteome analyses of human stem cells reveal source-dependent differences in their regenerative signature. Stem Cell Reports, 2022, , .	2.3	4
30982	Transcriptomic changes underlying glucocorticoid-induced suppression of milk production by dairy cows. Frontiers in Genetics, 0, 13, .	1.1	1
30983	Glycated Proteins, Glycine, Acetate, and Monounsaturated Fatty Acids May Act as New Biomarkers to Predict the Progression of Type 2 Diabetes: Secondary Analyses of a Randomized Controlled Trial. Nutrients, 2022, 14, 5165.	1.7	1
30984	Phenotypic analysis of Longya-10 Å— pale flax hybrid progeny and identification of candidate genes regulating prostrate/erect growth in flax plants. Frontiers in Plant Science, 0, 13, .	1.7	1
30985	High-Throughput Sequencing Reveals Novel microRNAs Involved in the Continuous Flowering Trait of Longan (Dimocarpus longan Lour.). International Journal of Molecular Sciences, 2022, 23, 15565.	1.8	3
30986	Bioinformatics-based analysis of potential candidates chromatin regulators for immune infiltration in osteoarthritis. BMC Musculoskeletal Disorders, 2022, 23, .	0.8	1
30987	Circulating miRNA Expression Profiles and Machine Learning Models in Association with Response to Irinotecan-Based Treatment in Metastatic Colorectal Cancer. International Journal of Molecular Sciences, 2023, 24, 46.	1.8	3
30988	Selective extracellular secretion of small double-stranded RNA by Tetragenococcus halophilus. Functional and Integrative Genomics, 2023, 23, .	1.4	1
30990	Single-cell transcriptome reveals dominant subgenome expression and transcriptional response to heat stress in Chinese cabbage. Genome Biology, 2022, 23, .	3.8	16
30991	Inhibiting Cyclin B1-treated Pontine Infarction by Suppressing Proliferation of SPP1+ Microglia. Molecular Neurobiology, 2023, 60, 1782-1796.	1.9	2
30992	Plantain flour: A potential anti-obesity ingredient for intestinal flora regulation and improved hormone secretion. Frontiers in Sustainable Food Systems, 0, 6, .	1.8	3
30993	Development of a Cancer-Associated Fibroblast-Related Prognostic Model in Breast Cancer via Bulk and Single-Cell RNA Sequencing. BioMed Research International, 2022, 2022, 1-26.	0.9	3
30994	Role of aerobic exercise in ameliorating NASH: Insights into the hepatic thyroid hormone signaling and circulating thyroid hormones. Frontiers in Endocrinology, 0, 13, .	1.5	1

#	ARTICLE	IF	CITATIONS
30995	Multi-scale pathology image texture signature is a prognostic factor for resectable lung adenocarcinoma: a multi-center, retrospective study. <i>Journal of Translational Medicine</i> , 2022, 20, .	1.8	3
30996	Common Assays in Mammalian Golgi Studies. <i>Methods in Molecular Biology</i> , 2023, , 303-332.	0.4	1
30997	Alterations in the serum proteome following electroconvulsive therapy for a major depressive episode: a longitudinal multicenter study. <i>Biological Psychiatry Global Open Science</i> , 2022, , .	1.0	0
30999	Molecular docking, ADMET profiling of gallic acid and its derivatives (N-alkyl gallamide) as an anti-breast cancer agent. <i>F1000Research</i> , 0, 11, 1453.	0.8	0
31001	Characterizing corn-straw-degrading actinomycetes and evaluating application efficiency in straw-returning experiments. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
31002	Synthetic lethal gene pairs: Experimental approaches and predictive models. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
31003	Autoencoder Networks Decipher the Association between Lung Cancer and Alzheimer's Disease. <i>Computational Intelligence and Neuroscience</i> , 2022, 2022, 1-11.	1.1	1
31005	Graphene quantum dots induce cascadic apoptosis via interaction with proteins associated with anti-oxidation after endocytosis by <i>Trypanosoma brucei</i> . <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
31007	Transcriptomic FHL1 ^{low} /pHER2 ^{high} signature as a predictive factor of outcome and immunotherapy response in non-small cell lung cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
31008	The SsAtg1 Activating Autophagy Is Required for Sclerotia Formation and Pathogenicity in <i>Sclerotinia sclerotiorum</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1314.	1.5	4
31010	Transcriptome Analysis for Flooding Stress-related Gene Identification in <i>Glycine soja</i> . <i>Han'guk Yukchong Hakhoe Chi</i> , 2022, 54, 315-330.	0.2	0
31011	Toxicogenomics Data for Chemical Safety Assessment and Development of New Approach Methodologies: An Adverse Outcome Pathway-Based Approach. <i>Advanced Science</i> , 2023, 10, .	5.6	7
31012	Testing the chilling-before drought-tolerance hypothesis in Pooideae grasses. <i>Molecular Ecology</i> , 2023, 32, 772-785.	2.0	1
31013	Differentially expressed gene profiles and associated ceRNA network in ATG7-Deficient lens epithelial cells under oxidative stress. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
31014	Baicalein Relieves Ferroptosis-Mediated Phagocytosis Inhibition of Macrophages in Ovarian Endometriosis. <i>Current Issues in Molecular Biology</i> , 2022, 44, 6189-6204.	1.0	5
31015	Fatty acids derived from the probiotic <i>Lactobacillus rhamnosus</i> HA-114 suppress age-dependent neurodegeneration. <i>Communications Biology</i> , 2022, 5, .	2.0	12
31017	Early prediction and longitudinal modeling of preeclampsia from multiomics. <i>Patterns</i> , 2022, 3, 100655.	3.1	18
31018	Dynamic chromatin organization and regulatory interactions in human endothelial cell differentiation. <i>Stem Cell Reports</i> , 2023, 18, 159-174.	2.3	3

#	ARTICLE	IF	CITATIONS
31019	A new framework for host-pathogen interaction research. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
31020	Transcriptome analysis provides insights into light condition effect on paclitaxel biosynthesis in yew saplings. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
31021	Overview of STEM Science as Process, Method, Material, and Data Named Entities. <i>Knowledge</i> , 2022, 2, 735-754.	0.7	0
31022	Senescence atlas reveals an aged-like inflamed niche that blunts muscle regeneration. <i>Nature</i> , 2023, 613, 169-178.	13.7	90
31024	Integrated analysis of necroptosis-related genes for evaluating immune infiltration and colon cancer prognosis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	6
31025	Cross-species cell-type assignment from single-cell RNA-seq data by a heterogeneous graph neural network. <i>Genome Research</i> , 2023, 33, 96-111.	2.4	11
31026	Integrating genome-wide methylation and transcriptome-wide analyses to reveal the genetic mechanism of milk traits in Kazakh horses. <i>Gene</i> , 2023, 856, 147143.	1.0	2
31027	Bioinformatics analysis of key biomarkers for bladder cancer. <i>Biomedical Reports</i> , 2022, 18, .	0.9	2
31028	SFRP2 Overexpression Induces an Osteoblast-like Phenotype in Prostate Cancer Cells. <i>Cells</i> , 2022, 11, 4081.	1.8	4
31031	Gene expression associations with body mass index in the Multi-Ethnic Study of Atherosclerosis. <i>International Journal of Obesity</i> , 2023, 47, 109-116.	1.6	1
31032	Comparative Proteomics Analysis of Growth-Primed Adult Dorsal Root Ganglia Reveals Key Molecular Mediators for Peripheral Nerve Regeneration. <i>ENeuro</i> , 2023, 10, ENEURO.0168-22.2022.	0.9	2
31033	Making sense of fragmentation and merging in lineage tracing experiments. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	2
31035	<scp>COLLAPSE</scp>: A representation learning framework for identification and characterization of protein structural sites. <i>Protein Science</i> , 2023, 32, .	3.1	4
31036	Ontology Completion with Graph-Based Machine Learning: A Comprehensive Evaluation. <i>Machine Learning and Knowledge Extraction</i> , 2022, 4, 1107-1123.	3.2	0
31038	CODA: a combo-Seq data analysis workflow. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	1
31039	Comprehensive Prognostic Analysis of Immune Implication Value and Oxidative Stress Significance of NECAP2 in Low-Grade Glioma. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-39.	1.9	3
31042	DNA methylation and hydroxymethylation characterize the identity of D1 and D2 striatal projection neurons. <i>Communications Biology</i> , 2022, 5, .	2.0	4
31043	A simplified and defined serum-free medium for cultivating fat across species. <i>IScience</i> , 2023, 26, 105822.	1.9	15

#	ARTICLE	IF	CITATIONS
31044	Proteomic Analysis of Meibomian Gland Secretions in Patients With Blepharokeratoconjunctivitis. <i>Translational Vision Science and Technology</i> , 2022, 11, 4.	1.1	0
31045	Physiological changes and gene responses during <i>Ganoderma lucidum</i> growth with selenium supplementation. <i>PeerJ</i> , 0, 10, e14488.	0.9	1
31046	Genome-wide identification, characterization, evolution, and expression pattern analyses of the typical thioredoxin gene family in wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
31049	mOWL: Python library for machine learning with biomedical ontologies. <i>Bioinformatics</i> , 2023, 39, .	1.8	1
31050	Proteomic Profiling Reveals Distinct Bacterial Extracellular Vesicle Subpopulations with Possibly Unique Functionality. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	1.4	4
31052	Co-expression of fibrotic genes in inflammatory bowel disease; A localized event?. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
31053	Therapeutic role of Artemether in the prevention of hepatic steatosis through miR-34a/PPAR γ pathway. <i>Drug Development Research</i> , 2023, 84, 156-171.	1.4	1
31054	Ecology, Not Host Phylogeny, Shapes the Oral Microbiome in Closely Related Species. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	8
31055	Isobaric labeling-based quantitative proteomics of FACS-purified immune cells and epithelial cells from the intestine of Crohn's disease patients reveals proteome changes of potential importance in disease pathogenesis. <i>Proteomics</i> , 0, , 2200366.	1.3	1
31057	The molecular evolution of spermatogenesis across mammals. <i>Nature</i> , 2023, 613, 308-316.	13.7	40
31058	Transcriptome profiling of two <i>Moringa</i> species and insights into their antihyperglycemic activity. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2
31059	Small RNA perspective of physical exercise-related improvement of male reproductive dysfunction due to obesity. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	0
31060	Interference with orco gene expression affects host recognition in <i>Diorhabda tarsalis</i> . <i>Frontiers in Physiology</i> , 0, 13, .	1.3	1
31061	Clinical proteomics towards multiomics in cancer. <i>Mass Spectrometry Reviews</i> , 0, , .	2.8	6
31062	Hsa-circ-0052001 promotes gastric cancer cell proliferation and invasion via the MAPK pathway. <i>Cancer Medicine</i> , 2023, 12, 7246-7257.	1.3	3
31063	A comprehensive review on rhubarb astringent/ laxative actions and the role of aquaporins as hub genes. <i>Phytochemistry Reviews</i> , 2023, 22, 565-586.	3.1	2
31064	RNA-Seq-based transcriptome analysis of methicillin-resistant <i>Staphylococcus aureus</i> growth inhibition by propionate. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
31065	miR-495-3p sensitizes BCR-ABL1-expressing leukemic cells to tyrosine kinase inhibitors by targeting multidrug resistance 1 gene in T3151 mutated cells. <i>Experimental Hematology</i> , 2023, 118, 40-52.	0.2	6

#	ARTICLE	IF	CITATIONS
31066	MycoCosm, the JGI's Fungal Genome Portal for Comparative Genomic and Multiomics Data Analyses. <i>Methods in Molecular Biology</i> , 2023, , 271-291.	0.4	7
31068	DrugCentral 2023 extends human clinical data and integrates veterinary drugs. <i>Nucleic Acids Research</i> , 2023, 51, D1276-D1287.	6.5	18
31069	Molecular cartooning with knowledge graphs. <i>Frontiers in Bioinformatics</i> , 0, 2, .	1.0	0
31070	Deep-Learning Algorithm and Concomitant Biomarker Identification for NSCLC Prediction Using Multi-Omics Data Integration. <i>Biomolecules</i> , 2022, 12, 1839.	1.8	7
31071	Polystyrene nanoplastics affect transcriptomic and epigenomic signatures of human fibroblasts and derived induced pluripotent stem cells: Implications for human health. <i>Environmental Pollution</i> , 2023, 320, 120849.	3.7	3
31072	RNA-Sequencing Muscle Plasticity to Resistance Exercise Training and Disuse in Youth and Older Age. <i>Physiologia</i> , 2022, 2, 164-179.	0.6	0
31074	Graph-based autoencoder integrates spatial transcriptomics with chromatin images and identifies joint biomarkers for Alzheimer's disease. <i>Nature Communications</i> , 2022, 13, .	5.8	14
31075	Differential methylation patterns in lean and obese non-alcoholic steatohepatitis-associated hepatocellular carcinoma. <i>BMC Cancer</i> , 2022, 22, .	1.1	5
31076	Environment and genotype predict the genomic nature of domestication of salmonids as revealed by gene expression. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	2
31077	High-Throughput DNA Metabarcoding as an Approach for Ichthyoplankton Survey in Oujiang River Estuary, China. <i>Diversity</i> , 2022, 14, 1111.	0.7	4
31079	Temporal Analysis Reveals the Transient Differential Expression of Transcription Factors That Underlie the Trans-Differentiation of Human Monocytes to Macrophages. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15830.	1.8	0
31080	Genome-wide identification, characterization, and evolutionary analysis of NBS genes and their association with disease resistance in <i>Musa</i> spp.. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	2
31081	Transcriptomic reveals the ferroptosis features of host response in a mouse model of Zika virus infection. <i>Journal of Medical Virology</i> , 2023, 95, .	2.5	6
31083	The transcriptomic landscape of neurons carrying PSEN1 mutations reveals changes in extracellular matrix components and non-coding gene expression. <i>Neurobiology of Disease</i> , 2023, 178, 105980.	2.1	6
31084	Transcriptomic analyses provide new insights into green and purple color pigmentation in <i>Rheum tanguticum</i> medicinal plants. <i>PeerJ</i> , 0, 10, e14265.	0.9	0
31085	Grain protein function prediction based on self-attention mechanism and bidirectional LSTM. <i>Briefings in Bioinformatics</i> , 0, , .	3.2	1
31086	Evaluation of Indian Mustard Genotypes for White Rust Resistance Using BjuWRR1 Gene and Their Phenotypic Performance. <i>Agronomy</i> , 2022, 12, 3122.	1.3	1
31087	CpG Site-Based Signature Predicts Survival of Colorectal Cancer. <i>Biomedicines</i> , 2022, 10, 3163.	1.4	3

#	ARTICLE	IF	CITATIONS
31088	How to survive in the world's third poplar: Insights from the genome of the highest altitude woody plant, <i>Hippophae tibetana</i> (Elaeagnaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
31089	Transcriptomic analysis of spleen B cell revealed the molecular basis of bursopentin on B cell differentiation. <i>Veterinary Research</i> , 2022, 53, .	1.1	0
31090	Population diversity analyses provide insights into key horticultural traits of Chinese native thymes. <i>Horticulture Research</i> , 2023, 10, .	2.9	2
31091	Common targetable inflammatory pathways in brain transcriptome of autism spectrum disorders and Tourette syndrome. <i>Frontiers in Neuroscience</i> , 0, 16, .	1.4	2
31092	Drug Repurposing Using Gene Co-Expression and Module Preservation Analysis in Acute Respiratory Distress Syndrome (ARDS), Systemic Inflammatory Response Syndrome (SIRS), Sepsis, and COVID-19. <i>Biology</i> , 2022, 11, 1827.	1.3	5
31094	Transcriptome analyses of different edible tissues of <i>Clanis bilineata tsingtauca</i> (Lepidoptera: Tj ETQq1 1 0,784314 rgBT /Ove	2.1	6
31097	Transcriptome analysis and cytochrome P450 monooxygenase reveal the molecular mechanism of Bisphenol A degradation by <i>Pseudomonas putida</i> strain YC-AE1. <i>BMC Microbiology</i> , 2022, 22, .	1.3	5
31099	A comparison of the genes and genesets identified by GWAS and EWAS of fifteen complex traits. <i>Nature Communications</i> , 2022, 13, .	5.8	6
31101	Thousands of human non-AUG extended proteoforms lack evidence of evolutionary selection among mammals. <i>Nature Communications</i> , 2022, 13, .	5.8	7
31102	Elucidating the Gene Signatures and Immune Cell Types in HIV-Infected Immunological Non-Responders by Bioinformatics Analyses. <i>International Journal of General Medicine</i> , 0, Volume 15, 8491-8507.	0.8	1
31103	Denisovan introgression has shaped the immune system of present-day Papuans. <i>PLoS Genetics</i> , 2022, 18, e1010470.	1.5	9
31104	<i>Syringa oblata</i> genome provides new insights into molecular mechanism of flower color differences among individuals and biosynthesis of its flower volatiles. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
31106	HEC-ASD: a hybrid ensemble-based classification model for predicting autism spectrum disorder disease genes. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	2
31107	Sex-stratified RNA-seq analysis reveals traumatic brain injury-induced transcriptional changes in the female hippocampus conducive to dementia. <i>Frontiers in Neurology</i> , 0, 13, .	1.1	0
31108	Tear-derived exosomal biomarkers of Graves' ophthalmopathy. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4
31110	Integrating unsupervised language model with triplet neural networks for protein gene ontology prediction. <i>PLoS Computational Biology</i> , 2022, 18, e1010793.	1.5	10
31111	A pyroptosis-related gene signature for prognostic and immunological evaluation in breast cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
31112	An improved assembly of the 'Cascade' hop (<i>Humulus lupulus</i>) genome uncovers signatures of molecular evolution and refines time of divergence estimates for the Cannabaceae family. <i>Horticulture Research</i> , 2023, 10, .	2.9	2

#	ARTICLE	IF	CITATIONS
31113	Ecological and Confined Domain Ontology Construction Scheme Using Concept Clustering for Knowledge Management. <i>Applied Sciences (Switzerland)</i> , 2023, 13, 32.	1.3	2
31114	Metagenomic characterization of the maternal prenatal gastrointestinal microbiome by pregravid BMI. <i>Obesity</i> , 2023, 31, 412-422.	1.5	1
31116	Early Diagnosis of Brain Diseases Using Artificial Intelligence and EV Molecular Data: A Proposed Noninvasive Repeated Diagnosis Approach. <i>Cells</i> , 2023, 12, 102.	1.8	0
31117	High throughput drug screening identifies resveratrol as suppressor of hepatic SELENOP expression. <i>Redox Biology</i> , 2023, 59, 102592.	3.9	5
31118	Identification of Key Genes from the Visceral Adipose Tissues of Overweight/Obese Adults with Hypertension through Transcriptome Sequencing. <i>Cytogenetic and Genome Research</i> , 2022, 162, 541-559.	0.6	1
31120	The immune landscape of high-grade brain tumor after treatment with immune checkpoint blockade. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
31121	Acute and chronic blood serum proteome changes in patients with methanol poisoning. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
31123	Genome-wide association studies on collagen contents trait for meat quality in Hanwoo.. <i>Journal of Animal Science and Technology</i> , 0, , .	0.8	0
31124	Anti-cancer effects of ginsenoside CK on acute myeloid leukemia in vitro and in vivo. <i>Heliyon</i> , 2022, 8, e12106.	1.4	1
31126	TYK2 correlates with immune infiltration: A prognostic marker for head and neck squamous cell carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
31128	The draft genome of the Tibetan partridge (<i>Perdix hodgsoniae</i>) provides insights into its phylogenetic position and high-altitude adaptation. <i>Journal of Heredity</i> , 0, , .	1.0	2
31130	Weighted gene co-expression network reveals driver genes contributing to phenotypes of anaplastic thyroid carcinoma and immune checkpoint identification for therapeutic targets. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	2
31131	Mitochondria and Endoplasmic Reticulum Stress in Retinal Organoids from Patients with Vision Loss. <i>American Journal of Pathology</i> , 2023, 193, 1721-1739.	1.9	6
31132	A Novel Immune Gene-Related Prognostic Score Predicts Survival and Immunotherapy Response in Glioma. <i>Medicina (Lithuania)</i> , 2023, 59, 23.	0.8	1
31133	Transcriptome analysis reveals differential transcription in tomato (<i>Solanum lycopersicum</i>) following inoculation with <i>Ralstonia solanacearum</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	2
31134	The Wu-Shi-Cha formula protects against ulcerative colitis by orchestrating immunity and microbiota homeostasis. <i>Journal of Ethnopharmacology</i> , 2023, 304, 116075.	2.0	2
31136	Genome-wide DNA methylation pattern in whole blood of patients with coal-burning arsenic poisoning. <i>Ecotoxicology and Environmental Safety</i> , 2022, 248, 114323.	2.9	1
31137	Gapless genome assembly of East Asian finless porpoise. <i>Scientific Data</i> , 2022, 9, .	2.4	1

#	ARTICLE	IF	CITATIONS
31138	Identification of significant genes associated with prognosis of gastric cancer by bioinformatics analysis. <i>Journal of the Egyptian National Cancer Institute</i> , 2022, 34, .	0.6	1
31139	Comparison of structural variants detected by PacBio-CLR and ONT sequencing in pear. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
31140	Transcriptome Analysis Reveals the Involvement of Alternative Splicing in the Nitrogen Starvation Response of <i>Chlamydomonas reinhardtii</i> . <i>Processes</i> , 2022, 10, 2719.	1.3	2
31141	Genetic evidence of aberrant striatal synaptic maturation and secretory pathway alteration in a dystonia mouse model. , 0, 1, .		1
31143	Multi-locus genome-wide association studies reveal genomic regions and putative candidate genes associated with leaf spot diseases in African groundnut (<i>Arachis hypogaea</i> L.) germplasm. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
31144	COVID-19 inhibits spermatogenesis in the testes by inducing cellular senescence. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
31145	Development and validation of a prognostic prediction model for iron metabolism-related genes in patients with pancreatic adenocarcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
31146	MicroRNAs Markedly Expressed in Apical Periodontitis Cooperatively Regulate Cytokines and Growth Factors Promoting an Anti-inflammatory Response. <i>Journal of Endodontics</i> , 2023, 49, 286-293.	1.4	6
31148	Physiological and Molecular Characterization of Yeast Cultures Pre-Adapted for Fermentation of Lignocellulosic Hydrolysate. <i>Fermentation</i> , 2023, 9, 72.	1.4	2
31149	Building Differential Co-expression Networks with Variable Selection and Regularization. <i>Studies in Computational Intelligence</i> , 2023, , 277-288.	0.7	0
31150	Text-Mining to Identify Gene Sets Involved in Biocorrosion by Sulfate-Reducing Bacteria: A Semi-Automated Workflow. <i>Microorganisms</i> , 2023, 11, 119.	1.6	5
31151	Unveiling the molecular mechanism involving anthocyanins in pineapple peel discoloration during fruit maturation. <i>Food Chemistry</i> , 2023, 412, 135482.	4.2	9
31152	Systematic evaluation of chromatin immunoprecipitation sequencing to study histone occupancy in dormancy transitions of grapevine buds. <i>Tree Physiology</i> , 0, , .	1.4	0
31153	ELOVL5 and IGFBP6 genes modulate sensitivity of breast cancer cells to ferroptosis. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	4
31154	CD4+ and CD8+ regulatory T cell characterization in the rat using a unique transgenic Foxp3-EGFP model. <i>BMC Biology</i> , 2023, 21, .	1.7	1
31156	Incorporating genome-wide and transcriptome-wide association studies to identify genetic elements of longissimus dorsi muscle in Huaxi cattle. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
31157	TSPAN4 is a prognostic and immune target in Glioblastoma multiforme. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	4
31158	Competing endogenous <i>scp>RNA</scp></i> network construction based on long non-coding <i>scp>RNAs</scp></i> , <i>scp>microRNAs</scp></i> , and <i>scp>mRNAs</scp></i> related to fat deposition in Songliao black swine. <i>Animal Genetics</i> , 0, , .	0.6	0

#	ARTICLE	IF	CITATIONS
31159	Autologous T cell therapy for MAGE-A4+ solid cancers in HLA-A*02+ patients: a phase 1 trial. <i>Nature Medicine</i> , 2023, 29, 104-114.	15.2	31
31160	Efficient querying of genomic reference databases with <i>gget</i> . <i>Bioinformatics</i> , 2023, 39, .	1.8	11
31161	Characterization and Analysis of the Full-Length Transcriptome Provide Insights into Fruit Quality Formation in Kiwifruit Cultivar <i>Actinidia arguta</i> cv. Qinzuyu. <i>Agronomy</i> , 2023, 13, 143.	1.3	0
31162	Lactylome analysis suggests lactylation-dependent mechanisms of metabolic adaptation in hepatocellular carcinoma. <i>Nature Metabolism</i> , 2023, 5, 61-79.	5.1	77
31163	ClonoCluster: A method for using clonal origin to inform transcriptome clustering. <i>Cell Genomics</i> , 2023, 3, 100247.	3.0	7
31164	Cardiac Transcriptome Remodeling and Impaired Bioenergetics in Single-Ventricle Congenital Heart Disease. <i>JACC Basic To Translational Science</i> , 2023, 8, 258-279.	1.9	3
31165	SPECC1L binds the myosin phosphatase complex MYPT1/PP1 ^β and can regulate its distribution between microtubules and filamentous actin. <i>Journal of Biological Chemistry</i> , 2023, 299, 102893.	1.6	4
31166	Prediction of ethanol fermentation under stressed conditions using yeast morphological data. <i>Journal of Bioscience and Bioengineering</i> , 2023, 135, 210-216.	1.1	7
31168	GWAS of depression in 4,520 individuals from the Russian population highlights the role of MAGI2 (S-SCAM) in the gut-brain axis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
31169	Transcriptome analysis reveals the effect of grafting on gossypol biosynthesis and gland formation in cotton. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	2
31170	Revealing the neurobiology underlying interpersonal neural synchronization with multimodal data fusion. <i>Neuroscience and Biobehavioral Reviews</i> , 2023, 146, 105042.	2.9	7
31171	SMRT and Illumina sequencing provide insights into mechanisms of lignin and terpenoids biosynthesis in <i>Pinus massoniana</i> Lamb. <i>International Journal of Biological Macromolecules</i> , 2023, 232, 123267.	3.6	3
31172	Spatially Resolved Top-Down Proteomics of Tissue Sections Based on a Microfluidic Nanodroplet Sample Preparation Platform. <i>Molecular and Cellular Proteomics</i> , 2023, 22, 100491.	2.5	6
31173	Altered transcriptome-proteome coupling indicates aberrant proteostasis in Parkinson's disease. <i>IScience</i> , 2023, 26, 105925.	1.9	2
31175	HS, an Ancient Molecular Recognition and Information Storage Glycosaminoglycan, Equips HS-Proteoglycans with Diverse Matrix and Cell-Interactive Properties Operative in Tissue Development and Tissue Function in Health and Disease. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1148.	1.8	7
31176	NucEnvDB: A Database of Nuclear Envelope Proteins and Their Interactions. <i>Membranes</i> , 2023, 13, 62.	1.4	0
31178	Transcriptome analysis of mesenteric arterioles changes and its mechanisms in cirrhotic rats with portal hypertension. <i>BMC Genomics</i> , 2023, 24, .	1.2	2
31179	Similar adaptative mechanism but divergent demographic history of four sympatric desert rodents in Eurasian inland. <i>Communications Biology</i> , 2023, 6, .	2.0	2

#	ARTICLE	IF	CITATIONS
31180	TIGIT agonism alleviates costimulation blockade-resistant rejection in a regulatory T cell–dependent manner. <i>American Journal of Transplantation</i> , 2023, 23, 180-189.	2.6	5
31181	A Nucleophilic Activity–Based Probe Enables Profiling of PLP–Dependent Enzymes. <i>ChemBioChem</i> , 2023, 24, .	1.3	0
31182	Sherlock: an open-source data platform to store, analyze and integrate Big Data for computational biologists. <i>F1000Research</i> , 0, 10, 409.	0.8	0
31183	Transposable elements are associated with genome-specific gene expression in bread wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
31184	<i>MaLAdapt</i> Reveals Novel Targets of Adaptive Introgression From Neanderthals and Denisovans in Worldwide Human Populations. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	7
31185	Identification of Differentially Expressed Proteins in Rats with Early Subacute Spinal Cord Injury Using an iTRAQ-based Quantitative Analysis. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2023, 26, .	0.6	2
31186	Prioritization of New Candidate Genes for Rare Genetic Diseases by a Disease-Aware Evaluation of Heterogeneous Molecular Networks. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1661.	1.8	1
31187	Maize cytolines as models to study the impact of different cytoplasm on gene expression under heat stress conditions. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	0
31188	Integrated DNA Methylation/RNA Profiling in Middle Temporal Gyrus of Alzheimer’s Disease. <i>Cellular and Molecular Neurobiology</i> , 0, , .	1.7	3
31189	psnGPCRdb: The Structure-network Database of G Protein Coupled Receptors. <i>Journal of Molecular Biology</i> , 2023, 435, 167950.	2.0	1
31190	Transcriptome analyses reveal the effects of mixed saline–alkali stress on indoleacetic acid and cytokinins in <i>Malus hupehensis</i> Rehd. leaves. <i>Physiology and Molecular Biology of Plants</i> , 2023, 29, 11-22.	1.4	1
31191	Profiling mouse brown and white adipocytes to identify metabolically relevant small ORFs and functional microproteins. <i>Cell Metabolism</i> , 2023, 35, 166-183.e11.	7.2	19
31192	Inferring cell developmental stage-specific lncRNA regulation in the developing human neocortex with CDSlncR. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	0
31193	Identification of potential visceral pain biomarkers in colon exudates from mice with experimental colitis: an exploratory in vitro study. <i>Journal of Pain</i> , 2023, , .	0.7	2
31194	Top-Down Proteomics Detection of Potential Salivary Biomarkers for Autoimmune Liver Diseases Classification. <i>International Journal of Molecular Sciences</i> , 2023, 24, 959.	1.8	6
31195	The human placenta shapes the phenotype of decidual macrophages. <i>Cell Reports</i> , 2023, 42, 111977.	2.9	12
31196	MAGNET: A web-based application for gene set enrichment analysis using macrophage data sets. <i>PLoS ONE</i> , 2023, 18, e0272166.	1.1	0
31197	Applications of transformer-based language models in bioinformatics: a survey. <i>Bioinformatics Advances</i> , 2023, 3, .	0.9	22

#	ARTICLE	IF	CITATIONS
31198	Genome-wide mapping of fluoroquinolone-stabilized DNA gyrase cleavage sites displays drug specific effects that correlate with bacterial persistence. <i>Nucleic Acids Research</i> , 2023, 51, 1208-1228.	6.5	2
31199	Molecular docking, network pharmacology and experimental verification to explore the mechanism of Wulongzhiyangwan in the treatment of pruritus. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31200	Investigation of early molecular alterations in tauopathy with generative adversarial networks. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31202	Saccharomyces genome database update: server architecture, pan-genome nomenclature, and external resources. <i>Genetics</i> , 2023, 224, .	1.2	12
31203	Phenotypic analysis and genome sequence of <i>Rhizopus oryzae</i> strain Y5, the causal agent of tobacco pole rot. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
31204	Genes related to N6-methyladenosine in the diagnosis and prognosis of idiopathic pulmonary fibrosis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
31205	A novel cuproptosis-related prognostic 2-lncRNAs signature in breast cancer. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	4
31207	MetaFunc: Taxonomic and Functional Analyses of High Throughput Sequencing for Microbiomes. <i>Gut Microbiome</i> , 0, , 1-41.	0.8	2
31208	Integrated Data Analysis Uncovers New COVID-19 Related Genes and Potential Drug Re-Purposing Candidates. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1431.	1.8	3
31209	Prediction and analysis of osteoarthritis hub genes with bioinformatics. <i>Annals of Translational Medicine</i> , 2023, 11, 66-66.	0.7	1
31210	Identification of oxidative stress-related genes and potential mechanisms in atherosclerosis. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
31211	Biallelic mutations in <i>CFAP54</i> cause male infertility with severe MMAF and NOA. <i>Journal of Medical Genetics</i> , 2023, 60, 827-834.	1.5	7
31212	Mapping the common gene networks that underlie related diseases. <i>Nature Protocols</i> , 2023, 18, 1745-1759.	5.5	3
31213	Effects of Resveratrol on Muscle Inflammation, Energy Utilisation, and Exercise Performance in an Eccentric Contraction Exercise Mouse Model. <i>Nutrients</i> , 2023, 15, 249.	1.7	4
31216	<i>Iris lactea</i> var. <i>chinensis</i> plant drought tolerance depends on the response of proline metabolism, transcription factors, transporters and the ROS-scavenging system. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	2
31218	One-step generation of core-shell biomimetic microspheres encapsulating double-layer cells using microfluidics for hair regeneration. <i>Biofabrication</i> , 2023, 15, 025007.	3.7	6
31219	MAGP1 maintains tumorigenicity and angiogenesis of laryngeal cancer by activating Wnt/catenin/MMP7 pathway. <i>Carcinogenesis</i> , 2024, 45, 220-234.	1.3	2
31220	Use of Apatinib as a Bait to Fish Its Unexpected Kinase Targets from the Hepatocellular Carcinoma Druggable Kinome. <i>Journal of Computational Biophysics and Chemistry</i> , 0, , .	1.0	0

#	ARTICLE	IF	CITATIONS
31221	Cardiac microRNA expression profile in response to estivation. <i>Biochimie</i> , 2023, 210, 22-34.	1.3	1
31222	A Comprehensive Exploration of the Transcriptomic Landscape in Multiple Sclerosis: A Systematic Review. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1448.	1.8	5
31223	The <scp>DNA</scp> binding high mobility group box protein family functionally binds <scp>RNA</scp>. <i>Wiley Interdisciplinary Reviews RNA</i> , 2023, 14, .	3.2	1
31224	Circulating immune response proteins predict the outcome following disease progression of osimertinib treated epidermal growth factor receptor-positive non-small-cell lung cancer patients. <i>Translational Lung Cancer Research</i> , 2023, 12, 14-26.	1.3	1
31225	Genome-wide association study of brain biochemical phenotypes reveals distinct genetic architecture of Alzheimerâ€™s disease related proteins. <i>Molecular Neurodegeneration</i> , 2023, 18, .	4.4	5
31226	Identification of Lipocalin 2 as a Ferroptosis-Related Key Gene Associated with Hypoxic-Ischemic Brain Damage via STAT3/NF-Î²B Signaling Pathway. <i>Antioxidants</i> , 2023, 12, 186.	2.2	6
31227	Adaptive Evolution Compensated for the Plasmid Fitness Costs Brought by Specific Genetic Conflicts. <i>Pathogens</i> , 2023, 12, 137.	1.2	1
31228	EGFL7 Secreted By Human Bone Mesenchymal Stem Cells Promotes Osteoblast Differentiation Partly Via Downregulation Of Notch1-Hes1 Signaling Pathway. <i>Stem Cell Reviews and Reports</i> , 2023, 19, 968-982.	1.7	2
31229	INTEGRATED BIOINFORMATIC ANALYSIS TO EVALUATE TARGET GENES AND PATHWAYS IN CHRONIC LYMPHOCYTIC LEUKEMIA. <i>Ankara Universitesi Eczacilik Fakultesi Dergisi</i> , 2023, 47, 22-22.	0.2	0
31230	GATA4 controls regionalization of tissue immunity and commensal-driven immunopathology. <i>Immunity</i> , 2023, 56, 43-57.e10.	6.6	8
31232	Transcriptome-wide characterization of alternative splicing in five drug-type cultivars of <i>Cannabis sativa</i> . <i>Botany</i> , 0, , .	0.5	0
31233	Comparative transcriptome analysis of <i>Callosobruchus chinensis</i> (L.) (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 307 103479.	1.1	3
31234	Comprehensive analysis of transcriptomics and metabolomics to understand tail-suspension-induced myocardial injury in rat. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	1
31235	Comparative phyloproteomics identifies conserved plasmodesmal proteins. <i>Journal of Experimental Botany</i> , 2023, 74, 1821-1835.	2.4	8
31236	Transcriptome analysis of hepatopancreas of Chinese grass shrimp, <i>Palaemonetes sinensis</i> , infected by <i>Enterocytophora artemiae</i> . <i>Fish and Shellfish Immunology</i> , 2023, 133, 108557.	1.6	3
31237	Using chemical and biological data to predict drug toxicity. <i>SLAS Discovery</i> , 2023, 28, 53-64.	1.4	17
31238	Full-length transcriptome analysis provides insights into larval shell formation in <i>Mulinia lateralis</i> . <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	4
31240	Predicting Modifiers of Genotype-Phenotype Correlations in Craniofacial Development. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1222.	1.8	0

#	ARTICLE	IF	CITATIONS
31241	Characterization of the innate immune response to <i>Streptococcus pneumoniae</i> infection in zebrafish. <i>PLoS Genetics</i> , 2023, 19, e1010586.	1.5	0
31243	Transcriptome analysis and gene expression analysis related to salinity-alkalinity and low temperature adaptation of <i>Triplophysa yarkandensis</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
31245	Transcriptomic analyses reveal three distinct molecular subgroups of Merkel cell carcinoma with differing prognoses. <i>International Journal of Cancer</i> , 2023, 152, 2099-2108.	2.3	2
31246	Î±-Synuclein Pathology and Reduced Neurogenesis in the Olfactory System Affect Olfaction in a Mouse Model of Parkinson's Disease. <i>Journal of Neuroscience</i> , 2023, 43, 1051-1071.	1.7	5
31248	Functional genomics provide key insights to improve the diagnostic yield of hereditary ataxia. <i>Brain</i> , 2023, 146, 2869-2884.	3.7	4
31251	Bioinformatic identification of potential biomarkers and therapeutic targets in carotid atherosclerosis and vascular dementia. <i>Frontiers in Neurology</i> , 0, 13, .	1.1	2
31252	Label-free quantitative proteomics of arbuscular mycorrhizal <i>Elaeagnus angustifolia</i> seedlings provides insights into salt-stress tolerance mechanisms. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
31253	Crystal Structure of the SH3 Domain of ASAP1 in Complex with the Proline Rich Motif (PRM) of MICAL1 Reveals a Unique SH3/PRM Interaction Mode. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1414.	1.8	2
31254	Proteomic analysis of protein lysine 2-hydroxyisobutyrylation (Khib) in soybean leaves. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	1
31255	Screening and identification of potential key biomarkers for glucocorticoid-induced osteonecrosis of the femoral head. <i>Journal of Orthopaedic Surgery and Research</i> , 2023, 18, .	0.9	1
31257	Network Pharmacology Analysis and Experimental Verification on Antiangiogenesis Mechanism of <i>Hedyotis diffusa</i> Willd in Liver Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2023, 2023, 1-11.	0.5	0
31259	Fc gamma receptor IIb in tumor-associated macrophages and dendritic cells drives poor prognosis of recurrent glioblastoma through immune-associated signaling pathways. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
31260	Mechanistic study of <i>Coriandrum sativum</i> on neuritogenesis and synaptogenesis based on computationally guided in vitro analyses. <i>Journal of Ethnopharmacology</i> , 2023, 306, 116165.	2.0	3
31261	Differential presence of exons (DPE): sequencing liquid biopsy by NGS. A new method for clustering colorectal Cancer patients. <i>BMC Cancer</i> , 2023, 23, .	1.1	2
31262	Integrated transcriptomic and metabolomic analyses revealed the molecular mechanism of terpenoid formation for salicylic acid resistance in <i>Pulsatilla chinensis</i> callus. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
31263	Comparative Transcriptome Analyses Reveal Genes Related to Spine Development in Cucumber (<i>Cucumis</i>) Tj ETQq _{1,1} 0.7843 _{0,4} 14 rgBT	1.1	0
31264	The venom composition and parthenogenesis mechanism of the parasitoid wasp <i>Microctonus</i> hyperodae, a declining biocontrol agent. <i>Insect Biochemistry and Molecular Biology</i> , 2023, 153, 103897.	1.2	3
31265	Prognosis, immune microenvironment, and personalized treatment prediction in Rho GTPase-activating protein 4-mutant cervical cancer: Computer strategies for precision oncology. <i>Life Sciences</i> , 2023, 315, 121360.	2.0	0

#	ARTICLE	IF	CITATIONS
31266	Expression landscapes in non-small cell lung cancer shaped by the thyroid transcription factor 1. <i>Lung Cancer</i> , 2023, 176, 121-131.	0.9	1
31267	TMT-based quantitative proteomic analysis reveals the underlying mechanisms of glycidyl methacrylate-induced 16HBE cell malignant transformation. <i>Toxicology</i> , 2023, 485, 153427.	2.0	1
31268	Biochemical mechanisms in pathogenesis of infantile epileptic spasm syndrome. <i>Seizure: the Journal of the British Epilepsy Association</i> , 2023, 105, 1-9.	0.9	4
31269	Integrated genomics and transcriptomics reveal the extreme heavy metal tolerance and adsorption potential of <i>Staphylococcus equorum</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 229, 388-400.	3.6	0
31270	A Baseline Cellular Antiviral State Is Maintained by cGAS and Its Most Frequent Naturally Occurring Variant rs610913. <i>Journal of Immunology</i> , 2022, 209, 535-547.	0.4	0
31271	The Chicken A and E Blood Systems Arise from Genetic Variation in and around the Regulators of Complement Activation Region. <i>Journal of Immunology</i> , 2022, 209, 1128-1137.	0.4	1
31272	Improving solution diversity on NSGA-II for multi-objective clustering problems. , 2022, , .		0
31273	Integrated Proteotranscriptomics of the Hypothalamus Reveals Altered Regulation Associated with the FecB Mutation in the BMPR1B Gene That Affects Prolificacy in Small Tail Han Sheep. <i>Biology</i> , 2023, 12, 72.	1.3	2
31274	DeepFusionGO: Protein function prediction by fusing heterogeneous features through deep learning. , 2022, , .		0
31275	Endogenous Retrovirus Elements Are Co-Expressed with IFN Stimulation Genes in the JAK-STAT Pathway. <i>Viruses</i> , 2023, 15, 60.	1.5	3
31276	Analysis of Staged Features of Gastritis-Cancer Transformation and Identification of Potential Biomarkers in Gastric Cancer. <i>Journal of Inflammation Research</i> , 0, Volume 15, 6857-6868.	1.6	0
31277	Association between microbial composition, diversity, and function of the maternal gastrointestinal microbiome with impaired glucose tolerance on the glucose challenge test. <i>PLoS ONE</i> , 2022, 17, e0271261.	1.1	4
31278	Transcriptomic and physiological analysis reveals crucial biological pathways associated with low-temperature stress in Tunisian soft-seed pomegranate (<i>Punica granatum</i> L.). <i>Journal of Plant Interactions</i> , 2023, 18, .	1.0	0
31279	A circadian clock translational control mechanism targets specific mRNAs to cytoplasmic messenger ribonucleoprotein granules. <i>Cell Reports</i> , 2022, 41, 111879.	2.9	4
31280	Deep learning-derived cardiovascular age shares a genetic basis with other cardiac phenotypes. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
31281	A multi-source fusion method to identify biomarkers for breast cancer prognosis based on dual-layer heterogeneous network. , 2022, , .		1
31282	Identification of miRNAs as Biomarkers of Cardiac Protection in Non-Genetically Modified Primary Human Cardiomyocytes Exposed to Halogenated Hypnotics in an In Vitro Model of Transfection and Ischemia/Reperfusion: A New Model in Translational Anesthesia. <i>Life</i> , 2023, 13, 64.	1.1	1
31283	Systemic Inflammation is Associated with Cardiometabolic Risk Factors and Clinical Outcomes. <i>Journal of Inflammation Research</i> , 0, Volume 15, 6891-6903.	1.6	1

#	ARTICLE	IF	CITATIONS
31284	Pathways Activated by Infected and Bystander Chondrocytes in Response to Ross River Virus Infection. <i>Viruses</i> , 2023, 15, 136.	1.5	0
31285	Zearalenone Regulates microRNA156 to Affect the Root Development of <i>Tetrastigma hemsleyanum</i> . <i>Tree Physiology</i> , 0, .	1.4	0
31286	Elucidation of the 1-phenethylisoquinoline pathway from an endemic conifer <i>Cephalotaxus hainanensis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	4
31287	A new method for predicting plant proteins function based on multi label classification algorithm. , 2022, , .		0
31288	Analyzing the multi-target pharmacological mechanism of folium <i>Artemisia argyi</i> acting on breast cancer: a network pharmacology approach. <i>Annals of Translational Medicine</i> , 2022, 10, 1368-1368.	0.7	3
31289	Whole-Exome Sequencing Identifies Genetic Variants for Severe Adolescent Idiopathic Scoliosis in a Taiwanese Population. <i>Journal of Personalized Medicine</i> , 2023, 13, 32.	1.1	3
31290	OpenGenomeBrowser: a versatile, dataset-independent and scalable web platform for genome data management and comparative genomics. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
31291	Prognostic value of des-γ-carboxyprothrombin in patients with AFP-negative HCC treated with TACE. <i>Oncology Letters</i> , 2022, 25, .	0.8	0
31292	Phylotranscriptomic Analyses of Mycoheterotrophic Monocots Show a Continuum of Convergent Evolutionary Changes in Expressed Nuclear Genes From Three Independent Nonphotosynthetic Lineages. <i>Genome Biology and Evolution</i> , 2023, 15, .	1.1	5
31293	Full-Length Transcriptome Characterization and Functional Analysis of Pathogenesis-Related Proteins in <i>Lilium Oriental Hybrid "Sorbonne"</i> Infected with <i>Botrytis elliptica</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 425.	1.8	1
31294	Analysis of network pharmacology and experimental verification to explore the mechanism of Modified <i>Guilu Erxian</i> Glue in the treatment of low immune function. <i>Pharmacological Research Modern Chinese Medicine</i> , 2023, 7, 100213.	0.5	0
31295	A morphometrics approach for inclusion of localised characteristics from medical imaging studies into genome-wide association studies. , 2022, , .		0
31296	Sympatric or micro-allopatric speciation in a glacial lake? Genomic islands support neither. <i>National Science Review</i> , 2022, 9, .	4.6	7
31297	The gold-ringed octopus (<i>Amphioctopus fangsiao</i>) genome and cerebral single-nucleus transcriptomes provide insights into the evolution of karyotype and neural novelties. <i>BMC Biology</i> , 2022, 20, .	1.7	6
31299	KL-RF: Predicting disease-gene associations with model fusion. , 2022, , .		0
31300	Antimicrobial resistance in <i>Klebsiella pneumoniae</i> : identification of bacterial DNA adenine methyltransferase as a novel drug target from hypothetical proteins using subtractive genomics. <i>Genomics and Informatics</i> , 2022, 20, e47.	0.4	3
31301	GCL-GO: A novel sequence-based hierarchy-aware method for protein function prediction. , 2022, , .		0
31303	Aortic Stress Activates an Adaptive Program in Thoracic Aortic Smooth Muscle Cells That Maintains Aortic Strength and Protects Against Aneurysm and Dissection in Mice. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2023, 43, 234-252.	1.1	5

#	ARTICLE	IF	CITATIONS
31304	Variation in heat shock protein 40 kDa relates to divergence in thermotolerance among cryptic rotifer species. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
31305	Positive Feature Values Prioritized Hierarchical Dependency Constrained Averaged One-dependence Estimators for Gene Ontology Feature Spaces. , 2022, , .		1
31306	Identification of the expression, prognostic value and cancer immunity of Gasdermin E based on multi-omics data, machine learning and gene ontology. , 2022, , .		0
31307	Multi-omics network model reveals key genes associated with p-coumaric acid stress response in an industrial yeast strain. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
31308	Diversity of Mixotrophic Neutrophilic Thiosulfate- and Iron-Oxidizing Bacteria from Deep-Sea Hydrothermal Vents. <i>Microorganisms</i> , 2023, 11, 100.	1.6	2
31309	Genome Sequence Resource of <i>Fusarium proliferatum</i> f. sp. <i>malus domestica</i> MR5, the Causative Agent of Apple Replant Disease. <i>Plant Disease</i> , 0, , .	0.7	0
31310	Zero Gravity is a Factor that Induces Negative Changes in Myelinated Fibers of the Spinal Tracts. <i>Bulletin of Experimental Biology and Medicine</i> , 2022, 174, 265-268.	0.3	0
31311	Chromosome-level genome and the identification of sex chromosomes in <i>Uloborus diversus</i> . <i>GigaScience</i> , 2022, 12, .	3.3	6
31312	Low-level cadmium exposure induced hormesis in peppermint young plant by constantly activating antioxidant activity based on physiological and transcriptomic analyses. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	6
31313	Physiological and Transcriptomic Response of Asiatic Hard Clam <i>Meretrix meretrix</i> to the Harmful Alga <i>Heterosigma akashiwo</i> . <i>Fishes</i> , 2023, 8, 67.	0.7	2
31314	Modular architecture and functional annotation of human RNA-binding proteins containing RNA recognition motif. <i>Biochimie</i> , 2023, 209, 116-130.	1.3	3
31315	Exploring the hub mechanisms of ischemic stroke based on protein-protein interaction networks related to ischemic stroke and inflammatory bowel disease. <i>Scientific Reports</i> , 2023, 13, .	1.6	4
31316	Genetic responses to adding nitrates to improve hydrophilic yellow pigment in <i>Monascus</i> fermentation. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 1341-1359.	1.7	4
31318	Binary Colloidal Crystals Promote Cardiac Differentiation of Human Pluripotent Stem Cells via Nuclear Accumulation of SETDB1. <i>ACS Nano</i> , 2023, 17, 3181-3193.	7.3	1
31319	Influence of sex, age and diabetes on brain transcriptome and proteome modifications following cerebral ischemia. <i>BMC Neuroscience</i> , 2023, 24, .	0.8	1
31321	TriTrypDB: An integrated functional genomics resource for kinetoplastida. <i>PLoS Neglected Tropical Diseases</i> , 2023, 17, e0011058.	1.3	27
31322	Identification of the egusi seed trait locus (<i>eg</i>) and its suppressor gene associated with the thin seed coat trait in watermelon. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
31323	<i>Lite-SeqCNN</i> : A Light-Weight Deep CNN Architecture for Protein Function Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 2242-2253.	1.9	1

#	ARTICLE	IF	CITATIONS
31324	PyGenePlexus: a Python package for gene discovery using network-based machine learning. <i>Bioinformatics</i> , 2023, 39, .	1.8	2
31325	De Novo Transcriptome Assembly and EST-SSR Marker Development and Application in <i>Chrysosplenium macrophyllum</i> . <i>Genes</i> , 2023, 14, 279.	1.0	2
31326	A Network of MicroRNAs and mRNAs Involved in Melanosome Maturation and Trafficking Defines the Lower Response of Pigmentable Melanoma Cells to Targeted Therapy. <i>Cancers</i> , 2023, 15, 894.	1.7	1
31329	Adriforant is a functional antagonist of histamine receptor 4 and attenuates itch and skin inflammation in mice. <i>European Journal of Pharmacology</i> , 2023, 945, 175533.	1.7	1
31330	Genomic and proteomic analysis of <i>Bacillus subtilis</i> as microplastic bioremediation agents. <i>AIP Conference Proceedings</i> , 2023, , .	0.3	0
31331	Molecular Characterization and Phylogenetic Analysis of Casein Gene Family in <i>Camelus ferus</i> . <i>Genes</i> , 2023, 14, 256.	1.0	1
31332	Genomic, Transcriptomic, and Proteomic Depiction of Induced Pluripotent Stem Cellsâ€œDerived Smooth Muscle Cells As Emerging Cellular Models for Arterial Diseases. <i>Hypertension</i> , 0, , .	1.3	4
31333	Identification of ULK1 as a novel mitophagy-related gene in diabetic nephropathy. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	3
31334	Single-cell analysis of myeloid cells in HPV+ tonsillar cancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
31336	Long-term potentiation and depression regulatory microRNAs were highlighted in Bisphenol A induced learning and memory impairment by microRNA sequencing and bioinformatics analysis. <i>PLoS ONE</i> , 2023, 18, e0279029.	1.1	3
31337	Maternal diet induces persistent DNA methylation changes in the muscle of beef calves. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
31339	Novel Genetic Variants Associated with Chronic Kidney Disease Progression. <i>Journal of the American Society of Nephrology: JASN</i> , 2023, 34, 857-875.	3.0	2
31340	Transcriptomic response of bioengineered human cartilage to parabolic flight microgravity is sex-dependent. <i>Npj Microgravity</i> , 2023, 9, .	1.9	5
31342	VIMâ€™AS1 promotes proliferation and drives enzalutamide resistance in prostate cancer via IGF2BP2â€™mediated HMCS1 mRNA stabilization. <i>International Journal of Oncology</i> , 2023, 62, .	1.4	2
31343	Melatonin Mitigates iNOS-Related Effects of HEMA and Camphorquinone in Human Dental Pulp Cells: Relevance for Postoperative Sensitivity Mechanism in Type 2 Diabetes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2562.	1.8	1
31345	Comparative Expression Profiling Reveals the Regulatory Effects of Dietary Mannan Oligosaccharides on the Intestinal Immune Response of Juvenile <i>Megalobrama amblycephala</i> against <i>Aeromonas hydrophila</i> Infection. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2207.	1.8	3
31346	The <i>Gynandropsis gynandra</i> genome provides insights into whole-genome duplications and the evolution of C4 photosynthesis in Cleomaceae. <i>Plant Cell</i> , 2023, 35, 1334-1359.	3.1	8
31347	Identification of New Candidate Genes Related to Semen Traits in Duroc Pigs through Weighted Single-Step GWAS. <i>Animals</i> , 2023, 13, 365.	1.0	5

#	ARTICLE	IF	CITATIONS
31349	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
31350	Molecular mechanisms of the Guizhi decoction on osteoarthritis based on an integrated network pharmacology and RNA sequencing approach with experimental validation. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
31351	Integration of proteomic and metabolomic analyses: New insights for mapping informal workers exposed to potentially toxic elements. <i>Frontiers in Public Health</i> , 0, 10, .	1.3	1
31352	Combined PD-1, BRAF and MEK inhibition in BRAFV600E colorectal cancer: a phase 2 trial. <i>Nature Medicine</i> , 2023, 29, 458-466.	15.2	28
31353	Prediction of Protein Molecular Functions Using Transformers. <i>Lecture Notes in Computer Science</i> , 2023, , 379-387.	1.0	0
31354	Characterization of proteome-size scaling by integrative omics reveals mechanisms of proliferation control in cancer. <i>Science Advances</i> , 2023, 9, .	4.7	6
31355	CD200 cytotoxic T lymphocytes in the tumor microenvironment are crucial for efficacious anti-PD-1/PD-L1 therapy. <i>Science Translational Medicine</i> , 2023, 15, .	5.8	12
31356	Cell Cycle-Related Gene SPC24: A Novel Potential Diagnostic and Prognostic Biomarker for Laryngeal Squamous Cell Cancer. <i>BioMed Research International</i> , 2023, 2023, 1-14.	0.9	1
31357	Genetic relationships of the Yucatan black hairless pig with Iberian breeds using single nucleotide polymorphisms. <i>Brazilian Journal of Veterinary Research and Animal Science</i> , 0, 60, e195697.	0.2	0
31358	Nematode gene annotation by machine-learning-assisted proteotranscriptomics enables proteome-wide evolutionary analysis. <i>Genome Research</i> , 2023, 33, 112-128.	2.4	1
31360	Expression profiles of lncRNAs and their possible regulatory role in monocrotaline-induced HSOS in rats. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
31361	Integration of chromatin accessibility and gene expression reveals new regulators of cold hardening to enhance freezing tolerance in <i>Prunus mume</i> . <i>Journal of Experimental Botany</i> , 2023, 74, 2173-2187.	2.4	4
31363	GOThrasher: a program to remove annotation biases from protein function annotation datasets. <i>Bioinformatics</i> , 2023, 39, .	1.8	0
31364	Gene Expression Profiles in Cancers and Their Therapeutic Implications. <i>Cancer Journal (Sudbury, Mass)</i> 11 0,784314,rgBT /Over	1.0	1
31365	CitrusGenome: A Bioinformatics Tool to Characterize, Visualize, and Explore Large Citrus Variant Datasets. <i>Communications in Computer and Information Science</i> , 2023, , 167-178.	0.4	0
31366	Follicular fluid progesterone down-regulated HPGD and COX2 in granulosa cells via suppressing NF- κ B in endometriosis. <i>Biology of Reproduction</i> , 0, , .	1.2	1
31367	Stelletin B Induces Cell Death in Bladder Cancer Via Activating the Autophagy/DAPK2/Apoptosis Signaling Cascade. <i>Marine Drugs</i> , 2023, 21, 73.	2.2	6
31368	Systematic comparison of transcriptomes of Caco-2 cells cultured under different cellular and physiological conditions. <i>Archives of Toxicology</i> , 0, , .	1.9	1

#	ARTICLE	IF	CITATIONS
31371	Network-based quantitative trait linkage analysis of microbiome composition in inflammatory bowel disease families. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
31372	Uncovering the effects and molecular mechanism of <i>Astragalus membranaceus</i> (Fisch.) Bunge and its bioactive ingredients formononetin and calycosin against colon cancer: An integrated approach based on network pharmacology analysis coupled with experimental validation and molecular docking. <i>Frontiers in Pharmacology</i> , 0, 14, .	1.6	4
31373	Transcriptome and metabolome profiling of the medicinal plant <i>Veratrum mengtzeanum</i> reveal key components of the alkaloid biosynthesis. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
31374	Comparative Analyses Reveal the Genetic Mechanism of Ambergris Production in the Sperm Whale Based on the Chromosome-Level Genome. <i>Animals</i> , 2023, 13, 361.	1.0	1
31375	Parkinsonâ€™s Disease Gene Biomarkers Screened by the LASSO and SVM Algorithms. <i>Brain Sciences</i> , 2023, 13, 175.	1.1	4
31376	PlantTribes2: Tools for comparative gene family analysis in plant genomics. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
31377	Analyzing RNAâ€“Protein Interactions by Crossâ€“Link Rates and CLIPâ€“seq Libraries. <i>Current Protocols</i> , 2023, 3, .	1.3	1
31378	Large language models generate functional protein sequences across diverse families. <i>Nature Biotechnology</i> , 2023, 41, 1099-1106.	9.4	213
31379	A targeted multi-proteomics approach generates a blueprint of the ciliary ubiquitinome. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	11
31380	Soil metatranscriptomics: An improved RNA extraction method toward functional analysis using nanopore direct RNA sequencing. <i>Phytobiomes Journal</i> , 0, , .	1.4	1
31381	Peptidomics analysis of plasma in patients with ankylosing spondylitis. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	3
31382	Identification of Long Noncoding RNAs That Exert Transcriptional Regulation by Forming RNAâ€“DNA Triplexes in Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2035.	1.8	2
31383	Time series transcriptome analysis implicates the circadian clock in the <i>Drosophila melanogaster</i> femaleâ€™s response to sex peptide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	5
31384	Self-assembly and self-delivery of the pure nanodrug dihydroartemisinin for tumor therapy and mechanism analysis. <i>Biomaterials Science</i> , 2023, 11, 2478-2485.	2.6	3
31385	Characterization and Application of EST-SSR Markers Developed from Transcriptome Sequences in <i>Elymus breviaristatus</i> (Poaceae: Triticeae). <i>Genes</i> , 2023, 14, 302.	1.0	1
31386	miRinGO: Prediction of Biological Processes Indirectly Targeted by Human microRNAs. <i>Non-coding RNA</i> , 2023, 9, 11.	1.3	1
31387	Addressing the pervasive scarcity of structural annotation in eukaryotic algae. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
31388	Comparative analysis of the chrysanthemum transcriptome with DNA methylation inhibitors treatment and silencing MET1 lines. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	0

#	ARTICLE	IF	CITATIONS
31389	DNA Methylation Dynamics During Esophageal Epithelial Regeneration Following Repair with Acellular Silk Fibroin Grafts in Rat. <i>Advanced Biology</i> , 0, , 2200160.	1.4	0
31390	scm6A-seq reveals single-cell landscapes of the dynamic m6A during oocyte maturation and early embryonic development. <i>Nature Communications</i> , 2023, 14, .	5.8	21
31391	Investigating nicotine pathway-related long non-coding RNAs in tobacco. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
31392	RNA sequencing indicates widespread conservation of circadian clocks in marine zooplankton. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	1.5	1
31393	Complete Genome Sequence of <i>Pantoea ananatis</i> strain LCFJ-001, Isolated from Bacterial Wilt Mulberry. <i>Plant Disease</i> , 0, , .	0.7	0
31397	Metrics for RNA Secondary Structure Comparison. <i>Methods in Molecular Biology</i> , 2023, , 79-88.	0.4	0
31398	Genome-wide genetic variation and comparative transcriptome analyses of citrus mutant Jeda-unshiu and wild-type Citrus unshiu. <i>Plant Biotechnology Reports</i> , 0, , .	0.9	0
31399	Correlated evolution of social organization and lifespan in mammals. <i>Nature Communications</i> , 2023, 14, .	5.8	7
31400	Endothelial cell-derived oxysterol ablation attenuates experimental autoimmune encephalomyelitis. <i>EMBO Reports</i> , 2023, 24, .	2.0	5
31401	Protein interaction studies in human induced neurons indicate convergent biology underlying autism spectrum disorders. <i>Cell Genomics</i> , 2023, 3, 100250.	3.0	12
31402	Physiological hypoxia improves growth and functional differentiation of human intestinal epithelial organoids. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	5
31403	Molecular Influence of Resiniferatoxin on the Urinary Bladder Wall Based on Differential Gene Expression Profiling. <i>Cells</i> , 2023, 12, 462.	1.8	1
31404	Transcriptome analysis reveals the key pathways and candidate genes involved in salt stress responses in <i>Cymbidium ensifolium</i> leaves. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	1
31405	Murine scald models characterize the role of neutrophils and neutrophil extracellular traps in severe burns. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
31406	A Tissue-Specific and Toxicology-Focused Knowledge Graph. <i>Information (Switzerland)</i> , 2023, 14, 91.	1.7	0
31407	Genome-wide screening reveals the genetic basis of mammalian embryonic eye development. <i>BMC Biology</i> , 2023, 21, .	1.7	1
31409	Using Ontologies to Create Machine-Actionable Datasets: Two Case Studies. <i>Metrology</i> , 2023, 3, 65-80.	0.9	2
31410	Integrative pathway and network analysis provide insights on flooding-tolerance genes in soybean. <i>Scientific Reports</i> , 2023, 13, .	1.6	1

#	ARTICLE	IF	CITATIONS
31411	Membranome Similarity between Glioblastoma Multiforme Cell Lines and Primary Tumors. <i>OBM Neurobiology</i> , 2023, 07, 1-8.	0.2	0
31412	KRT17 serves as an oncogene biomarker of poor survival in patients with hepatocellular carcinoma. , 2023, 3, 18-25.		1
31413	Therapeutic effects and mechanisms of Ku-Gan formula on atopic dermatitis: A pilot clinical study and modular pharmacology analysis with animal validation. <i>Journal of Ethnopharmacology</i> , 2023, 307, 116194.	2.0	3
31414	Using ontologies for life science text-based resource organization. <i>Artificial Intelligence in the Life Sciences</i> , 2023, 3, 100059.	1.6	1
31415	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
31416	Utility of proteomics and phosphoproteomics in the tailored medication of cancer. , 2023, , 319-332.		0
31417	Combined analysis of chromatin accessibility and gene expression profiles provide insight into Fucoxanthin biosynthesis in <i>Isochrysis galbana</i> under green light. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	0
31418	Databases and prospects of dynamic gene regulation in eukaryotes: A mini review. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 2147-2159.	1.9	1
31419	Physiological and transcriptomic responses to cold waves of the most cold-tolerant mangrove, <i>Kandelia obovata</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
31420	Quantitative analysis of high-throughput biological data. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2023, 13, .	6.2	2
31421	Single-cell sequencing of ascites fluid illustrates heterogeneity and therapy-induced evolution during gastric cancer peritoneal metastasis. <i>Nature Communications</i> , 2023, 14, .	5.8	14
31423	<i>vicR</i> overexpression in <i>Streptococcus mutans</i> causes aggregation and affects interspecies competition. <i>Molecular Oral Microbiology</i> , 2023, 38, 224-236.	1.3	2
31427	Endocrine Disrupting Chemicals Influence Hub Genes Associated with Aggressive Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3191.	1.8	3
31428	A novel approach to interrogating the effects of chemical warfare agent exposure using organ-on-a-chip technology and multiomic analysis. <i>PLoS ONE</i> , 2023, 18, e0280883.	1.1	3
31429	Identification of <i>IGF2</i> as Genomic Driver and Actionable Therapeutic Target in Hepatoblastoma. <i>Molecular Cancer Therapeutics</i> , 2023, 22, 485-498.	1.9	4
31430	Large-Scale Quantitative Proteomic Analysis during Different Stages of Somatic Embryogenesis in <i>Larix olgensis</i> . <i>Current Issues in Molecular Biology</i> , 2023, 45, 2021-2034.	1.0	1
31431	Spatial transcriptomics using multiplexed deterministic barcoding in tissue. <i>Nature Communications</i> , 2023, 14, .	5.8	5
31432	Full-length transcriptome profiling for fruit development in <i>Diospyros oleifera</i> using nanopore sequencing. <i>BMC Genomic Data</i> , 2023, 24, .	0.7	1

#	ARTICLE	IF	CITATIONS
31433	Gene expression reveals immune response strategies of naïve Hawaiian honeycreepers experimentally infected with introduced avian malaria. <i>Journal of Heredity</i> , 2023, 114, 326-340.	1.0	3
31434	Identification of key genes and imbalance of immune cell infiltration in immunoglobulin A associated vasculitis nephritis by integrated bioinformatic analysis. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
31435	Network Pharmacology and Molecular Modeling to Elucidate the Potential Mechanism of Neem Oil against <i>Acne vulgaris</i> . <i>Molecules</i> , 2023, 28, 2849.	1.7	1
31436	Identification of fatty acid metabolism-based molecular subtypes and prognostic signature to predict immune landscape and guide clinical drug treatment in renal clear cell carcinoma. <i>International Immunopharmacology</i> , 2023, 116, 109735.	1.7	4
31438	Low-dose of caffeine alleviates high altitude pulmonary edema via regulating mitochondrial quality control process in AT1 cells. <i>Frontiers in Pharmacology</i> , 0, 14, .	1.6	0
31439	Construction and validation of a hypoxia-related risk signature identified EXO1 as a prognostic biomarker based on 12 genes in lung adenocarcinoma. <i>Aging</i> , 2023, 15, 2293-2307.	1.4	0
31440	Effect of fermented soy beverage in aged female mice model. <i>Food Research International</i> , 2023, 169, 112745.	2.9	2
31441	Genome graphs detect human polymorphisms in active epigenomic state during influenza infection. <i>Cell Genomics</i> , 2023, 3, 100294.	3.0	3
31442	Clinical prognostic value of OSGIN2 in gastric cancer and its proliferative effect in vitro. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
31443	PGC-1s shape epidermal physiology by modulating keratinocyte proliferation and terminal differentiation. <i>iScience</i> , 2023, 26, 106314.	1.9	3
31444	Breast cancer cell secretome analysis to decipher miRNA regulating the tumor microenvironment and discover potential biomarkers. <i>Heliyon</i> , 2023, 9, e15421.	1.4	0
31446	Genome-scale CRISPR screen reveals neddylation to contribute to cisplatin resistance of testicular germ cell tumours. <i>British Journal of Cancer</i> , 2023, 128, 2270-2282.	2.9	2
31447	Developing a Knowledge Graph for Pharmacokinetic Natural Product-Drug Interactions. <i>Journal of Biomedical Informatics</i> , 2023, 140, 104341.	2.5	4
31448	Bioinformatics and computational chemistry approaches to explore the mechanism of the anti-depressive effect of ligustilide. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31449	Estradiol cycling drives female obesogenic adipocyte hyperplasia. <i>Cell Reports</i> , 2023, 42, 112390.	2.9	3
31450	Unified access to up-to-date residue-level annotations from UniProtKB and other biological databases for PDB data. <i>Scientific Data</i> , 2023, 10, .	2.4	2
31452	Probe-based bacterial single-cell RNA sequencing predicts toxin regulation. <i>Nature Microbiology</i> , 2023, 8, 934-945.	5.9	14
31454	Cellular Proteomic Profiling Using Proximity Labeling by TurboID-NES in Microglial and Neuronal Cell Lines. <i>Molecular and Cellular Proteomics</i> , 2023, 22, 100546.	2.5	5

#	ARTICLE	IF	CITATIONS
31455	Comparative- and network-based proteomic analysis of bacterial chondronecrosis with osteomyelitis lesions in broilerâ€™s proximal tibiae identifies new molecular signatures of lameness. Scientific Reports, 2023, 13, .	1.6	2
31456	Comparative genomics analyses reveal sequence determinants underlying interspecies variations in injury-responsive enhancers. BMC Genomics, 2023, 24, .	1.2	1
31457	Digital light processing-bioprinted poly-NAGA-GelMA-based hydrogel lenticule for precise refractive errors correction. Biofabrication, 2023, 15, 035011.	3.7	4
31459	Network pharmacology-integrated molecular docking analysis of phytochemicals of <i>Caesalpinia pulcherrima</i> (peacock flower) as potential anti-metastatic agents. Journal of Biomolecular Structure and Dynamics, 2024, 42, 1778-1794.	2.0	2
31460	Draft Genome Sequence of <i>Enterobacter cloacae</i> S23 a Plant Growth-promoting Passenger Endophytic Bacterium Isolated from Groundnut Nodule Possesses Stress Tolerance Traits. Current Genomics, 2023, 24, .	0.7	0
31462	Introducing multi-dimensional hierarchical classification: Characterization, solving strategies and performance measures. Neurocomputing, 2023, 533, 141-160.	3.5	1
31463	Mechanisms of <i>Phaeocystis globosa</i> blooms in the Beibu Gulf revealed by metatranscriptome analysis. Harmful Algae, 2023, 124, 102407.	2.2	3
31464	Revealing holistic metabolic responses associated with lipid and docosahexaenoic acid (DHA) production in <i>Aurantiochytrium</i> sp. SW1. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2023, 1868, 159306.	1.2	2
31465	Whole-genome sequencing of a biocontrol <i>Myxococcus xanthus</i> R31 isolate and comparative genomic analysis. Gene, 2023, 863, 147286.	1.0	5
31466	HER2 as a potential therapeutic target on quiescent prostate cancer cells. Translational Oncology, 2023, 31, 101642.	1.7	2
31467	The cotton miR530-SAP6 module activated by systemic acquired resistance mediates plant defense against <i>Verticillium dahliae</i> . Plant Science, 2023, 330, 111647.	1.7	6
31468	Transcriptome response of Antarctic <i>Phaeodactylum tricorutum</i> ICE-H producing dimethylsulphoniopropionate to hypersaline stress. Process Biochemistry, 2023, 128, 206-217.	1.8	0
31469	REL-NPMI: Exploring genotype and phenotype relationship of pancreatitis based on improved normalized point-by-point mutual information. Computers in Biology and Medicine, 2023, 158, 106868.	3.9	0
31470	Proteomic and phosphoproteomic analyses of Jurkat T-cell treated with 2â€™3â€™ cGAMP reveals various signaling axes impacted by cyclic dinucleotides. Journal of Proteomics, 2023, 279, 104869.	1.2	0
31471	Overall mortality risk analysis for rectal cancer using deep learning-based fuzzy systems. Computers in Biology and Medicine, 2023, 157, 106706.	3.9	1
31472	Whole genome sequencing identified candidate genes related to litter size of Qinghai fine wool sheep under artificial selection. Small Ruminant Research, 2023, 223, 106969.	0.6	0
31473	Clustering of multi-layer networks with structural relations and conservation of features. Applied Soft Computing Journal, 2023, 140, 110272.	4.1	0
31474	Rare earth elements detoxification mechanism in the hyperaccumulator <i>Dicranopteris linearis</i> : [silicon-pectin] matrix fixation. Journal of Hazardous Materials, 2023, 452, 131254.	6.5	5

#	ARTICLE	IF	CITATIONS
31475	Dietary intake of household cadmium-contaminated rice caused genome-wide DNA methylation changes on gene/hubs related to metabolic disorders and cancers. <i>Environmental Pollution</i> , 2023, 327, 121553.	3.7	0
31476	A deep transcriptome meta-analysis reveals sex differences in multiple sclerosis. <i>Neurobiology of Disease</i> , 2023, 181, 106113.	2.1	7
31477	Identification of genes responsible for the social skill in the earthworm, <i>Eudrilus eugeniae</i> . <i>Gene Reports</i> , 2023, 31, 101774.	0.4	0
31478	Metabolic regulation mechanism of <i>Trametes gibbosa</i> CB1 on lignin. <i>International Journal of Biological Macromolecules</i> , 2023, 240, 124189.	3.6	2
31479	Role of N6-adenosine-methyltransferase subunits METTL3 and METTL14 in the biological properties of periodontal ligament cells. <i>Tissue and Cell</i> , 2023, 82, 102081.	1.0	2
31480	Complete genome sequence of <i>Lactobacillus fermentum</i> 9-4, a purine-degrading <i>Lactobacillus</i> probiotic isolated from Chinese fermented rice-flour noodles. <i>Journal of Future Foods</i> , 2023, 3, 169-174.	2.0	1
31481	Saikosaponin A and D attenuate skeletal muscle atrophy in chronic kidney disease by reducing oxidative stress through activation of PI3K/AKT/Nrf2 pathway. <i>Phytomedicine</i> , 2023, 114, 154766.	2.3	4
31482	Enantioselectivity effects of energy metabolism in honeybees (<i>Apis mellifera</i>) by triticonazole. <i>Science of the Total Environment</i> , 2023, 877, 162884.	3.9	1
31483	Microglia-containing cerebral organoids derived from induced pluripotent stem cells for the study of neurological diseases. <i>IScience</i> , 2023, 26, 106267.	1.9	13
31484	Morphology-guided transcriptomic analysis of human pancreatic cancer organoids reveals microenvironmental signals that enhance invasion. <i>Journal of Clinical Investigation</i> , 2023, 133, .	3.9	4
31485	NetGO 3.0: Protein Language Model Improves Large-Scale Functional Annotations. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 349-358.	3.0	7
31486	Identification of key genes involved in neural regeneration and the repairing effect of BDNF-overexpressed BMSCs on spinal cord ischemia-reperfusion injury in rats. <i>Biomedicine and Pharmacotherapy</i> , 2023, 160, 114293.	2.5	4
31487	Combined Study of Transcriptome and Metabolome Reveals Involvement of Metabolites and Candidate Genes in Flavonoid Biosynthesis in <i>Prunus avium</i> L.. <i>Horticulturae</i> , 2023, 9, 463.	1.2	0
31488	The viral packaging motor potentiates Kaposi's sarcoma-associated herpesvirus gene expression late in infection. <i>PLoS Pathogens</i> , 2023, 19, e1011163.	2.1	1
31489	The genome and transcriptome of <i>Sarocladium terricola</i> provide insight into ergosterol biosynthesis. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	0
31490	Identification of Candidate Genes Involved in the Determinism of Pollen Grain Aperture Morphology by Comparative Transcriptome Analysis in <i>Papaveraceae</i> . <i>Plants</i> , 2023, 12, 1570.	1.6	0
31491	Understanding the response in <i>Pugionium cornutum</i> (L.) Gaertn. seedling leaves under drought stress using transcriptome and proteome integrated analysis. <i>PeerJ</i> , 0, 11, e15165.	0.9	0
31492	Chromosome-level genome assembly and population genomic resource to accelerate orphan crop lablab breeding. <i>Nature Communications</i> , 2023, 14, .	5.8	10

#	ARTICLE	IF	CITATIONS
31493	Regulation of neural stem cell self-renewal, proliferation and differentiation by the RhoA guanine nucleotide exchange factor Arhgef 1. <i>Gene</i> , 2023, 863, 147306.	1.0	0
31494	Insights into identifying resistance genes for cold and disease stresses through chromosome-level reference genome analyses of <i>Poncirus polyandra</i> . <i>Genomics</i> , 2023, 115, 110617.	1.3	1
31495	A pathogenic variant in the uncharacterized RNF212B gene results in severe aneuploidy male infertility and repeated IVF failure. <i>Human Genetics and Genomics Advances</i> , 2023, 4, 100189.	1.0	1
31496	A herbal product inhibits carbon tetrachloride-induced liver fibrosis by suppressing the epidermal growth factor receptor signaling pathway. <i>Journal of Ethnopharmacology</i> , 2023, 311, 116419.	2.0	1
31508	The genome of <i>Lignosus tigris</i> : Uncovering its hidden nutraceutical potential. <i>South African Journal of Botany</i> , 2023, 154, 108-119.	1.2	2
31509	Investigation of the keratinocyte transcriptome altered in high-glucose environment: An in-vitro model system for precision medicine. <i>Journal of Dermatological Science</i> , 2023, 109, 37-46.	1.0	3
31510	Toxicologic effect of short-term enrofloxacin exposure on brain of <i>Carassius auratus</i> var. <i>Pengze</i> . <i>Science of the Total Environment</i> , 2023, 869, 161730.	3.9	3
31511	Systems vaccinology for the design of rational vaccines against protozoan parasites. , 2022, , 297-334.		0
31512	Neuro-immune deconvolution analysis of OAS3 as a transcriptomic central node in HIV-associated neurocognitive disorders. <i>Journal of the Neurological Sciences</i> , 2023, 446, 120562.	0.3	1
31513	Prognostic value of nuclear morphometry in myxoid liposarcoma. <i>Cancer Science</i> , 2023, 114, 2178-2188.	1.7	4
31514	FirmTruss Community Search in Multilayer Networks. <i>Proceedings of the VLDB Endowment</i> , 2022, 16, 505-518.	2.1	4
31516	BIRCH: An Automated Workflow for Evaluation, Correction, and Visualization of Batch Effect in Bottom-Up Mass Spectrometry-Based Proteomics Data. <i>Journal of Proteome Research</i> , 2023, 22, 471-481.	1.8	1
31517	Identifying molecular targets of Aspiletrein-derived steroidal saponins in lung cancer using network pharmacology and molecular docking-based assessments. <i>Scientific Reports</i> , 2023, 13, .	1.6	7
31519	Alterations in platelet proteome signature and impaired platelet integrin α IIb β 3 activation in patients with COVID-19. <i>Journal of Thrombosis and Haemostasis</i> , 2023, 21, 1307-1321.	1.9	6
31520	Causal knowledge graph construction and evaluation for clinical decision support of diabetic nephropathy. <i>Journal of Biomedical Informatics</i> , 2023, 139, 104298.	2.5	8
31521	Surfaceome Profiling of Cell Lines and Patient-Derived Xenografts Confirm FGFR4, NCAM1, CD276, and Highlight AGRL2, JAM3, and L1CAM as Surface Targets for Rhabdomyosarcoma. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2601.	1.8	6
31522	Molecular mechanisms of environmental exposures and human disease. <i>Nature Reviews Genetics</i> , 2023, 24, 332-344.	7.7	29
31523	Computational Approaches to Enzyme Inhibition by Marine Natural Products in the Search for New Drugs. <i>Marine Drugs</i> , 2023, 21, 100.	2.2	4

#	ARTICLE	IF	CITATIONS
31524	BPDE, the Migration and Invasion of Human Trophoblast Cells, and Occurrence of Miscarriage in Humans: Roles of a Novel <i>lncRNA-HZ09</i> . <i>Environmental Health Perspectives</i> , 2023, 131, .	2.8	14
31525	Proteome-Wide Detection and Annotation of Receptor Tyrosine Kinases (RTKs): RTK-PRED and the TyReK Database. <i>Biomolecules</i> , 2023, 13, 270.	1.8	0
31526	CP204L Is a Multifunctional Protein of African Swine Fever Virus That Interacts with the VPS39 Subunit of the Homotypic Fusion and Vacuole Protein Sorting Complex and Promotes Lysosome Clustering. <i>Journal of Virology</i> , 2023, 97, .	1.5	2
31527	Upregulation of GALNT7 in prostate cancer modifies O-glycosylation and promotes tumour growth. <i>Oncogene</i> , 2023, 42, 926-937.	2.6	12
31528	De Novo Assembly of an Allotetraploid <i>Artemisia argyi</i> Genome. <i>Agronomy</i> , 2023, 13, 436.	1.3	1
31529	Systematic approach to identify therapeutic targets and functional pathways for the cervical cancer. <i>Journal of Genetic Engineering and Biotechnology</i> , 2023, 21, 10.	1.5	1
31530	Elucidating the functional roles of prokaryotic proteins using big data and artificial intelligence. <i>FEMS Microbiology Reviews</i> , 2023, 47, .	3.9	4
31531	Transcriptome and methylome dynamics in the gills of large yellow croaker (<i>Larimichthys crocea</i>) during low-salinity adaption. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	1
31533	Integrative Analysis of Proteome-wide Association Studies and Functional Enrichment Analysis to Identify Genes and Chemicals Associated with Alcohol Dependence. <i>Journal of Addiction Medicine</i> , 2023, 17, 319-325.	1.4	0
31534	Predictive model of transcriptional elongation control identifies trans regulatory factors from chromatin signatures. <i>Nucleic Acids Research</i> , 2023, 51, 1608-1624.	6.5	1
31536	Epstein-Barr Virus Synergizes with BRD7 to Conquer c-Myc-Mediated Viral Latency Maintenance via Chromatin Remodeling. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	5
31537	Pan-cancer molecular subtypes of metastasis reveal distinct and evolving transcriptional programs. <i>Cell Reports Medicine</i> , 2023, 4, 100932.	3.3	5
31538	Linking chemicals, genes and morphological perturbations to diseases. <i>Toxicology and Applied Pharmacology</i> , 2023, 461, 116407.	1.3	1
31539	A proteomic analysis of NETosis in trauma: Emergence of serpinB1 as a key player. <i>Journal of Trauma and Acute Care Surgery</i> , 2023, 94, 361-370.	1.1	5
31540	Pan-genome and transcriptome analyses provide insights into genomic variation and differential gene expression profiles related to disease resistance and fatty acid biosynthesis in eastern black walnut (<i>Juglans nigra</i>). <i>Horticulture Research</i> , 2023, 10, .	2.9	11
31541	Recent development of machine learning models for the prediction of drug-drug interactions. <i>Korean Journal of Chemical Engineering</i> , 2023, 40, 276-285.	1.2	5
31542	Computer-Aided Screening and Revealing Action Mechanism of Green Tea Polyphenols Intervention in Alzheimer's Disease. <i>Foods</i> , 2023, 12, 635.	1.9	2
31544	Chromosome-Level Assembly of Flowering Cherry (<i>Prunus campanulata</i>) Provides Insight into Anthocyanin Accumulation. <i>Genes</i> , 2023, 14, 389.	1.0	1

#	ARTICLE	IF	CITATIONS
31545	Reversal of hyperactive higher-order thalamus attenuates defensiveness in a mouse model of PTSD. <i>Science Advances</i> , 2023, 9, .	4.7	4
31546	Differentially expression analyses in fruit of cultivated and wild species of grape and peach. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31547	microRNAs profiling of small extracellular vesicles from midbrain tissue of Parkinson's disease. <i>Frontiers in Molecular Neuroscience</i> , 0, 16, .	1.4	1
31548	Evolved bacterial resistance to the chemotherapy gemcitabine modulates its efficacy in co-cultured cancer cells. <i>ELife</i> , 0, 12, .	2.8	6
31553	Genome-Wide Identification of Sweet Orange WRKY Transcription Factors and Analysis of Their Expression in Response to Infection by <i>Penicillium digitatum</i> . <i>Current Issues in Molecular Biology</i> , 2023, 45, 1250-1271.	1.0	5
31554	Exhaustion-like dysfunction of T and NKT cells in a linked severe combined immunodeficiency patient with maternal engraftment by single-cell analysis. <i>International Journal of Molecular Medicine</i> , 2023, 51, .	1.8	0
31555	Reading bots: The implication of deep learning on guided reading. <i>Frontiers in Psychology</i> , 0, 14, .	1.1	1
31556	Comparative proteome analysis of different <i>Saccharomyces cerevisiae</i> strains during growth on sucrose and glucose. <i>Scientific Reports</i> , 2023, 13, .	1.6	5
31557	Ageotypes revisited: The brain and central nervous system dysfunction as a major nutritional and lifestyle target for healthy aging. <i>Maturitas</i> , 2023, 170, 51-57.	1.0	2
31558	YAP/TAZ activation predicts clinical outcomes in mesothelioma and is conserved in in vitro model of driver mutations. <i>Clinical and Translational Medicine</i> , 2023, 13, .	1.7	1
31559	Identification of Hub Genes for Colorectal Cancer with Liver Metastasis Using miRNA-mRNA Network. <i>Disease Markers</i> , 2023, 2023, 1-14.	0.6	1
31560	The association of gene polymorphisms with milk production and mastitis resistance phenotypic traits in dairy cattle. <i>Annals of Animal Science</i> , 2023, 23, 419-430.	0.6	0
31561	Linking Phenotypes and Genotypes with Matrix Factorizations. <i>Current Pharmaceutical Biotechnology</i> , 2023, 24, .	0.9	0
31562	Identification of SARS-CoV-2 Main Protease (Mpro) Cleavage Sites Using Two-Dimensional Electrophoresis and In Silico Cleavage Site Prediction. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3236.	1.8	2
31563	Myocardial Infarction-Induced INSL6 Decrease Contributes to Breast Cancer Progression. <i>Disease Markers</i> , 2023, 2023, 1-33.	0.6	1
31564	Cytohesin-4 Upregulation in Glioma-Associated M2 Macrophages Is Correlated with Pyroptosis and Poor Prognosis. <i>Journal of Molecular Neuroscience</i> , 0, , .	1.1	2
31565	A Monoclonal Human Alveolar Epithelial Cell Line (AELo) with Pronounced Barrier Function for Studying Drug Permeability and Viral Infections. <i>Advanced Science</i> , 2023, 10, .	5.6	6
31567	Transcriptome sequencing of <i>Cocos nucifera</i> leaves in response to <i>Rhynchophorus ferrugineus</i> infestation. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0

#	ARTICLE	IF	CITATIONS
31568	PRSet: Pathway-based polygenic risk score analyses and software. <i>PLoS Genetics</i> , 2023, 19, e1010624.	1.5	28
31570	Interaction-integrated linear mixed model reveals 3D-genetic basis underlying Autism. <i>Genomics</i> , 2023, 115, 110575.	1.3	3
31571	Moesin is an effector of tau-induced actin overstabilization, cell cycle activation, and neurotoxicity in Alzheimer's disease. <i>IScience</i> , 2023, 26, 106152.	1.9	5
31572	Whole genome sequence of <i>Cryptosphaeria pullmanensis</i> , an important pathogenic fungus potentially threatening crop and forestry production. <i>Genomics</i> , 2023, 115, 110576.	1.3	2
31573	The Usher syndrome 1C protein harmonin regulates canonical Wnt signaling. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	3
31574	Single-nucleus Atlas of Sevoflurane-induced Hippocampal Cell Type and Sex-specific Effects during Development in Mice. <i>Anesthesiology</i> , 2023, 138, 477-495.	1.3	6
31575	The scalable precision medicine open knowledge engine (SPOKE): a massive knowledge graph of biomedical information. <i>Bioinformatics</i> , 2023, 39, .	1.8	16
31576	An EMS-induced allele of the <i>brachytic2</i> gene can reduce plant height in maize. <i>Plant Cell Reports</i> , 2023, 42, 749-761.	2.8	1
31577	N-Linked Glycoproteome Analysis of <i>Dioscorea alata</i> Tuber Shows Atypical Glycosylation and Indicates Central Role of Glycosylated Proteins in Tuber Maturation. <i>Protein Journal</i> , 2023, 42, 78-93.	0.7	2
31578	Combination IFN γ and Membrane-Stable CD40L Maximize Tumor Dendritic Cell Activation and Lymph Node Trafficking to Elicit Systemic T-cell Immunity. <i>Cancer Immunology Research</i> , 2023, 11, 466-485.	1.6	1
31579	Identification of phenotypic and genotypic properties and cold adaptive mechanisms of novel freeze-thaw stress-resistant strain <i>Pseudomonas mandelii</i> from Antarctica. <i>Polar Biology</i> , 2023, 46, 169-183.	0.5	0
31580	Epitranscriptomic regulation of cortical neurogenesis via <i>Mettl8</i> -dependent mitochondrial tRNA m ³ C modification. <i>Cell Stem Cell</i> , 2023, 30, 300-311.e11.	5.2	10
31581	Single-cell multi-omic analysis profiles defective genome activation and epigenetic reprogramming associated with human pre-implantation embryo arrest. <i>Cell Reports</i> , 2023, 42, 112100.	2.9	5
31583	Human <i>RSPO1</i> Mutation Represses Beige Adipocyte Thermogenesis and Contributes to Diet-Induced Adiposity. <i>Advanced Science</i> , 2023, 10, .	5.6	5
31584	Artificial Intelligence in the Genetic Diagnosis of Rare Disease. <i>Clinics in Laboratory Medicine</i> , 2023, 43, 127-143.	0.7	2
31585	684. Genome-wide association studies for maturity rate in grazing dairy cows. , 2022, , .		0
31586	373. Fine-mapping young-stock survival QTL on chromosome 6 in Nordic Red Dairy Cattle. , 2022, , .		0
31587	Responses of carbapenemase-producing and non-producing carbapenem-resistant <i>Pseudomonas aeruginosa</i> strains to meropenem revealed by quantitative tandem mass spectrometry proteomics. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1

#	ARTICLE	IF	CITATIONS
31588	Genome-wide identification and characterization of parthenocarpic fruit set-related gene homologs in cucumber (<i>Cucumis sativus</i> L.). <i>Scientific Reports</i> , 2023, 13, .	1.6	5
31590	Enabling Single-Cell Drug Response Annotations from Bulk RNA-Seq Using SCAD. <i>Advanced Science</i> , 2023, 10, .	5.6	5
31591	Multilingual translation for zero-shot biomedical classification using BioTranslator. <i>Nature Communications</i> , 2023, 14, .	5.8	4
31592	Microbial community succession patterns and drivers of Luxiang-flavor Jiupei during long fermentation. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	5
31594	Transcriptomic and physiological analysis reveal phytohormone and phenylpropanoid biosynthesis in root of <i>Cynanchum auriculatum</i> . <i>Plant Growth Regulation</i> , 2023, 101, 67-85.	1.8	5
31596	SARS-CoV-2 leverages airway epithelial protective mechanism for viral infection. <i>IScience</i> , 2023, 26, 106175.	1.9	2
31597	Altered microRNA Transcriptome in Cultured Human Airway Cells upon Infection with SARS-CoV-2. <i>Viruses</i> , 2023, 15, 496.	1.5	2
31598	HMM-based profiling identifies the binding to divalent cations and nucleotides as common denominators of suramin targets. <i>Frontiers in Drug Discovery</i> , 0, 3, .	1.1	0
31599	Identification of potential biomarkers for colorectal cancer by clinical database analysis and Kaplan-Meier curves analysis. <i>Medicine (United States)</i> , 2023, 102, e32877.	0.4	4
31600	Label-Free Mass Spectrometry Proteomics Reveals Different Pathways Modulated in THP-1 Cells Infected with Therapeutic Failure and Drug Resistance <i>Leishmania infantum</i> Clinical Isolates. <i>ACS Infectious Diseases</i> , 2023, 9, 470-485.	1.8	0
31605	Integrated transcriptomic and metabolomic analyses reveal key metabolic pathways in response to potassium deficiency in coconut (<i>Cocos nucifera</i> L.) seedlings. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
31606	Exploring conserved and novel MicroRNA-like small RNAs from stress tolerant <i>Trichoderma fusants</i> and parental strains during interaction with fungal phytopathogen <i>Sclerotium rolfsii</i> Sacc.. <i>Pesticide Biochemistry and Physiology</i> , 2023, 191, 105368.	1.6	4
31607	Identification of Salt Tolerance Related Candidate Genes in Sea Rice 86™ at the Seedling and Reproductive Stages Using QTL-Seq and BSA-Seq. <i>Genes</i> , 2023, 14, 458.	1.0	7
31608	Modeling Blast Crisis Using Mutagenized Chronic Myeloid Leukemia-Derived Induced Pluripotent Stem Cells (iPSCs). <i>Cells</i> , 2023, 12, 598.	1.8	6
31609	SARSMutOnto: An Ontology for SARS-CoV-2 Lineages and Mutations. <i>Viruses</i> , 2023, 15, 505.	1.5	1
31610	GO Bench: shared hub for universal benchmarking of machine learning-based protein functional annotations. <i>Bioinformatics</i> , 2023, 39, .	1.8	1
31611	A Hybrid Machine Learning Approach to Screen Optimal Predictors for the Classification of Primary Breast Tumors from Gene Expression Microarray Data. <i>Diagnostics</i> , 2023, 13, 708.	1.3	6
31612	Identification of Hub Genes Associated with Breast Cancer Using Integrated Gene Expression Data with Protein-Protein Interaction Network. <i>Applied Sciences (Switzerland)</i> , 2023, 13, 2403.	1.3	4

#	ARTICLE	IF	CITATIONS
31613	Investigation of distinct gene expression profile patterns that can improve the classification of intermediate-risk prognosis in AML patients. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	2
31614	Single-nucleus RNA sequencing in ischemic cardiomyopathy reveals common transcriptional profile underlying end-stage heart failure. <i>Cell Reports</i> , 2023, 42, 112086.	2.9	9
31615	Leveraging massively parallel reporter assays for evolutionary questions. <i>Genome Biology</i> , 2023, 24, .	3.8	10
31616	Bronchial epithelial cell transcriptional responses to inhaled corticosteroids dictate severe asthmatic outcomes. <i>Journal of Allergy and Clinical Immunology</i> , 2023, 151, 1513-1524.	1.5	3
31618	Genome-wide analysis of long non-coding RNAs in sugar beet (<i>Beta vulgaris</i> L.) under drought stress. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
31620	Shared Biological Pathways and Processes in Patients with Intellectual Disability: A Multicenter Study. <i>Neuropediatrics</i> , 0, , .	0.3	0
31621	DNA methylation profiling reveals novel pathway implicated in cardiovascular diseases of diabetes. <i>Frontiers in Endocrinology</i> , 0, 14, .	1.5	2
31622	Germline variation in <i>RASAL2</i> may predict survival in patients with <i>RAS</i> -activated colorectal cancer. <i>Genes Chromosomes and Cancer</i> , 2023, 62, 332-341.	1.5	0
31624	Phylogeny, transcriptional profile, and auxin-induced phosphorylation modification characteristics of conserved PIN proteins in Moso bamboo (<i>Phyllostachys edulis</i>). <i>International Journal of Biological Macromolecules</i> , 2023, 234, 123671.	3.6	6
31625	Transcriptome analysis of putative key signaling pathways and genes in the nidamental gland tissue associated with reproductive regulation of golden cuttlefish (<i>Sepia esculenta</i> Hoyle). <i>Aquaculture Reports</i> , 2023, 29, 101494.	0.7	0
31626	Transcriptional dynamics of maize leaves, pollens and ovules to gain insights into heat stress-related responses. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	4
31627	Processing of carbon-reinforced construction materials releases PM2.5 inducing inflammation and (secondary) genotoxicity in human lung epithelial cells and fibroblasts. <i>Environmental Toxicology and Pharmacology</i> , 2023, 98, 104079.	2.0	2
31628	Deficiency of primate-specific <i>SSX1</i> induced asthenoteratozoospermia in infertile men and cynomolgus monkey and tree shrew models. <i>American Journal of Human Genetics</i> , 2023, 110, 516-530.	2.6	5
31629	Artificial intelligence assessment of the potential of tocilizumab along with corticosteroids therapy for the management of COVID-19 evoked acute respiratory distress syndrome. <i>PLoS ONE</i> , 2023, 18, e0280677.	1.1	2
31631	Gcap14 is a microtubule plus-end-tracking protein coordinating microtubule-actin crosstalk during neurodevelopment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	2
31633	Identification and validation of a novel ubiquitination-related gene <i>UBE2T</i> in Ewing's sarcoma. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	0
31635	De Novo Assembly and Characterization of the Transcriptome of an Omnivorous Camel Cricket (<i>Tachycines meditationis</i>). <i>International Journal of Molecular Sciences</i> , 2023, 24, 4005.	1.8	0
31636	Chromosome-scale genome assembly and insights into the metabolome and gene regulation of leaf color transition in an important oak species, <i>Quercus dentata</i> . <i>New Phytologist</i> , 2023, 238, 2016-2032.	3.5	13

#	ARTICLE	IF	CITATIONS
31638	IRF4 as a novel target involved in malignant transformation of oral submucous fibrosis into oral squamous cell carcinoma. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
31640	Computational identification and systematic classification of cytochrome P450 genes in <i>Pogostemon cablin</i> provide insights into flavonoids biosynthesis. <i>Acta Physiologiae Plantarum</i> , 2023, 45, .	1.0	1
31641	Transcriptional Profiling Supports the Notochordal Origin of Chordoma and Its Dependence on a TGF β 1-TBXT Network. <i>American Journal of Pathology</i> , 2023, 193, 532-547.	1.9	1
31642	Cardiomyocyte Pdk4 response is associated with metabolic maladaptation in aging. <i>Aging Cell</i> , 2023, 22, .	3.0	7
31643	Long noncoding RNA GATA2-AS1 augments endothelial hypoxia inducible factor 1- α induction and regulates hypoxic signaling. <i>Journal of Biological Chemistry</i> , 2023, 299, 103029.	1.6	4
31644	Hypothesis-free phenotype prediction within a genetics-first framework. <i>Nature Communications</i> , 2023, 14, .	5.8	1
31645	Exploration and identification of anoikis-related genes in polycythemia vera. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
31646	Genome-Wide Gene-Set Analysis Identifies Molecular Mechanisms Associated with ALS. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4021.	1.8	1
31647	Confusoside from <i>Anneslea fragrans</i> Alleviates Acetaminophen-Induced Liver Injury in HepG2 via PI3K-CASP3 Signaling Pathway. <i>Molecules</i> , 2023, 28, 1932.	1.7	2
31650	Potential Early Markers for Breast Cancer: A Proteomic Approach Comparing Saliva and Serum Samples in a Pilot Study. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4164.	1.8	5
31651	Transcriptome-based variations effectively untangling the intraspecific relationships and selection signals in Xinyang Maojian tea population. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
31652	Transcriptomic analysis reveals differentially expressed genes associated with pine wood nematode resistance in resistant <i>Pinus thunbergii</i> . <i>Tree Physiology</i> , 2023, 43, 995-1008.	1.4	3
31653	Genome Size Changes by Duplication, Divergence, and Insertion in <i>Caenorhabditis</i> Worms. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	0
31654	Comprehensive chromatin proteomics resolves functional phases of pluripotency and identifies changes in regulatory components. <i>Nucleic Acids Research</i> , 2023, 51, 2671-2690.	6.5	2
31655	FLI1 and FRA1 transcription factors drive the transcriptional regulatory networks characterizing muscle invasive bladder cancer. <i>Communications Biology</i> , 2023, 6, .	2.0	4
31657	Comprehensive analysis of PHGDH for predicting prognosis and immunotherapy response in patients with endometrial carcinoma. <i>BMC Medical Genomics</i> , 2023, 16, .	0.7	1
31658	A compilation of bioinformatic approaches to identify novel downstream targets for the detection and prophylaxis of cancer. <i>Advances in Protein Chemistry and Structural Biology</i> , 2023, , 75-113.	1.0	0
31659	Leveraging GWAS data derived from a large cooperative group trial to assess the risk of taxane-induced peripheral neuropathy (TIPN) in patients being treated for breast cancer: Part 2—functional implications of a SNP cluster associated with TIPN risk in patients being treated for breast cancer. <i>Supportive Care in Cancer</i> , 2023, 31, .	1.0	1

#	ARTICLE	IF	CITATIONS
31661	A proteomics approach to identify COPD-related changes in lung fibroblasts. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2023, 324, L521-L535.	1.3	1
31662	A guide to current methodology and usage of reverse vaccinology towards <i>in silico</i> vaccine discovery. <i>FEMS Microbiology Reviews</i> , 2023, 47, .	3.9	14
31663	Genome-wide analysis of R2R3-MYB transcription factors in <i>Boehmeria nivea</i> (L.) gaudich revealed potential cadmium tolerance and anthocyanin biosynthesis genes. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	5
31664	Identification and validation of ferroptosis-related genes and immune infiltration in ischemic cardiomyopathy. <i>Frontiers in Cardiovascular Medicine</i> , 0, 10, .	1.1	1
31665	Genome assembly of <i>Musa beccarii</i> shows extensive chromosomal rearrangements and genome expansion during evolution of Musaceae genomes. <i>GigaScience</i> , 2022, 12, .	3.3	4
31666	Uncovering the complex genetic architecture of human plasma lipidome using machine learning methods. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31667	Integrated transcriptome analysis reveals roles of long non-coding RNAs (lncRNAs) in caprine skeletal muscle mass and meat quality. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	4
31669	Exploiting moderate hypoxia to benefit patients with brain disease: Molecular mechanisms and translational research in progress. , 2023, 1, 55-65.		6
31670	Whole-Genome Sequence of <i>Lactiplantibacillus plantarum</i> Mut-3, Isolated from Indonesian Fermented Soybean (Tempeh). <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	1
31671	Integrated transcriptomics and metabolomics analyses provide insights into salt-stress response in germination and seedling stage of wheat (<i>Triticum aestivum</i> L.). <i>Current Plant Biology</i> , 2023, 33, 100274.	2.3	6
31673	Addressing Tumor Heterogeneity by Sensitizing Resistant Cancer Cells to T cellâ€‘Secreted Cytokines. <i>Cancer Discovery</i> , 2023, 13, 1186-1209.	7.7	1
31674	Comparative transcriptome analysis of adult worker bees under short-term heat stress. <i>Frontiers in Ecology and Evolution</i> , 0, 11, .	1.1	0
31675	Selection signature analysis reveals <i>RDH5</i> performed key function in vision during sheep domestication process. <i>Archives Animal Breeding</i> , 2023, 66, 81-91.	0.5	1
31676	<i>Radiobacillus kansasensis</i> sp. nov., a halotolerant bacterium isolated from woodland soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
31678	LINC01798/miR-17-5p axis regulates ITGA8 and causes changes in tumor microenvironment and stemness in lung adenocarcinoma. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	4
31679	BEAR: A Novel Virtual Screening Method Based on Large-Scale Bioactivity Data. <i>Journal of Chemical Information and Modeling</i> , 2023, 63, 1429-1437.	2.5	3
31680	AURKA Identified as Potential Lung Cancer Marker through Comprehensive Bioinformatic Analysis and Experimental Verification. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2023, 33, 39-59.	0.4	1
31681	PriPath: identifying dysregulated pathways from differential gene expression via grouping, scoring, and modeling with an embedded feature selection approach. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	8

#	ARTICLE	IF	CITATIONS
31682	Neuroligins facilitate the development of bone cancer pain via regulating synaptic transmission: an experimental study. <i>Brazilian Journal of Anesthesiology</i> (Elsevier), 2023, , 744422.	0.2	0
31683	Using protein-per-mRNA differences among human tissues in codon optimization. <i>Genome Biology</i> , 2023, 24, .	3.8	7
31684	Clustering of Human Gene Expression Stimulated by Bacterial Infection from Microarray Analysis. , 2022, , .		0
31685	Transcriptomic thermal plasticity underlying gonadal development in a turtle with <i><scp>ZZ</scp>/<scp>ZW</scp></i> sex chromosomes despite canalized genotypic sex determination. <i>Ecology and Evolution</i> , 2023, 13, .	0.8	5
31687	A genome and singleâ€nucleus cerebral cortex transcriptome atlas of the shortâ€finned pilot whale <i><i>Globicephala macrorhynchus</i></i> . <i>Molecular Ecology Resources</i> , 2023, 23, 1108-1123.	2.2	1
31688	Transcriptomic changes in single yeast cells under various stress conditions. <i>BMC Genomics</i> , 2023, 24, .	1.2	0
31689	Gene profiling reveals the role of inflammation, abnormal uterine muscle contraction and vascularity in recurrent implantation failure. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	3
31690	Photosynthetic and transcriptomic responses of <i>Chlorella</i> sp. to tigecycline. <i>Algal Research</i> , 2023, 71, 103033.	2.4	3
31692	MSC-CSMC: A multi-objective semi-supervised clustering algorithm based on constraints selection and multi-source constraints for gene expression data. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
31693	Proteinfer, deep neural networks for protein functional inference. <i>ELife</i> , 0, 12, .	2.8	31
31694	Draft Genome and Biological Characteristics of <i>Fusarium solani</i> and <i>Fusarium oxysporum</i> Causing Black Rot in <i>Gastrodia elata</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 4545.	1.8	0
31695	Comparative transcriptomic and metabolomic analyses reveal differences in flavonoid biosynthesis between PCNA and PCA persimmon fruit. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	5
31696	Transcriptomic Analyses of Brains of RBM8A Conditional Knockout Mice at Different Developmental Stages Reveal Conserved Signaling Pathways Contributing to Neurodevelopmental Diseases. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4600.	1.8	1
31697	Analysis of proteomesâ€”i. , 2023, , 111-138.		0
31698	Functional genomics of <i>Chlamydomonas reinhardtii</i> . , 2023, , 65-84.		0
31699	COL12A1 Acts as a Novel Prognosis Biomarker and Activates Cancer-Associated Fibroblasts in Pancreatic Cancer through Bioinformatics and Experimental Validation. <i>Cancers</i> , 2023, 15, 1480.	1.7	2
31700	PrismEXP: gene annotation prediction from stratified gene-gene co-expression matrices. <i>PeerJ</i> , 0, 11, e14927.	0.9	2
31701	Nicotinamide riboside supplementation is not associated with altered methylation homeostasis in Parkinsonâ€™s disease. <i>IScience</i> , 2023, 26, 106278.	1.9	4

#	ARTICLE	IF	CITATIONS
31703	Consensus Clustering and Survival-Related Genes of Cuproptosis in Cutaneous Melanoma. Mediators of Inflammation, 2023, 2023, 1-15.	1.4	4
31704	Using the Proteomics Toolbox to Resolve Topology and Dynamics of Compartmentalized cAMP Signaling. International Journal of Molecular Sciences, 2023, 24, 4667.	1.8	4
31705	The early neutrophil-committed progenitors aberrantly differentiate into immunoregulatory monocytes during emergency myelopoiesis. Cell Reports, 2023, 42, 112165.	2.9	11
31707	Evaluation of Genetic Testing in a Cohort of Diverse Pediatric Patients in the United States with Congenital Cataracts. Genes, 2023, 14, 608.	1.0	0
31709	Ontology Assisted Unsupervised Clustering for Interpreting Microarray Gene Expression Profiles. , 2022, , .		0
31710	Role of hypoxia-inducible factor-1 α and survivin in breast cancer recurrence and prognosis. Heliyon, 2023, 9, e14132.	1.4	2
31711	Effects of allicin on human Simpson-Golabi-Behmel syndrome cells in mediating browning phenotype. Frontiers in Endocrinology, 0, 14, .	1.5	0
31712	ALMedGraph: a comprehensive multi-relational knowledge graph for precision medicine. Database: the Journal of Biological Databases and Curation, 2023, 2023, .	1.4	2
31713	Construction of a fatty acid metabolism-related gene signature for predicting prognosis and immune response in breast cancer. Frontiers in Genetics, 0, 14, .	1.1	4
31714	The RNA binding protein DND1 is elevated in a subpopulation of pro-spermatogonia and targets chromatin modifiers and translational machinery during late gestation. PLoS Genetics, 2023, 19, e1010656.	1.5	0
31715	The ion channel <sc>CALHM6</sc> controls bacterial infection-induced cellular cross-talk at the immunological synapse. EMBO Journal, 2023, 42, .	3.5	5
31718	Small Brown Planthopper Nymph Infestation Regulates Plant Defenses by Affecting Secondary Metabolite Biosynthesis in Rice. International Journal of Molecular Sciences, 2023, 24, 4764.	1.8	0
31719	Transcriptome Analysis of Differentially Expressed Genes Associated with Salt Stress in Cowpea (Vigna Tj ETQq0 0 0 rgBT /Overlock 10 24, 4762.	1.8	7
31720	Pan-Cancer Analysis Reveals Functional Similarity of Three lncRNAs across Multiple Tumors. International Journal of Molecular Sciences, 2023, 24, 4796.	1.8	1
31721	Artificial intelligence and machine learning in pain research: a data scientometric analysis. Pain Reports, 2022, 7, e1044.	1.4	16
31722	The enormous repetitive Antarctic krill genome reveals environmental adaptations and population insights. Cell, 2023, 186, 1279-1294.e19.	13.5	23
31723	Comparative Genomic and Transcriptomic Analyses Reveal the Impacts of Genetic Admixture in Kazaks, Uyghurs, and Huis. Molecular Biology and Evolution, 2023, 40, .	3.5	4
31725	The Gene Ontology knowledgebase in 2023. Genetics, 2023, 224, .	1.2	253

#	ARTICLE	IF	CITATIONS
31726	From multiallele fish to nonstandard environments, how ZFIN assigns phenotypes, human disease models, and gene expression annotations to genes. <i>Genetics</i> , 0, , .	1.2	2
31727	Hepatic gene expression profiles during fedâ€“fastedâ€“refed state in mice. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	3
31728	Differentially Expressed Genes Analysis in the Human Small Airway Epithelium of Healthy Smokers Shows Potential Risks of Disease Caused by Oxidative Stress and Inflammation and the Potentiality of Astaxanthin as an Anti-Inflammatory Agent. <i>International Journal of Inflammation</i> , 2023, 2023, 1-10.	0.9	0
31729	Identification of GNG7 as a novel biomarker and potential therapeutic target for gastric cancer via bioinformatic analysis and in vitro experiments. <i>Aging</i> , 0, , .	1.4	0
31732	Gene Functional Networks from Time Expression Profiles: A Constructive Approach Demonstrated in Chili Pepper (<i>Capsicum annuum</i> L.). <i>Plants</i> , 2023, 12, 1148.	1.6	0
31733	Biomedical Knowledge Graphs: Context, Queries and Complexity. <i>Studies in Big Data</i> , 2022, , 529-567.	0.8	0
31734	<i>DIS3</i> Variants are Associated With Primary Ovarian Insufficiency: Importance of Transcription/Translation in Oogenesis. <i>Journal of Clinical Endocrinology and Metabolism</i> , 0, , .	1.8	0
31736	Single-cell sequencing reveals peritoneal environment and insights into fibrosis in CAPD patients. <i>IScience</i> , 2023, 26, 106336.	1.9	2
31737	Validation of the new EPIC DNA methylation microarray (900K EPIC v2) for high-throughput profiling of the human DNA methylome. <i>Epigenetics</i> , 2023, 18, .	1.3	13
31738	Metatranscriptomics and metabarcoding reveal spatiotemporal shifts in fungal communities and their activities in Chinese coastal waters. <i>Molecular Ecology</i> , 2023, 32, 2750-2765.	2.0	6
31739	Exosomal Mir-3613-3p derived from oxygenâ€“glucose deprivation-treated brain microvascular endothelial cell promotes microglial M1 polarization. <i>Cellular and Molecular Biology Letters</i> , 2023, 28, .	2.7	6
31740	Insights into Online microRNA Bioinformatics Tools. <i>Non-coding RNA</i> , 2023, 9, 18.	1.3	3
31741	Full-Length Transcriptome of the Great Himalayan Leaf-Nosed Bats (<i>Hipposideros armiger</i>) Optimized Genome Annotation and Revealed the Expression of Novel Genes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4937.	1.8	0
31742	Identification of Selection Signatures and Loci Associated with Important Economic Traits in Yunan Black and Huainan Pigs. <i>Genes</i> , 2023, 14, 655.	1.0	1
31743	Integrating Multi-Omics Analysis Reveals the Regulatory Mechanisms of Whiteâ€“Violet Mutant Flowers in Grape Hyacinth (<i>Muscari latifolium</i>). <i>International Journal of Molecular Sciences</i> , 2023, 24, 5044.	1.8	1
31745	<sc>MFN2</sc> deficiency affects calcium homeostasis in lung adenocarcinoma cells via downregulation of <sc>UCP4</sc>. <i>FEBS Open Bio</i> , 2023, 13, 1107-1124.	1.0	0
31746	Genome-wide association study to identify SNPs and candidate genes associated with body size traits in donkeys. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	3
31747	A Specific High Toxicity of Xinjunan (Diocetyl diethylenetriamine) to <i>Xanthomonas</i> by Affecting the Iron Metabolism. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	3

#	ARTICLE	IF	CITATIONS
31748	Transcriptome analysis reveals the crucial function of hyperoside in inhibiting anthocyanin accumulation in grape (<i>Vitis vinifera</i> L.) fruits by inducing VvMYB62. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
31749	Translating Ribosome Affinity Purification (TRAP) and Bioinformatic RNA-Seq Analysis in Post-metamorphic <i>Xenopus laevis</i> . <i>Methods in Molecular Biology</i> , 2023, , 279-310.	0.4	0
31750	CD24-associated ceRNA network reveals prognostic biomarkers in breast carcinoma. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
31751	Quantitative Proteomics of Nervous System Regeneration: From Sample Preparation to Functional Data Analyses. <i>Methods in Molecular Biology</i> , 2023, , 343-366.	0.4	0
31753	Cooperative driver pathways discovery by multiplex network embedding. <i>Briefings in Bioinformatics</i> , 0, , .	3.2	0
31754	Histone H3-wild type diffuse midline gliomas with H3K27me3 loss are a distinct entity with exclusive EGFR or ACVR1 mutation and differential methylation of homeobox genes. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31755	Sex-Specific Effects of Early-Life Iron Deficiency and Prenatal Choline Treatment on Adult Rat Hippocampal Transcriptome. <i>Nutrients</i> , 2023, 15, 1316.	1.7	1
31757	Exploring the components and mechanism of <i>Solanum nigrum</i> L. for colon cancer treatment based on network pharmacology and molecular docking. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	2
31758	Transcriptomic analysis of pea plant responses to chitoooligosaccharidesâ€™™ treatment revealed stimulation of mitogen-activated protein kinase cascade. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
31760	Transcriptomic analysis of the Non-Obstructive Azoospermia (NOA) to address gene expression regulation in human testis. <i>Systems Biology in Reproductive Medicine</i> , 2023, 69, 196-214.	1.0	1
31763	A mitochondrial function-related LncRNA signature predicts prognosis and immune microenvironment for breast cancer. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
31764	Clinical and prognostic associations of autoantibodies recognizing adrenergic/muscarinic receptors in patients with heart failure. <i>Cardiovascular Research</i> , 0, , .	1.8	2
31765	CFAGO: cross-fusion of network and attributes based on attention mechanism for protein function prediction. <i>Bioinformatics</i> , 2023, 39, .	1.8	6
31766	Higher-order modular regulation of the human proteome. <i>Molecular Systems Biology</i> , 2023, 19, .	3.2	4
31767	Potential biomarker proteins for aspiration pneumonia detected by shotgun proteomics using buccal mucosa samples: a cross-sectional case-control study. <i>Clinical Proteomics</i> , 2023, 20, .	1.1	2
31768	Analysis of context-specific KRAS effector (sub)complexes in Caco-2 cells. <i>Life Science Alliance</i> , 2023, 6, e202201670.	1.3	1
31769	Prognosis and Characterization of Microenvironment in Cervical Cancer Influenced by Fatty Acid Metabolism-Related Genes. <i>Journal of Oncology</i> , 2023, 2023, 1-34.	0.6	2
31770	Comprehensive bioinformatic analysis constructs a CXCL model for predicting survival and immunotherapy effectiveness in ovarian cancer. <i>Frontiers in Pharmacology</i> , 0, 14, .	1.6	1

#	ARTICLE	IF	CITATIONS
31771	Digital spatial profiling of human parathyroid tumors reveals cellular and molecular alterations linked to vitamin D deficiency. , 2023, 2, .		1
31774	Molecular and network-level mechanisms explaining individual differences in autism spectrum disorder. <i>Nature Neuroscience</i> , 2023, 26, 650-663.	7.1	24
31775	A crowdsourcing database for the copy-number variation of the Spanish population. <i>Human Genomics</i> , 2023, 17, .	1.4	2
31776	Telomere-related genes as potential biomarkers to predict endometriosis and immune response: Development of a machine learning-based risk model. <i>Frontiers in Medicine</i> , 0, 10, .	1.2	3
31778	Ginseng-based carbon dots inhibit the growth of squamous cancer cells by increasing ferroptosis. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	4
31780	Bioinformatics analysis and verification of <scp>m6A</scp> related genes based on the construction of keloid diagnostic model. <i>International Wound Journal</i> , 2023, 20, 2700-2717.	1.3	1
31781	An integrated approach of high-performance liquid chromatography-mass spectrometry-based chemical profiling, network pharmacology, and molecular docking to reveal the potential mechanisms of Qishen Gubiao granules for treating coronavirus disease 2019. <i>Journal of Separation Science</i> , 2023, 46, .	1.3	4
31782	End-to-end interpretable disease-gene association prediction. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	4
31787	Screening and identification of key biomarkers of depression using bioinformatics. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31788	Content and quality of physical activity ontologies: a systematic review. <i>International Journal of Behavioral Nutrition and Physical Activity</i> , 2023, 20, .	2.0	0
31790	Integrated analysis and clinical correlation analysis of hub genes, immune infiltration, and potential therapeutic agents related to lupus nephritis. <i>Lupus</i> , 0, , 096120332311615.	0.8	0
31791	Proteomic characterisation of perhexiline treatment on THP-1 M1 macrophage differentiation. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	3
31792	Lipid extract derived from newly isolated <i>Rhodotorula toruloides</i> LAB-07 for cosmetic applications. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 2009-2017.	1.9	3
31794	Analysis of gene expression and use of connectivity mapping to identify drugs for treatment of human glomerulopathies. <i>Frontiers in Medicine</i> , 0, 10, .	1.2	2
31795	A preliminary study on the root-knot nematode resistance of a cherry plum cultivar Mirabolano 29C. <i>Czech Journal of Genetics and Plant Breeding</i> , 2023, 59, 133-140.	0.4	1
31796	Strategy for the Adaptation to Stressful Conditions of the Novel Isolated Conditional Piezophilic Strain <i>Halomonas titanicae</i> ANRCS81. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	1.4	4
31797	The potential value of cuproptosis in myocardial immune infiltration that occurs in pediatric congenital heart disease in response to surgery with cardiopulmonary bypass. <i>Immunity, Inflammation and Disease</i> , 2023, 11, .	1.3	0
31798	Identification of potential biomarkers and therapeutic targets for posttraumatic acute respiratory distress syndrome. <i>BMC Medical Genomics</i> , 2023, 16, .	0.7	0

#	ARTICLE	IF	CITATIONS
31800	Lymphocytic Choriomeningitis Virus Clone 13 Infection Results in CD8 T Cell-Mediated Host Mortality in Diacylglycerol Kinase Deficient Mice. <i>Journal of Immunology</i> , 2023, 210, 1281-1291.	0.4	0
31801	The Josephin domain (JD) containing proteins are predicted to bind to the same interactors: Implications for spinocerebellar ataxia type 3 (SCA3) studies using <i>Drosophila melanogaster</i> mutants. <i>Frontiers in Molecular Neuroscience</i> , 0, 16, .	1.4	2
31802	Radical-Scavenging and Subchondral Bone-Regenerating Nanomedicine for Osteoarthritis Treatment. <i>ACS Nano</i> , 2023, 17, 6131-6146.	7.3	15
31806	Bioinformatics approach to identify the impacts of microgravity on the development of bone and joint diseases. <i>Informatics in Medicine Unlocked</i> , 2023, 38, 101211.	1.9	0
31808	Different Resistance Exercise Loading Paradigms Similarly Affect Skeletal Muscle Gene Expression Patterns of Myostatin-Related Targets and mTORC1 Signaling Markers. <i>Cells</i> , 2023, 12, 898.	1.8	3
31809	Convergent <i>Aedes</i> and <i>Drosophila</i> CidB interactomes suggest cytoplasmic incompatibility targets are conserved. <i>Insect Biochemistry and Molecular Biology</i> , 2023, 155, 103931.	1.2	3
31810	Identification of five hub immune genes and characterization of two immune subtypes of osteoarthritis. <i>Frontiers in Endocrinology</i> , 0, 14, .	1.5	0
31811	Using a whole genome co-expression network to inform the functional characterisation of predicted genomic elements from <i>Mycobacterium tuberculosis</i> transcriptomic data. <i>Molecular Microbiology</i> , 2023, 119, 381-400.	1.2	1
31812	Shared Genes of PPARG and NOS2 in Alzheimer's Disease and Ulcerative Colitis Drive Macrophages and Microglia Polarization: Evidence from Bioinformatics Analysis and Following Validation. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5651.	1.8	4
31813	In silico analysis to identify miR-1271-5p/PLCB4 (phospholipase C Beta 4) axis mediated oxaliplatin resistance in metastatic colorectal cancer. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31814	Exogenous L-lactate administration in rat hippocampus increases expression of key regulators of mitochondrial biogenesis and antioxidant defense. <i>Frontiers in Molecular Neuroscience</i> , 0, 16, .	1.4	8
31816	Pharmacogenomic and Statistical Analysis. <i>Methods in Molecular Biology</i> , 2023, , 305-330.	0.4	0
31817	The MicroRNA Ame-Bantam-3p Controls Larval Pupal Development by Targeting the Multiple Epidermal Growth Factor-like Domains 8 Gene (<i>megf8</i>) in the Honeybee, <i>Apis mellifera</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 5726.	1.8	1
31818	spSeudoMap: cell type mapping of spatial transcriptomics using unmatched single-cell RNA-seq data. <i>Genome Medicine</i> , 2023, 15, .	3.6	3
31819	Comprehensive analysis of the expression, prognostic value and biological importance of OVO-like proteins in clear cell renal cell carcinoma. <i>Oncology Letters</i> , 2023, 25, .	0.8	1
31820	Integrin β 3-Mediated Cell Senescence Associates with Gut Inflammation and Intestinal Degeneration in Models of Alzheimer's Disease. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5697.	1.8	3
31821	Analyzing CRISPR screens in non-conventional microbes. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2023, 50, .	1.4	2
31822	Susceptibility and Permissivity of Zebrafish (<i>Danio rerio</i>) Larvae to Cypriniviruses. <i>Viruses</i> , 2023, 15, 768.	1.5	2

#	ARTICLE	IF	CITATIONS
31823	DIAPH1 mediates progression of atherosclerosis and regulates hepatic lipid metabolism in mice. <i>Communications Biology</i> , 2023, 6, .	2.0	3
31824	An informatic workflow for the enhanced annotation of excretory/secretory proteins of <i>Haemonchus contortus</i> . <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 2696-2704.	1.9	1
31826	Identification of new potential downstream transcriptional targets of the strigolactone pathway including glucosinolate biosynthesis. <i>Plant Direct</i> , 2023, 7, .	0.8	6
31827	Resistance in pea (<i>Pisum sativum</i>) genetic resources to the pea aphid, <i>Acyrtosiphon pisum</i> . <i>Entomologia Experimentalis Et Applicata</i> , 2023, 171, 435-448.	0.7	1
31828	Reduced Transcriptome Analysis of Zebrafish Embryos Prioritizes Environmental Compounds with Adverse Cardiovascular Activities. <i>Environmental Science & Technology</i> , 2023, 57, 4959-4970.	4.6	0
31829	Immune Activation following Irbesartan Treatment in a Colorectal Cancer Patient: A Case Study. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5869.	1.8	1
31830	De Novo Transcriptome Sequencing of <i>Codonopsis lanceolata</i> for Identification of Triterpene Synthase and Triterpene Acetyltransferase. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5769.	1.8	1
31831	Comparative proteome profiles of <i>Polygonatum cyrtoneura</i> Hua rhizomes (<i>Rhizoma Polygonati</i>) in response to different levels of cadmium stress. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	2
31832	Integrative transcriptome and proteome analysis reveals maize responses to <i>Fusarium verticillioides</i> infection inside the stalks. <i>Molecular Plant Pathology</i> , 2023, 24, 693-710.	2.0	7
31833	Integration of Stemness Gene Signatures Reveals Core Functional Modules of Stem Cells and Potential Novel Stemness Genes. <i>Genes</i> , 2023, 14, 745.	1.0	5
31835	Whole Genome Resequencing Revealed the Effect of Helicase <i>yqhH</i> Gene on Regulating <i>Bacillus thuringiensis</i> LLP29 against Ultraviolet Radiation Stress. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5810.	1.8	4
31836	Gene augmentation for autosomal dominant retinitis pigmentosa using rhodopsin genomic loci nanoparticles in the P23H/ β knock-in murine model. <i>Gene Therapy</i> , 2023, 30, 628-640.	2.3	1
31837	Integrated Multi-Omics Techniques and Network Pharmacology Analysis to Explore the Material Basis and Mechanism of Simiao Pill in the Treatment of Rheumatoid Arthritis. <i>ACS Omega</i> , 2023, 8, 11138-11150.	1.6	2
31839	Integrative comparative analysis of avian chromosome evolution by in-silico mapping of the gene ontology of homologous synteny blocks and evolutionary breakpoint regions. <i>Genetica</i> , 0, .	0.5	0
31840	Icariin Induces Triple-Negative Breast Cancer Cell Apoptosis and Suppresses Invasion by Inhibiting the JNK/c-Jun Signaling Pathway. <i>Drug Design, Development and Therapy</i> , 0, Volume 17, 821-836.	2.0	4
31841	Automated assembly of molecular mechanisms at scale from text mining and curated databases. <i>Molecular Systems Biology</i> , 2023, 19, .	3.2	9
31842	Computational Approaches Drive Developments in Immune-Oncology Therapies for PD-1/PD-L1 Immune Checkpoint Inhibitors. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5908.	1.8	4
31843	Transcriptome sequencing identifies prognostic genes involved in gastric adenocarcinoma. <i>Molecular and Cellular Biochemistry</i> , 0, .	1.4	0

#	ARTICLE	IF	CITATIONS
31845	Intraspecific Comparative Analysis Reveals Genomic Variation of <i>Didymella arachidicola</i> and Pathogenicity Factors Potentially Related to Lesion Phenotype. <i>Biology</i> , 2023, 12, 476.	1.3	0
31846	Elucidating the patterns of pleiotropy and its biological relevance in maize. <i>PLoS Genetics</i> , 2023, 19, e1010664.	1.5	0
31847	Endosymbiont-containing germarium transcriptional survey in a cereal weevil depicts downregulation of immune effectors at the onset of sexual maturity. <i>Frontiers in Physiology</i> , 0, 14, .	1.3	2
31848	Stromal Senescence following Treatment with the CDK4/6 Inhibitor Palbociclib Alters the Lung Metastatic Niche and Increases Metastasis of Drug-Resistant Mammary Cancer Cells. <i>Cancers</i> , 2023, 15, 1908.	1.7	5
31849	NaRnEA: An Information Theoretic Framework for Gene Set Analysis. <i>Entropy</i> , 2023, 25, 542.	1.1	2
31850	Growth rate-associated transcriptome reorganization in response to genomic, environmental, and evolutionary interruptions. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
31851	Distinct function of SPL genes in age-related resistance in <i>Arabidopsis</i> . <i>PLoS Pathogens</i> , 2023, 19, e1011218.	2.1	8
31852	Construction and analysis of protein-protein interaction networks based on nuclear proteomics data of the desiccation-tolerant <i>Xerophyta schlechteri</i> leaves subjected to dehydration stress. <i>Communicative and Integrative Biology</i> , 2023, 16, .	0.6	1
31853	Adaptation of the Porcine Pituitary Transcriptome, Spliceosome and Editome during Early Pregnancy. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5946.	1.8	4
31854	Assembly and Analysis of <i>Haemonchus contortus</i> Transcriptome as a Tool for the Knowledge of Ivermectin Resistance Mechanisms. <i>Pathogens</i> , 2023, 12, 499.	1.2	6
31855	Influence of Scaffold Microarchitecture on Angiogenesis and Regulation of Cell Differentiation during the Early Phase of Bone Healing: A Transcriptomics and Histological Analysis. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6000.	1.8	3
31856	Draft genome sequence resource of sweet cherry virescence phytoplasma strain SCV-TA2020 associated with sweet cherry virescence disease in China. <i>Plant Disease</i> , 0, , .	0.7	0
31857	Primate protein-ligand interfaces exhibit significant conservation and unveil human-specific evolutionary drivers. <i>PLoS Computational Biology</i> , 2023, 19, e1010966.	1.5	0
31858	SERPINE1 and its co-expressed genes are associated with the progression of clear cell renal cell carcinoma. <i>BMC Urology</i> , 2023, 23, .	0.6	3
31859	Sex differences of signal complexity at resting-state functional magnetic resonance imaging and their associations with the estrogen-signaling pathway in the brain. <i>Cognitive Neurodynamics</i> , 0, , .	2.3	0
31860	The m6A methylation landscape, molecular characterization and clinical relevance in prostate adenocarcinoma. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	0
31861	Enterohemorrhagic <i>Escherichia coli</i> responds to gut microbiota metabolites by altering metabolism and activating stress responses. <i>Gut Microbes</i> , 2023, 15, .	4.3	1
31862	Urea cycle activation triggered by host-microbiota maladaptation driving colorectal tumorigenesis. <i>Cell Metabolism</i> , 2023, 35, 651-666.e7.	7.2	15

#	ARTICLE	IF	CITATIONS
31863	Complete genome of <i>Sphingomonas paucimobilis</i> ZJSH1, an endophytic bacterium from <i>Dendrobium officinale</i> with stress resistance and growth promotion potential. <i>Archives of Microbiology</i> , 2023, 205, .	1.0	7
31864	The DREAM complex functions as conserved master regulator of somatic DNA-repair capacities. <i>Nature Structural and Molecular Biology</i> , 2023, 30, 475-488.	3.6	18
31866	Integrative identification of hub genes in development of atrial fibrillation related stroke. <i>PLoS ONE</i> , 2023, 18, e0283617.	1.1	0
31867	Upregulation of Biomarker <i>Limd1</i> Was Correlated with Immune Infiltration in Doxorubicin-Related Cardiotoxicity. <i>Mediators of Inflammation</i> , 2023, 2023, 1-23.	1.4	0
31869	Identification of two unannotated miRNAs in classic Hodgkin lymphoma cell lines. <i>PLoS ONE</i> , 2023, 18, e0283186.	1.1	0
31870	Transcriptomic Analyses of Exercise Training in Alzheimer's Disease Cerebral Cortex. <i>Journal of Alzheimer's Disease</i> , 2023, 93, 349-363.	1.2	2
31871	A novel method to identify and characterize personalized functional driver lncRNAs in cancer samples. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 2471-2482.	1.9	1
31872	Integrated analysis of transcriptome, small RNA, and phytohormonal content changes between <i>Artemisia annua</i> Linn. and <i>Nicotiana benthamiana</i> Domin in heterogeneous grafting. , 2023, 2, 0-0.		0
31875	Identification of prognostic and therapeutic biomarkers in type 2 papillary renal cell carcinoma. <i>World Journal of Surgical Oncology</i> , 2023, 21, .	0.8	2
31876	The oncogenic properties of the <i>EWSR1::CREM</i> fusion gene are associated with polyamine metabolism. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31877	Fusion gene <i>4CL-CCR</i> promotes lignification in tobacco suspension cells. <i>Plant Cell Reports</i> , 2023, 42, 939-952.	2.8	3
31878	Antiviral activity of glucosylceramide synthase inhibitors in alphavirus infection of the central nervous system. <i>Brain Communications</i> , 2023, 5, .	1.5	2
31879	Fast and accurate protein function prediction from sequence through pretrained language model and homology-based label diffusion. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	12
31881	Downregulation of <i>PSAT1</i> inhibits cell proliferation and migration in uterine corpus endometrial carcinoma. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
31882	Physiological, transcriptome and co-expression network analysis of chlorophyll-deficient mutants in flue-cured tobacco. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	1
31883	Proximity proteome mapping reveals PD-L1-dependent pathways disrupted by anti-PD-L1 antibody specifically in EGFR-mutant lung cancer cells. <i>Cell Communication and Signaling</i> , 2023, 21, .	2.7	1
31884	PI3K/AKT/mTOR inhibitors as potential extracellular matrix modulators for targeting EMT subtype gastric tumors. , 2023, 40, .		1
31885	Integrating AI/ML Models for Patient Stratification Leveraging Omics Dataset and Clinical Biomarkers from COVID-19 Patients: A Promising Approach to Personalized Medicine. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6250.	1.8	3

#	ARTICLE	IF	CITATIONS
31886	Whole-genome sequencing analysis of two heat-evolved <i>Escherichia coli</i> strains. <i>BMC Genomics</i> , 2023, 24, .	1.2	1
31887	Impaired Reorganization of Centrosome Structure Underlies Human Infantile Dilated Cardiomyopathy. <i>Circulation</i> , 2023, 147, 1291-1303.	1.6	3
31888	RAS and PP2A activities converge on epigenetic gene regulation. <i>Life Science Alliance</i> , 2023, 6, e202301928.	1.3	5
31889	Proteomic Landscape of Human Sperm in Patients with Different Spermatogenic Impairments. <i>Cells</i> , 2023, 12, 1017.	1.8	4
31890	Discovery of SNP Molecular Markers and Candidate Genes Associated with Sacbrood Virus Resistance in <i>Apis cerana cerana</i> Larvae by Whole-Genome Resequencing. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6238.	1.8	0
31891	Transcriptomics Reveals the Molecular Basis for Methyl Jasmonate to Promote the Synthesis of Monoterpenoids in <i>Schizonepeta tenuifolia</i> Briq.. <i>Current Issues in Molecular Biology</i> , 2023, 45, 2738-2756.	1.0	1
31892	Integrated Physiological and Transcriptomic Analyses Revealed Improved Cold Tolerance in Cucumber (<i>Cucumis sativus</i> L.) by Exogenous Chitosan Oligosaccharide. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6202.	1.8	7
31893	Uncovering biomarkers for potential therapeutic targeting for COVID-19-related acute kidney injury: A bioinformatic approach. <i>Journal of Translational Critical Care Medicine</i> , 2023, 5, .	0.0	0
31894	Identification of gene networks mediating regional resistance to tauopathy in late-onset Alzheimer's disease. <i>PLoS Genetics</i> , 2023, 19, e1010681.	1.5	1
31895	BioASQ-QA: A manually curated corpus for Biomedical Question Answering. <i>Scientific Data</i> , 2023, 10, .	2.4	3
31896	Identifying molecular and functional similarities and differences between human primary cardiac valve interstitial cells and ventricular fibroblasts. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 11, .	2.0	1
31897	Characterization and Genome Analysis of <i>Cladobotryum mycophilum</i> , the Causal Agent of Cobweb Disease of <i>Morchella sextelata</i> in China. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 411.	1.5	1
31898	Genetic risk of depression is different in subgroups of dietary ratio of tryptophan to large neutral amino acids. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
31899	Identifying potential biomarkers for the diagnosis and treatment of IgA nephropathy based on bioinformatics analysis. <i>BMC Medical Genomics</i> , 2023, 16, .	0.7	0
31900	Convergent Within-Host Adaptation of <i>Pseudomonas aeruginosa</i> through the Transcriptional Regulatory Network. <i>MSystems</i> , 0, , .	1.7	0
31901	Single Nucleotide Polymorphism rs9277336 Controls the Nuclear Alpha Actinin 4 Human Leukocyte Antigen-DPA1 Axis and Pulmonary Endothelial Pathophenotypes in Pulmonary Arterial Hypertension. <i>Journal of the American Heart Association</i> , 2023, 12, .	1.6	1
31902	Functional Annotation Routines Used by ABRF Bioinformatics Core Facilities - Observations, Comparisons, and Considerations. <i>Journal of Biomolecular Techniques</i> , 2023, 34, 3fc1f5fe.0b74b9db.	0.8	0
31903	X chromosome dosage and the genetic impact across human tissues. <i>Genome Medicine</i> , 2023, 15, .	3.6	8

#	ARTICLE	IF	CITATIONS
31905	Identification of transcription factors related to diabetic tubulointerstitial injury. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	4
31906	Whole exome sequencing reveals novel variants associated with diminished ovarian reserve in young women. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	2
31907	Tracking of activated cTfh cells following sequential influenza vaccinations reveals transcriptional profile of clonotypes driving a vaccine-induced immune response. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
31908	Chromosome-level genome assembly of the critically endangered Baer's pochard (<i>Aythya baeri</i>). <i>Scientific Data</i> , 2023, 10, .	2.4	1
31909	FN (Fibronectin)-Integrin β 5 Signaling Promotes Thoracic Aortic Aneurysm in a Mouse Model of Marfan Syndrome. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2023, 43, .	1.1	5
31910	Identification of cancer-related genes FGFR2 and CEBPB in choledochal cyst via RNA sequencing of patient-derived liver organoids. <i>PLoS ONE</i> , 2023, 18, e0283737.	1.1	0
31911	Transcriptome Analysis of Resistant and Susceptible Pecan (<i>Carya illinoensis</i>) Reveals the Mechanism of Resistance to Black Spot Disease (<i>Colletotrichum fioriniae</i>). <i>Journal of Agricultural and Food Chemistry</i> , 2023, 71, 5812-5822.	2.4	2
31912	Best practices for single-cell analysis across modalities. <i>Nature Reviews Genetics</i> , 2023, 24, 550-572.	7.7	128
31914	Antibiotic resistance in <i>Neisseria gonorrhoeae</i> : broad-spectrum drug target identification using subtractive genomics. <i>Genomics and Informatics</i> , 2023, 21, e5.	0.4	1
31915	Insight into the mechanism of DNA methylation and miRNA-mRNA regulatory network in ischemic stroke. <i>Mathematical Biosciences and Engineering</i> , 2023, 20, 10264-10283.	1.0	2
31917	Transcriptomic data in tumor-adjacent normal tissues harbor prognostic information on multiple cancer types. <i>Cancer Medicine</i> , 0, , .	1.3	0
31918	Distinct cervical tissue-adherent and luminal microbiome communities correlate with mucosal host gene expression and protein levels in Kenyan sex workers. <i>Microbiome</i> , 2023, 11, .	4.9	0
31921	Transcriptomic data meta-analysis reveals common and injury model specific gene expression changes in the regenerating zebrafish heart. <i>Scientific Reports</i> , 2023, 13, .	1.6	5
31922	Metaboverse enables automated discovery and visualization of diverse metabolic regulatory patterns. <i>Nature Cell Biology</i> , 2023, 25, 616-625.	4.6	4
31923	Profiling proteomic responses to hexokinase-II depletion in terpene-producing <i>Saccharomyces cerevisiae</i> . <i>Engineering Microbiology</i> , 2023, 3, 100079.	2.2	2
31924	Human Adult Astrocyte Extracellular Vesicle Transcriptomics Study Identifies Specific RNAs Which Are Preferentially Secreted as EV Luminal Cargo. <i>Genes</i> , 2023, 14, 853.	1.0	0
31925	SARS-CoV-2 <i>ORF3A</i> interacts with the Clc-like chloride channel-1 (<i>CLCC1</i>) and triggers an unfolded protein response. <i>PeerJ</i> , 0, 11, e15077.	0.9	2
31926	A look under the hood of genomic-estimated breed compositions for brangus cattle: What have we learned?. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	2

#	ARTICLE	IF	CITATIONS
31927	Insights on the Biomarker Potential of Exosomal Non-Coding RNAs in Colorectal Cancer: An In Silico Characterization of Related Exosomal lncRNA/circRNAâ€“miRNAâ€“Target Axis. <i>Cells</i> , 2023, 12, 1081.	1.8	4
31928	A complete gap-free diploid genome in <i>Saccharum</i> complex and the genomic footprints of evolution in the highly polyploid <i>Saccharum</i> genus. <i>Nature Plants</i> , 2023, 9, 554-571.	4.7	7
31932	Digital research environments: a requirements analysis. , 0, , .		0
31933	Pregnancy-specific responses to COVID-19 revealed by high-throughput proteomics of human plasma. <i>Communications Medicine</i> , 2023, 3, .	1.9	4
31935	Identification of candidate genes responsible for chasmogamy in wheat. <i>BMC Genomics</i> , 2023, 24, .	1.2	1
31938	K-RET: knowledgeable biomedical relation extraction system. <i>Bioinformatics</i> , 2023, 39, .	1.8	1
31939	Combining GS-assisted GWAS and transcriptome analysis to mine candidate genes for nitrogen utilization efficiency in <i>Populus cathayana</i> . <i>BMC Plant Biology</i> , 2023, 23, .	1.6	1
31940	clusterMaker2: a major update to clusterMaker, a multi-algorithm clustering app for Cytoscape. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	3
31941	A high-quality chromosome-level <i>Eutrema salsugineum</i> genome, an extremophile plant model. <i>BMC Genomics</i> , 2023, 24, .	1.2	4
31942	Identification of new immune subtypes of renal injury associated with anti-neutrophil cytoplasmic antibodyâ€“associated vasculitis based on integrated bioinformatics analysis. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
31943	Integrated enzymes activity and transcriptome reveal the effect of exogenous melatonin on the strain degeneration of <i>Cordyceps militaris</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3
31944	Unraveling astrocyte behavior in the space brain: Radiation response of primary astrocytes. <i>Frontiers in Public Health</i> , 0, 11, .	1.3	2
31946	Gonadal transcriptomes reveal sex-biased expression genes associated with sex determination and differentiation in red-tail catfish (<i>Hemibagrus wyckioides</i>). <i>BMC Genomics</i> , 2023, 24, .	1.2	6
31947	Combined PacBio Iso-Seq and Illumina RNA-Seq Analysis of the <i>Tuta absoluta</i> (Meyrick) Transcriptome and Cytochrome P450 Genes. <i>Insects</i> , 2023, 14, 363.	1.0	1
31949	Proof-of-concept study for liver-directed miQURE technology in a dyslipidemic mouse model. <i>Molecular Therapy - Nucleic Acids</i> , 2023, 32, 454-467.	2.3	0
31950	N-arachidonylglycine is a caloric state-dependent circulating metabolite which regulates human CD4+T cell responsiveness. <i>IScience</i> , 2023, 26, 106578.	1.9	4
31951	Modeling of clinical phenotypes in systemic lupus erythematosus based on the platelet transcriptome and FCGR2a genotype. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	1
31952	RNAlysis: analyze your RNA sequencing data without writing a single line of code. <i>BMC Biology</i> , 2023, 21, .	1.7	4

#	ARTICLE	IF	CITATIONS
31955	N-glycoproteomics of brain synapses and synaptic vesicles. <i>Cell Reports</i> , 2023, 42, 112368.	2.9	5
31957	The effect of temperature and invasive alien predator on genetic and phenotypic variation in the damselfly <i>Ischnura elegans</i> : cross-latitude comparison. <i>Frontiers in Zoology</i> , 2023, 20, .	0.9	1
31958	Population genomics reveals demographic history and selection signatures of hazelnut (<i>Corylus</i>). <i>Horticulture Research</i> , 0, , .	2.9	0
31960	Ancestry-related differences in chromatin accessibility and gene expression of <i>APOE</i> ϵ 4 are associated with Alzheimer's disease risk. <i>Alzheimer's and Dementia</i> , 2023, 19, 3902-3915.	0.4	2
31962	METTL3 enhances dentinogenesis differentiation of dental pulp stem cells via increasing GDF6 and STC1 mRNA stability. <i>BMC Oral Health</i> , 2023, 23, .	0.8	2
31963	Gender trend of monkeypox virus infection. <i>Expert Review of Anti-Infective Therapy</i> , 2023, 21, 571-576.	2.0	1
31964	Single-nucleus gene and gene set expression-based similarity network fusion identifies autism molecular subtypes. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	0
31965	Activation of AMPK promotes cardiac differentiation by stimulating the autophagy pathway. <i>Journal of Cell Communication and Signaling</i> , 2023, 17, 939-955.	1.8	2
31967	Immune profiling in Puerto Rican injection drug users with and without HIV-1 infection. <i>Journal of Leukocyte Biology</i> , 0, , .	1.5	0
31969	RoPE: A robust profile likelihood method for differential gene expression analysis. <i>Genetic Epidemiology</i> , 2023, 47, 379-393.	0.6	1
31970	Latent disease similarities and therapeutic repurposing possibilities uncovered by multi-modal generative topic modeling of human diseases. <i>Bioinformatics Advances</i> , 0, , .	0.9	2
31971	The dcGO Domain-Centric Ontology Database in 2023: New Website and Extended Annotations for Protein Structural Domains. <i>Journal of Molecular Biology</i> , 2023, 435, 168093.	2.0	2
31972	Comprehensive Metabolomic and Transcriptomic Analysis of the Regulatory Network of Volatile Terpenoid Formation during the Growth and Development of Pears (<i>Pyrus</i> spp. "Panguxiang"). <i>Horticulturae</i> , 2023, 9, 483.	1.2	0
31973	Eta polycaprolactone (ϵ -PCL) implants appear to cause a partial differentiation of breast cancer lung metastasis in a murine model. <i>BMC Cancer</i> , 2023, 23, .	1.1	0
31974	Integrated Metabolome and Transcriptome Analysis Reveals a Potential Mechanism for Water Accumulation Mediated Translucency in Pineapple (<i>Ananas comosus</i> (L.) Merr.) Fruit. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7199.	1.8	3
31975	β -tocotrienol regulates gastric cancer by targeting notch signaling pathway. <i>Hereditas</i> , 2023, 160, .	0.5	0
31976	Peptidoglycan Recognition Protein S5 of <i>Bombyx mori</i> Facilitates the Proliferation of <i>Bombyx mori</i> Cypovirus 1. <i>Journal of Agricultural and Food Chemistry</i> , 0, , .	2.4	0
31977	Transcriptome analysis reveals the molecular mechanisms of adaptation to high temperatures in <i>Gracilaria bailinae</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0

#	ARTICLE	IF	CITATIONS
31978	Unveiling DNA damage repair-based molecular subtypes, tumor microenvironment and pharmacogenomic landscape in gastric cancer. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	2
31979	An Anatomical Ontology for the Class Collembola (Arthropoda: Hexapoda). <i>Brazilian Archives of Biology and Technology</i> , 0, 66, .	0.5	1
31980	A chromosome-scale genome assembly of <i>Malus domestica</i> , a multi-stress resistant apple variety. <i>Genomics</i> , 2023, 115, 110627.	1.3	6
31982	Transcriptomic analysis of <i>Andrias davidianus</i> meat and experimental validation for exploring its bioactive components as functional foods. , 2023, , 1-13.		1
31983	Fe/S Redox-Coupled Mercury Transformation Mediated by <i>Acidithiobacillus ferrooxidans</i> ATCC 23270 under Aerobic and/or Anaerobic Conditions. <i>Microorganisms</i> , 2023, 11, 1028.	1.6	1
31984	Alveolar Capillary Barrier Protection In Vitro: Lung Cell Type-Specific Effects and Molecular Mechanisms Induced by 1 α , 25-Dihydroxyvitamin D ₃ . <i>International Journal of Molecular Sciences</i> , 2023, 24, 7298.	1.8	1
31985	Analysis of Nipah Virus Replication and Host Proteome Response Patterns in Differentiated Porcine Airway Epithelial Cells Cultured at the Air-Liquid Interface. <i>Viruses</i> , 2023, 15, 961.	1.5	0
31986	A Transcriptome-Based Precision Oncology Platform for Patient Therapy Alignment in a Diverse Set of Treatment-Resistant Malignancies. <i>Cancer Discovery</i> , 2023, 13, 1386-1407.	7.7	8
31987	Investigation of Diagnostic and Prognostic Value of CLEC4M of Non-Small Cell Lung Carcinoma Associated with Immune Microenvironment. <i>International Journal of General Medicine</i> , 0, Volume 16, 1317-1332.	0.8	0
31988	Drug Discovery in Canine Pyometra Disease Identified by Text Mining and Microarray Data Analysis. <i>BioMed Research International</i> , 2023, 2023, 1-11.	0.9	0
31990	Identification of novel pathways and immune profiles related to sarcopenia. <i>Frontiers in Medicine</i> , 0, 10, .	1.2	3
31991	Comparative Tumor Microenvironment Analysis of Primary and Recurrent Ovarian Granulosa Cell Tumors. <i>Molecular Cancer Research</i> , 2023, 21, 483-494.	1.5	0
31992	Genealyzer: web application for the analysis and comparison of gene expression data. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	0
31994	Identification of NETs-related biomarkers and molecular clusters in systemic lupus erythematosus. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	23
31995	Integrative analysis of TP53 mutations in lung adenocarcinoma for immunotherapies and prognosis. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	1
31996	A robust reprogramming strategy for generating hepatocyte-like cells usable in pharmaco-toxicological studies. <i>Stem Cell Research and Therapy</i> , 2023, 14, .	2.4	2
31997	Elucidating the role of two types of essential oils in regulating antibiotic resistance in soil. <i>Journal of Hazardous Materials</i> , 2023, 454, 131443.	6.5	1
31998	The Effects of a Multi-Ingredient Supplement Containing <i>Wasabia Japonica</i> Extract, Theacrine, and Copper (I) Niacin Chelate on Peripheral Blood Mononuclear Cell DNA Methylation, Transcriptomics, and Sirtuin Activity. <i>Physiologia</i> , 2023, 3, 233-246.	0.6	0

#	ARTICLE	IF	CITATIONS
31999	Nuciferine Effectively Protects Mice against Acetaminophen-Induced Liver Injury. <i>Antioxidants</i> , 2023, 12, 949.	2.2	2
32001	Cyclic GMP-AMP Synthase (cGAS) Deletion Reduces Severity in Bilateral Nephrectomy Mice through Changes in Neutrophil Extracellular Traps and Mitochondrial Respiration. <i>Biomedicines</i> , 2023, 11, 1208.	1.4	1
32002	Multi-omic underpinnings of epigenetic aging and human longevity. <i>Nature Communications</i> , 2023, 14, .	5.8	5
32003	Mass Spectrometry based identification of site-specific proteomic alterations and potential pathways underlying the pathophysiology of schizophrenia. <i>Molecular Biology Reports</i> , 0, .	1.0	0
32004	Integrated metabolome and transcriptome analysis provides insights on the floral scent formation in <i>Hydrangea arborescens</i> . <i>Physiologia Plantarum</i> , 2023, 175, .	2.6	4
32005	Latent generative landscapes as maps of functional diversity in protein sequence space. <i>Nature Communications</i> , 2023, 14, .	5.8	7
32006	Plant-on-chip: Core morphogenesis processes in the tiny plant <i>Wolffia australiana</i> . , 2023, 2, .		2
32007	Oncogenic <i>CDK13</i> mutations impede nuclear RNA surveillance. <i>Science</i> , 2023, 380, .	6.0	9
32008	CD103+ regulatory T cells underlie resistance to radio-immunotherapy and impair CD8+ T cell activation in glioblastoma. <i>Nature Cancer</i> , 2023, 4, 665-681.	5.7	12
32009	Sequencing and bioinformatics analysis of miRNA from rat endplate chondrogenic exosomes. <i>Experimental and Therapeutic Medicine</i> , 2023, 25, .	0.8	0
32010	DeepSG2PPI: A Protein-Protein Interaction Prediction Method Based on Deep Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 2907-2919.	1.9	1
32011	Metabolomic and transcriptomic analyses of the flavonoid biosynthetic pathway in blueberry (<i>Vaccinium</i> spp.). <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	5
32013	A systematic pan-cancer analysis reveals the clinical prognosis and immunotherapy value of C-X3-C motif ligand 1 (<i>CX3CL1</i>). <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
32014	Effects of Atherogenic Factors on Endothelial Cells: Bioinformatics Analysis of Differentially Expressed Genes and Signaling Pathways. <i>Biomedicines</i> , 2023, 11, 1216.	1.4	0
32015	Clinically Relevant Biology of Hyaluronic Acid in the Desmoplastic Stroma of Pancreatic Ductal Adenocarcinoma. <i>Pancreas</i> , 2022, 51, 1092-1104.	0.5	0
32016	A non-canonical role of ATG8 in Golgi recovery from heat stress in plants. <i>Nature Plants</i> , 2023, 9, 749-765.	4.7	15
32017	Differential expression of microRNAs and target genes analysis in olfactory ensheathing cell-derived extracellular vesicles versus olfactory ensheathing cells. <i>Current Stem Cell Research and Therapy</i> , 2023, 18, .	0.6	0
32018	In Ovo Injection of CHIR-99021 Promotes Feather Follicle Development via Modulating the Wnt Signaling Pathway and Transcriptome in Goose Embryos (<i>Anser cygnoides</i>). <i>Frontiers in Physiology</i> , 0, 13, .	1.3	6

#	ARTICLE	IF	CITATIONS
32019	Identification of miRNAs Involved in Male Fertility and Pollen Development in Brassica oleracea var. capitata L. by High-Throughput Sequencing. Horticulturae, 2023, 9, 515.	1.2	1
32021	PRDM1 DNA-binding zinc finger domain is required for normal limb development and is disrupted in split hand/foot malformation. DMM Disease Models and Mechanisms, 2023, 16, .	1.2	5
32022	Informatics and computational methods in natural product drug discovery. , 2023, , 147-166.		0
32023	Systematic elucidation of genetic mechanisms underlying cholesterol uptake. Cell Genomics, 2023, , 100304.	3.0	2
32024	Deep learning on graphs for multi-omics classification of COPD. PLoS ONE, 2023, 18, e0284563.	1.1	2
32025	Cortical glia in SOD1(G93A) mice are subtly affected by ALS-like pathology. Scientific Reports, 2023, 13, .	1.6	1
32026	Mitoregulin Contributes to Creatine Shuttling and Cardiolipin Protection in Mice Muscle. International Journal of Molecular Sciences, 2023, 24, 7589.	1.8	2
32028	The mechanism of peach kernel and safflower herb-pair for the treatment of liver fibrosis based on network pharmacology and molecular docking technology: A review. Medicine (United States), 2023, 102, e33593.	0.4	2
32029	The Neurogenetics of Functional Connectivity Alterations in Autism: Insights From Subtyping in 657 Individuals. Biological Psychiatry, 2023, 94, 804-813.	0.7	4
32030	Causal feature selection using a knowledge graph combining structured knowledge from the biomedical literature and ontologies: A use case studying depression as a risk factor for Alzheimer's disease. Journal of Biomedical Informatics, 2023, 142, 104368.	2.5	2
32035	Ontology Partitioning for Managing Change Effects. Lecture Notes in Networks and Systems, 2023, , 132-146.	0.5	0
32038	MaSS: Model-agnostic, Semantic and Stealthy Data Poisoning Attack on Knowledge Graph Embedding. , 2023, , .		0
32079	Machine Learning in Drug Design. , 2023, , 231-264.		0
32084	Poem-Like<i>Tolls</i>3. , 2023, , 253-258.		0
32235	Identification of Expressed, Mutated Genes and Binding Sites of DNA Associated Proteins in Alzheimer's Disease. , 2023, , 50-64.		0
32322	Mass Spectrometry-Based Vitreous Proteomics: Validated Methods and Analysis Pipeline. Methods in Molecular Biology, 2023, , 157-167.	0.4	0
32365	Ontological Modelling and Social Networks: From Expert Validation to Consolidated Domains. Lecture Notes in Computer Science, 2023, , 672-687.	1.0	0
32366	Relation Predictions in Comorbid Disease Centric Knowledge Graph Using Heterogeneous GNN Models. Lecture Notes in Computer Science, 2023, , 343-356.	1.0	0

#	ARTICLE	IF	CITATIONS
32456	Double Binds of Science. , 2023, , 80-101.		0
32459	Solicitude. , 2023, , 183-220.		0
32460	Labyrinth Life. , 2023, , 42-79.		0
32462	Poem-Like<i>Tolls</i>1. , 2023, , 1-10.		0
32463	Curation. , 2023, , 111-140.		0
32466	Scrupulousness. , 2023, , 141-182.		0
32467	Poem-Like<i>Tolls</i>2. , 2023, , 103-107.		0
32471	Fors. , 2023, , 13-41.		0
32570	Uncovering the genetics of the human connectome. , 2023, , 309-341.		0
32660	Biomedical Ontologies. Computers in Health Care, 2023, , 125-169.	0.2	0
32802	Identification of potential inhibitor(s) against phospholipase A2 using a network pharmacology-based approach. , 2023, , 15-38.		0
32833	Understanding and applying biological resilience, from genes to ecosystems. , 2023, 2, .		3
32842	BERT-based classification of fungi protein sequences with multiple GO labels. , 2023, , .		0
32916	Myokines, Measurement, and Technical Considerations. Neuromethods, 2023, , 215-241.	0.2	0
32931	Dissecting key regulators of transcriptome kinetics through scalable single-cell RNA profiling of pooled CRISPR screens. Nature Biotechnology, 0, , .	9.4	3
32958	NCSML-HDTD: Network Centrality and Sequence-Based Machine Learning Methodology for Human Drug Targets Discovery of COVID-19. Lecture Notes in Networks and Systems, 2023, , 515-523.	0.5	0
32980	Machine Learning for Protein Engineering. Challenges and Advances in Computational Chemistry and Physics, 2023, , 277-311.	0.6	1
33007	Multiobjective Differential Evolution for Predicting Protein-Protein Interactions Using GO-Based Semantic Similarity Measures. Lecture Notes in Networks and Systems, 2023, , 463-472.	0.5	0

#	ARTICLE	IF	CITATIONS
33013	Resources and tools for studying convergent evolution in different lineages of smut fungi. <i>Mycological Progress</i> , 2023, 22, .	0.5	0
33031	Drug Repurposing Using Knowledge Graph Embeddings with a Focus on Vector-Borne Diseases: A Model Comparison. <i>Communications in Computer and Information Science</i> , 2023, , 105-117.	0.4	0
33051	Literature Review on the Development of Visualization Studies (2012–2022). , 0, , .		0
33079	Knowledge Management in the Context of Toxicity Testing. , 0, , .		0
33133	Controlled Vocabularies and Semantics in Systems Biology. , 2023, , 136-149.		0
33135	Drug Repositioning Using Genome-wide Screening and Systems Biology Approaches and Applications. , 2023, , 31-51.		0
33136	Molecular Investigation of Protein–Protein Interaction Candidates Related to the Mammalian Brain. , 2023, , 81-107.		0
33167	Invited: Accelerating Genome Analysis via Algorithm-Architecture Co-Design. , 2023, , .		1
33169	BacWGSpipe: A Snakemake Workflow for a Complete Analysis of Bacterial Whole-Genome Sequencing Data. , 2023, , .		0
33186	A New Model Based on Differential Evolutionary Algorithm and Markov Clustering for Identifying Protein Complexes. , 2023, , .		0
33204	Computational and Informatics Methodologies in Drug Discovery, with Focus on Natural Products. , 2023, , 1-22.		0
33240	Bioinformatics: Theory and Applications. , 2023, , 539-555.		0
33257	Deep learning-based survival prediction using DNA methylation-derived 3D genomic information. , 2023, , .		0
33258	Leveraging Large Language Models for Predicting Microbial Virulence from Protein Structure and Sequence. , 2023, , .		1
33274	Clique-Based Topological Characterization of Chromatin Interaction Hubs. <i>Lecture Notes in Computer Science</i> , 2023, , 476-486.	1.0	0
33277	RIMBO - An Ontology for Model Revision Databases. <i>Lecture Notes in Computer Science</i> , 2023, , 523-534.	1.0	0
33278	A Brief Study of Gene Co-expression Thresholding Algorithms. <i>Lecture Notes in Computer Science</i> , 2023, , 420-430.	1.0	0
33376	Synergistic Disease Similarity Measurement via Unifying Hierarchical Relation Perception and Association Capturing. , 2023, , .		0

#	ARTICLE	IF	CITATIONS
33387	The Genetics of Alcohol-Related Liver Disease. , 2023, , 975-996.		0
33409	Protein Sorting Prediction. Methods in Molecular Biology, 2024, , 27-63.	0.4	0
33515	Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry with Re-Engineered 2, a 5-Dihydroxypheny Acid Derivative. , 2024, , 313-337.		0
33540	SORBET: A Siamese Network for Ontology Embeddings Using a Distance-Based Regression Loss and BERT. Lecture Notes in Computer Science, 2023, , 561-578.	1.0	0
33608	Models and Diagrams in Biology. , 2023, , 25-47.		0
33609	Ontologies and Similar Artefacts. , 2023, , 81-114.		0
33724	Masked Language Modeling for Resource Constrained Biological Natural Language Processing. , 2023, , .		0
33765	Differential Co-expression Analysis of Breast Cancer Based on a Meta-module Recovery Method. , 2023, , .		0
33770	How to Define a Multi-modal Knowledge Graph?. Communications in Computer and Information Science, 2024, , 78-95.	0.4	0
33831	Machine Learning for the Evaluation and Detection of Key Markers in Dilated Cardiomyopathy. Lecture Notes in Electrical Engineering, 2023, , 515-525.	0.3	0
33927	Best practices for the ATAC-seq assay and its data analysis. , 2024, , 285-318.		0
33947	Introduction to the Industrial Application of Semantic Technologies. Springer Series in Advanced Manufacturing, 2024, , 23-65.	0.2	0
34051	SLPFA: Protein Structure-Label Embedding Attention Network for Protein Function Annotation. , 2023, , .		0
34052	Disease Treatment Key Genes Identification In Heterogeneous Interaction Networks. , 2023, , .		0
34053	Identification of risk genes and biological pathways influencing myopia via transcriptome association study and biomedical ontology methods. , 2023, , .		0
34055	Predicting the effect of genes on longevity with novel hierarchical dependency-constrained tree augmented naive Bayes classifiers. , 2023, , .		0
34056	Enhancing ProteinBERT: Integrating Intrinsically Disordered Proteins for Comprehensive Proteomic Predictions. , 2023, , .		0
34057	Identifying Disease-related Brain Imaging Quantitative Traits and Related Genetic Variations via A Bidirectional Association Learning Method. , 2023, , .		0

#	ARTICLE	IF	CITATIONS
34059	Interpretable Graph Convolutional Network for Alzheimer's Disease Diagnosis using Multi-Modal Imaging Genetics. , 2023, , .		0
34060	Integrating Heterogeneous Biological Networks and Ontologies for Improved Protein Function Prediction with Graph Neural Networks. , 2023, , .		0
34061	Prediction of Non-coding Driver Mutations Using Ensemble Learning. , 2023, , .		0
34062	Construction for ontology of stroke in Traditional Chinese Medicine. , 2023, , .		0
34064	Latent space feature representation on multiple biological network for synthetic lethality interaction prediction. , 2023, , .		0
34066	Auto-GO: Reproducible, Robust and High Quality Ontology Enrichment Visualizations. , 2023, , .		0
34067	Evolutionary Graph-Clustering vs Evolutionary Cluster-Detection Approaches for Community Identification in PPI Networks. Lecture Notes in Business Information Processing, 2024, , 98-113.	0.8	0
34084	Transcriptomic profiling-based identification of biomarkers of stem cells. , 2024, , 203-214.		0
34185	Bioinformatics in Pathway Identification, Design, Modelling, and Simulation. , 2024, , 181-198.		0
34188	Simultaneous nanopore profiling of mRNA m6A and pseudouridine reveals translation coordination. Nature Biotechnology, 0, , .	9.4	0
34200	Identification of drought stress genes expressed in Jatropha curcas by using RNA sequencing. AIP Conference Proceedings, 2024, , .	0.3	0
34258	Machine learning for functional protein design. Nature Biotechnology, 2024, 42, 216-228.	9.4	1
34266	Introduction to sample preparation for proteomics and mass spectrometry. , 2024, , 7-32.		0
34301	Functional overrepresentation analysis and their application in microbial pathogenesis. , 2024, , 171-179.		0
34307	Host-pathogen interactions: databases and approaches for data generation. , 2024, , 15-51.		0
34328	Exploring the Sit-and-Wait Potential of the Bacterial Pathogen Shigella flexneri: A Comparative Genomic Study. , 0, , .		0
34354	Data Preparation, Transforms, Quality, and Management. Computers in Health Care, 2024, , 377-413.	0.2	0
34487	Dissecting the Immune System through Gene Regulation. Advances in Experimental Medicine and Biology, 2024, , 219-235.	0.8	0

#	ARTICLE	IF	CITATIONS
---	---------	----	-----------