## Gene Ontology Consortium: going forward

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**Citation Report** 

#	Article	IF	CITATIONS
4	"On the Power of Penetrating into Space― The Telescopes of William Herschel. Journal for the History of Astronomy, 1976, 7, 75-108.	0.1	38
5	dicty <scp>B</scp> ase 2015: Expanding data and annotations in a new software environment. Genesis, 2015, 53, 523-534.	0.8	29
6	SmedGD 2.0: The <i>Schmidtea mediterranea</i> genome database. Genesis, 2015, 53, 535-546.	0.8	114
7	Mouse Genome Database: From sequence to phenotypes and disease models. Genesis, 2015, 53, 458-473.	0.8	13
8	Prediction of Scaffold Proteins based on Protein Interaction and Domain Architectures. , 2015, , .		0
9	An Antifungal Combination Matrix Identifies a Rich Pool of Adjuvant Molecules that Enhance Drug Activity against Diverse Fungal Pathogens. Cell Reports, 2015, 13, 1481-1492.	2.9	68
10	Constraint methods that accelerate free-energy simulations of biomolecules. Journal of Chemical Physics, 2015, 143, 243143.	1.2	1
11	A large-scale crop protection bioassay data set. Scientific Data, 2015, 2, 150032.	2.4	18
12	Prediction of tissue-specific effects of gene knockout on apoptosis in different anatomical structures of human brain. BMC Genomics, 2015, 16, S3.	1.2	8
13	The administration of intranasal live attenuated influenza vaccine induces changes in the nasal microbiota and nasal epithelium gene expression profiles. Microbiome, 2015, 3, 74.	4.9	64
14	Complete genome sequence of Staphylococcus aureus, strain ILRI_Eymole1/1, isolated from a Kenyan dromedary camel. Standards in Genomic Sciences, 2015, 10, 109.	1.5	16
15	HitPredict version 4: comprehensive reliability scoring of physical protein–protein interactions from more than 100 species. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav117.	1.4	92
16	Into the blue: the importance of murine <i>lacZ</i> gene expression profiling in understanding and treating human disease. DMM Disease Models and Mechanisms, 2015, 8, 1341-1343.	1.2	1
17	IRES-dependent translated genes in fungi: computational prediction, phylogenetic conservation and functional association. BMC Genomics, 2015, 16, 1059.	1.2	10
18	Characterization of genome-wide H3K27ac profiles reveals a distinct PM2.5-associated histone modification signature. Environmental Health, 2015, 14, 65.	1.7	37
19	Phenotype-driven strategies for exome prioritization of human Mendelian disease genes. Genome Medicine, 2015, 7, 81.	3.6	97
20	Mathematical models of cancer metabolism. Cancer & Metabolism, 2015, 3, 14.	2.4	27
21	GESearch: An Interactive GUI Tool for Identifying Gene Expression Signature. BioMed Research International, 2015, 2015, 1-8.	0.9	2

#	Article	IF	CITATIONS
22	On the genetics of sleep disorders: genome-wide association studies and beyond. Advances in Genomics and Genetics, 0, , 293.	0.8	9
23	In Silico Analysis of Correlations between Protein Disorder and Post-Translational Modifications in Algae. International Journal of Molecular Sciences, 2015, 16, 19812-19835.	1.8	20
24	Proteins and Their Interacting Partners: An Introduction to Protein–Ligand Binding Site Prediction Methods. International Journal of Molecular Sciences, 2015, 16, 29829-29842.	1.8	66
25	Integrated inference and evaluation of host–fungi interaction networks. Frontiers in Microbiology, 2015, 6, 764.	1.5	63
26	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
27	MicroRNA Expression Profile in Penile Cancer Revealed by Next-Generation Small RNA Sequencing. PLoS ONE, 2015, 10, e0131336.	1.1	30
28	The Esg Gene Is Involved in Nicotine Sensitivity in Drosophila melanogaster. PLoS ONE, 2015, 10, e0133956.	1.1	16
29	Small RNAs and Gene Network in a Durable Disease Resistance Gene—Mediated Defense Responses in Rice. PLoS ONE, 2015, 10, e0137360.	1.1	20
30	Modeling the Regulatory Mechanisms by Which NLRX1 Modulates Innate Immune Responses to Helicobacter pylori Infection. PLoS ONE, 2015, 10, e0137839.	1.1	32
31	Genome-Wide Assessment of Outer Membrane Vesicle Production in Escherichia coli. PLoS ONE, 2015, 10, e0139200.	1.1	79
32	orthoFind Facilitates the Discovery of Homologous and Orthologous Proteins. PLoS ONE, 2015, 10, e0143906.	1.1	3
33	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. Current Genomics, 2015, 17, 33-61.	0.7	3
34	Application of Functional Genomics for Bovine Respiratory Disease Diagnostics. Bioinformatics and Biology Insights, 2015, 9s2, BBI.S30525.	1.0	7
35	Visual annotation display (VLAD): a tool for finding functional themes in lists of genes. Mammalian Genome, 2015, 26, 567-573.	1.0	37
36	Global alterations of the transcriptional landscape during yeast growth and development in the absence of Ume6-dependent chromatin modification. Molecular Genetics and Genomics, 2015, 290, 2031-2046.	1.0	11
37	Exploiting information content and semantics to accurately compute similarity of GO-based annotated entities. , 2015, , .		2
38	Identification of Potential Non-invasive Biomarkers for Breast Cancer Prognosis and Treatment by Systematic Bioinformatics Analysis. , 2015, , .		1
39	TAF1 Variants Are Associated with Dysmorphic Features, Intellectual Disability, and Neurological Manifestations. American Journal of Human Genetics, 2015, 97, 922-932.	2.6	101

#	Article	IF	CITATIONS
40	Next-generation diagnostics and disease-gene discovery with the Exomiser. Nature Protocols, 2015, 10, 2004-2015.	5.5	296
41	Transcriptional program for nitrogen starvation-induced lipid accumulation in Chlamydomonas reinhardtii. Biotechnology for Biofuels, 2015, 8, 207.	6.2	60
42	An integrative measure of graph- and vector-based semantic similarity using information content distance. , 2015, , .		3
43	Semantic mapping to align PPI networks and predict conserved protein complexes. , 2015, , .		Ο
44	A web tool for measuring gene semantic similarities by combining gene ontology and gene co-function networks. , 2015, , .		0
45	Stress-induced DNA damage biomarkers: applications and limitations. Frontiers in Chemistry, 2015, 3, 35.	1.8	149
46	High-quality draft genome sequences of five anaerobic oral bacteria and description of Peptoanaerobacter stomatis gen. nov., sp. nov., a new member of the family Peptostreptococcaceae. Standards in Genomic Sciences, 2015, 10, 37.	1.5	21
47	Application of comparative biology in GO functional annotation: the mouse model. Mammalian Genome, 2015, 26, 574-583.	1.0	11
48	The history of the CATH structural classification of protein domains. Biochimie, 2015, 119, 209-217.	1.3	34
49	Databases for Microbiologists. Journal of Bacteriology, 2015, 197, 2458-2467.	1.0	39
49 50	Databases for Microbiologists. Journal of Bacteriology, 2015, 197, 2458-2467. Bacterial reference genes for gene expression studies by RT-qPCR: survey and analysis. Antonie Van Leeuwenhoek, 2015, 108, 685-693.	1.0 0.7	39 121
	Bacterial reference genes for gene expression studies by RT-qPCR: survey and analysis. Antonie Van		
50	Bacterial reference genes for gene expression studies by RT-qPCR: survey and analysis. Antonie Van Leeuwenhoek, 2015, 108, 685-693.	0.7	121
50 51	Bacterial reference genes for gene expression studies by RT-qPCR: survey and analysis. Antonie Van Leeuwenhoek, 2015, 108, 685-693. FAST: FAST Analysis of Sequences Toolbox. Frontiers in Genetics, 2015, 6, 172.	0.7	121 29
50 51 52	Bacterial reference genes for gene expression studies by RT-qPCR: survey and analysis. Antonie Van Leeuwenhoek, 2015, 108, 685-693.         FAST: FAST Analysis of Sequences Toolbox. Frontiers in Genetics, 2015, 6, 172.         GXD: a community resource of mouse Gene Expression Data. Mammalian Genome, 2015, 26, 314-324.	0.7 1.1 1.0	121 29 23
50 51 52 53	Bacterial reference genes for gene expression studies by RT-qPCR: survey and analysis. Antonie Van Leeuwenhoek, 2015, 108, 685-693.         FAST: FAST Analysis of Sequences Toolbox. Frontiers in Genetics, 2015, 6, 172.         GXD: a community resource of mouse Gene Expression Data. Mammalian Genome, 2015, 26, 314-324.         Biological Databases for Human Research. Genomics, Proteomics and Bioinformatics, 2015, 13, 55-63.         Allorecognition, via TgrB1 and TgrC1, mediates the transition from unicellularity to multicellularity	0.7 1.1 1.0 3.0	121 29 23 84
50 51 52 53 54	Bacterial reference genes for gene expression studies by RT-qPCR: survey and analysis. Antonie Van Leeuwenhoek, 2015, 108, 685-693.         FAST: FAST Analysis of Sequences Toolbox. Frontiers in Genetics, 2015, 6, 172.         CXD: a community resource of mouse Gene Expression Data. Mammalian Genome, 2015, 26, 314-324.         Biological Databases for Human Research. Genomics, Proteomics and Bioinformatics, 2015, 13, 55-63.         Allorecognition, via TgrB1 and TgrC1, mediates the transition from unicellularity to multicellularity in the social amoebae <i>Dictyostellum discoideum </i> Orthology for comparative genomics in the mouse genome database. Mammalian Genome, 2015, 26, 315, 26, 314, 324.	0.7 1.1 1.0 3.0 1.2	121 29 23 84 34

#	Article	IF	CITATIONS
58	Molecular inhibitors of DNA repair: searching for the ultimate tumor killing weapon. Future Medicinal Chemistry, 2015, 7, 1543-1558.	1.1	14
59	Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2207-2217.	1.1	101
60	ProtPhylo: identification of protein–phenotype and protein–protein functional associations via phylogenetic profiling. Nucleic Acids Research, 2015, 43, W160-W168.	6.5	26
61	Genetic, epigenetic, and molecular landscapes of multifocal and multicentric glioblastoma. Acta Neuropathologica, 2015, 130, 587-597.	3.9	68
62	Rat malignant fibrous histiocytoma (MFH)-derived cloned cell lines (MT-8 and MT-9) show different differentiation in mesenchymal stem cell lineage. Experimental and Toxicologic Pathology, 2015, 67, 499-507.	2.1	4
63	Genetic variation in <i>IL-1β, IL-2, IL-6, TSPO</i> and <i>BDNF</i> and response to duloxetine or placebo treatment in major depressive disorder. Pharmacogenomics, 2015, 16, 1919-1929.	0.6	19
64	Differences in somatic mutation landscape of hepatocellular carcinoma in Asian American and European American populations. Oncotarget, 2016, 7, 40491-40499.	0.8	32
65	Application of MATLAB in -Omics and Systems Biology. , 0, , .		Ο
66	Differences in reproductive toxicology between alopecia drugs: an analysis on adverse events among female and male cases. Oncotarget, 2016, 7, 82074-82084.	0.8	26
67	CASTIN: a system for comprehensive analysis of cancer-stromal interactome. BMC Genomics, 2016, 17, 899.	1.2	10
68	Interconnections Between RNA-Processing Pathways Revealed by a Sequencing-Based Genetic Screen for Pre-mRNA Splicing Mutants in Fission Yeast. G3: Genes, Genomes, Genetics, 2016, 6, 1513-1523.	0.8	14
69	Piecemeal Buildup of the Genetic Code, Ribosomes, and Genomes from Primordial tRNA Building Blocks. Life, 2016, 6, 43.	1.1	38
70	Knowledge Representation and Management: a Linked Data Perspective. Yearbook of Medical Informatics, 2016, 25, 178-183.	0.8	17
71	ExSurv: A Web Resource for Prognostic Analyses of Exons across Human Cancers Using Clinical Transcriptomes. Cancer Informatics, 2016, 15s2, CIN.S39367.	0.9	3
72	Differentially Expressed miRNAs in Tumor, Adjacent, and Normal Tissues of Lung Adenocarcinoma. BioMed Research International, 2016, 2016, 1-10.	0.9	28
73	Integrated Approaches to Drug Discovery for Oxidative Stress-Related Retinal Diseases. Oxidative Medicine and Cellular Longevity, 2016, 2016, 1-9.	1.9	12
74	Identification of crucial microRNAs and genes in hypoxia-induced human lung adenocarcinoma cells. OncoTargets and Therapy, 2016, Volume 9, 4605-4616.	1.0	28
75	Lamina Associated Polypeptide 1 (LAP1) Interactome and Its Functional Features. Membranes, 2016, 6, 8.	1.4	19

ARTICLE IF CITATIONS Order, Disorder, and Everything in Between. Molecules, 2016, 21, 1090. 1.7 72 76 N6-methyladenosine of HIV-1 RNA regulates viral infection and HIV-1 Gag protein expression. ELife, 2016, 2.8 Assembly, Assessment, and Availability of De novo Generated Eukaryotic Transcriptomes. Frontiers in 78 1.1 57 Genetics, 2015, 6, 361. Whole-Transcriptome Analysis of Verocytotoxigenic Escherichia coli O157:H7 (Sakai) Suggests Plant-Species-Specific Metábolic Responses on Exposure to Spinach and Lettuce Extracts. Frontiers in 34 Microbiology, 2016, 7, 1088. Differential Biphasic Transcriptional Host Response Associated with Coevolution of Hemagglutinin 80 1.5 11 Quasispecies of Influenza A Virus. Frontiers in Microbiology, 2016, 7, 1167. Stable Gene Regulatory Network Modeling From Steady-State Data. Bioengineering, 2016, 3, 12. 1.6 82 Expression Profiles and Biological Roles of miR-196a in Swine. Genes, 2016, 7, 5. 1.0 10 Microarray Expression Profiling of Long Non-Coding RNAs Involved in Nasopharyngeal Carcinoma Metastasis. International Journal of Molecular Sciences, 2016, 17, 1956. 1.8 Human Intervention Study to Assess the Effects of Supplementation with Olive Leaf Extract on 84 Peripheral Blood Mononuclear Cell Gene Expression. International Journal of Molecular Sciences, 1.8 24 2016, 17, 2019. Generalized enrichment analysis improves the detection of adverse drug events from the biomedical 1.2 literature. BMC Bioinformatics, 2016, 17, 250. GeneSCF: a real-time based functional enrichment tool with support for multiple organisms. BMC 1.2 86 87 Bioinformatics, 2016, 17, 365. The effects of lymph node status on predicting outcome in ER+ /HER2- tamoxifen treated breast cancer 1.1 patients using gene signatures. BMC Cancer, 2016, 16, 555. Model organism databases: essential resources that need the support of both funders and users. BMC 88 1.7 46 Biology, 2016, 14, 49. Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and 89 1.5 Multi-layered Scaffolding. PLoS Genetics, 2016, 12, e1005954. Activation of Myenteric Glia during Acute Inflammation In Vitro and In Vivo. PLoS ONE, 2016, 11, 90 69 1.1 e0151335. Differential RNA-seq, Multi-Network Analysis and Metabolic Regulation Analysis of Kluyveromyces marxianus Reveals a Compartmentalised Response to Xylose. PLoS ONE, 2016, 11, e0156242. GenToS: Use of Orthologous Gene Information to Prioritize Signals from Human GWAS. PLoS ONE, 92 1.1 2 2016, 11, e0162466. omicsNPC: Applying the Non-Parametric Combination Methodology to the Integrative Analysis of 1.1 Heterogeneous Omics Data. PLoS ONE, 2016, 11, e0165545.

	CITATION RE	CITATION REPORT	
#	Article	IF	Citations
94	EP300 Protects from Light-Induced Retinopathy in Zebrafish. Frontiers in Pharmacology, 2016, 7, 126.	1.6	13
95	VESPUCCI: Exploring Patterns of Gene Expression in Grapevine. Frontiers in Plant Science, 2016, 7, 633.	1.7	65
96	Identification of Key Proteins and Networks Related to Grain Development in Wheat (Triticum) Tj ETQq0 0 0 rgBT Frontiers in Plant Science, 2016, 7, 922.	/Overlocl 1.7	k 10 Tf 50 66 23
97	Highlighting the Need for Systems-Level Experimental Characterization of Plant Metabolic Enzymes. Frontiers in Plant Science, 2016, 7, 1127.	1.7	2
98	Comparative Characterization of the Leaf Tissue of Physalis alkekengi and Physalis peruviana Using RNA-seq and Metabolite Profiling. Frontiers in Plant Science, 2016, 7, 1883.	1.7	27
99	Bioinformatics for RNAâ€Seq Data Analysis. , 2016, , .		6
100	Seven protective miRNA signatures for prognosis of cervical cancer. Oncotarget, 2016, 7, 56690-56698.	0.8	31
101	DUCTAL CARCINOMA IN SITU AND INVASIVE BREAST CANCER-BASED DIFFERENTIAL GENE EXPRESSION STUDY FOR THERAPEUTIC DEVELOPMENT. Asian Journal of Pharmaceutical and Clinical Research, 2016, 9, 48.	0.3	1
102	Molecular serum signature of treatment resistant depression. Psychopharmacology, 2016, 233, 3051-3059.	1.5	20
103	Role of Altered Expression of miR-146a, miR-155, and miR-122 in Pediatric Patients with Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2016, 22, 327-335.	0.9	63
104	Avoiding common pitfalls when clustering biological data. Science Signaling, 2016, 9, re6.	1.6	118
105	Alignment of PPI Networks Using Semantic Similarity for Conserved Protein Complex Prediction. IEEE Transactions on Nanobioscience, 2016, 15, 380-389.	2.2	5
106	High-throughput sequencing and de novo transcriptome assembly of Swertia japonica to identify genes involved in the biosynthesis of therapeutic metabolites. Plant Cell Reports, 2016, 35, 2091-2111.	2.8	38
107	Analysis of microRNA expression during the torpor-arousal cycle of a mammalian hibernator, the 13-lined ground squirrel. Physiological Genomics, 2016, 48, 388-396.	1.0	31
108	<scp>GAMDB</scp> : a web resource to connect microRNAs with autophagy in gerontology. Cell Proliferation, 2016, 49, 246-251.	2.4	10
109	Adaptation to nocturnality – learning from avian genomes. BioEssays, 2016, 38, 694-703.	1.2	13
110	ICEPO: the ion channel electrophysiology ontology. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw017.	1.4	9
111	bioassayR: Cross-Target Analysis of Small Molecule Bioactivity. Journal of Chemical Information and Modeling, 2016, 56, 1237-1242.	2.5	13

#	Article	IF	CITATIONS
112	Regions of variable DNA methylation in human placenta associated with newborn neurobehavior. Epigenetics, 2016, 11, 603-613.	1.3	91
113	ATtRACT—a database of RNA-binding proteins and associated motifs. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw035.	1.4	215
114	MINERVA—a platform for visualization and curation of molecular interaction networks. Npj Systems Biology and Applications, 2016, 2, 16020.	1.4	68
115	Large-scale gene co-expression network as a source of functional annotation for cattle genes. BMC Genomics, 2016, 17, 846.	1.2	18
116	A systematic study on drug-response associated genes using baseline gene expressions of the Cancer Cell Line Encyclopedia. Scientific Reports, 2016, 6, 22811.	1.6	54
117	Systems-level effects of ectopic galectin-7 reconstitution in cervical cancer and its microenvironment. BMC Cancer, 2016, 16, 680.	1.1	26
118	A Module-Based Approach for Evaluating Differential Genome-Wide Expression Profiles. , 2016, , .		0
119	De-novo protein function prediction using DNA binding and RNA binding proteins as a test case. Nature Communications, 2016, 7, 13424.	5.8	22
120	Driver gene classification reveals a substantial overrepresentation of tumor suppressors among very large chromatin-regulating proteins. Scientific Reports, 2016, 6, 38988.	1.6	22
121	FARNA: knowledgebase of inferred functions of non-coding RNA transcripts. Nucleic Acids Research, 2017, 45, gkw973.	6.5	30
122	SNP-Seek II: A resource for allele mining and analysis of big genomic data in Oryza sativa. Current Plant Biology, 2016, 7-8, 16-25.	2.3	48
123	ThaleMine: A Warehouse for Arabidopsis Data Integration and Discovery. Plant and Cell Physiology, 2017, 58, pcw200.	1.5	39
124	From comorbidities of chronic obstructive pulmonary disease to identification of shared molecular mechanisms by data integration. BMC Bioinformatics, 2016, 17, 441.	1.2	20
125	Microarray data analysis to identify crucial genes regulated by CEBPB in human SNB19 glioma cells. World Journal of Surgical Oncology, 2016, 14, 258.	0.8	19
126	Zinc finger protein 407 overexpression upregulates PPAR target gene expression and improves glucose homeostasis in mice. American Journal of Physiology - Endocrinology and Metabolism, 2016, 311, E869-E880.	1.8	13
127	Exploring FlyBase Data Using QuickSearch. Current Protocols in Bioinformatics, 2016, 56, 1.31.1-1.31.23.	25.8	6
128	Modern Proteomics – Sample Preparation, Analysis and Practical Applications. Advances in Experimental Medicine and Biology, 2016, , .	0.8	13
129	Bioinformatics Tools for Proteomics Data Interpretation. Advances in Experimental Medicine and Biology, 2016, 919, 281-341.	0.8	20

#	Article	IF	CITATIONS
130	Developing integrated crop knowledge networks to advance candidate gene discovery. Applied & Translational Genomics, 2016, 11, 18-26.	2.1	66
131	Identification of critical paralog groups with indispensable roles in the regulation of signaling flow. Scientific Reports, 2016, 6, 38588.	1.6	8
132	Effects of hibernation on bone marrow transcriptome in thirteen-lined ground squirrels. Physiological Genomics, 2016, 48, 513-525.	1.0	29
133	Ontology extension based on axiomatic cognitive model for Ontology learning. , 2016, , .		1
134	Filtering association rules in Gene Ontology based on term specificity. , 2016, , .		0
135	Screening and analysis of breast cancer genes regulated by the human mammary microenvironment in a humanized mouse model. Oncology Letters, 2016, 12, 5261-5268.	0.8	5
136	Exploring human disease using the Rat Genome Database. DMM Disease Models and Mechanisms, 2016, 9, 1089-1095.	1.2	27
137	Integrative Biological Databases. Translational Bioinformatics, 2016, , 295-307.	0.0	0
138	Multiclassifier combinatorial proteomics of organelle shadows at the example of mitochondria in chromatin data. Proteomics, 2016, 16, 393-401.	1.3	12
139	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	9.0	198
140	Genome-wide functional annotation of Phomopsis longicolla isolate MSPL 10-6. Genomics Data, 2016, 8, 67-69.	1.3	2
141	Gene expression profiling reveals novel protective effects of Aminaphtone on ECV304 endothelial cells. European Journal of Pharmacology, 2016, 782, 59-69.	1.7	7
142	Transcriptome analysis of cortical tissue reveals shared sets of downregulated genes in autism and schizophrenia. Translational Psychiatry, 2016, 6, e817-e817.	2.4	38
143	Altered gene expression in the lower respiratory tract of Car6 â^'/â^' mice. Transgenic Research, 2016, 25, 649-664.	1.3	7
144	Open PHACTS computational protocols for in silico target validation of cellular phenotypic screens: knowing the knowns. MedChemComm, 2016, 7, 1237-1244.	3.5	18
145	Guidelines for the functional annotation of microRNAs using the Gene Ontology. Rna, 2016, 22, 667-676.	1.6	35
146	Protein-protein interactions among signaling pathways may become new therapeutic targets in liver cancer (Review). Oncology Reports, 2016, 35, 625-638.	1.2	8
147	DCIdb 2.0: mining clinically relevant drug–gene interactions. Nucleic Acids Research, 2016, 44, D1036-D1044.	6.5	359

#	Article	IF	Citations
148	Unipept web services for metaproteomics analysis. Bioinformatics, 2016, 32, 1746-1748.	1.8	44
149	Expression profiles of long noncoding RNAs in cutaneous squamous cell carcinoma. Epigenomics, 2016, 8, 501-518.	1.0	26
150	Exploring information from the topology beneath the Gene Ontology terms to improve semantic similarity measures. Gene, 2016, 586, 148-157.	1.0	5
151	The Reactome pathway Knowledgebase. Nucleic Acids Research, 2016, 44, D481-D487.	6.5	3,319
152	A flexible method for estimating the fraction of fitness influencing mutations from large sequencing data sets. Genome Research, 2016, 26, 834-843.	2.4	10
153	MouseNet v2: a database of gene networks for studying the laboratory mouse and eight other model vertebrates. Nucleic Acids Research, 2016, 44, D848-D854.	6.5	40
154	Beef quality with different intramuscular fat content and proteomic analysis using isobaric tag for relative and absolute quantitation of differentially expressed proteins. Meat Science, 2016, 118, 96-102.	2.7	30
155	Network-based metabolic analysis and microbial community modeling. Current Opinion in Microbiology, 2016, 31, 124-131.	2.3	79
156	FunTree: advances in a resource for exploring and contextualising protein function evolution. Nucleic Acids Research, 2016, 44, D317-D323.	6.5	13
157	COMBREX-DB: an experiment centered database of protein function: knowledge, predictions and knowledge gaps. Nucleic Acids Research, 2016, 44, D330-D335.	6.5	47
158	FAM46 proteins are novel eukaryotic non-canonical poly(A) polymerases. Nucleic Acids Research, 2016, 44, 3534-3548.	6.5	60
159	QuickRNASeq lifts large-scale RNA-seq data analyses to the next level of automation and interactive visualization. BMC Genomics, 2016, 17, 39.	1.2	37
160	Molecular characterization of Gleason patterns 3 and 4 prostate cancer using reverse Warburg effect-associated genes. Cancer & Metabolism, 2016, 4, 8.	2.4	17
161	Complete genome sequence of an agr-dysfunctional variant of the ST239 lineage of the methicillin-resistant Staphylococcus aureus strain GV69 from Brazil. Standards in Genomic Sciences, 2016, 11, 34.	1.5	4
162	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	6.0	1,398
163	The omic approach to parasitic trematode research—a review of techniques and developments within the past 5Ayears. Parasitology Research, 2016, 115, 2523-2543.	0.6	10
164	Whole organism transcriptome analysis of zebrafish models of Bardet-Biedl Syndrome and Alstr¶m Syndrome provides mechanistic insight into shared and divergent phenotypes. BMC Genomics, 2016, 17, 318.	1.2	15
165	Protein–protein interaction inference based on semantic similarity of Gene Ontology terms. Journal of Theoretical Biology, 2016, 401, 30-37.	0.8	51

#	Article	IF	CITATIONS
166	<i>Companion</i> : a web server for annotation and analysis of parasite genomes. Nucleic Acids Research, 2016, 44, W29-W34.	6.5	127
167	Network-driven plasma proteomics expose molecular changes in the Alzheimer's brain. Molecular Neurodegeneration, 2016, 11, 31.	4.4	34
168	Homology-Based Annotation of Large Protein Datasets. Methods in Molecular Biology, 2016, 1415, 153-176.	0.4	0
169	GEneSTATION 1.0: a synthetic resource of diverse evolutionary and functional genomic data for studying the evolution of pregnancy-associated tissues and phenotypes. Nucleic Acids Research, 2016, 44, D908-D916.	6.5	6
170	An Integrative Proteomic Approach Identifies Novel Cellular SMYD2 Substrates. Journal of Proteome Research, 2016, 15, 2052-2059.	1.8	21
171	Complex Sources of Variation in Tissue Expression Data: Analysis of the GTEx Lung Transcriptome. American Journal of Human Genetics, 2016, 99, 624-635.	2.6	65
173	The Cell Ontology 2016: enhanced content, modularization, and ontology interoperability. Journal of Biomedical Semantics, 2016, 7, 44.	0.9	201
174	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
175	Arthrogryposis as a Syndrome: Gene Ontology Analysis. Molecular Syndromology, 2016, 7, 101-109.	0.3	49
176	Transcriptome sequencing reveals genome-wide variation in molecular evolutionary rate among ferns. BMC Genomics, 2016, 17, 692.	1.2	16
177	How to Identify Pathogenic Mutations among All Those Variations: Variant Annotation and Filtration in the Genome Sequencing Era. Human Mutation, 2016, 37, 1272-1282.	1.1	28
178	Analyzing and interpreting genome data at the network level with ConsensusPathDB. Nature Protocols, 2016, 11, 1889-1907.	5.5	364
179	The Role of Retrotransposons in Gene Family Expansions in the Human and Mouse Genomes. Genome Biology and Evolution, 2016, 8, 2632-2650.	1.1	23
180	Label-free quantitative proteomic analysis of the inhibitory activities of juglone against translation and energy metabolism in Escherichia coli. Phytochemistry Letters, 2016, 18, 55-58.	0.6	11
181	Mutual enrichment in aggregated ranked lists with applications to gene expression regulation. Bioinformatics, 2016, 32, i464-i472.	1.8	5
182	Formation of the Embryonic Head in the Mouse. Current Topics in Developmental Biology, 2016, 117, 497-521.	1.0	5
183	Creating NoSQL Biological Databases with Ontologies for Query Relaxation. Procedia Computer Science, 2016, 91, 460-469.	1.2	17
184	Proteomic comparison of near-isogenic barley (Hordeum vulgare L.) germplasm differing in the allelic state of a major senescence QTL identifies numerous proteins involved in plant pathogen defense. Plant Physiology and Biochemistry, 2016, 109, 114-127.	2.8	9

		CITATION REP	ORT	
#	Article		IF	CITATIONS
185	The effect of host genetics on the gut microbiome. Nature Genetics, 2016, 48, 1407-14	12.	9.4	672
187	A systems biology-led insight into the role of the proteome in neurodegenerative disease Review of Proteomics, 2016, 13, 845-855.	es. Expert	1.3	22
188	NET-GE: a web-server for NETwork-based human gene enrichment. Bioinformatics, 2016	32, 3489-3491.	1.8	14
189	An approach to comprehensive genome and proteome expression analyses in Schwann neurons during peripheral nerve myelin formation. Journal of Neurochemistry, 2016, 138	cells and 8, 830-844.	2.1	10
190	Integrated DB for Bioinformatics: A Case Study on Analysis of Functional Effect of MiRN. Cancer. Lecture Notes in Computer Science, 2016, , 214-222.	A SNPs in	1.0	5
191	Computational assessment of feature combinations for pathogenic variant prediction. N Genetics & amp; Genomic Medicine, 2016, 4, 431-446.	1olecular	0.6	13
192	Representing and querying disease networks using graph databases. BioData Mining, 20	016, 9, 23.	2.2	75
193	Transcriptome analysis reveals rod/cone photoreceptor specific signatures across mamn Human Molecular Genetics, 2016, 25, ddw268.	nalian retinas.	1.4	36
194	Computational determination of the effects of virulent Escherichia coli and salmonella bacteriophages on human gut. Computer Methods and Programs in Biomedicine, 2016,	135, 27-35.	2.6	5
195	Computational Approaches for Functional Prediction and Characterisation of Long None Trends in Genetics, 2016, 32, 620-637.	oding RNAs.	2.9	89
196	<scp>RNA</scp> â€sequencing profiles hippocampal gene expression in a validated moc cancerâ€induced depression. Genes, Brain and Behavior, 2016, 15, 711-721.	el of	1.1	10
197	Leaf apoplastic proteome composition in UV-B treated Arabidopsis thaliana mutants imperative extracellular glutathione degradation. Data in Brief, 2016, 6, 368-377.	paired in	0.5	3
198	miRNA Profiling in Plants: Current Identification and Expression Approaches. , 2016, , 18	9-215.		0
199	RSAT::Plants: Motif Discovery Within Clusters of Upstream Sequences in Plant Genomes Molecular Biology, 2016, 1482, 279-295.	. Methods in	0.4	8
200	Coding and noncoding variants in <i>HFM1</i> , <i>MLH3</i> , <i>MSH4</i> , <i>MSH5&lt; and <i>RNF212B</i> affect recombination rate in cattle. Genome Research, 2016, 26, 1</i>		2.4	77
201	Quantitative profiling of glycans and glycopeptides: an informatics' perspective. Cu Structural Biology, 2016, 40, 70-80.	rent Opinion in	2.6	29
202	Transcriptomic analysis of skin in a case of ichthyosis Curth-Macklin caused by a <i>KRT1 British Journal of Dermatology, 2016, 175, 1372-1375.</i>	mutation.	1.4	2
203	Identification of compound–protein interactions through the analysis of gene ontolog enrichment for proteins and molecular fragments of compounds. Molecular Genetics an 2016, 291, 2065-2079.		1.0	62

#	Article	IF	CITATIONS
204	Genomics of the Effect of Spinal Cord Stimulation on an Animal Model of Neuropathic Pain. Neuromodulation, 2016, 19, 576-586.	0.4	48
205	Network-assisted investigation of virulence and antibiotic-resistance systems in Pseudomonas aeruginosa. Scientific Reports, 2016, 6, 26223.	1.6	28
206	MathIOmica: An Integrative Platform for Dynamic Omics. Scientific Reports, 2016, 6, 37237.	1.6	35
207	Genome-wide transcriptome analysis revealed organelle specific responses to temperature variations in algae. Scientific Reports, 2016, 6, 37770.	1.6	38
208	Candidate egg case silk genes for the spider <i>Argiope argentata</i> from differential gene expression analyses. Insect Molecular Biology, 2016, 25, 757-768.	1.0	11
209	Protein–RNA interactions: structural biology and computational modeling techniques. Biophysical Reviews, 2016, 8, 359-367.	1.5	23
210	Inhibition of mTOR induces a paused pluripotent state. Nature, 2016, 540, 119-123.	13.7	191
211	Systems analysis identifies miR-29b regulation of invasiveness in melanoma. Molecular Cancer, 2016, 15, 72.	7.9	21
212	Draft genome of the living fossil Ginkgo biloba. GigaScience, 2016, 5, 49.	3.3	232
213	Local Cellular and Cytokine Cues in the Spleen Regulate In Situ T Cell Receptor Affinity, Function, and Fate of CD8 + T Cells. Immunity, 2016, 45, 988-998.	6.6	25
214	Head regeneration in hemichordates is not a strict recapitulation of development. Developmental Dynamics, 2016, 245, 1159-1175.	0.8	28
215	Tissue enrichment analysis for C. elegans genomics. BMC Bioinformatics, 2016, 17, 366.	1.2	155
216	Predicting protein subcellular localization based on information content of gene ontology terms. Computational Biology and Chemistry, 2016, 65, 1-7.	1.1	10
217	Mutational patterns in oncogenes and tumour suppressors. Biochemical Society Transactions, 2016, 44, 925-931.	1.6	16
218	Proximity Labeling Reveals Molecular Determinants of FGFR4 Endosomal Transport. Journal of Proteome Research, 2016, 15, 3841-3855.	1.8	14
219	The Resistome: A Comprehensive Database ofEscherichia coliResistance Phenotypes. ACS Synthetic Biology, 2016, 5, 1566-1577.	1.9	17
220	Time-course gene expression data on the transcriptional effects of Aminaphtone on ECV304 endothelial cells. Data in Brief, 2016, 8, 836-850.	0.5	3
221	Progress Towards Computational 3-D Multicellular Systems Biology. Advances in Experimental Medicine and Biology, 2016, 936, 225-246.	0.8	27

#	Article	IF	CITATIONS
222	Rapid evolutionary response to a transmissible cancer in Tasmanian devils. Nature Communications, 2016, 7, 12684.	5.8	162
223	Ancestral light and chloroplast regulation form the foundations for C4 gene expression. Nature Plants, 2016, 2, 16161.	4.7	32
224	Multiparameter functional diversity of human C2H2 zinc finger proteins. Genome Research, 2016, 26, 1742-1752.	2.4	131
225	A protein network descriptor server and its use in studying protein, disease, metabolic and drug targeted networks. Briefings in Bioinformatics, 2017, 18, bbw071.	3.2	34
226	A New Method for Identifying Essential Proteins by Measuring Co-Expression and Functional Similarity. IEEE Transactions on Nanobioscience, 2016, 15, 939-945.	2.2	10
227	Global phylogeography and evolutionary history of Shigella dysenteriae type 1. Nature Microbiology, 2016, 1, 16027.	5.9	65
228	Identifying and removing the cell-cycle effect from single-cell RNA-Sequencing data. Scientific Reports, 2016, 6, 33892.	1.6	97
229	Dynamic DNA methylation regulates neuronal intrinsic membrane excitability. Science Signaling, 2016, 9, ra83.	1.6	64
230	Quorum sensing activity of Citrobacter amalonaticus L8A, a bacterium isolated from dental plaque. Scientific Reports, 2016, 6, 20702.	1.6	18
231	eSNPO: An eQTL-based SNP Ontology and SNP functional enrichment analysis platform. Scientific Reports, 2016, 6, 30595.	1.6	9
232	Mapping wild-type and R345W fibulin-3 intracellular interactomes. Experimental Eye Research, 2016, 153, 165-169.	1.2	6
233	Multi-omics integration accurately predicts cellular state in unexplored conditions for Escherichia coli. Nature Communications, 2016, 7, 13090.	5.8	123
234	Transfer learning across ontologies for phenome–genome association prediction. Bioinformatics, 2017, 33, 529-536.	1.8	35
235	Ontologies in bioinformatics and systems biology. Russian Journal of Genetics: Applied Research, 2016, 6, 749-758.	0.4	1
236	A transcription factor hierarchy defines an environmental stress response network. Science, 2016, 354, .	6.0	394
237	Identification of differentially expressed genes from multipotent epithelia at the onset of an asexual development. Scientific Reports, 2016, 6, 27357.	1.6	17
238	Obtaining Human Ischemic Stroke Gene Expression Biomarkers from Animal Models: A Cross-species Validation Study. Scientific Reports, 2016, 6, 29693.	1.6	17
239	Comprehensive coverage of cardiovascular disease data in the disease portals at the Rat Genome Database. Physiological Genomics, 2016, 48, 589-600.	1.0	3

#	Article	IF	CITATIONS
240	Metagenomics, Metatranscriptomics, and Metabolomics Approaches for Microbiome Analysis. Evolutionary Bioinformatics, 2016, 12s1, EBO.S36436.	0.6	227
241	Genetic analysis of variation in lifespan using a multiparental advanced intercross Drosophila mapping population. BMC Genetics, 2016, 17, 113.	2.7	22
242	The Proteasix Ontology. Journal of Biomedical Semantics, 2016, 7, 33.	0.9	8
243	InteGO2: a web tool for measuring and visualizing gene semantic similarities using Gene Ontology. BMC Genomics, 2016, 17, 530.	1.2	26
244	Tribbles ortholog NIPI-3 and bZIP transcription factor CEBP-1 regulate a Caenorhabditis elegans intestinal immune surveillance pathway. BMC Biology, 2016, 14, 105.	1.7	35
245	The quality of metabolic pathway resources depends on initial enzymatic function assignments: a case for maize. BMC Systems Biology, 2016, 10, 129.	3.0	15
246	Complex systems analysis of bladder cancer susceptibility reveals a role for decarboxylase activity in two genome-wide association studies. BioData Mining, 2016, 9, 40.	2.2	6
247	Learning mixed graphical models with separate sparsity parameters and stability-based model selection. BMC Bioinformatics, 2016, 17, 175.	1.2	53
248	Prediction of scaffold proteins based on protein interaction and domain architectures. BMC Bioinformatics, 2016, 17, 220.	1.2	6
249	ToxEvaluator: an integrated computational platform to aid the interpretation of toxicology study-related findings. Database: the Journal of Biological Databases and Curation, 2016, 2016, .	1.4	7
250	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
251	Training and evaluation corpora for the extraction of causal relationships encoded in biological expression language (BEL). Database: the Journal of Biological Databases and Curation, 2016, 2016, baw113.	1.4	24
252	Modeling biochemical pathways in the gene ontology. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw126.	1.4	11
253	ToxReporter: viewing the genome through the eyes of a toxicologist. Database: the Journal of Biological Databases and Curation, 2016, 2016, .	1.4	1
254	Increased Intestinal Microbial Diversity Following Fecal Microbiota Transplant for Active Crohn's Disease. Inflammatory Bowel Diseases, 2016, 22, 2182-2190.	0.9	175
255	Efficient Exploration of Biological Data Using Semantic Web Compatible Databases. , 2016, , .		0
256	A Hitchhiker's Guide to Metatranscriptomics. , 2016, , 313-342.		8
257	Genome-wide association study of pathological gambling. European Psychiatry, 2016, 36, 38-46.	0.1	82

		CITATION REPORT		
#	Article		IF	Citations
258	TBR1 regulates autism risk genes in the developing neocortex. Genome Research, 201	6, 26, 1013-1022.	2.4	71
259	MUFFINN: cancer gene discovery via network analysis of somatic mutation data. Geno 17, 129.	me Biology, 2016,	3.8	126
260	Predicting drug–target interaction using positive-unlabeled learning. Neurocomputir 50-57.	ıg, 2016, 206,	3.5	83
261	The blister fluid proteome of paediatric burns. Journal of Proteomics, 2016, 146, 122-1	32.	1.2	10
262	The Perseus computational platform for comprehensive analysis of (prote)omics data. Methods, 2016, 13, 731-740.	Nature	9.0	6,181
263	Pairwise comparison of mammalian transcriptomes associated with the effect of polyp expression activity of developmental gene modules. Cell and Tissue Biology, 2016, 10,	loidy on the 122-132.	0.2	2
264	Identifying candidate genes for wood formation in poplar based on microarray networl graph theory. Tree Genetics and Genomes, 2016, 12, 1.	۲ analysis and	0.6	7
265	Accelerating Adverse Outcome Pathway Development Using Publicly Available Data Sc Environmental Health Reports, 2016, 3, 53-63.	urces. Current	3.2	64
266	Next-Generation Sequencing and the Crustacean Immune System: The Need for Altern Gene Annotation. Integrative and Comparative Biology, 2016, 56, 1113-1130.	atives in Immune	0.9	24
267	g:Profiler—a web server for functional interpretation of gene lists (2016 update). Nu Research, 2016, 44, W83-W89.	cleic Acids	6.5	1,179
268	PathwAX: a web server for network crosstalk based pathway annotation. Nucleic Acids 44, W105-W109.	Research, 2016,	6.5	36
269	Differential burden of rare protein truncating variants in Alzheimer's disease patier centenarians. Human Molecular Genetics, 2016, 25, ddw150.	its compared to	1.4	10
270	Utilization of HPASubC for the Identification of Sinusoid-Specific Proteins in the Liver. Proteome Research, 2016, 15, 1623-1629.	ournal of	1.8	9
271	Epigenome overlap measure (EPOM) for comparing tissue/cell types based on chromat Genomics, 2016, 17, 10.	in states. BMC	1.2	7
272	A review of the new HGNC gene family resource. Human Genomics, 2016, 10, 6.		1.4	68
273	Novel function discovery through sequence and structural data mining. Current Opinic Structural Biology, 2016, 38, 53-61.	on in	2.6	32
274	Candidate gene prioritization with Endeavour. Nucleic Acids Research, 2016, 44, W11	7-W121.	6.5	111
275	Mouse genome database 2016. Nucleic Acids Research, 2016, 44, D840-D847.		6.5	80

#	Article	IF	CITATIONS
276	DESM: portal for microbial knowledge exploration systems. Nucleic Acids Research, 2016, 44, D624-D633.	6.5	12
277	CAMP <sub>R3</sub> : a database on sequences, structures and signatures of antimicrobial peptides: Table 1 Nucleic Acids Research, 2016, 44, D1094-D1097.	6.5	521
278	PhytoPath: an integrative resource for plant pathogen genomics. Nucleic Acids Research, 2016, 44, D688-D693.	6.5	42
279	Representation and inference of cellular architecture for metabolic reconstruction and modeling. Bioinformatics, 2016, 32, 1074-1079.	1.8	0
280	Recurrent Fusions in <i>MYB</i> and <i>MYBL1</i> Define a Common, Transcription Factor–Driven Oncogenic Pathway in Salivary Gland Adenoid Cystic Carcinoma. Cancer Discovery, 2016, 6, 176-187.	7.7	179
281	MitoMiner v3.1, an update on the mitochondrial proteomics database. Nucleic Acids Research, 2016, 44, D1258-D1261.	6.5	182
282	The Transporter Classification Database (TCDB): recent advances. Nucleic Acids Research, 2016, 44, D372-D379.	6.5	711
283	PCOSKB: A KnowledgeBase on genes, diseases, ontology terms and biochemical pathways associated with PolyCystic Ovary Syndrome. Nucleic Acids Research, 2016, 44, D1032-D1035.	6.5	46
284	On the linkage between the ubiquitin-proteasome system and the mitochondria. Biochemical and Biophysical Research Communications, 2016, 473, 80-86.	1.0	39
285	RNA-seq reveals a diminished acclimation response to the combined effects of ocean acidification and elevated seawater temperature in Pagothenia borchgrevinki. Marine Genomics, 2016, 28, 87-97.	0.4	34
286	LegumelP 2.0—a platform for the study of gene function and genome evolution in legumes. Nucleic Acids Research, 2016, 44, D1189-D1194.	6.5	23
287	The <i><scp>A</scp>rabidopsis</i> transcriptional regulator <scp>DPB</scp> 3â€4 enhances heat stress tolerance without growth retardation in rice. Plant Biotechnology Journal, 2016, 14, 1756-1767.	4.1	55
288	Pharmacodynamics of Dimethyl Fumarate Are Tissue Specific and Involve NRF2-Dependent and -Independent Mechanisms. Antioxidants and Redox Signaling, 2016, 24, 1058-1071.	2.5	49
289	UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB. Bioinformatics, 2016, 32, 2264-2271.	1.8	37
290	Hymenoptera Genome Database: integrating genome annotations in HymenopteraMine. Nucleic Acids Research, 2016, 44, D793-D800.	6.5	105
291	GeneWeaver: data driven alignment of cross-species genomics in biology and disease. Nucleic Acids Research, 2016, 44, D555-D559.	6.5	30
292	Long-noncoding RNAs in basal cell carcinoma. Tumor Biology, 2016, 37, 10595-10608.	0.8	35
293	Multi-task consensus clustering of genome-wide transcriptomes from related biological conditions. Bioinformatics, 2016, 32, 1509-1517.	1.8	6

#	Article	IF	CITATIONS
294	The Human Physiome: how standards, software and innovative service infrastructures are providing the building blocks to make it achievable. Interface Focus, 2016, 6, 20150103.	1.5	30
295	Ensembl Genomes 2016: more genomes, more complexity. Nucleic Acids Research, 2016, 44, D574-D580.	6.5	530
296	WormBase 2016: expanding to enable helminth genomic research. Nucleic Acids Research, 2016, 44, D774-D780.	6.5	329
297	Using the Gene Ontology to Annotate Key Players in Parkinson's Disease. Neuroinformatics, 2016, 14, 297-304.	1.5	20
298	Strategies in functional proteomics: Unveiling the pathways to precision oncology. Cancer Letters, 2016, 382, 86-94.	3.2	7
299	The genomic basis of parasitism in the Strongyloides clade of nematodes. Nature Genetics, 2016, 48, 299-307.	9.4	226
300	Epigenome-wide profiling of DNA methylation in paired samples of adipose tissue and blood. Epigenetics, 2016, 11, 227-236.	1.3	59
301	Quality assurance of the gene ontology using abstraction networks. Journal of Bioinformatics and Computational Biology, 2016, 14, 1642001.	0.3	24
302	Translation of Genotype to Phenotype by a Hierarchy of Cell Subsystems. Cell Systems, 2016, 2, 77-88.	2.9	72
303	Extending gene ontology with gene association networks. Bioinformatics, 2016, 32, 1185-1194.	1.8	42
304	The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	6.5	64
305	Multidimensional Screening Platform for Simultaneously Targeting Oncogenic KRAS and Hypoxia-Inducible Factors Pathways in Colorectal Cancer. ACS Chemical Biology, 2016, 11, 1322-1331.	1.6	28
306	Gene regulatory mechanisms underpinning prostate cancer susceptibility. Nature Genetics, 2016, 48, 387-397.	9.4	119
307	Stable engineered vascular networks from human induced pluripotent stem cell-derived endothelial cells cultured in synthetic hydrogels. Acta Biomaterialia, 2016, 35, 32-41.	4.1	86
308	Harnessing QbD, Programming Languages, and Automation for Reproducible Biology. Trends in Biotechnology, 2016, 34, 214-227.	4.9	44
309	Hepatitis E virus ORF1 encoded non structural protein–host protein interaction network. Virus Research, 2016, 213, 195-204.	1.1	15
310	Exome arrays capture polygenic rare variant contributions to schizophrenia. Human Molecular Genetics, 2016, 25, 1001-1007.	1.4	54
311	PlanMine – a mineable resource of planarian biology and biodiversity. Nucleic Acids Research, 2016, 44, D764-D773.	6.5	130

		CITATION REPORT	
# 312	ARTICLE eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. Nucleic Acids Research, 2016, 44, D286-D293.	IF 6.5	Citations 1,937
313	Whole-Exome Sequencing in Familial Parkinson Disease. JAMA Neurology, 2016, 73, 68.	4.5	71
314	Enhanced annotations and features for comparing thousands of <i>Pseudomonas</i> genomes in the Pseudomonas genome database. Nucleic Acids Research, 2016, 44, D646-D653.	6.5	929
315	Recent Advances and Emerging Applications in Text and Data Mining for Biomedical Discovery. Briefings in Bioinformatics, 2016, 17, 33-42.	3.2	131
316	Bovine Genome Database: new tools for gleaning function from the <i>Bos taurus</i> genome. Nucleic Acids Research, 2016, 44, D834-D839.	6.5	87
317	PPIXpress: construction of condition-specific protein interaction networks based on transcript expression. Bioinformatics, 2016, 32, 571-578.	1.8	21
318	SIGNOR: a database of causal relationships between biological entities. Nucleic Acids Research, 2016, 44, D548-D554.	6.5	243
319	SILAC-based proteomic analysis reveals that salidroside antagonizes cobalt chloride-induced hypoxic effects by restoring the tricarboxylic acid cycle in cardiomyocytes. Journal of Proteomics, 2016, 130, 211-220.	1.2	33
320	Single ell transcriptomics and functional target validation of brown adipocytes show their complex roles in metabolic homeostasis. FASEB Journal, 2016, 30, 81-92.	0.2	39
321	Profiling the proteomics in honeybee worker brains submitted to the proboscis extension reflex. Journal of Proteomics, 2017, 151, 131-144.	1.2	7
322	Physiological adjustments and transcriptome reprogramming are involved in the acclimation to salinity gradients in diatoms. Environmental Microbiology, 2017, 19, 909-925.	1.8	29
323	The antineoplastic drug, trastuzumab, dysregulates metabolism in iPSCâ€derived cardiomyocytes. Clinical and Translational Medicine, 2017, 6, 5.	1.7	48
324	Primary Cell Culture of Live Neurosurgically Resected Aged Adult Human Brain Cells and Single Cell Transcriptomics. Cell Reports, 2017, 18, 791-803.	2.9	60
325	The protein expression landscape of mitosis and meiosis in diploid budding yeast. Journal of Proteomics, 2017, 156, 5-19.	1.2	7
326	Mutations at protein-protein interfaces: Small changes over big surfaces have large impacts on human health. Progress in Biophysics and Molecular Biology, 2017, 128, 3-13.	1.4	129
327	Protein–glycosaminoglycan interaction networks: Focus on heparan sulfate. Perspectives in Science, 2017, 11, 62-69.	0.6	13
328	Functional Transcriptomics in Diverse Intestinal Epithelial Cell Types Reveals Robust MicroRNA Sensitivity in Intestinal Stem Cells to Microbial Status. Journal of Biological Chemistry, 2017, 292, 2586-2600.	1.6	105
329	The 24th annual <i>Nucleic Acids Research</i> database issue: a look back and upcoming changes. Nucleic Acids Research, 2017, 45, D1-D11.	6.5	144

#	Article	IF	CITATIONS
330	Pathway analysis of complex diseases for GWAS, extending to consider rare variants, multi-omics and interactions. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 335-353.	1.1	54
331	Supra-operonic clusters of functionally related genes (SOCs) are a source of horizontal gene co-transfers. Scientific Reports, 2017, 7, 40294.	1.6	11
332	ontologyX: a suite of R packages for working with ontological data. Bioinformatics, 2017, 33, 1104-1106.	1.8	86
333	ORCAN—a web-based meta-server for real-time detection and functional annotation of orthologs. Bioinformatics, 2017, 33, 1224-1226.	1.8	11
334	Get GO! Retrieving GO Data Using AmiGO, QuickGO, API, Files, and Tools. Methods in Molecular Biology, 2017, 1446, 149-160.	0.4	28
335	MalaCards: an amalgamated human disease compendium with diverse clinical and genetic annotation and structured search. Nucleic Acids Research, 2017, 45, D877-D887.	6.5	398
336	TP53 Modulates Oxidative Stress in Gata1 + Erythroid Cells. Stem Cell Reports, 2017, 8, 360-372.	2.3	8
337	Uniclust databases of clustered and deeply annotated protein sequences and alignments. Nucleic Acids Research, 2017, 45, D170-D176.	6.5	520
338	Impairment of Host Liver Repopulation by Transplanted Hepatocytes in Aged Rats and the Release by Short-Term Growth Hormone Treatment. American Journal of Pathology, 2017, 187, 553-569.	1.9	2
339	PHI-base: a new interface and further additions for the multi-species pathogen–host interactions database. Nucleic Acids Research, 2017, 45, D604-D610.	6.5	231
340	Brief exposure to small molecules allows induction of mouse embryonic fibroblasts into neural crestâ€ike precursors. FEBS Letters, 2017, 591, 590-602.	1.3	11
341	Plasticity in gene transcription explains the differential performance of two invasive fish species. Evolutionary Applications, 2017, 10, 563-576.	1.5	51
342	Predicting disease-related genes using integrated biomedical networks. BMC Genomics, 2017, 18, 1043.	1.2	46
343	Plasmodium falciparum CRK4 directs continuous rounds of DNA replication during schizogony. Nature Microbiology, 2017, 2, 17017.	5.9	79
344	Expansion of the Gene Ontology knowledgebase and resources. Nucleic Acids Research, 2017, 45, D331-D338.	6.5	1,838
345	Gene expression metadata analysis reveals molecular mechanisms employed by Phanerochaete chrysosporium during lignin degradation and detoxification of plant extractives. Current Genetics, 2017, 63, 877-894.	0.8	34
346	Identifying the Metabolic Differences of a Fast-Growth Phenotype in Synechococcus UTEX 2973. Scientific Reports, 2017, 7, 41569.	1.6	56
347	Genetic loci associated with chronic obstructive pulmonary disease overlap with loci for lung function and pulmonary fibrosis. Nature Genetics, 2017, 49, 426-432.	9.4	306

#	Article	IF	CITATIONS
348	A combined large-scale meta-analysis identifies <i>COG6</i> as a novel shared risk <i>locus</i> for rheumatoid arthritis and systemic lupus erythematosus. Annals of the Rheumatic Diseases, 2017, 76, 286-294.	0.5	58
349	Hypoxiaâ€induced <scp>HIF</scp> 1 <i>α</i> targets in melanocytes reveal a molecular profile associated with poor melanoma prognosis. Pigment Cell and Melanoma Research, 2017, 30, 339-352.	1.5	29
351	Annotation of functional impact of voltage-gated sodium channel mutations. Human Mutation, 2017, 38, 485-493.	1.1	12
352	A Circadian Genomic Signature Common to Ketamine and Sleep Deprivation in the Anterior Cingulate Cortex. Biological Psychiatry, 2017, 82, 351-360.	0.7	82
353	Genome content analysis yields new insights into the relationship between the human malaria parasite Plasmodium falciparum and its anopheline vectors. BMC Genomics, 2017, 18, 205.	1.2	2
354	Evolution of complexity in the zebrafish synapse proteome. Nature Communications, 2017, 8, 14613.	5.8	112
355	From sequencing data to gene functions: co-functional network approaches. Animal Cells and Systems, 2017, 21, 77-83.	0.8	27
356	InterPred: A pipeline to identify and model protein–protein interactions. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1159-1170.	1.5	32
357	Expression profiling-based clustering of healthy subjects recapitulates classifications defined by clinical observation in Chinese medicine. Journal of Genetics and Genomics, 2017, 44, 191-197.	1.7	22
358	Proteome scale identification, classification and structural analysis of iron-binding proteins in bread wheat. Journal of Inorganic Biochemistry, 2017, 170, 63-74.	1.5	12
359	Overcoming the divide between ataxias and spastic paraplegias: Shared phenotypes, genes, and pathways. Movement Disorders, 2017, 32, 332-345.	2.2	144
360	Phenotype-Specific Association of Single-Nucleotide Polymorphisms with Heart Failure and Preserved Ejection Fraction: a Genome-Wide Association Analysis of the Cardiovascular Health Study. Journal of Cardiovascular Translational Research, 2017, 10, 285-294.	1.1	16
361	Genomic Comparison of Indigenous African and Northern European Chickens Reveals Putative Mechanisms of Stress Tolerance Related to Environmental Selection Pressure. G3: Genes, Genomes, Genetics, 2017, 7, 1525-1537.	0.8	38
362	Insights into the human brain proteome: Disclosing the biological meaning of protein networks in cerebrospinal fluid. Critical Reviews in Clinical Laboratory Sciences, 2017, 54, 185-204.	2.7	29
363	Matrix Metalloproteinase-28 Is a Key Contributor to Emphysema Pathogenesis. American Journal of Pathology, 2017, 187, 1288-1300.	1.9	25
364	The genome sequence of the wisent (Bison bonasus). GigaScience, 2017, 6, 1-5.	3.3	22
365	Identification of protein features encoded by alternative exons using Exon Ontology. Genome Research, 2017, 27, 1087-1097.	2.4	45
366	Transcriptome Analysis of Mango (Mangifera indica L.) Fruit Epidermal Peel to Identify Putative Cuticle-Associated Genes. Scientific Reports, 2017, 7, 46163.	1.6	68

щ		15	CITATIONS
#	ARTICLE Mps1 Regulates Kinetochore-Microtubule Attachment Stability via the Ska Complex to Ensure	IF	CITATIONS
367	Error-Free Chromosome Segregation. Developmental Cell, 2017, 41, 143-156.e6.	3.1	73
368	The BRENDA enzyme information system–From a database to an expert system. Journal of Biotechnology, 2017, 261, 194-206.	1.9	136
369	KLRG1 impairs regulatory Tâ€cell competitive fitness in the gut. Immunology, 2017, 152, 65-73.	2.0	17
370	Tumourâ€associated changes in intestinal epithelial cells cause local accumulation of <scp>KLRG</scp> 1 <sup>+</sup> <scp>GATA</scp> 3 <sup>+</sup> regulatory T cells in mice. Immunology, 2017, 152, 74-88.	2.0	14
371	goSTAC: gene ontology subtrees to tag and annotate genes within a set. Source Code for Biology and Medicine, 2017, 12, 6.	1.7	10
372	Identification of breast cancer prognostic modules based on weighted protein-protein interaction networks. Oncology Letters, 2017, 13, 3935-3941.	0.8	5
373	A subcellular map of the human proteome. Science, 2017, 356, .	6.0	2,079
374	Gremlin Language for Querying the BiographDB Integrated Biological Database. Lecture Notes in Computer Science, 2017, , 303-313.	1.0	2
375	Neuropeptides predicted from the transcriptome analysis of the gray garden slug Deroceras reticulatum. Peptides, 2017, 93, 51-65.	1.2	50
376	Interactive Toxicogenomics: Gene set discovery, clustering and analysis in Toxygates. Scientific Reports, 2017, 7, 1390.	1.6	18
377	AptRank: an adaptive PageRank model for protein function prediction on  bi-relational graphs. Bioinformatics, 2017, 33, 1829-1836.	1.8	40
378	Navigating through the Jungle of Allergens: Features and Applications of Allergen Databases. International Archives of Allergy and Immunology, 2017, 173, 1-11.	0.9	16
380	Tradict enables accurate prediction of eukaryotic transcriptional states from 100 marker genes. Nature Communications, 2017, 8, 15309.	5.8	18
381	Identification of a target protein of Hydra actinoporin-like toxin-1 (HALT-1) using GST affinity purification and SILAC-based quantitative proteomics. Toxicon, 2017, 133, 153-161.	0.8	6
382	BioMake: a GNU make-compatible utility for declarative workflow management. Bioinformatics, 2017, 33, 3502-3504.	1.8	5
383	Identification of molecular characteristics induced by radiotherapy in rectal cancer based on microarray data. Oncology Letters, 2017, 13, 2777-2783.	0.8	6
384	Cascading Effects of Nanoparticle Coatings: Surface Functionalization Dictates the Assemblage of Complexed Proteins and Subsequent Interaction with Model Cell Membranes. ACS Nano, 2017, 11, 5489-5499.	7.3	57
385	Altered interactions between unicellular and multicellular genes drive hallmarks of transformation in a diverse range of solid tumors. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6406-6411.	3.3	159

#	Article	IF	CITATIONS
386	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. Molecular Biology and Evolution, 2017, 34, 2115-2122.	3.5	2,156
387	MARRVEL: Integration of Human and Model Organism Genetic Resources to Facilitate Functional Annotation of the Human Genome. American Journal of Human Genetics, 2017, 100, 843-853.	2.6	181
388	From Gene Annotation to Function Prediction for Metagenomics. Methods in Molecular Biology, 2017, 1611, 27-34.	0.4	12
389	The Bologna Annotation Resource (BAR 3.0): improving protein functional annotation. Nucleic Acids Research, 2017, 45, W285-W290.	6.5	18
390	Maintenance of neural activities in torpid Rhinolophus ferrumequinum bats revealed by 2D gel-based proteome analysis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1004-1019.	1.1	4
391	Insights into Ciliary Genes and Evolution from Multi-Level Phylogenetic Profiling. Molecular Biology and Evolution, 2017, 34, 2016-2034.	3.5	54
392	Microarray Analysis Reveals Increased Expression of Matrix Metalloproteases and Cytokines of Interleukin-20 Subfamily in the Kidneys of Neonate Rats Underwent Unilateral Ureteral Obstruction: A Potential Role of IL-24 in the Regulation of Inflammation and Tissue Remodeling. Kidney and Blood Pressure Research, 2017, 42, 16-32.	0.9	6
393	Molecular characterization and expression analysis of pearl millet plasma membrane proteolipid 3 () Tj ETQq1	1 0.784314 1.4	rgॺॖॖॖॖҬॖ /Overloo
394	MPFit: Computational Tool for Predicting Moonlighting Proteins. Methods in Molecular Biology, 2017, 1611, 45-57.	0.4	4
395	Network-Based Gene Function Prediction in Mouse and Other Model Vertebrates Using MouseNet Server. Methods in Molecular Biology, 2017, 1611, 183-198.	0.4	3
396	Protein Function Prediction. Methods in Molecular Biology, 2017, , .	0.4	15
397	PARP3 is a promoter of chromosomal rearrangements and limits G4 DNA. Nature Communications, 2017, 8, 15110.	5.8	32
398	IGF2BP3 functions as a potential oncogene and is a crucial target of miR-34a in gastric carcinogenesis. Molecular Cancer, 2017, 16, 77.	7.9	115
399	Neuro-symbolic representation learning on biological knowledge graphs. Bioinformatics, 2017, 33, 2723-2730.	1.8	92
400	DisProt 7.0: a major update of the database of disordered proteins. Nucleic Acids Research, 2017, 45, D219-D227.	6.5	242
401	Variability in Metagenomic Count Data and Its Influence on the Identification of Differentially Abundant Genes. Journal of Computational Biology, 2017, 24, 311-326.	0.8	19
402	Green listed—a CRISPR screen tool. Bioinformatics, 2017, 33, 1099-1100.	1.8	12
403	The Zebrafish Model Organism Database: new support for human disease models, mutation details, gene expression phenotypes and searching. Nucleic Acids Research, 2017, 45, D758-D768.	6.5	71

#	Article	IF	CITATIONS
404	Integrative Analysis of Transcriptomics and Proteomics Data for the Characterization of Brain Tissue After Ischemic Stroke. Trends in Mathematics, 2017, , 21-27.	0.1	0
405	Integrated Servers for Structure-Informed Function Prediction. , 2017, , 427-448.		0
406	Clustering and Network Analysis of Reverse Phase Protein Array Data. Methods in Molecular Biology, 2017, 1606, 171-191.	0.4	6
407	Sma3s: A universal tool for easy functional annotation of proteomes and transcriptomes. Proteomics, 2017, 17, 1700071.	1.3	71
408	Macroanalysis in the Arts and Sciences. , 2017, , 87-100.		0
409	Identifying key nodes in multilayer networks based on tensor decomposition. Chaos, 2017, 27, 063108.	1.0	42
410	Temperature-responsive miRNAs in Drosophila orchestrate adaptation to different ambient temperatures. Rna, 2017, 23, 1352-1364.	1.6	23
411	Cognitive Characterization of Schizophrenia Risk Variants Involved in Synaptic Transmission: Evidence of CACNA1C's Role in Working Memory. Neuropsychopharmacology, 2017, 42, 2612-2622.	2.8	28
412	RNAseq based transcriptomics study of SMCs from carotid atherosclerotic plaque: BMP2 and IDs proteins are crucial regulators of plaque stability. Scientific Reports, 2017, 7, 3470.	1.6	21
413	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. Sexual Development, 2017, 11, 94-108.	1.1	0
414	Bioinformatics in translational drug discovery. Bioscience Reports, 2017, 37, .	1.1	68
415	Dynamic regulation of Nanog and stem cell-signaling pathways by Hoxa1 during early neuro-ectodermal differentiation of ES cells. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5838-5845.	3.3	54
416	RCAS: an RNA centric annotation system for transcriptome-wide regions of interest. Nucleic Acids Research, 2017, 45, e91-e91.	6.5	23
417	A resource of potential drug targets and strategic decisionâ€making for obstructive sleep apnoea pharmacotherapy. Respirology, 2017, 22, 861-873.	1.3	50
418	The long non-coding RNA LINC00152 is essential for cell cycle progression through mitosis in HeLa cells. Scientific Reports, 2017, 7, 2265.	1.6	51
419	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
420	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. Journal of Experimental Medicine, 2017, 214, 2073-2088.	4.2	30
421	Histone H3 lysine 36 methylation affects temperature-induced alternative splicing and flowering in plants. Genome Biology, 2017, 18, 102.	3.8	146

#	ARTICLE	IF	CITATIONS
422	Structure of the Transcriptional Regulatory Network Correlates with Regulatory Divergence in Drosophila. Molecular Biology and Evolution, 2017, 34, 1352-1362.	3.5	24
423	RefBool: a reference-based algorithm for discretizing gene expression data. Bioinformatics, 2017, 33, 1953-1962.	1.8	7
424	An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. Cell, 2017, 169, 350-360.e12.	13.5	322
425	Large-Scale Profiling Reveals the Influence of Genetic Variation on Gene Expression in Human Induced Pluripotent Stem Cells. Cell Stem Cell, 2017, 20, 533-546.e7.	5.2	157
426	Cytosolic YB-1 and NSUN2 are the only proteins recognizing specific motifs present in mRNAs enriched in exosomes. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 664-673.	1.1	84
427	Comparison of global gene expression profiles of microdissected human foetal Leydig cells with their normal and hyperplastic adult equivalents. Molecular Human Reproduction, 2017, 23, 339-354.	1.3	14
428	TOMATOMICS: A Web Database for Integrated Omics Information in Tomato. Plant and Cell Physiology, 2017, 58, pcw207.	1.5	29
429	The Transcriptome of the Zebrafish Embryo After Chemical Exposure: A Meta-Analysis. Toxicological Sciences, 2017, 157, 291-304.	1.4	35
430	DES-ncRNA: A knowledgebase for exploring information about human micro and long noncoding RNAs based on literature-mining. RNA Biology, 2017, 14, 963-971.	1.5	21
431	Connecting myelin-related and synaptic dysfunction in schizophrenia with SNP-rich gene expression hubs. Scientific Reports, 2017, 7, 45494.	1.6	9
432	eTumorType, An Algorithm of Discriminating Cancer Types for Circulating Tumor Cells or Cell-free DNAs in Blood. Genomics, Proteomics and Bioinformatics, 2017, 15, 130-140.	3.0	15
433	Transcriptome-based investigation of cirrus development and identifying microsatellite markers in rattan (Daemonorops jenkinsiana). Scientific Reports, 2017, 7, 46107.	1.6	16
434	CHK2 is involved in the p53-independent radiosensitizing effects of valproic acid. Oncology Letters, 2017, 13, 2591-2598.	0.8	5
435	Identification of novel cancer therapeutic targets using a designed and pooled shRNA library screen. Scientific Reports, 2017, 7, 43023.	1.6	33
436	Comparative transcriptome analyses of flower development in four species of Achimenes (Gesneriaceae). BMC Genomics, 2017, 18, 240.	1.2	41
437	Identification of genes associated with tongue cancer in patients with a history of tobacco and/or alcohol use. Oncology Letters, 2017, 13, 629-638.	0.8	8
438	Gene Expression Profiling with Cre-Conditional Pseudorabies Virus Reveals a Subset of Midbrain Neurons That Participate in Reward Circuitry. Journal of Neuroscience, 2017, 37, 4128-4144.	1.7	47
439	Mitochondrial chaperone <scp>HSP</scp> â€60 regulates antiâ€bacterial immunity via p38 <scp>MAP</scp> kinase signaling. EMBO Journal, 2017, 36, 1046-1065.	3.5	66

ARTICLE IF CITATIONS Bioinformatics identification of new targets for improving low temperature stress tolerance in 440 1.2 8 spring and winter wheat. BMC Bioinformatics, 2017, 18, 174. De novo transcriptome assembly reveals high transcriptional complexity in Pisum sativum axillary 441 1.2 24 buds and shows rapid changes in expression of diurnally regulated genes. BMC Genomics, 2017, 18, 221. Systematic protein–protein interaction mapping for clinically relevant human <scp>GPCR</scp>s. 442 3.2 63 Molecular Systems Biology, 2017, 13, 918. Evolution of plant conducting cells: perspectives from key regulators of vascular cell 443 2.4 differentiation. Journal of Experimental Botany, 2017, 68, 17-26. Nitric Oxide Modulates Histone Acetylation at Stress Genes by Inhibition of Histone Deacetylases. 444 2.3 114 Plant Physiology, 2017, 173, 1434-1452. Altered mucosal expression of microRNAs in pediatric patients with inflammatory bowel disease. Digestive and Liver Disease, 2017, 49, 378-387. 0.4 The BioGRID interaction database: 2017 update. Nucleic Acids Research, 2017, 45, D369-D379. 446 6.5 920 A Genome-wide Association Study Identifies Risk Alleles in Plasminogen and P4HA2 Associated with 447 2.6 78 Giant Cell Arteritis. American Journal of Human Genetics, 2017, 100, 64-74. A Multi-step Transcriptional and Chromatin State Cascade Underlies Motor Neuron Programming 448 5.2 86 from Embryonic Stem Cells. Cell Stem Cell, 2017, 20, 205-217.e8. Open Targets: a platform for therapeutic target identification and validation. Nucleic Acids Research, 449 6.5 2017, 45, D985-D994. Using Baseline Transcriptional Connectomes in Rat to Identify Genetic Pathways Associated with 450 2 0.4 Predisposition to Complex Traits. Methods in Molecular Biology, 2017, 1488, 299-317. Landscape of Pleiotropic Proteins Causing Human Disease: Structural and System Biology Insights. 1.1 Human Mutation, 2017, 38, 289-296. The Monarch Initiative: an integrative data and analytic platform connecting phenotypes to genotypes 452 6.5 306 across species. Nucleic Acids Research, 2017, 45, D712-D722. Social Interactions and Indirect Genetic Effects on Complex Juvenile and Adult Traits. Methods in 0.4 Molecular Biology, 2017, 1488, 499-517. Distinct global binding patterns of the Wilms tumor gene 1 (WT1) â<sup>°</sup>KTS and +KTS isoforms in leukemic cells. Haematologica, 2017, 102, 336-345. 454 12 1.7 Decoding the role of regulatory element polymorphisms in complex disease. Current Opinion in 30 Genetics and Development, 2017, 43, 38-45. Meta-analysis of transcriptomic datasets identifies genes enriched in the mammalian circadian 456 6.5 29 pacemaker. Nucleic Acids Research, 2017, 45, 9860-9873. Depletion of Myofibril-Associated Proteins Using Selective Protein Extraction as a Tool in Cardiac 0.4 Proteomics. Methods in Molecular Biology, 2017, 1788, 1-9.

#	Article	IF	CITATIONS
458	MARK3-mediated phosphorylation of ARHGEF2 couples microtubules to the actin cytoskeleton to establish cell polarity. Science Signaling, 2017, 10, .	1.6	52
459	Biological network border detection. Integrative Biology (United Kingdom), 2017, 9, 947-955.	0.6	1
460	Peripheral blood micro <scp>RNA</scp> and <i><scp>VEGFA</scp></i> <scp>mRNA</scp> changes following electroconvulsive therapy: implications for psychotic depression. Acta Psychiatrica Scandinavica, 2017, 136, 594-606.	2.2	32
461	A Bayesian approach for estimating protein–protein interactions by integrating structural and non-structural biological data. Molecular BioSystems, 2017, 13, 2592-2602.	2.9	1
462	The Arabidopsis MOS4-Associated Complex Promotes MicroRNA Biogenesis and Precursor Messenger RNA Splicing. Plant Cell, 2017, 29, 2626-2643.	3.1	81
463	SMARCB1 is required for widespread BAF complex–mediated activation of enhancers and bivalent promoters. Nature Genetics, 2017, 49, 1613-1623.	9.4	207
464	Constrained vertebrate evolution by pleiotropic genes. Nature Ecology and Evolution, 2017, 1, 1722-1730.	3.4	72
465	Inflammasome-driven catecholamine catabolism in macrophages blunts lipolysis during ageing. Nature, 2017, 550, 119-123.	13.7	329
466	Analysis of dermal fibroblasts isolated from neonatal and child cleft lip and adult skin: Developmental implications on reconstructive surgery. International Journal of Molecular Medicine, 2017, 40, 1323-1334.	1.8	17
467	Transcriptomic Analysis of Octanoic Acid Response in <i>Drosophila sechellia</i> Using RNA-Sequencing. G3: Genes, Genomes, Genetics, 2017, 7, 3867-3873.	0.8	21
468	Genomeâ€wide characterization of differential transcript usage in <i>Arabidopsis thaliana</i> . Plant Journal, 2017, 92, 1218-1231.	2.8	31
469	Widespread Post-transcriptional Attenuation of Genomic Copy-Number Variation in Cancer. Cell Systems, 2017, 5, 386-398.e4.	2.9	102
470	A genome-wide comparison of mesenchymal stem cells derived from human placenta and umbilical cord. Taiwanese Journal of Obstetrics and Gynecology, 2017, 56, 664-671.	0.5	9
471	Hemodynamic Forces Sculpt Developing Heart Valves through a KLF2-WNT9B Paracrine Signaling Axis. Developmental Cell, 2017, 43, 274-289.e5.	3.1	114
472	Modulation of Global Transcriptional Regulatory Networks as a Strategy for Increasing Kanamycin Resistance of the Translational Elongation Factor-G Mutants in <i>Escherichia coli</i> . G3: Genes, Genomes, Genetics, 2017, 7, 3955-3966.	0.8	11
473	A Problem-Driven Approach for Building a Bioinformatics GraphDB. Lecture Notes in Computer Science, 2017, , 134-144.	1.0	0
474	Early Life Exposure to Low Levels of AHR Agonist PCB126 (3,3′,4,4′,5-Pentachlorobiphenyl) Reprograms Gene Expression in Adult Brain. Toxicological Sciences, 2017, 160, 386-397.	1.4	21
475	Congenic mice demonstrate the presence of QTLs conferring obesity and hypercholesterolemia on chromosome 1 in the TALLYHO mouse. Mammalian Genome, 2017, 28, 487-497.	1.0	9

#	Article	IF	CITATIONS
476	Single-Nucleotide Polymorphisms in Vitamin D–Related Genes May Modify Vitamin D–Breast Cancer Associations. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1761-1771.	1.1	15
477	mRNA-Seq reveals accumulation followed by reduction of small nuclear and nucleolar RNAs in yeast exposed to antiviral ribavirin. FEMS Yeast Research, 2017, 17, .	1.1	1
478	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. Science Advances, 2017, 3, e1700299.	4.7	142
479	Rule Mining Techniques to Predict Prokaryotic Metabolic Pathways. Methods in Molecular Biology, 2017, 1613, 311-331.	0.4	2
480	Identification of prognostic markers of high grade prostate cancer through an integrated bioinformatics approach. Journal of Cancer Research and Clinical Oncology, 2017, 143, 2571-2579.	1.2	34
481	Multiplexed quantification of proteins and transcripts in single cells. Nature Biotechnology, 2017, 35, 936-939.	9.4	684
482	Rat Genome and Model Resources. ILAR Journal, 2017, 58, 42-58.	1.8	38
483	Liver transcriptome analysis reveals important factors involved in the metabolic adaptation of the transition cow. Journal of Dairy Science, 2017, 100, 9311-9323.	1.4	24
484	INDEX: Incremental depth extension approach for protein–protein interaction networks alignment. BioSystems, 2017, 162, 24-34.	0.9	17
485	Identifying consistent disease subnetworks using DNet. Methods, 2017, 131, 104-110.	1.9	16
486	Microbial diversity in the hypersaline Lake Meyghan, Iran. Scientific Reports, 2017, 7, 11522.	1.6	76
487	<scp>APE</scp> 1/Refâ€1 knockdown in pancreatic ductal adenocarcinoma – characterizing gene expression changes and identifying novel pathways using singleâ€cell <scp>RNA</scp> sequencing. Molecular Oncology, 2017, 11, 1711-1732.	2.1	27
488	Global organization of a binding site network gives insight into evolution and structure-function relationships of proteins. Scientific Reports, 2017, 7, 11652.	1.6	4
489	Global Analysis of Membrane-associated Protein Oligomerization Using Protein Correlation Profiling. Molecular and Cellular Proteomics, 2017, 16, 1972-1989.	2.5	32
490	A meta-analysis of genome-wide association studies identifies 17 new Parkinson's disease risk loci. Nature Genetics, 2017, 49, 1511-1516.	9.4	944
491	Data Analysis Pipeline for RNAâ€seq Experiments: From Differential Expression to Cryptic Splicing. Current Protocols in Bioinformatics, 2017, 59, 11.15.1-11.15.21.	25.8	35
492	Unravelling the biology of chromatin in health and cancer using proteomic approaches. Expert Review of Proteomics, 2017, 14, 905-915.	1.3	5
493	Impaired expressions of the beta and delta isoforms of vacuolar processing enzymes compromise the basal defenses of Arabidopsis thaliana against the phloem-feeding insect Myzus persicae. Acta Physiologiae Plantarum, 2017, 39, 1.	1.0	3

#	Article	IF	CITATIONS
494	Multiomics Analysis of Tumor Microenvironment Reveals Gata2 and miRNA-124-3p as Potential Novel Biomarkers in Ovarian Cancer. OMICS A Journal of Integrative Biology, 2017, 21, 603-615.	1.0	42
495	FunctionAnnotator, a versatile and efficient web tool for non-model organism annotation. Scientific Reports, 2017, 7, 10430.	1.6	29
496	Semantic Data Integration and Knowledge Management to Represent Biological Network Associations. Methods in Molecular Biology, 2017, 1613, 403-423.	0.4	11
497	Proteomic Analysis of Secreted Proteins from Cell Microenvironment. Methods in Molecular Biology, 2017, 1662, 45-58.	0.4	4
498	Transcriptome analysis of inflammation-related gene expression in endothelial cells activated by complement MASP-1. Scientific Reports, 2017, 7, 10462.	1.6	14
499	Genome reconstruction in Cynara cardunculus taxa gains access to chromosome-scale DNA variation. Scientific Reports, 2017, 7, 5617.	1.6	30
500	The yeast noncoding RNA interaction network. Rna, 2017, 23, 1479-1492.	1.6	25
501	Mutation intolerant genes and targets of FMRP are enriched for nonsynonymous alleles in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 724-731.	1.1	19
502	Using the hierarchy of biological ontologies to identify mechanisms in flat networks. Biology and Philosophy, 2017, 32, 627-649.	0.7	9
503	Proteomic analysis of the secretome of human bone marrow-derived mesenchymal stem cells primed by pro-inflammatory cytokines. Journal of Proteomics, 2017, 166, 115-126.	1.2	80
504	Activating transcription factor 3 promotes loss of the acinar cell phenotype in response to cerulein-induced pancreatitis in mice. Molecular Biology of the Cell, 2017, 28, 2347-2359.	0.9	21
505	Screening disrupted molecular functions and pathways associated with clear cell renal cell carcinoma using Gibbs sampling. Computational Biology and Chemistry, 2017, 70, 15-20.	1.1	1
506	Microarray analysis reveals key genes and pathways in Tetralogy of Fallot. Molecular Medicine Reports, 2017, 16, 2707-2713.	1.1	1
507	Full Characterization of Localization Diversity in the Human Protein Interactome. Journal of Proteome Research, 2017, 16, 3019-3029.	1.8	22
508	Dynamic regulation of lysine acetylation: the balance between acetyltransferase and deacetylase activities. American Journal of Physiology - Renal Physiology, 2017, 313, F842-F846.	1.3	34
509	Energy metabolism and whole-exome sequencing-based analysis of Sasang constitution: a pilot study. Integrative Medicine Research, 2017, 6, 165-178.	0.7	4
511	Rapid evolution of female-biased genes among four species of <i>Anopheles</i> malaria mosquitoes. Genome Research, 2017, 27, 1536-1548.	2.4	60
512	Quantitative Temporal in Vivo Proteomics Deciphers the Transition of Virus-Driven Myeloid Cells into M2 Macrophages. Journal of Proteome Research, 2017, 16, 3391-3406.	1.8	15

#	Article	IF	CITATIONS
513	DES-TOMATO: A Knowledge Exploration System Focused On Tomato Species. Scientific Reports, 2017, 7, 5968.	1.6	8
514	Active nuclear transcriptome analysis reveals inflammasome-dependent mechanism for early neutrophil response to Mycobacterium marinum. Scientific Reports, 2017, 7, 6505.	1.6	26
515	High-Coverage Whole-Exome Sequencing Identifies Candidate Genes for Suicide in Victims with Major Depressive Disorder. Scientific Reports, 2017, 7, 7106.	1.6	56
516	Ensembl core software resources: storage and programmatic access for DNA sequence and genome annotation. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	56
517	Strategies and tools to improve crop productivity by targeting photosynthesis. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160377.	1.8	19
518	Bioinformatics Resources for Interpreting Proteomics Mass Spectrometry Data. Methods in Molecular Biology, 2017, 1647, 267-295.	0.4	1
519	PlantExpress: A Database Integrating OryzaExpress and ArthaExpress for Single-species and Cross-species Gene Expression Network Analyses with Microarray-Based Transcriptome Data. Plant and Cell Physiology, 2017, 58, e1-e1.	1.5	23
520	Inhibition of β-Catenin Signaling in the Skin Rescues Cutaneous Adipogenesis in Systemic Sclerosis: A Randomized, Double-Blind, Placebo-Controlled Trial of C-82. Journal of Investigative Dermatology, 2017, 137, 2473-2483.	0.3	43
521	Complete Genome Sequence of Achromobacter denitrificans PR1. Genome Announcements, 2017, 5, .	0.8	12
522	Integrative gene network analysis identifies key signatures, intrinsic networks and host factors for influenza virus A infections. Npj Systems Biology and Applications, 2017, 3, 35.	1.4	11
523	MPK1/SLT2 Links Multiple Stress Responses with Gene Expression in Budding Yeast by Phosphorylating Tyr1 of the RNAP II CTD. Molecular Cell, 2017, 68, 913-925.e3.	4.5	32
524	Transcriptomics reveal an integrative role for maternal thyroid hormones during zebrafish embryogenesis. Scientific Reports, 2017, 7, 16657.	1.6	14
525	Exome array analysis identifies GPR35 as a novel susceptibility gene for anthracycline-induced cardiotoxicity in childhood cancer. Pharmacogenetics and Genomics, 2017, 27, 445-453.	0.7	22
526	Leveraging Stacked Denoising Autoencoder in Prediction of Pathogen-Host Protein-Protein Interactions. , 2017, , .		9
527	Novel Common Variants Associated with Obesity and Type 2 Diabetes Detected Using a cFDR Method. Scientific Reports, 2017, 7, 16397.	1.6	11
528	From the research laboratory to the database: the <i>Caenorhabditis elegans</i> kinome in UniProtKB. Biochemical Journal, 2017, 474, 493-515.	1.7	9
529	Analysis of gene expression profiling variations induced by hsa-miR-145-5p-overexpression in laryngeal squamous cell carcinoma cell line Tu-177. Molecular Medicine Reports, 2017, 16, 5863-5870.	1.1	7
530	GRAFENE: Graphlet-based alignment-free network approach integrates 3D structural and sequence (residue order) data to improve protein structural comparison. Scientific Reports, 2017, 7, 14890.	1.6	21

#	Article	IF	CITATIONS
531	Quantitative chemoproteomic profiling reveals multiple target interactions of spongiolactone derivatives in leukemia cells. Chemical Communications, 2017, 53, 12818-12821.	2.2	10
532	Genomic history of the seventh pandemic of cholera in Africa. Science, 2017, 358, 785-789.	6.0	255
533	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature Genetics, 2017, 49, 1231-1238.	9.4	216
534	Time-matched analysis of DNA adduct formation and early gene expression as predictive tool for renal carcinogenesis in methylazoxymethanol acetate treated Eker rats. Archives of Toxicology, 2017, 91, 3427-3438.	1.9	8
535	Assessing glycolytic flux alterations resulting from genetic perturbations in E. coli using a biosensor. Metabolic Engineering, 2017, 42, 194-202.	3.6	22
536	Systematic discovery of novel eukaryotic transcriptional regulators using sequence homology independent prediction. BMC Genomics, 2017, 18, 480.	1.2	12
537	Scalable FRaC Variants: Anomaly Detection for Precision Medicine. , 2017, , .		0
538	Reactome enhanced pathway visualization. Bioinformatics, 2017, 33, 3461-3467.	1.8	140
539	Best Practices in Manual Annotation with the Gene Ontology. Methods in Molecular Biology, 2017, 1446, 41-54.	0.4	21
540	How Does the Scientific Community Contribute to Gene Ontology?. Methods in Molecular Biology, 2017, 1446, 85-93.	0.4	9
541	Dynamic changes in murine forebrain miR-211 expression associate with cholinergic imbalances and epileptiform activity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4996-E5005.	3.3	45
542	DIGNiFI: Discovering causative genes for orphan diseases using protein-protein interaction networks. BMC Systems Biology, 2017, 11, 23.	3.0	12
543	SEQUOIA: significance enhanced network querying through context-sensitive random walk and minimization of network conductance. BMC Systems Biology, 2017, 11, 20.	3.0	6
544	Ontological interpretation of biomedical database content. Journal of Biomedical Semantics, 2017, 8, 24.	0.9	7
545	Two-way learning with one-way supervision for gene expression data. BMC Bioinformatics, 2017, 18, 150.	1.2	2
546	QueryOR: a comprehensive web platform for genetic variant analysis and prioritization. BMC Bioinformatics, 2017, 18, 225.	1.2	20
547	WebGIVI: a web-based gene enrichment analysis and visualization tool. BMC Bioinformatics, 2017, 18, 237.	1.2	12
548	A machine learning classifier trained on cancer transcriptomes detects NF1 inactivation signal in glioblastoma. BMC Genomics, 2017, 18, 127.	1.2	30

#	Article	IF	CITATIONS
549	Genomic adaptation to agricultural environments: cabbage white butterflies (Pieris rapae) as a case study. BMC Genomics, 2017, 18, 412.	1.2	13
550	Comparative analysis of the root transcriptomes of cultivated sweetpotato (Ipomoea batatas [L.] Lam) and its wild ancestor (Ipomoea trifida [Kunth] G. Don). BMC Plant Biology, 2017, 17, 9.	1.6	50
551	CottonFGD: an integrated functional genomics database for cotton. BMC Plant Biology, 2017, 17, 101.	1.6	271
552	Prior knowledge guided active modules identification: an integrated multi-objective approach. BMC Systems Biology, 2017, 11, 8.	3.0	14
553	An additional k-means clustering step improves the biological features of WGCNA gene co-expression networks. BMC Systems Biology, 2017, 11, 47.	3.0	253
554	N-of-1-pathways MixEnrich: advancing precision medicine via single-subject analysis in discovering dynamic changes of transcriptomes. BMC Medical Genomics, 2017, 10, 27.	0.7	29
555	Transcriptome modulation by hydrocortisone in severe burn shock: ancillary analysis of a prospective randomized trial. Critical Care, 2017, 21, 158.	2.5	17
556	GLADIATOR: a global approach for elucidating disease modules. Genome Medicine, 2017, 9, 48.	3.6	23
557	Toward a comprehensive drug ontology: extraction of drug-indication relations from diverse information sources. Journal of Biomedical Semantics, 2017, 8, 2.	0.9	24
558	Therapeutic indications and other use-case-driven updates in the drug ontology: anti-malarials, anti-hypertensives, opioid analgesics, and a large term request. Journal of Biomedical Semantics, 2017, 8, 10.	0.9	14
559	Proteome-pl: proteome isoelectric point database. Nucleic Acids Research, 2017, 45, D1112-D1116.	6.5	209
560	mirDNMR: a gene-centered database of background <i>de novo</i> mutation rates in human. Nucleic Acids Research, 2017, 45, D796-D803.	6.5	33
561	Plant Reactome: a resource for plant pathways and comparative analysis. Nucleic Acids Research, 2017, 45, D1029-D1039.	6.5	95
562	The Gene Ontology Handbook. Methods in Molecular Biology, 2017, , .	0.4	63
563	Proteomic Analysis, Immune Dysregulation, and Pathway Interconnections with Obesity. Journal of Proteome Research, 2017, 16, 274-287.	1.8	8
564	Name-calling in the hippocampus (and beyond): coming to terms with neuron types and properties. Brain Informatics, 2017, 4, 1-12.	1.8	31
565	Primer on the Gene Ontology. Methods in Molecular Biology, 2017, 1446, 25-37.	0.4	63
566	Behavior change interventions: the potential of ontologies for advancing science and practice. Journal of Behavioral Medicine, 2017, 40, 6-22.	1.1	135

#	Article	IF	CITATIONS
567	Identification of key genes involved in nasopharyngeal carcinoma. Brazilian Journal of Otorhinolaryngology, 2017, 83, 670-676.	0.4	13
568	ccNET: Database of co-expression networks with functional modules for diploid and polyploid <i>Gossypium</i> . Nucleic Acids Research, 2017, 45, D1090-D1099.	6.5	89
569	Immunoproteomic analysis of house dust mite antigens reveals distinct classes of dominant T cell antigens according to function and serological reactivity. Clinical and Experimental Allergy, 2017, 47, 577-592.	1.4	26
570	COEXPEDIA: exploring biomedical hypotheses via co-expressions associated with medical subject headings (MeSH). Nucleic Acids Research, 2017, 45, D389-D396.	6.5	84
571	Proteomics of human mitochondria. Mitochondrion, 2017, 33, 2-14.	1.6	44
572	The genome of Onchocerca volvulus, agent of river blindness. Nature Microbiology, 2017, 2, 16216.	5.9	107
573	SoyNet: a database of co-functional networks for soybeanGlycine max. Nucleic Acids Research, 2017, 45, D1082-D1089.	6.5	56
574	T <scp>ranslational</scp> A <scp>dvances</scp> <scp>in</scp> <scp>the</scp> F <scp>ield</scp> <scp>of</scp> P <scp>ulmonary</scp> H <scp>ypertension</scp> .Translating MicroRNA Biology in Pulmonary Hypertension. It Will Take More Than "miR―Words. American Journal of Respiratory and Critical Care Medicine. 2017. 195. 167-178.	2.5	70
575	The PathoYeastract database: an information system for the analysis of gene and genomic transcription regulation in pathogenic yeasts. Nucleic Acids Research, 2017, 45, D597-D603.	6.5	35
576	BiRWLGO: A global network-based strategy for IncRNA function annotation using bi-random walk. , 2017, , .		3
577	Mining cross-ontology weighted association rules between GO and HPO. , 2017, , .		0
578	Associating Genomics and Clinical Information by Means of Semantic Based Ranking. , 2017, , .		0
579	Decellularization and Solubilization of Porcine Liver for Use as a Substrate for Porcine Hepatocyte Culture. Cell Transplantation, 2017, 26, 1840-1854.	1.2	69
580	A flexible ontology for inference of emergent whole cell function from relationships between subcellular processes. Scientific Reports, 2017, 7, 17689.	1.6	25
581	Phosphoproteomics of cAMP signaling of Bordetella adenylate cyclase toxin in mouse dendritic cells. Scientific Reports, 2017, 7, 16298.	1.6	7
582	Conserved Transcription Factors Steer Growth-Related Genomic Programs in Daphnia. Genome Biology and Evolution, 2017, 9, 1821-1842.	1.1	13
583	Modulation of nonsense mediated decay by rapamycin. Nucleic Acids Research, 2017, 45, 3448-3459.	6.5	26
584	Monitoring of the spatial and temporal dynamics of BER/SSBR pathway proteins, including MYH, UNG2, MPG, NTH1 and NEIL1-3, during DNA replication. Nucleic Acids Research, 2017, 45, 8291-8301.	6.5	25

#	Article	IF	CITATIONS
585	Creating a Structured Adverse Outcome Pathway Knowledgebase via Ontology-Based Annotations. Applied in Vitro Toxicology, 2017, 3, 298-311.	0.6	49
586	Cell Cycle Model System for Advancing Cancer Biomarker Research. Scientific Reports, 2017, 7, 17989.	1.6	7
587	Subchronic olanzapine exposure leads to increased expression of myelination-related genes in rat fronto-medial cortex. Translational Psychiatry, 2017, 7, 1262.	2.4	16
588	CUFID-query: accurate network querying through random walk based network flow estimation. BMC Bioinformatics, 2017, 18, 500.	1.2	1
589	Sex differences in microRNA-mRNA networks: examination of novel epigenetic programming mechanisms in the sexually dimorphic neonatal hypothalamus. Biology of Sex Differences, 2017, 8, 27.	1.8	27
590	Collaborative data analytics towards prediction on pathogen-host protein-protein interactions. , 2017, , .		2
591	Epistasis analysis of microRNAs on pathological stages in colon cancer based on anÂEmpirical Bayesian Elastic Net method. BMC Genomics, 2017, 18, 756.	1.2	4
592	Exploring digenic inheritance in arrhythmogenic cardiomyopathy. BMC Medical Genetics, 2017, 18, 145.	2.1	14
593	Identification and analysis of key genes in osteosarcoma using bioinformatics. Oncology Letters, 2018, 15, 2789-2794.	0.8	29
594	Combining ATAC-seq with nuclei sorting for discovery of cis-regulatory regions in plant genomes. Nucleic Acids Research, 2017, 45, e41-e41.	6.5	231
595	A molecular signature of lung cancer: potential biomarkers for adenocarcinoma and squamous cell carcinoma. Oncotarget, 2017, 8, 105492-105509.	0.8	23
596	Molecular architecture underlying fluid absorption by the developing inner ear. ELife, 2017, 6, .	2.8	43
597	Wegweiser durch den Allergendschungel: Allergendatenbanken, ihre Merkmale und Anwendungsgebiete. Karger Kompass Pneumologie, 2017, 5, 138-148.	0.0	0
598	Evaluating the contributions of GO term properties to semantic similarity measurement. International Journal of Data Mining and Bioinformatics, 2017, 18, 240.	0.1	0
599	Histological and transcriptomic effects of 17α-methyltestosterone on zebrafish gonad development. BMC Genomics, 2017, 18, 557.	1.2	52
600	Update on 13 Syndromes Affecting Craniofacial and Dental Structures. Frontiers in Physiology, 2017, 8, 1038.	1.3	32
601	Development of an Efficient Protein Extraction Method Compatible with LC-MS/MS for Proteome Mapping in Two Australian Seagrasses Zostera muelleri and Posidonia australis. Frontiers in Plant Science, 2017, 8, 1416.	1.7	20
602	eQTLs Regulating Transcript Variations Associated with Rapid Internode Elongation in Deepwater Rice. Frontiers in Plant Science, 2017, 8, 1753.	1.7	29

#	Article	IF	CITATIONS
603	The Functional Genetics of Handedness and Language Lateralization: Insights from Gene Ontology, Pathway and Disease Association Analyses. Frontiers in Psychology, 2017, 8, 1144.	1.1	28
604	iTRAQ-based Proteomic Analysis of APPSw,Ind Mice Provides Insights into the Early Changes in Alzheimer's Disease. Current Alzheimer Research, 2017, 14, 1109-1122.	0.7	8
605	Ancient human miRNAs are more likely to have broad functions and disease associations than young miRNAs. BMC Genomics, 2017, 18, 672.	1.2	11
606	Identification of epigenetically altered genes and potential gene targets in melanoma using bioinformatic methods. OncoTargets and Therapy, 2018, Volume 11, 9-15.	1.0	5
608	Detecting Disease Specific Pathway Substructures through an Integrated Systems Biology Approach. Non-coding RNA, 2017, 3, 20.	1.3	25
609	Exploring Wound-Healing Genomic Machinery with a Network-Based Approach. Pharmaceuticals, 2017, 10, 55.	1.7	6
610	The human cytoplasmic dynein interactome reveals novel activators of motility. ELife, 2017, 6, .	2.8	120
611	Integrative Bioinformatic Analysis of Transcriptomic Data Identifies Conserved Molecular Pathways Underlying Ionizing Radiation-Induced Bystander Effects (RIBE). Cancers, 2017, 9, 160.	1.7	5
612	Saliva as a Blood Alternative for Genome-Wide DNA Methylation Profiling by Methylated DNA Immunoprecipitation (MeDIP) Sequencing. Epigenomes, 2017, 1, 14.	0.8	8
613	Identification of Key Candidate Genes and Pathways in Colorectal Cancer by Integrated Bioinformatical Analysis. International Journal of Molecular Sciences, 2017, 18, 722.	1.8	132
614	Inferring Genes and Biological Functions That Are Sensitive to the Severity of Toxicity Symptoms. International Journal of Molecular Sciences, 2017, 18, 755.	1.8	2
615	Identifying and Analyzing Novel Epilepsy-Related Genes Using Random Walk with Restart Algorithm. BioMed Research International, 2017, 2017, 1-13.	0.9	19
616	Comparative Pan-Genome Analysis of Piscirickettsia salmonis Reveals Genomic Divergences within Genogroups. Frontiers in Cellular and Infection Microbiology, 2017, 7, 459.	1.8	52
617	A Preliminary List of Horizontally Transferred Genes in Prokaryotes Determined by Tree Reconstruction and Reconciliation. Frontiers in Genetics, 2017, 8, 112.	1.1	11
618	A Poly(Lactic-co-Glycolic) Acid Nanovaccine Based on Chimeric Peptides from Different Leishmania infantum Proteins Induces Dendritic Cells Maturation and Promotes Peptide-Specific IFNÎ <sup>3</sup> -Producing CD8+ T Cells Essential for the Protection against Experimental Visceral Leishmaniasis. Frontiers in Immunology, 2017, 8, 684.	2.2	58
619	Identification of New Features from Known Bacterial Protective Vaccine Antigens Enhances Rational Vaccine Design. Frontiers in Immunology, 2017, 8, 1382.	2.2	25
620	Comparative Genomics Analysis of a New Exiguobacterium Strain from Salar de Huasco Reveals a Repertoire of Stress-Related Genes and Arsenic Resistance. Frontiers in Microbiology, 2017, 8, 456.	1.5	55
621	Bacterial colonization stimulates a complex physiological response in the immature human intestinal epithelium. ELife, 2017, 6, .	2.8	132

#	Article	IF	CITATIONS
622	Molecular Genetic Analysis of Human Endometrial Mesenchymal Stem Cells That Survived Sublethal Heat Shock. Stem Cells International, 2017, 2017, 1-14.	1.2	10
623	Fish Oil Feeding Modulates the Expression of Hepatic MicroRNAs in a Western-Style Diet-Induced Nonalcoholic Fatty Liver Disease Rat Model. BioMed Research International, 2017, 2017, 1-11.	0.9	16
624	Proteomics in non-human primates: utilizing RNA-Seq data to improve protein identification by mass spectrometry in vervet monkeys. BMC Genomics, 2017, 18, 877.	1.2	17
625	Bridging Chromosomal Architecture and Pathophysiology of Streptococcus pneumoniae. Genome Biology and Evolution, 2017, 9, 350-361.	1.1	9
626	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. Molecular Medicine Reports, 2017, 15, 3231-3238.	1.1	27
627	Assisted clustering of gene expression data using ANCut. BMC Genomics, 2017, 18, 623.	1.2	10
628	Specific MicroRNA Pattern in Colon Tissue of Young Children with Eosinophilic Colitis. International Journal of Molecular Sciences, 2017, 18, 1050.	1.8	2
629	Transcriptome and proteome responses in RNAlater preserved tissue of Arabidopsis thaliana. PLoS ONE, 2017, 12, e0175943.	1.1	38
630	A new two-stage method for revealing missing parts of edges in protein-protein interaction networks. PLoS ONE, 2017, 12, e0177029.	1.1	1
631	A network-based method using a random walk with restart algorithm and screening tests to identify novel genes associated with Menière's disease. PLoS ONE, 2017, 12, e0182592.	1.1	41
632	Transcriptomic profiling in muscle and adipose tissue identifies genes related to growth and lipid deposition. PLoS ONE, 2017, 12, e0184120.	1.1	25
633	Prediction and analysis of essential genes using the enrichments of gene ontology and KEGG pathways. PLoS ONE, 2017, 12, e0184129.	1.1	202
634	Chronic obstructive pulmonary disease candidate gene prioritization based on metabolic networks and functional information. PLoS ONE, 2017, 12, e0184299.	1.1	6
635	Mapping the STK4/Hippo signaling network in prostate cancer cell. PLoS ONE, 2017, 12, e0184590.	1.1	22
636	Relating protein functional diversity to cell type number identifies genes that determine dynamic aspects of chromatin organisation as potential contributors to organismal complexity. PLoS ONE, 2017, 12, e0185409.	1.1	4
637	Loci and pathways associated with uterine capacity for pregnancy and fertility in beef cattle. PLoS ONE, 2017, 12, e0188997.	1.1	46
638	Resolving host–pathogen interactions by dual RNA-seq. PLoS Pathogens, 2017, 13, e1006033.	2.1	245
639	The integrative omics of white-rot fungus Pycnoporus coccineus reveals co-regulated CAZymes for orchestrated lignocellulose breakdown. PLoS ONE, 2017, 12, e0175528.	1.1	64

#	Article	IF	CITATIONS
640	Detecting similar binding pockets to enable systems polypharmacology. PLoS Computational Biology, 2017, 13, e1005522.	1.5	35
641	Fast and general tests of genetic interaction for genome-wide association studies. PLoS Computational Biology, 2017, 13, e1005556.	1.5	1
642	A composite network of conserved and tissue specific gene interactions reveals possible genetic interactions in glioma. PLoS Computational Biology, 2017, 13, e1005739.	1.5	15
643	TrypsNetDB: An integrated framework for the functional characterization of trypanosomatid proteins. PLoS Neglected Tropical Diseases, 2017, 11, e0005368.	1.3	15
644	Vulvar squamous cell carcinoma aggressiveness is associated with differential expression of collagen and STAT1. Clinical Proteomics, 2017, 14, 40.	1.1	2
645	Guanylate-binding protein-1 is a potential new therapeutic target for triple-negative breast cancer. BMC Cancer, 2017, 17, 727.	1.1	34
646	RNA sequencing identifies novel non-coding RNA and exon-specific effects associated with cigarette smoking. BMC Medical Genomics, 2017, 10, 58.	0.7	48
647	Integrated network analysis to explore the key genes regulated by parathyroid hormone receptor 1 in osteosarcoma. World Journal of Surgical Oncology, 2017, 15, 177.	0.8	10
648	Metabolic responses to ethanol and butanol in Chlamydomonas reinhardtii. Biotechnology for Biofuels, 2017, 10, 239.	6.2	9
649	Granatum: a graphical single-cell RNA-Seq analysis pipeline for genomics scientists. Genome Medicine, 2017, 9, 108.	3.6	63
650	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. Genome Medicine, 2017, 9, 114.	3.6	86
651	Epigenome-wide association study of asthma and wheeze in childhood and adolescence. Clinical Epigenetics, 2017, 9, 112.	1.8	60
652	The bacterial interlocked process ONtology (BiPON): a systemic multi-scale unified representation of biological processes in prokaryotes. Journal of Biomedical Semantics, 2017, 8, 53.	0.9	5
653	The Gene Ontology of eukaryotic cilia and flagella. Cilia, 2017, 6, 10.	1.8	6
654	A rapid and accurate approach for prediction of interactomes from co-elution data (PrInCE). BMC Bioinformatics, 2017, 18, 457.	1.2	54
655	ADAGE signature analysis: differential expression analysis with data-defined gene sets. BMC Bioinformatics, 2017, 18, 512.	1.2	17
656	Identifying term relations cross different gene ontology categories. BMC Bioinformatics, 2017, 18, 573.	1.2	46
657	Semantic biclustering for finding local, interpretable and predictive expression patterns. BMC Genomics, 2017, 18, 752.	1.2	3

# 658	ARTICLE FNSemSim: An improved disease similarity method based on network fusion. , 2017, , .	IF	CITATIONS 8
659	O rpheus DB. Proceedings of the VLDB Endowment, 2017, 10, 1130-1141.	2.1	24
660	GOstruct 2.0. , 2017, , .		8
661	Cell-surface marker discovery for lung cancer. Oncotarget, 2017, 8, 113373-113402.	0.8	36
662	Epigenetic mechanisms underlying maternal diabetes-associated risk of congenital heart disease. JCI Insight, 2017, 2, .	2.3	59
663	Genome-wide DNA methylation analysis in permanent atrial fibrillation. Molecular Medicine Reports, 2017, 16, 5505-5514.	1.1	23
664	PCOSBase: a manually curated database of polycystic ovarian syndrome. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	10
665	Mouse Genome Database (MGD)-2017: community knowledge resource for the laboratory mouse. Nucleic Acids Research, 2017, 45, D723-D729.	6.5	255
666	Digoxin-induced anemia among patients with atrial fibrillation and heart failure: clinical data analysis and drug-gene interaction network. Oncotarget, 2017, 8, 57003-57011.	0.8	11
667	BRENDA in 2017: new perspectives and new tools in BRENDA. Nucleic Acids Research, 2017, 45, D380-D388.	6.5	251
668	The neXtProt knowledgebase on human proteins: 2017 update. Nucleic Acids Research, 2017, 45, D177-D182.	6.5	145
669	SUBA4: the interactive data analysis centre for Arabidopsis subcellular protein locations. Nucleic Acids Research, 2017, 45, D1064-D1074.	6.5	390
670	Exploring biomedical ontology mappings with graph theory methods. PeerJ, 2017, 5, e2990.	0.9	2
671	Exploring targeted therapy of osteosarcoma using proteomics data. OncoTargets and Therapy, 2017, Volume 10, 565-577.	1.0	22
672	Identification of Proteases and Protease Inhibitors in Allergenic and Non-Allergenic Pollen. International Journal of Molecular Sciences, 2017, 18, 1199.	1.8	19
673	Alga-PrAS (Algal Protein Annotation Suite): A Database of Comprehensive Annotation in Algal Proteomes. Plant and Cell Physiology, 2017, 58, pcw212.	1.5	11
674	cFLIP critically modulates apoptotic resistance in epithelial-to-mesenchymal transition. Oncotarget, 2017, 8, 101072-101086.	0.8	6
675	TcoF-DB v2: update of the database of human and mouse transcription co-factors and transcription factor interactions. Nucleic Acids Research, 2017, 45, D145-D150.	6.5	63

#	Article	IF	CITATIONS
676	CDCA2 promotes lung adenocarcinoma cell proliferation and predicts poor survival in lung adenocarcinoma patients. Oncotarget, 2017, 8, 19768-19779.	0.8	28
677	Know Me! Unraveling the Riddle of Calcific Aortic Valve Disease by Bioinformatics. Tohoku Journal of Experimental Medicine, 2017, 243, 255-261.	0.5	6
678	About miRNAs, miRNA seeds, target genes and target pathways. Oncotarget, 2017, 8, 107167-107175.	0.8	115
679	IAS: Interaction Specific GO Term Associations for Predicting Protein-Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1247-1258.	1.9	11
680	Exploring autophagy with Gene Ontology. Autophagy, 2018, 14, 419-436.	4.3	64
681	Gene expression in retinal ischemic post-conditioning. Graefe's Archive for Clinical and Experimental Ophthalmology, 2018, 256, 935-949.	1.0	8
682	Gene expression of indoor fungal communities under damp building conditions: Implications for human health. Indoor Air, 2018, 28, 548-558.	2.0	34
683	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. Scientific Reports, 2018, 8, 3434.	1.6	43
684	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. Nature Genetics, 2018, 50, 381-389.	9.4	1,332
685	Analysis of the miRNA–mRNA–IncRNA network in human estrogen receptor-positive and estrogen receptor-negative breast cancer based on TCGA data. Gene, 2018, 658, 28-35.	1.0	67
686	Prediction and characterization of human ageing-related proteins by using machine learning. Scientific Reports, 2018, 8, 4094.	1.6	44
687	A Novel Five-Node Feed-Forward Loop Unravels miRNA-Gene-TF Regulatory Relationships in Ischemic Stroke. Molecular Neurobiology, 2018, 55, 8251-8262.	1.9	12
688	PAGER 2.0: an update to the pathway, annotated-list and gene-signature electronic repository for Human Network Biology. Nucleic Acids Research, 2018, 46, D668-D676.	6.5	18
689	SECLAF: a webserver and deep neural network design tool for hierarchical biological sequence classification. Bioinformatics, 2018, 34, 2487-2489.	1.8	21
690	Gene expression models based on a reference laboratory strain are poor predictors of Mycobacterium tuberculosis complex transcriptional diversity. Scientific Reports, 2018, 8, 3813.	1.6	14
691	Interleukins and their signaling pathways in the Reactome biological pathway database. Journal of Allergy and Clinical Immunology, 2018, 141, 1411-1416.	1.5	11
692	Rfam 13.0: shifting to a genome-centric resource for non-coding RNA families. Nucleic Acids Research, 2018, 46, D335-D342.	6.5	819
693	Using deep learning to model the hierarchical structure and function of a cell. Nature Methods, 2018, 15, 290-298.	9.0	292

#	Article	IF	CITATIONS
694	Comparative transcriptome analysis to investigate the potential role of miRNAs in milk protein/fat quality. Scientific Reports, 2018, 8, 6250.	1.6	17
695	Multiple large-scale gene and genome duplications during the evolution of hexapods. Proceedings of the United States of America, 2018, 115, 4713-4718.	3.3	151
696	Menin regulates the serine biosynthetic pathway in Ewing sarcoma. Journal of Pathology, 2018, 245, 324-336.	2.1	35
697	Differential transcriptome analysis of zebrafish ( <i>Danio rerio</i> ) larvae challenged by <i>Vibrio parahaemolyticus</i> . Journal of Fish Diseases, 2018, 41, 1049-1062.	0.9	17
698	Cardiac recovery via extended cell-free delivery of extracellular vesicles secreted by cardiomyocytes derived from induced pluripotent stem cells. Nature Biomedical Engineering, 2018, 2, 293-303.	11.6	249
699	An epistatic effect of KRT25 on SP6 is involved in curly coat in horses. Scientific Reports, 2018, 8, 6374.	1.6	18
700	Functional characterization of transposon-tagged abiotic stress-responsive rice genes and their molecular polymorphisms among various stress-tolerant genotypes. Molecular Breeding, 2018, 38, 1.	1.0	0
701	A comparative analysis of rod bipolar cell transcriptomes identifies novel genes implicated in night vision. Scientific Reports, 2018, 8, 5506.	1.6	12
702	Developing reduced <scp>SNP</scp> assays from wholeâ€genome sequence data to estimate introgression in an organism with complex genetic patterns, the Iberian honeybee ( <i>Apis mellifera) Tj ETQq0 0</i>	0 ng:BT /Ov	ver <b>2</b> øck 10 Tf
703	Transcriptomics reveals a cross-modulatory effect between riboflavin and iron and outlines responses to riboflavin biosynthesis and uptake in Vibrio cholerae. Scientific Reports, 2018, 8, 3149.	1.6	17
704	WNT ligands control initiation and progression of human papillomavirus-driven squamous cell carcinoma. Oncogene, 2018, 37, 3753-3762.	2.6	24
705	Cri-du-Chat Syndrome interactome network: Correlating genotypic variations to associated phenotypes. Gene Reports, 2018, 11, 179-187.	0.4	2
706	Searching and Extracting Data from the EMBL-EBI Complex Portal. Methods in Molecular Biology, 2018, 1764, 377-390.	0.4	7
707	Baseline mRNA expression differs widely between common laboratory strains of zebrafish. Scientific Reports, 2018, 8, 4780.	1.6	18
708	Global and gene-specific DNA methylation effects of different asbestos fibres on human bronchial epithelial cells. Environment International, 2018, 115, 301-311.	4.8	10
709	Highly parallel genome variant engineering with CRISPR–Cas9. Nature Genetics, 2018, 50, 510-514.	9.4	73
710	The role of epistatic interactions underpinning resistance to parasitic <i>Varroa</i> mites in haploid honey bee ( <i>Apis mellifera</i> ) drones. Journal of Evolutionary Biology, 2018, 31, 801-809.	0.8	21
711	Open chromatin dynamics reveals stage-specific transcriptional networks in hiPSC-based neurodevelopmental model. Stem Cell Research, 2018, 29, 88-98.	0.3	18

#	Article	IF	CITATIONS
712	Crossâ€ŧalk between monocyte invasion and astrocyte proliferation regulates scarring in brain injury. EMBO Reports, 2018, 19, .	2.0	98
713	Comprehensive pathway analyses of schizophrenia risk loci point to dysfunctional postsynaptic signaling. Schizophrenia Research, 2018, 199, 195-202.	1.1	26
714	Molecular Correlates of In Vitro Responses to Dacomitinib and Afatinib in Bladder Cancer. Bladder Cancer, 2018, 4, 77-90.	0.2	19
715	araGWAB: Network-based boosting of genome-wide association studies in Arabidopsis thaliana. Scientific Reports, 2018, 8, 2925.	1.6	21
716	Linking dendroecology and association genetics in natural populations: Stress responses archived in tree rings associate with <scp>SNP</scp> genotypes in silver fir ( <i>Abies alba</i> Mill.). Molecular Ecology, 2018, 27, 1428-1438.	2.0	56
717	Statistical approach for selection of biologically informative genes. Gene, 2018, 655, 71-83.	1.0	12
718	AOP-DB: A database resource for the exploration of Adverse Outcome Pathways through integrated association networks. Toxicology and Applied Pharmacology, 2018, 343, 71-83.	1.3	59
719	A community approach to mortality prediction in sepsis via gene expression analysis. Nature Communications, 2018, 9, 694.	5.8	178
720	FGF2 and FAM201A affect the development of osteonecrosis of the femoral head after femoral neck fracture. Gene, 2018, 652, 39-47.	1.0	31
721	DNA methylation profiling in nonfunctioning pituitary adenomas. Molecular and Cellular Endocrinology, 2018, 473, 194-204.	1.6	34
722	Systematic Gene-to-Phenotype Arrays: A High-Throughput Technique for Molecular Phenotyping. Molecular Cell, 2018, 69, 321-333.e3.	4.5	7
723	DIBS: a repository of disordered binding sites mediating interactions with ordered proteins. Bioinformatics, 2018, 34, 535-537.	1.8	72
724	Genomic resequencing combined with quantitative proteomic analyses elucidate the survival mechanisms of Lactobacillus plantarum P-8 in a long-term glucose-limited experiment. Journal of Proteomics, 2018, 176, 37-45.	1.2	9
726	Integrative Genomic and Proteomic Analysis of the Response ofLactobacillus caseiZhang to Glucose Restriction. Journal of Proteome Research, 2018, 17, 1290-1299.	1.8	5
727	Toward Dynamic Resources Management for IoT-Based Manufacturing. , 2018, 56, 52-59.		132
728	Diverse Regulators of Human Ribosome Biogenesis Discovered by Changes in Nucleolar Number. Cell Reports, 2018, 22, 1923-1934.	2.9	92
729	Approaches to target tractability assessment – a practical perspective. MedChemComm, 2018, 9, 606-613.	3.5	50
730	Revealing the action mechanisms of dexamethasone on the birth weight of infant using RNA-sequencing data of trophoblast cells. Medicine (United States), 2018, 97, e9653.	0.4	2

#	Article	IF	CITATIONS
731	Ribosome Incorporation into Somatic Cells Promotes Lineage Transdifferentiation towards Multipotency. Scientific Reports, 2018, 8, 1634.	1.6	17
732	A novel approach for analysing evolutional motivation of empirical engineering knowledge. International Journal of Production Research, 2018, 56, 2897-2923.	4.9	21
733	miRâ€29 contributes to normal endothelial function and can restore it in cardiometabolic disorders. EMBO Molecular Medicine, 2018, 10, .	3.3	72
734	Identification of 22q13 genes most likely to contribute to Phelan McDermid syndrome. European Journal of Human Genetics, 2018, 26, 293-302.	1.4	54
735	Proteomic analysis reveals distinctive protein profiles involved in CD8+ T cell-mediated murine autoimmune cholangitis. Cellular and Molecular Immunology, 2018, 15, 756-767.	4.8	9
736	Enhancer redundancy provides phenotypic robustness in mammalian development. Nature, 2018, 554, 239-243.	13.7	514
737	Comparative Genomics Reveals Accelerated Evolution in Conserved Pathways during the Diversification of Anole Lizards. Genome Biology and Evolution, 2018, 10, 489-506.	1.1	43
738	DGIdb 3.0: a redesign and expansion of the drug–gene interaction database. Nucleic Acids Research, 2018, 46, D1068-D1073.	6.5	686
739	Polysome-profiling in small tissue samples. Nucleic Acids Research, 2018, 46, e3-e3.	6.5	53
740	Transcriptomic signatures of cellular and humoral immune responses in older adults after seasonal influenza vaccination identified by data-driven clustering. Scientific Reports, 2018, 8, 739.	1.6	34
741	Insights from Ion Binding Site Network Analysis into Evolution and Functions of Proteins. Molecular Informatics, 2018, 37, e1700144.	1.4	4
742	Atomic structures of low-complexity protein segments reveal kinked β sheets that assemble networks. Science, 2018, 359, 698-701.	6.0	376
743	Region-Specific Methylation Profiling in Acute Myeloid Leukemia. Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 33-42.	2.2	11
744	Genome-Wide Association Study in African Americans with Acute Respiratory Distress Syndrome Identifies the Selectin P Ligand Gene as a Risk Factor. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1421-1432.	2.5	50
745	Differential gene expression induced by anti-cancer agent plumbagin is mediated by androgen receptor in prostate cancer cells. Scientific Reports, 2018, 8, 2694.	1.6	20
746	A novel approach to wildlife transcriptomics provides evidence of diseaseâ€mediated differential expression and changes to the microbiome of amphibian populations. Molecular Ecology, 2018, 27, 1413-1427.	2.0	32
747	Comparative genomics reveals new single-nucleotide polymorphisms that can assist in identification of adherent-invasive Escherichia coli. Scientific Reports, 2018, 8, 2695.	1.6	46
748	Human Cervical Mucus Plugs Exhibit Insufficiencies in Antimicrobial Activity Towards Group B Streptococcus. Journal of Infectious Diseases, 2018, 217, 1626-1636.	1.9	19

		15	<u></u>
#	ARTICLE	IF	CITATIONS
749	Differential proteomic analysis of synovial fluid from hip arthroplasty patients with a pseudotumor vs. Periprosthetic osteolysis. Journal of Orthopaedic Research, 2018, 36, 1849-1859.	1.2	7
751	Identification of differential proteinâ€coding gene expressions in early phase lung adenocarcinoma. Thoracic Cancer, 2018, 9, 234-240.	0.8	4
752	Network-based method for mining novel HPV infection related genes using random walk with restart algorithm. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2376-2383.	1.8	31
753	Clinical and RNA expression integrated signature for urothelial bladder cancer prognosis. Cancer Biomarkers, 2018, 21, 535-546.	0.8	6
754	Identification of the functional alteration signatures across different cancer types with support vector machine and feature analysis. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2218-2227.	1.8	20
755	Benefit of Apabetalone on Plasma Proteins in Renal Disease. Kidney International Reports, 2018, 3, 711-721.	0.4	31
756	Women-specific risk factors for heart failure: A genetic approach. Maturitas, 2018, 109, 104-111.	1.0	10
757	EZH2 Represses the B Cell Transcriptional Program and Regulates Antibody-Secreting Cell Metabolism and Antibody Production. Journal of Immunology, 2018, 200, 1039-1052.	0.4	99
758	ATTED-II in 2018: A Plant Coexpression Database Based on Investigation of the Statistical Property of the Mutual Rank Index. Plant and Cell Physiology, 2018, 59, e3-e3.	1.5	235
759	Upregulation of CDCA5 promotes gastric cancer malignant progression via influencing cyclin E1. Biochemical and Biophysical Research Communications, 2018, 496, 482-489.	1.0	45
760	What do the genetic association data say about the high risk of suicide in people with depression? A novel network-based approach to find common molecular basis for depression and suicidal behavior and related therapeutic targets. Journal of Affective Disorders, 2018, 229, 463-468.	2.0	12
761	Large-scale aggregation analysis of eukaryotic proteins reveals an involvement of intrinsically disordered regions in protein folding. Scientific Reports, 2018, 8, 678.	1.6	26
762	Identification of genes related to proliferative diabetic retinopathy through RWR algorithm based on protein–protein interaction network. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2369-2375.	1.8	33
763	A network approach to exploring the functional basis of gene–gene epistatic interactions in disease susceptibility. Bioinformatics, 2018, 34, 1741-1749.	1.8	11
764	Rapid genome shrinkage in a self-fertile nematode reveals sperm competition proteins. Science, 2018, 359, 55-61.	6.0	102
765	A novel gene signature based on five glioblastoma stem-like cell relevant genes predicts the survival of primary glioblastoma. Journal of Cancer Research and Clinical Oncology, 2018, 144, 439-447.	1.2	36
766	FunGeneNet: a web tool to estimate enrichment of functional interactions in experimental gene sets. BMC Genomics, 2018, 19, 76.	1.2	7
767	Adaptations in energy metabolism and gene family expansions revealed by comparative transcriptomics of three Chagas disease triatomine vectors. BMC Genomics, 2018, 19, 296.	1.2	12

#	Article	IF	CITATIONS
768	Annotating activation/inhibition relationships to protein-protein interactions using gene ontology relations. BMC Systems Biology, 2018, 12, 9.	3.0	8
769	QSurface: fast identification of surface expression markers in cancers. BMC Systems Biology, 2018, 12, 17.	3.0	6
770	Epigenetic impacts of stress priming of the neuroinflammatory response to sarin surrogate in mice: a model of Gulf War illness. Journal of Neuroinflammation, 2018, 15, 86.	3.1	47
771	Gene-level differential analysis at transcript-level resolution. Genome Biology, 2018, 19, 53.	3.8	108
772	Sensing the cilium, digital capture of ciliary data for comparative genomics investigations. Cilia, 2018, 7, 3.	1.8	3
773	Differences in MWCNT- and SWCNT-induced DNA methylation alterations in association with the nuclear deposition. Particle and Fibre Toxicology, 2018, 15, 11.	2.8	57
774	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. Nucleic Acids Research, 2018, 46, D718-D725.	6.5	90
775	Knockout of the <i>Gsta4</i> Gene in Male Mice Leads to an Altered Pattern of Hepatic Protein Carbonylation and Enhanced Inflammation Following Chronic Consumption of an Ethanol Diet. Alcoholism: Clinical and Experimental Research, 2018, 42, 1192-1205.	1.4	10
776	Bioinformatics challenges and perspectives when studying the effect of epigenetic modifications on alternative splicing. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20170073.	1.8	13
777	Identification of diverse target RNAs that are functionally regulated by human Pumilio proteins. Nucleic Acids Research, 2018, 46, 362-386.	6.5	80
778	Germline pathogenic variants in PALB2 and other cancer-predisposing genes in families with hereditary diffuse gastric cancer without CDH1 mutation: a whole-exome sequencing study. The Lancet Gastroenterology and Hepatology, 2018, 3, 489-498.	3.7	87
779	A Strategy for Discovery of Endocrine Interactions with Application to Whole-Body Metabolism. Cell Metabolism, 2018, 27, 1138-1155.e6.	7.2	58
780	Genome-wide transcriptomic analysis of BR-deficient Micro-Tom reveals correlations between drought stress tolerance and brassinosteroid signaling in tomato. Plant Physiology and Biochemistry, 2018, 127, 553-560.	2.8	39
781	Functional and structural characterization of osteocytic MLO-Y4 cell proteins encoded by genes differentially expressed in response to mechanical signals in vitro. Scientific Reports, 2018, 8, 6716.	1.6	11
782	An Ontology of Psychological Barriers to Support Behaviour Change. , 2018, , .		6
783	Tumor-Independent Host Secretomes Induced By Angiogenesis and Immune-Checkpoint Inhibitors. Molecular Cancer Therapeutics, 2018, 17, 1602-1612.	1.9	6
785	Automated Computational Inference of Multi-protein Assemblies from Biochemical Co-purification Data. Methods in Molecular Biology, 2018, 1764, 391-399.	0.4	1
786	Identification of PP1–Gadd34 substrates involved in the unfolded protein response using K-BIPS, a method for phosphatase substrate identification. Molecular Omics, 2018, 14, 121-133.	1.4	11

#	Article	IF	CITATIONS
787	A comprehensive evaluation of module detection methods for gene expression data. Nature Communications, 2018, 9, 1090.	5.8	229
788	Systematic characterization of pan ancer mutation clusters. Molecular Systems Biology, 2018, 14, e7974.	3.2	39
789	Identification of IncRNAs by microarray analysis reveals the potential role of IncRNAs in cervical cancer pathogenesis. Oncology Letters, 2018, 15, 5584-5592.	0.8	18
790	Elucidating the Impact of CHO Cell Culture Media on Tryptophan Oxidation of a Monoclonal Antibody Through Gene Expression Analyses. Biotechnology Journal, 2018, 13, e1700254.	1.8	9
791	Disease genes prediction by HMM based PU-learning using gene expression profiles. Journal of Biomedical Informatics, 2018, 81, 102-111.	2.5	18
792	Systematic Characterization of Stress-Induced RNA Granulation. Molecular Cell, 2018, 70, 175-187.e8.	4.5	190
793	Evolutionary Interplay between Symbiotic Relationships and Patterns of Signal Peptide Gain and Loss. Genome Biology and Evolution, 2018, 10, 928-938.	1.1	9
794	An LaeA- and BrlA-Dependent Cellular Network Governs Tissue-Specific Secondary Metabolism in the Human Pathogen Aspergillus fumigatus. MSphere, 2018, 3, .	1.3	58
795	GENEASE: real time bioinformatics tool for multi-omics and disease ontology exploration, analysis and visualization. Bioinformatics, 2018, 34, 3160-3168.	1.8	13
796	PRR4: A novel downregulated gene in laryngeal cancer. Oncology Letters, 2018, 15, 4669-4675.	0.8	5
797	Exploring the oncoproteomic response of human prostate cancer to therapeutic radiation using dataâ€independent acquisition (DIA) mass spectrometry. Prostate, 2018, 78, 563-575.	1.2	23
798	Chromatin Immunoprecipitation Sequencing (ChIP-Seq) for Transcription Factors and Chromatin Factors in Arabidopsis thaliana Roots: From Material Collection to Data Analysis. Methods in Molecular Biology, 2018, 1761, 231-248.	0.4	11
799	Detecting Essential Proteins Based on Network Topology, Gene Expression Data, and Gene Ontology Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 109-116.	1.9	44
800	Regularized Non-Negative Matrix Factorization for Identifying Differentially Expressed Genes and Clustering Samples: A Survey. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 974-987.	1.9	52
801	How to use and integrate bioinformatics tools to compare proteomic data from distinct conditions? A tutorial using the pathological similarities between Aortic Valve Stenosis and Coronary Artery Disease as a case-study. Journal of Proteomics, 2018, 171, 37-52.	1.2	8
802	The benefits (and misfortunes) of SDS in top-down proteomics. Journal of Proteomics, 2018, 175, 75-86.	1.2	25
803	Transcriptional Changes in the Mouse Retina after Ocular Blast Injury: A Role for the Immune System. Journal of Neurotrauma, 2018, 35, 118-129.	1.7	26
804	DUSP1 and KCNJ2 mRNA upregulation can serve as a biomarker of mechanical asphyxia-induced death in cardiac tissue. International Journal of Legal Medicine, 2018, 132, 655-665.	1.2	10

		CITATION REP	ORT	
#	ARTICLE		IF	CITATIONS
805	Near perfect protein multi-label classification with deep neural networks. Methods, 201	8, 132, 50-56.	1.9	31
806	BioGrakn: A Knowledge Graph-Based Semantic Database for Biomedical Sciences. Advar Intelligent Systems and Computing, 2018, , 299-309.	nces in	0.5	13
807	BioPlex Display: An Interactive Suite for Large-Scale AP–MS Protein–Protein Interac of Proteome Research, 2018, 17, 722-726.	tion Data. Journal	1.8	59
808	Expanded and updated data and a query pipeline for iBeetle-Base. Nucleic Acids Researce D831-D835.	h, 2018, 46,	6.5	35
809	Microarray analysis to identify the similarities and differences of pathogenesis between occlusive disease and abdominal aortic aneurysm. Vascular, 2018, 26, 301-314.	aortic	0.4	6
810	Group spike-and-slab lasso generalized linear models for disease prediction and associat detection by incorporating pathway information. Bioinformatics, 2018, 34, 901-910.	ted genes	1.8	33
811	The Transcriptional Landscape of Radiation-Treated Human Prostate Cancer: Analysis of Tissue Cohort. International Journal of Radiation Oncology Biology Physics, 2018, 100,		0.4	24
812	Synaptic proteomics as a means to identify the molecular basis of mental illness: Are we there?. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2018, 84, 353		2.5	23
813	Deciphering the electric code of Geobacter sulfurreducens in cocultures with Pseudomo aeruginosa via SWATH-MS proteomics. Bioelectrochemistry, 2018, 119, 150-160.	onas	2.4	24
814	A proteomic portrait of dinoflagellate chromatin reveals abundant RNA-binding proteins Chromosoma, 2018, 127, 29-43.		1.0	13
815	Systematic-analysis of mRNA expression profiles in skeletal muscle of patients with type glucocorticoid was central in pathogenesis. Journal of Cellular Physiology, 2018, 233, 4		2.0	8
816	S-FLN: A sequence-based hierarchical approach for functional linkage network construct of Theoretical Biology, 2018, 437, 149-162.	tion. Journal	0.8	0
817	A Workflow Guide to RNA-seq Analysis of Chaperone Function and Beyond. Methods in Biology, 2018, 1709, 233-252.	Molecular	0.4	3
818	Post-translational regulation of metabolism in fumarate hydratase deficient cancer cells Engineering, 2018, 45, 149-157.	. Metabolic	3.6	27
819	Chemical reaction vector embeddings: towards predicting drug metabolism in the huma microbiome. , 2018, , .	an gut		12
820	Integrated analysis of motif activity and gene expression changes of transcription facto Research, 2018, 28, 243-255.	rs. Genome	2.4	58
821	Association of Rare Predicted Loss-of-Function Variants in Cellular Pathways with Sub-P Age-Related Macular Degeneration. Ophthalmology, 2018, 125, 398-406.	nenotypes in	2.5	12
822	Integration of ENCODE RNAseq and eCLIP Data Sets. Methods in Molecular Biology, 20	18, 1720, 111-129.	0.4	5

#	Article	IF	CITATIONS
824	MicroRNA dynamics at the onset of primordial germ and somatic cell sex differentiation during mouse embryonic gonad development. Rna, 2018, 24, 287-303.	1.6	32
825	Prediction of potential drivers connecting different dysfunctional levels in lung adenocarcinoma via a protein–protein interaction network. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2284-2293.	1.8	18
826	Expanding horizons: new roles for non-canonical RNA-binding proteins in cancer. Current Opinion in Genetics and Development, 2018, 48, 112-120.	1.5	58
827	Gene expression differs in codominant prairie grasses under drought. Molecular Ecology Resources, 2018, 18, 334-346.	2.2	6
828	Cln5 is secreted and functions as a glycoside hydrolase in Dictyostelium. Cellular Signalling, 2018, 42, 236-248.	1.7	45
829	Whole-Genome Characterization of Bacillus cereus Associated with Specific Disease Manifestations. Infection and Immunity, 2018, 86, .	1.0	11
830	A computational method using the random walk with restart algorithm for identifying novel epigenetic factors. Molecular Genetics and Genomics, 2018, 293, 293-301.	1.0	32
831	Identification of Mature Atherosclerotic Plaque Proteome Signatures Using Data-Independent Acquisition Mass Spectrometry. Journal of Proteome Research, 2018, 17, 164-176.	1.8	24
832	The axonal endoplasmic reticulum: One organelle—many functions in development, maintenance, and plasticity. Developmental Neurobiology, 2018, 78, 181-208.	1.5	44
833	Identification of a myofibroblast-specific expression signature in skin wounds. Matrix Biology, 2018, 65, 59-74.	1.5	57
834	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. Molecular Psychiatry, 2018, 23, 1169-1180.	4.1	32
835	Oxidative stress in female cancers. Oncotarget, 2018, 9, 23824-23842.	0.8	68
836	Making deep learning models transparent. Journal of Medical Artificial Intelligence, 2018, 1, 1-1.	1.1	2
837	TSGOE: A web tool for tissue-specific gene ontology enrichment. , 2018, , .		0
838	Optimizing gene set annotations combining GO structure and gene expression data. BMC Systems Biology, 2018, 12, 133.	3.0	0
839	Bioinformatics methodologies for coeliac disease and its comorbidities. Briefings in Bioinformatics, 2018, , .	3.2	6
840	Genomics of neonatal sepsis: has-miR-150 targeting BCL11B functions in disease progression. Italian Journal of Pediatrics, 2018, 44, 145.	1.0	18
842	HPO2GO: prediction of human phenotype ontology term associations for proteins using cross ontology annotation co-occurrences. PeerJ, 2018, 6, e5298.	0.9	27

#	Article	IF	CITATIONS
843	Networkâ€ʿbased gene function inference method to predict optimal gene functions associated with fetal growth restriction. Molecular Medicine Reports, 2018, 18, 3003-3010.	1.1	3
844	System analysis of the regulation of the immune response by CD147 and FOXC1 in cancer cell lines. Oncotarget, 2018, 9, 12918-12931.	0.8	8
846	Application of Biomedical Text Mining. , 0, , .		4
847	Reconstruction of avian ancestral karyotypes reveals differences in the evolutionary history of macro- and microchromosomes. Genome Biology, 2018, 19, 155.	3.8	44
848	Identification of critically carcinogenesis-related genes in basal cell carcinoma. OncoTargets and Therapy, 2018, Volume 11, 6957-6967.	1.0	7
849	Integrated Bioinformatics Analysis for Identificating the Therapeutic Targets of Aspirin in Small Cell Lung Cancer. Journal of Biomedical Informatics, 2018, 88, 20-28.	2.5	26
850	SWRL Reasoning Using Decision Tables. Lecture Notes in Computer Science, 2018, , 68-82.	1.0	0
851	funcExplorer: a tool for fast data-driven functional characterisation of high-throughput expression data. BMC Genomics, 2018, 19, 817.	1.2	5
852	Adipocyte-secreted BMP8b mediates adrenergic-induced remodeling of the neuro-vascular network in adipose tissue. Nature Communications, 2018, 9, 4974.	5.8	104
853	Identification of common coexpression modules based on quantitative network comparison. BMC Bioinformatics, 2018, 19, 213.	1.2	5
854	A new method for evaluating the impacts of semantic similarity measures on the annotation of gene sets. PLoS ONE, 2018, 13, e0208037.	1.1	3
855	Detection of correlated hidden factors from single cell transcriptomes using Iteratively Adjusted-SVA (IA-SVA). Scientific Reports, 2018, 8, 17040.	1.6	8
856	Dynamics of the Phanerochaete carnosa transcriptome during growth on aspen and spruce. BMC Genomics, 2018, 19, 815.	1.2	15
857	Lung fibroblasts express a miR-19a-19b-20a sub-cluster to suppress TGF-β-associated fibroblast activation in murine pulmonary fibrosis. Scientific Reports, 2018, 8, 16642.	1.6	22
858	Born to Cry: A Genetic Dissection of Infant Vocalization. Frontiers in Behavioral Neuroscience, 2018, 12, 250.	1.0	24
859	Arabidopsis thaliana responds to colonisation of Piriformospora indica by secretion of symbiosis-specific proteins. PLoS ONE, 2018, 13, e0209658.	1.1	17
860	Genome survey sequencing for the characterization of genetic background of Dracaena cambodiana and its defense response during dragon's blood formation. PLoS ONE, 2018, 13, e0209258.	1.1	16
861	Sex-Specific Transcriptome Differences in Substantia Nigra Tissue: A Meta-Analysis of Parkinson's Disease Data. Genes, 2018, 9, 275.	1.0	16

	CHAI	ION REPORT	
#	Article	IF	CITATIONS
862	FELLA: an R package to enrich metabolomics data. BMC Bioinformatics, 2018, 19, 538.	1.2	61
863	Bone Marrow–Derived Proangiogenic Cells Mediate Pulmonary Arteriole Stiffening via Serotonin 2B Receptor Dependent Mechanism. Circulation Research, 2018, 123, e51-e64.	2.0	17
864	Comprehensive Analysis of <i>BAP1</i> Somatic Mutation in Clear Cell Renal Cell Carcinoma to Explore Potential Mechanisms <i>in Silico</i> . Journal of Cancer, 2018, 9, 4108-4116.	1.2	17
865	Selective expansion of myeloid and NK cells in humanized mice yields human-like vaccine responses. Nature Communications, 2018, 9, 5031.	5.8	39
866	Comparative Proteomic Analysis. , 2018, , .		2
867	BioGraph: a web application and a graph database for querying and analyzing bioinformatics resources. BMC Systems Biology, 2018, 12, 98.	3.0	28
868	Prediction of gene regulatory enhancers across species reveals evolutionarily conserved sequence properties. PLoS Computational Biology, 2018, 14, e1006484.	1.5	71
869	Fenretinide targeting of human colon cancer sphere cells through cell cycle regulation and stress‑responsive activities. Oncology Letters, 2018, 16, 5339-5348.	0.8	3
870	Identification of Moonlighting Proteins in Genomes Using Text Mining Techniques. Proteomics, 2018, 18, 1800083.	1.3	6
871	The FAK inhibitor BI 853520 exerts anti-tumor effects in breast cancer. Oncogenesis, 2018, 7, 73.	2.1	63
872	Analysis of porcine body size variation using re-sequencing data of miniature and large pigs. BMC Genomics, 2018, 19, 687.	1.2	12
873	Identification of <scp>tRNA</scp> â€derived small noncoding <scp>RNA</scp> s as potential biomarkers for prediction of recurrence in tripleâ€negative breast cancer. Cancer Medicine, 2018, 7, 5130-5144.	1.3	28
874	Conditional and interaction gene-set analysis reveals novel functional pathways for blood pressure. Nature Communications, 2018, 9, 3768.	5.8	50
875	Comparative genomic analysis of the human and nematode <i>Caenorhabditis elegans</i> uncovers potential reproductive genes and disease associations in humans. Physiological Genomics, 2018, 50, 1002-1014.	1.0	21
876	Topological alternate centrality measure capturing drug targets in the network of MAPK pathways. IET Systems Biology, 2018, 12, 226-232.	0.8	1
877	Reprogramming of regulatory network using expression uncovers sex-specific gene regulation in Drosophila. Nature Communications, 2018, 9, 4061.	5.8	23
878	Neurogenetic profiles delineate large-scale connectivity dynamics of the human brain. Nature Communications, 2018, 9, 3876.	5.8	48
879	Improved ontology-based similarity calculations using a study-wise annotation model. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	11

#	Article	IF	CITATIONS
880	PalmXplore: oil palm gene database. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	19
881	Identification of key genes and long non‑coding RNAs in celecoxib‑treated lung squamous cell carcinoma cell line by RNA‑sequencing. Molecular Medicine Reports, 2018, 17, 6456-6464.	1.1	6
882	Artificial Intelligence for Cloud-Assisted Smart Factory. IEEE Access, 2018, 6, 55419-55430.	2.6	92
883	Single cell molecular alterations reveal target cells and pathways of concussive brain injury. Nature Communications, 2018, 9, 3894.	5.8	113
884	Classification, Ontology, and Precision Medicine. New England Journal of Medicine, 2018, 379, 1452-1462.	13.9	220
885	Computational Strategy to Predict Possible Protein Function Using an Evolutionary Algorithm Implement in SIFTER Tool. , 2018, , .		0
886	The biological embedding of early-life socioeconomic status and family adversity in children's genome-wide DNA methylation. Epigenomics, 2018, 10, 1445-1461.	1.0	92
887	Cytogenetic and Transcriptomic Analysis of Human Endometrial MSC Retaining Proliferative Activity after Sublethal Heat Shock. Cells, 2018, 7, 184.	1.8	10
888	Comparative Gene Expression Analysis in WM164 Melanoma Cells Revealed That Î <sup>2</sup> -Î <sup>2</sup> -Dimethylacrylshikonin Leads to ROS Generation, Loss of Mitochondrial Membrane Potential, and Autophagy Induction. Molecules, 2018, 23, 2823.	1.7	17
889	WEADE: A workflow for enrichment analysis and data exploration. PLoS ONE, 2018, 13, e0204016.	1.1	3
890	Host Proteins Identified in Extracellular Viral Particles as Targets for Broad-Spectrum Antiviral Inhibitors. Journal of Proteome Research, 2018, 18, 7-17.	1.8	7
891	Genome-scale analysis of <i>Acetobacterium bakii</i> reveals the cold adaptation of psychrotolerant acetogens by post-transcriptional regulation. Rna, 2018, 24, 1839-1855.	1.6	10
892	Overlapping Patterns of Gene Expression Between Gametophyte and Sporophyte Phases in the Fern Polypodium amorphum (Polypodiales). Frontiers in Plant Science, 2018, 9, 1450.	1.7	19
893	Studying how genetic variants affect mechanism in biological systems. Essays in Biochemistry, 2018, 62, 575-582.	2.1	0
894	Identifying the dynamic gene regulatory network during latent HIV-1 reactivation using high-dimensional ordinary differential equations. International Journal of Computational Biology and Drug Design, 2018, 11, 135.	0.3	1
895	Identification of key differentially expressed MicroRNAs in cancer patients through pan-cancer analysis. Computers in Biology and Medicine, 2018, 103, 183-197.	3.9	28
896	Species-level functional profiling of metagenomes and metatranscriptomes. Nature Methods, 2018, 15, 962-968.	9.0	1,125
897	Overlapping clustering of gene expression data using penalized weighted normalized cut. Genetic Epidemiology, 2018, 42, 796-811.	0.6	5

#	Article	IF	CITATIONS
898	Improving Interpretation of Cardiac Phenotypes and Enhancing Discovery With Expanded Knowledge in the Gene Ontology. Circulation Genomic and Precision Medicine, 2018, 11, e001813.	1.6	24
899	Predicting bioprocess targets of chemical compounds through integration of chemical-genetic and genetic interactions. PLoS Computational Biology, 2018, 14, e1006532.	1.5	13
900	Trendy: segmented regression analysis of expression dynamics in high-throughput ordered profiling experiments. BMC Bioinformatics, 2018, 19, 380.	1.2	24
901	The Future of Computational Chemogenomics. Methods in Molecular Biology, 2018, 1825, 425-450.	0.4	7
902	Clobal identification and characterization of IncRNAs that control inflammation in malignant cholangiocytes. BMC Genomics, 2018, 19, 735.	1.2	22
903	ADAM protein family – its role in tumorigenesis, mechanisms of chemoresistance and potential as diagnostic and prognostic factors. Neoplasma, 2018, 65, 823-839.	0.7	13
904	Unveiling gibberellin-responsive coding and long noncoding RNAs in maize. Plant Molecular Biology, 2018, 98, 427-438.	2.0	14
905	An integrative tissue-network approach to identify and test human disease genes. Nature Biotechnology, 2018, 36, 1091-1099.	9.4	54
906	Nuclear Factor I Represses the Notch Effector HEY1 in Glioblastoma. Neoplasia, 2018, 20, 1023-1037.	2.3	24
907	PGD: Pineapple Genomics Database. Horticulture Research, 2018, 5, 66.	2.9	25
908	DNA methylation in adolescents with anxiety disorder: a longitudinal study. Scientific Reports, 2018, 8, 13800.	1.6	13
909	Molecular Networks of Postia placenta Involved in Degradation of Lignocellulosic Biomass Revealed from Metadata Analysis of Open Access Gene Expression Data. International Journal of Biological Sciences, 2018, 14, 237-252.	2.6	11
910	Model organism data evolving in support of translational medicine. Lab Animal, 2018, 47, 277-289.	0.2	35
911	Discovery and characterization of conserved binding of eIF4E 1 (CBE1), a eukaryotic translation initiation factor 4E–binding plant protein. Journal of Biological Chemistry, 2018, 293, 17240-17247.	1.6	25
912	Gene set enrichment analysis of <scp>SNP</scp> data in dairy and beef cattle with bovine respiratory disease. Animal Genetics, 2018, 49, 527-538.	0.6	25
913	Additional common variants associated with type 2 diabetes and coronary artery disease detected using a pleiotropic cFDR method. Journal of Diabetes and Its Complications, 2018, 32, 1105-1112.	1.2	5
914	An integrated genomic analysis of anaplastic meningioma identifies prognostic molecular signatures. Scientific Reports, 2018, 8, 13537.	1.6	49
915	Higher-order molecular organization as a source of biological function. Bioinformatics, 2018, 34, i944-i953.	1.8	32

	CITATION REP	PORT	
#	Article	IF	CITATIONS
916	DES-Mutation: System for Exploring Links of Mutations and Diseases. Scientific Reports, 2018, 8, 13359.	1.6	13
917	Translation Stress Positively Regulates MscL-Dependent Excretion of Cytoplasmic Proteins. MBio, 2018, 9, .	1.8	19
918	ANNOgesic: a Swiss army knife for the RNA-seq based annotation of bacterial/archaeal genomes. GigaScience, 2018, 7, .	3.3	60
919	Comprehensive innate immune profiling of chikungunya virus infection in pediatric cases. Molecular Systems Biology, 2018, 14, e7862.	3.2	66
920	Numerous recursive sites contribute to accuracy of splicing in long introns in flies. PLoS Genetics, 2018, 14, e1007588.	1.5	18
921	Exploration of gene functions for esophageal squamous cell carcinoma using network-based guilt by association principle. Brazilian Journal of Medical and Biological Research, 2018, 51, e6801.	0.7	2
922	A multi-objective gene clustering algorithm guided by apriori biological knowledge with intensification and diversification strategies. BioData Mining, 2018, 11, 16.	2.2	17
923	Roles and mechanisms of action of HNFâ€ʻ4α in�the�hepatic differentiation of WBâ€ʻF344 cells. Internation Journal of Molecular Medicine, 2019, 43, 1021-1032.	al 1.8	2
924	Regulatory RNAs in Virulence and Host-Microbe Interactions. , 2018, , 305-337.		4
925	The UCSC Genome Browser database: 2018 update. Nucleic Acids Research, 2018, 46, D762-D769.	6.5	476
926	Mouse Genome Database (MGD)-2018: knowledgebase for the laboratory mouse. Nucleic Acids Research, 2018, 46, D836-D842.	6.5	241
927	PDBe: towards reusable data delivery infrastructure at protein data bank in Europe. Nucleic Acids Research, 2018, 46, D486-D492.	6.5	76
928	Minimotif Miner 4: a million peptide minimotifs and counting. Nucleic Acids Research, 2018, 46, D465-D470.	6.5	15
929	FunCoup 4: new species, data, and visualization. Nucleic Acids Research, 2018, 46, D601-D607.	6.5	44
930	EuPathDB: The Eukaryotic Pathogen Genomics Database Resource. Methods in Molecular Biology, 2018, 1757, 69-113.	0.4	80
931	Bovine Genome Database: Tools for Mining the Bos taurus Genome. Methods in Molecular Biology, 2018, 1757, 211-249.	0.4	5
932	Altered mitochondrial acetylation profiles in a kainic acid model of temporal lobe epilepsy. Free Radical Biology and Medicine, 2018, 123, 116-124.	1.3	37
933	A genome-wide cross-trait analysis from UK Biobank highlights the shared genetic architecture of asthma and allergic diseases. Nature Genetics, 2018, 50, 857-864.	9.4	191

#	Article	IF	CITATIONS
934	Using WormBase: A Genome Biology Resource for Caenorhabditis elegans and Related Nematodes. Methods in Molecular Biology, 2018, 1757, 399-470.	0.4	28
935	WEGO 2.0: a web tool for analyzing and plotting GO annotations, 2018 update. Nucleic Acids Research, 2018, 46, W71-W75.	6.5	473
936	Urinary transcriptomics reveals patterns associated with subclinical injury of the renal allograft. Biomarkers in Medicine, 2018, 12, 427-438.	0.6	3
937	PomBase: The Scientific Resource for Fission Yeast. Methods in Molecular Biology, 2018, 1757, 49-68.	0.4	32
938	Statistical and artificial neural network-based analysis to understand complexity and heterogeneity in preeclampsia. Computational Biology and Chemistry, 2018, 75, 222-230.	1.1	23
939	Identification and bioinformatics analysis of overlapping differentially expressed genes in depression, papillary thyroid cancer and uterine fibroids. Experimental and Therapeutic Medicine, 2018, 15, 4810-4816.	0.8	9
940	The SS18-SSX Fusion Oncoprotein Hijacks BAF Complex Targeting and Function to Drive Synovial Sarcoma. Cancer Cell, 2018, 33, 1128-1141.e7.	7.7	169
941	Clinical Correlations of Transcriptional Profile in Patients Infected With Avian Influenza H7N9 Virus. Journal of Infectious Diseases, 2018, 218, 1238-1248.	1.9	18
942	Hymenoptera Genome Database: Using HymenopteraMine to Enhance Genomic Studies of Hymenopteran Insects. Methods in Molecular Biology, 2018, 1757, 513-556.	0.4	12
943	The Ensembl Genome Browser: Strategies for Accessing Eukaryotic Genome Data. Methods in Molecular Biology, 2018, 1757, 115-139.	0.4	13
944	Exploring the role of low-frequency and rare exonic variants in alcohol and tobacco use. Drug and Alcohol Dependence, 2018, 188, 94-101.	1.6	10
945	Computational Approach to Investigating Key GO Terms and KEGG Pathways Associated with CNV. BioMed Research International, 2018, 2018, 1-9.	0.9	3
946	Quantifying compartmentâ€associated variations ofÂprotein abundance in proteomics data. Molecular Systems Biology, 2018, 14, e8131.	3.2	14
947	A General Framework for Interrogation of mRNA Stability Programs Identifies RNA-Binding Proteins that Govern Cancer Transcriptomes. Cell Reports, 2018, 23, 1639-1650.	2.9	56
948	E47 Governs the MYC-CDKN1B/p27 KIP1 -RB Network to Growth Arrest PDA Cells Independent of CDKN2A/p16 INK4A and Wild-Type p53. Cellular and Molecular Gastroenterology and Hepatology, 2018, 6, 181-198.	2.3	14
949	Gene prioritization using Bayesian matrix factorization with genomic and phenotypic side information. Bioinformatics, 2018, 34, i447-i456.	1.8	32
950	Functional genomics of lipid metabolism in the oleaginous yeast Rhodosporidium toruloides. ELife, 2018, 7, .	2.8	98
951	Identification of the potential oncogenes in glioblastoma based on bioinformatic analysis and elucidation of the underlying mechanisms. Oncology Reports, 2018, 40, 715-725.	1.2	15

#	Article	IF	CITATIONS
952	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. Nature Genetics, 2018, 50, 937-943.	9.4	55
953	Clustering huge protein sequence sets in linear time. Nature Communications, 2018, 9, 2542.	5.8	497
954	A Domain-Specific Terminology for Retinopathy of Prematurity and Its Applications in Clinical Settings. Journal of Healthcare Engineering, 2018, 2018, 1-6.	1.1	3
956	PrimAlign: PageRank-inspired Markovian alignment for large biological networks. Bioinformatics, 2018, 34, i537-i546.	1.8	25
958	Differential aging of growth plate cartilage underlies differences in bone length and thus helps determine skeletal proportions. PLoS Biology, 2018, 16, e2005263.	2.6	48
959	TelNet - a database for human and yeast genes involved in telomere maintenance. BMC Genetics, 2018, 19, 32.	2.7	36
960	Phenotype-driven gene prioritization for rare diseases using graph convolution on heterogeneous networks. BMC Medical Genomics, 2018, 11, 57.	0.7	30
961	PanACEA: a bioinformatics tool for the exploration and visualization of bacterial pan-chromosomes. BMC Bioinformatics, 2018, 19, 246.	1.2	9
962	Gene Discovery of Characteristic Metabolic Pathways in the Tea Plant (Camellia sinensis) Using â€~Omics'-Based Network Approaches: A Future Perspective. Frontiers in Plant Science, 2018, 9, 480.	1.7	33
963	MU-LOC: A Machine-Learning Method for Predicting Mitochondrially Localized Proteins in Plants. Frontiers in Plant Science, 2018, 9, 634.	1.7	29
964	Long non-coding RNAs RP5-821D11.7, APCDD1L-AS1 and RP11-277P12.9 were associated with the prognosis of lung squamous cell carcinoma. Molecular Medicine Reports, 2018, 17, 7238-7248.	1.1	16
965	Construction of ParÃ; rubber tree genome and multi-transcriptome database accelerates rubber researches. BMC Genomics, 2018, 19, 922.	1.2	31
966	A new bioinformatics tool to help assess the significance of BRCA1 variants. Human Genomics, 2018, 12, 36.	1.4	10
967	Cigarette Smoke–Induced Emphysema Exhausts Early Cytotoxic CD8+ T Cell Responses against Nascent Lung Cancer Cells. Journal of Immunology, 2018, 201, 1558-1569.	0.4	19
968	MaxMIF: A New Method for Identifying Cancer Driver Genes through Effective Data Integration. Advanced Science, 2018, 5, 1800640.	5.6	37
969	Application of Transcriptomics to Compare the Carbohydrate Active Enzymes That Are Expressed by Diverse Genera of Anaerobic Fungi to Degrade Plant Cell Wall Carbohydrates. Frontiers in Microbiology, 2018, 9, 1581.	1.5	58
970	Large-Scale Ontology Matching. ACM Computing Surveys, 2019, 51, 1-35.	16.1	32
971	Network Modularity and Hierarchical Structure in Breast Cancer Molecular Subtypes. Springer Proceedings in Complexity, 2018, , 352-358.	0.2	18

#	Article	IF	CITATIONS
972	Lossless Compression of Binary Trees With Correlated Vertex Names. IEEE Transactions on Information Theory, 2018, 64, 6070-6080.	1.5	10
973	Whole-genome resequencing of Ujumqin sheep to investigate the determinants of the multi-vertebral trait. Genome, 2018, 61, 653-661.	0.9	8
974	ExAtlas. , 2018, , 73-104.		1
975	Delineating the underlying molecular mechanisms and key genes involved in metastasis of colorectal cancer via bioinformatics analysis. Oncology Reports, 2018, 39, 2297-2305.	1.2	5
976	DNA methylation and gene expression profiling reveal <i>MFAP5</i> as a regulatory driver of extracellular matrix remodeling in varicose vein disease. Epigenomics, 2018, 10, 1103-1119.	1.0	21
977	Integrative analysis of promising molecular biomarkers and pathways for coronary artery disease using WGCNA and MetaDE methods. Molecular Medicine Reports, 2018, 18, 2789-2797.	1.1	12
978	MGOGP: a gene module-based heuristic algorithm for cancer-related gene prioritization. BMC Bioinformatics, 2018, 19, 215.	1.2	6
979	CoNVaQ: a web tool for copy number variation-based association studies. BMC Genomics, 2018, 19, 369.	1.2	29
980	Metazoan Parasite Vaccines: Present Status and Future Prospects. Frontiers in Cellular and Infection Microbiology, 2018, 8, 67.	1.8	59
981	The Use of CRISPR/Cas9 Gene Editing to Confirm Congenic Contaminations in Host-Pathogen Interaction Studies. Frontiers in Cellular and Infection Microbiology, 2018, 8, 87.	1.8	3
982	Phosphatidylserine-Liposomes Promote Tolerogenic Features on Dendritic Cells in Human Type 1 Diabetes by Apoptotic Mimicry. Frontiers in Immunology, 2018, 9, 253.	2.2	58
983	Differential Phagocytic Properties of CD45low Microglia and CD45high Brain Mononuclear Phagocytes—Activation and Age-Related Effects. Frontiers in Immunology, 2018, 9, 405.	2.2	102
984	Analyzing AbrB-Knockout Effects through Genome and Transcriptome Sequencing of Bacillus licheniformis DW2. Frontiers in Microbiology, 2018, 9, 307.	1.5	24
985	Reduction of Proliferating Olfactory Cells and Low Expression of Extracellular Matrix Genes Are Hallmarks of the Aged Olfactory Mucosa. Frontiers in Aging Neuroscience, 2018, 10, 86.	1.7	33
986	Sphingolipid Metabolism Is Dysregulated at Transcriptomic and Metabolic Levels in the Spinal Cord of an Animal Model of Amyotrophic Lateral Sclerosis. Frontiers in Molecular Neuroscience, 2017, 10, 433.	1.4	52
987	Decoding the chromatin proteome of a single genomic locus by DNA sequencing. PLoS Biology, 2018, 16, e2005542.	2.6	14
988	Genomeâ€wide association metaâ€analysis of age at first cannabis use. Addiction, 2018, 113, 2073-2086.	1.7	24
989	Elevated Nrf-2 responses are insufficient to mitigate protein carbonylation in hepatospecific PTEN deletion mice. PLoS ONE, 2018, 13, e0198139.	1.1	12

#	Article	IF	CITATIONS
990	dropEst: pipeline for accurate estimation of molecular counts in droplet-based single-cell RNA-seq experiments. Genome Biology, 2018, 19, 78.	3.8	159
991	Regulatory RNAs in Virulence and Host-Microbe Interactions. Microbiology Spectrum, 2018, 6, .	1.2	34
992	The Complex Interaction of Mitochondrial Genetics and Mitochondrial Pathways in Psychiatric Disease. Molecular Neuropsychiatry, 2018, 4, 52-69.	3.0	42
993	Potential biomarkers and therapeutic targets in cervical cancer: Insights from the meta-analysis of transcriptomics data within network biomedicine perspective. PLoS ONE, 2018, 13, e0200717.	1.1	89
994	Combinatorial Targeting by MicroRNAs Co-ordinates Post-transcriptional Control of EMT. Cell Systems, 2018, 7, 77-91.e7.	2.9	92
995	Regulation of osteogenesis by long noncoding RNAs: An epigenetic mechanism contributing to bone formation. Connective Tissue Research, 2018, 59, 35-41.	1.1	21
996	Next generation sequencing for miRNA profile of spleen CD4 <sup>+</sup> T cells in the murine model of acute asthma. Epigenomics, 2018, 10, 1071-1083.	1.0	8
997	Systematic target function annotation of human transcription factors. BMC Biology, 2018, 16, 4.	1.7	12
998	ASGDB: a specialised genomic resource for interpreting Anopheles sinensis insecticideÂresistance. Parasites and Vectors, 2018, 11, 32.	1.0	2
999	Integrated multi-omic analysis of host-microbiota interactions in acute oak decline. Microbiome, 2018, 6, 21.	4.9	49
1000	Phenotypic Screening. Methods in Molecular Biology, 2018, , .	0.4	0
1001	Bio-SimVerb and Bio-SimLex: wide-coverage evaluation sets of word similarity in biomedicine. BMC Bioinformatics, 2018, 19, 33.	1.2	21
1002	Structural biology data archiving – where we are and what lies ahead. FEBS Letters, 2018, 592, 2153-2167.	1.3	11
1003	Riboflavin Depletion Promotes Tumorigenesis in HEK293T and NIH3T3 Cells by Sustaining Cell Proliferation and Regulating Cell Cycle–Related Gene Transcription. Journal of Nutrition, 2018, 148, 834-843.	1.3	13
1004	Computational Methods for Understanding Mass Spectrometry–Based Shotgun Proteomics Data. Annual Review of Biomedical Data Science, 2018, 1, 207-234.	2.8	108
1005	Quantitative Prioritization of Tool Compounds for Phenotypic Screening. Methods in Molecular Biology, 2018, 1787, 195-206.	0.4	3
1006	Efficient proximity labeling in living cells and organisms with TurboID. Nature Biotechnology, 2018, 36, 880-887.	9.4	1,103
1007	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. Nature Genetics, 2018, 50, 1240-1246.	9.4	199

		CITATION RE	EPORT	
# 1008	ARTICLE An Introduction to Tools, Databases, and Practical Guidelines for NGS Data Analysis. , 2	2018, , 61-89.	IF	Citations
1009	CellBIC: bimodality-based top-down clustering of single-cell RNA sequencing data revea structure of the cell type. Nucleic Acids Research, 2018, 46, e124-e124.	als hierarchical	6.5	15
1010	Comprehensive analysis of gene expression profiles provides insight into the pathogen disease. Molecular Medicine Reports, 2018, 18, 2643-2650.	esis of Crohn's	1.1	5
1011	Creating Transparent and Reproducible Pipelines: Best Practices for Tools, Data, and W Management Systems. , 2018, , 15-43.	Vorkflow		1
1012	Proteomic distinction of renal oncocytomas and chromophobe renal cell carcinomas. C Proteomics, 2018, 15, 25.	Clinical	1.1	8
1013	Databases and Tools for the Analysis of the Barley Genome. Compendium of Plant Gen 377-394.	omes, 2018, ,	0.3	1
1014	Discovering Putative Prion-Like Proteins in Plasmodium falciparum: A Computational a Analysis. Frontiers in Microbiology, 2018, 9, 1737.	nd Experimental	1.5	42
1015	Divergent brain gene expression patterns associate with distinct cell-specific tau neuro traits in progressive supranuclear palsy. Acta Neuropathologica, 2018, 136, 709-727.	pathology	3.9	47
1016	Comparative transcriptomic analyses and single-cell RNA sequencing of the freshwater Schmidtea mediterranea identify major cell types and pathway conservation. Genome 124.		3.8	44
1017	The inconsistent regulation of HOXC13 on different keratins and the regulation mecha in cashmere goat (Capra hircus). BMC Genomics, 2018, 19, 630.	inism on HOXC13	1.2	21
1018	Functional implication of celiac disease associated lncRNAs in disease pathogenesis. C Biology and Medicine, 2018, 102, 369-375.	omputers in	3.9	6
1019	Data mining of the cancer-related lncRNAs GO terms and KEGG pathways by using mR Mathematical Biosciences, 2018, 304, 1-8.	MR method.	0.9	29
1020	Epigenetic Variability Confounds Transcriptome but Not Proteome Profiling for Coexpr Gene Function Prediction. Molecular and Cellular Proteomics, 2018, 17, 2082-2090.	ession-based	2.5	9
1021	Impulse model-based differential expression analysis of time course sequencing data. N Research, 2018, 46, e119.	Nucleic Acids	6.5	81
1022	Direct measurement of pervasive weak repression by microRNAs and their role at the mBMC Genomics, 2018, 19, 362.	ietwork level.	1.2	9
1023	De novo Transcriptome Assembly of the Clown Anemonefish (Amphiprion percula): A N Study the Evolution of Fish Color. Frontiers in Marine Science, 2018, 5, .	lew Resource to	1.2	15
1024	Whole genome sequencing of the monomorphic pathogen Mycobacterium bovis revea differentiation of cattle clinical isolates. BMC Genomics, 2018, 19, 2.	als local	1.2	36
1025	LncRNAs KB‑1836B5, LINC00566 and FAM27L are associated with the survival time ovarian cancer. Oncology Letters, 2018, 16, 3735-3745.	of patients with	0.8	5

#	Article	IF	CITATIONS
1026	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
1027	Using RegulonDB, the <i>Escherichia coli</i> Kâ€12 Gene Regulatory Transcriptional Network Database. Current Protocols in Bioinformatics, 2018, 61, 1.32.1-1.32.30.	25.8	8
1028	Fractal dimension analysis reveals skeletal muscle disorganization in mdx mice. Biochemical and Biophysical Research Communications, 2018, 503, 109-115.	1.0	17
1029	Secretome Screening Reveals Fibroblast Growth Factors as Novel Inhibitors of Viral Replication. Journal of Virology, 2018, 92, .	1.5	32
1030	Bioinformatics and genomic databases. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2018, 147, 75-92.	1.0	15
1031	VarAFT: a variant annotation and filtration system for human next generation sequencing data. Nucleic Acids Research, 2018, 46, W545-W553.	6.5	136
1032	Cellular stress alters 3′UTR landscape through alternative polyadenylation and isoform-specific degradation. Nature Communications, 2018, 9, 2268.	5.8	104
1033	Regular aspirin use and gene expression profiles in prostate cancer patients. Cancer Causes and Control, 2018, 29, 775-784.	0.8	3
1034	Developments in toxicogenomics: understanding and predicting compound-induced toxicity from gene expression data. Molecular Omics, 2018, 14, 218-236.	1.4	90
1035	Dynamic genome wide expression profiling of Drosophila head development reveals a novel role of Hunchback in retinal glia cell development and blood-brain barrier integrity. PLoS Genetics, 2018, 14, e1007180.	1.5	11
1036	Proteomic Architecture of Human Coronary and Aortic Atherosclerosis. Circulation, 2018, 137, 2741-2756.	1.6	100
1037	Functional Enrichment Analysis. , 2019, , 218-229.		2
1038	Beyond Homology Transfer: Deep Learning for Automated Annotation of Proteins. Journal of Grid Computing, 2019, 17, 225-237.	2.5	29
1039	Elevated histone H3 acetylation is associated with genes involved in T lymphocyte activation and glutamate decarboxylase antibody production in patients with type 1 diabetes. Journal of Diabetes Investigation, 2019, 10, 51-61.	1.1	15
1040	The combined effects of FADS gene variation and dietary fats in obesity-related traits in a population from the far north of Sweden: the GLACIER Study. International Journal of Obesity, 2019, 43, 808-820.	1.6	15
1041	Prediction of skin antiâ€aging clinical benefits of an association of ingredients from marine and maritime origins: Ex vivo evaluation using a labelâ€free quantitative proteomic and customized data processing approach. Journal of Cosmetic Dermatology, 2019, 18, 355-370.	0.8	6
1042	The Gene Ontology. , 2019, , 1-7.		3
1043	Genome-Wide Scanning of Gene Expression. , 2019, , 452-462.		0

	CITATION R	EPORT	
# 1044	ARTICLE Biological and Medical Ontologies: Protein Ontology (PRO). , 2019, , 832-837.	IF	CITATIONS
1045	Identification and interaction analysis of key genes and microRNAs in atopic dermatitis by bioinformatics analysis. Clinical and Experimental Dermatology, 2019, 44, 257-264.	0.6	23
1046	Identification of synthetic lethality based on a functional network by using machine learning algorithms. Journal of Cellular Biochemistry, 2019, 120, 405-416.	1.2	102
1047	Phylo-PFP: improved automated protein function prediction using phylogenetic distance of distantly related sequences. Bioinformatics, 2019, 35, 753-759.	1.8	29
1048	Computational resources associating diseases with genotypes, phenotypes and exposures. Briefings in Bioinformatics, 2019, 20, 2098-2115.	3.2	27
1049	Bioinformatics analysis to reveal the key genes related to obstructive sleep apnea. Sleep and Breathing, 2019, 23, 259-267.	0.9	5
1050	ToBio: Global Pathway Similarity Search Based on Topological and Biological Features. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 336-349.	1.9	4
1051	PathEmb: Random Walk Based Document Embedding for Global Pathway Similarity Search. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 1329-1335.	3.9	5
1052	CAG Repeat Not Polyglutamine Length Determines Timing of Huntington's Disease Onset. Cell, 2019, 178, 887-900.e14.	13.5	301
1053	Analysis of Protein–Protein Functional Associations by Using Gene Ontology and KEGG Pathway. BioMed Research International, 2019, 2019, 1-10.	0.9	18
1054	Avian Binocularity and Adaptation to Nocturnal Environments: Genomic Insights from a Highly Derived Visual Phenotype. Genome Biology and Evolution, 2019, 11, 2244-2255.	1.1	12
1055	The evolution of gene duplicates in angiosperms and the impact of protein-protein interactions and the mechanism of duplication. Genome Biology and Evolution, 2019, 11, 2292-2305.	1.1	48
1056	Guideline for comparing functional enrichment of biological network modular structures. Applied Network Science, 2019, 4, .	0.8	4
1057	A Nutrigenomics Approach Using RNA Sequencing Technology to Study Nutrient–Gene Interactions in Agricultural Animals. Current Developments in Nutrition, 2019, 3, nzz082.	0.1	13
1058	Replication timing networks reveal a link between transcription regulatory circuits and replication timing control. Genome Research, 2019, 29, 1415-1428.	2.4	12
1059	Cholestatic liver disease results increased production of reactive aldehydes and an atypical periportal hepatic antioxidant response. Free Radical Biology and Medicine, 2019, 143, 101-114.	1.3	13
1060	Five genes may predict metastasis in non‑small cell lung cancer using bioinformatics analysis. Oncology Letters, 2019, 18, 1723-1732.	0.8	9
1061	Inferring novel genes related to colorectal cancer via random walk with restart algorithm. Gene Therapy, 2019, 26, 373-385.	2.3	3

#	Article	IF	CITATIONS
1062	Head Start Immunity: Characterizing the Early Protection of C Strain Vaccine Against Subsequent Classical Swine Fever Virus Infection. Frontiers in Immunology, 2019, 10, 1584.	2.2	9
1063	A gene expression network analysis of the pancreatic islets from lean and obese mice identifies complement 1qÂlike-3 secreted protein as a regulator of β-cell function. Scientific Reports, 2019, 9, 10119.	1.6	8
1064	Graphical models for zero-inflated single cell gene expression. Annals of Applied Statistics, 2019, 13, 848-873.	0.5	19
1065	Inhibiting ubiquitination causes an accumulation of SUMOylated newly synthesized nuclear proteins at PML bodies. Journal of Biological Chemistry, 2019, 294, 15218-15234.	1.6	37
1066	Sirius: A Resource for Analyzing Drug-Disease Relationships for Drug Repositioning. Lecture Notes in Electrical Engineering, 2019, , 235-244.	0.3	0
1067	SMAC, a computational system to link literature, biomedical and expression data. Scientific Reports, 2019, 9, 10480.	1.6	3
1068	Identification of Key Genes and Candidated Pathways in Human Autosomal Dominant Polycystic Kidney Disease by Bioinformatics Analysis. Kidney and Blood Pressure Research, 2019, 44, 533-552.	0.9	14
1069	Precise and systematic survey of the efficacy of multicomponent drugs against functional dyspepsia. Scientific Reports, 2019, 9, 10713.	1.6	16
1070	Improved detection of common variants in coronary artery disease and blood pressure using a pleiotropy cFDR method. Scientific Reports, 2019, 9, 10340.	1.6	1
1071	Convergent horizontal gene transfer and cross-talk of mobile nucleic acids in parasitic plants. Nature Plants, 2019, 5, 991-1001.	4.7	72
1072	Experimental Acute Exposure to Thirdhand Smoke and Changes in the Human Nasal Epithelial Transcriptome. JAMA Network Open, 2019, 2, e196362.	2.8	11
1073	Ontology mapping for semantically enabled applications. Drug Discovery Today, 2019, 24, 2068-2075.	3.2	25
1074	A systems biology pipeline identifies regulatory networks for stem cell engineering. Nature Biotechnology, 2019, 37, 810-818.	9.4	18
1075	Selective Killing of RAS-Malignant Tissues by Exploiting Oncogene-Induced DNA Damage. Cell Reports, 2019, 28, 119-131.e4.	2.9	18
1076	Selection at behavioural, developmental and metabolic genes is associated with the northward expansion of a successful tropical colonizer. Molecular Ecology, 2019, 28, 3523-3543.	2.0	7
1077	GAIL: An interactive webserver for inference and dynamic visualization of gene-gene associations based on gene ontology guided mining of biomedical literature. PLoS ONE, 2019, 14, e0219195.	1.1	5
1078	Identification of an early cell fate regulator by detecting dynamics in transcriptional heterogeneity and co-regulation during astrocyte differentiation. Npj Systems Biology and Applications, 2019, 5, 18.	1.4	10
1079	Integrating proteomics and transcriptomics for the identification of potential targets in early colorectal cancer. International Journal of Oncology, 2019, 55, 439-450.	1.4	15

#	Article	IF	CITATIONS
1080	Chromatin profiling of cortical neurons identifies individual epigenetic signatures in schizophrenia. Translational Psychiatry, 2019, 9, 256.	2.4	18
1081	Changes of Gene Expression in Euglena gracilis Obtained During the 29th DLR Parabolic Flight Campaign. Scientific Reports, 2019, 9, 14260.	1.6	10
1082	Transcriptional Regulator TonEBP Mediates Oxidative Damages in Ischemic Kidney Injury. Cells, 2019, 8, 1284.	1.8	2
1083	Astrovirus replication in human intestinal enteroids reveals multi-cellular tropism and an intricate host innate immune landscape. PLoS Pathogens, 2019, 15, e1008057.	2.1	69
1084	Rewiring of Cancer Cell Metabolism by Mitochondrial VDAC1 Depletion Results in Time-Dependent Tumor Reprogramming: Glioblastoma as a Proof of Concept. Cells, 2019, 8, 1330.	1.8	18
1085	Bioinformatics for Marine Products: An Overview of Resources, Bottlenecks, and Perspectives. Marine Drugs, 2019, 17, 576.	2.2	26
1086	Jointly integrating VCF-based variants and OWL-based biomedical ontologies in MongoDB. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	1.9	7
1087	SIGNOR 2.0, the SIGnaling Network Open Resource 2.0: 2019 update. Nucleic Acids Research, 2020, 48, D504-D510.	6.5	160
1088	Translational offsetting as a mode of estrogen receptor αâ€dependent regulation of geneÂexpression. EMBO Journal, 2019, 38, e101323.	3.5	33
1089	Elevated serum alpha-1 antitrypsin is a major component of GlycA-associated risk for future morbidity and mortality. PLoS ONE, 2019, 14, e0223692.	1.1	14
1090	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. Nucleic Acids Research, 2020, 48, D489-D497.	6.5	161
1091	Compositional epistasis detection using a few prototype disease models. PLoS ONE, 2019, 14, e0213236.	1.1	1
1092	Gene Cascade Finder: A tool for identification of gene cascades and its application in Caenorhabditis elegans. PLoS ONE, 2019, 14, e0215187.	1.1	5
1093	Druggable genome in attention deficit/hyperactivity disorder and its co-morbid conditions. New avenues for treatment. Molecular Psychiatry, 2021, 26, 4004-4015.	4.1	27
1094	Toward understanding the origin and evolution of cellular organisms. Protein Science, 2019, 28, 1947-1951.	3.1	2,262
1095	Identification of Genes and Pathways Associated with Acne Using Integrated Bioinformatics Methods. Dermatology, 2019, 235, 445-455.	0.9	14
1096	Tumor Transcriptome Reveals High Expression of IL-8 in Non-Small Cell Lung Cancer Patients with Low Pectoralis Muscle Area and Reduced Survival. Cancers, 2019, 11, 1251.	1.7	26
1097	Exploring the Pathological Mechanism of Bladder Cancer Based on Tumor Mutational Burden Analysis. BioMed Research International, 2019, 2019, 1-9.	0.9	9

#	Article	IF	CITATIONS
1098	SamPler – a novel method for selecting parameters for gene functional annotation routines. BMC Bioinformatics, 2019, 20, 454.	1.2	5
1099	Inferring novel genes related to oral cancer with a network embedding method and one-class learning algorithms. Gene Therapy, 2019, 26, 465-478.	2.3	14
1100	Gene-diet interactions associated with complex trait variation in an advanced intercross outbred mouse line. Nature Communications, 2019, 10, 4097.	5.8	35
1101	Low complexity regions in the proteins of prokaryotes perform important functional roles and are highly conserved. Nucleic Acids Research, 2019, 47, 9998-10009.	6.5	44
1102	Extensive Thioautotrophic Gill Endosymbiont Diversity within a Single <i>Ctena orbiculata</i> (Bivalvia: Lucinidae) Population and Implications for Defining Host-Symbiont Specificity and Species Recognition. MSystems, 2019, 4, .	1.7	7
1103	Enabling Web-scale data integration in biomedicine through Linked Open Data. Npj Digital Medicine, 2019, 2, 90.	5.7	19
1104	Integrative approaches to reconstruct regulatory networks from multi-omics data: A review of state-of-the-art methods. Computational Biology and Chemistry, 2019, 83, 107120.	1.1	35
1105	LINC00461 affects the survival of patients with renal cell carcinoma by acting as a competing endogenous RNA for microRNA‑942. Oncology Reports, 2019, 42, 1924-1934.	1.2	19
1106	Construction and analysis of a diabetic nephropathy related protein-protein interaction network reveals nine critical and functionally associated genes. Computational Biology and Chemistry, 2019, 83, 107115.	1.1	1
1107	Proteomic analysis of the rice (Oryza officinalis) provides clues on molecular tagging of proteins for brown planthopper resistance. BMC Plant Biology, 2019, 19, 30.	1.6	13
1108	Impact of human milk on the transcriptomic response of fetal intestinal epithelial cells reveals expression changes of immune-related genes. Food and Function, 2019, 10, 140-150.	2.1	8
1109	Deterministic column subset selection for single-cell RNA-Seq. PLoS ONE, 2019, 14, e0210571.	1.1	0
1110	Epigallocatechin‑3‑gallate modulates long non‑coding RNA and mRNA expression profiles in lung cancer cells. Molecular Medicine Reports, 2019, 19, 1509-1520.	1.1	18
1111	GOTrapper: a tool to navigate through branches of gene ontology hierarchy. BMC Bioinformatics, 2019, 20, 20.	1.2	11
1112	Identification of Prognostic Biomarker Signatures and Candidate Drugs in Colorectal Cancer: Insights from Systems Biology Analysis. Medicina (Lithuania), 2019, 55, 20.	0.8	51
1113	The Genetic Structures of an Extensively Drug Resistant (XDR) Klebsiella pneumoniae and Its Plasmids. Frontiers in Cellular and Infection Microbiology, 2018, 8, 446.	1.8	28
1114	Transcriptome Analysis of Mesenchymal Stem Cells from Multiple Myeloma Patients Reveals Downregulation of Genes Involved in Cell Cycle Progression, Immune Response, and Bone Metabolism. Scientific Reports, 2019, 9, 1056.	1.6	28
1115	DEEPred: Automated Protein Function Prediction with Multi-task Feed-forward Deep Neural Networks. Scientific Reports, 2019, 9, 7344.	1.6	80

#	Article	IF	CITATIONS
1116	A hypergraph-based method for large-scale dynamic correlation study at the transcriptomic scale. BMC Genomics, 2019, 20, 397.	1.2	6
1117	Retinal Gene Distribution and Functionality Implicated in Inherited Retinal Degenerations Can Reveal Disease-Relevant Pathways for Pharmacologic Intervention. Pharmaceuticals, 2019, 12, 74.	1.7	5
1118	Transcriptional Regulatory Network Analysis to Reveal the Key Genes Involved in Skeletal Muscle Injury. Journal of Computational Biology, 2019, 26, 1090-1099.	0.8	3
1119	Whole-genome deep-learning analysis identifies contribution of noncoding mutations to autism risk. Nature Genetics, 2019, 51, 973-980.	9.4	216
1120	Using a Multi-Stage hESC Model to Characterize BDE-47 Toxicity During Neurogenesis. Toxicological Sciences, 2019, 171, 221-234.	1.4	20
1121	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	5.8	240
1122	Expanding Alternative Splicing Identification by Integrating Multiple Sources of Transcription Data in Tomato. Frontiers in Plant Science, 2019, 10, 689.	1.7	26
1123	metaQuantome: An Integrated, Quantitative Metaproteomics Approach Reveals Connections Between Taxonomy and Protein Function in Complex Microbiomes. Molecular and Cellular Proteomics, 2019, 18, S82-S91.	2.5	26
1124	Computational identification of protein-protein interactions in model plant proteomes. Scientific Reports, 2019, 9, 8740.	1.6	56
1125	Method for Generalization of Fuzzy Sets. Lecture Notes in Computer Science, 2019, , 273-286.	1.0	0
1126	Transcriptomics Analysis Reveals New Insights into the Roles of Notch1 Signaling on Macrophage Polarization. Scientific Reports, 2019, 9, 7999.	1.6	23
1127	Maize transcriptomic repertoires respond to gibberellin stimulation. Molecular Biology Reports, 2019, 46, 4409-4421.	1.0	5
1128	Recent trends in molecular diagnostics of yeast infections: from PCR to NGS. FEMS Microbiology Reviews, 2019, 43, 517-547.	3.9	77
1129	Integrating yeast chemical genomics and mammalian cell pathway analysis. Acta Pharmacologica Sinica, 2019, 40, 1245-1255.	2.8	2
1130	Pathway-specific protein domains are predictive for human diseases. PLoS Computational Biology, 2019, 15, e1007052.	1.5	8
1131	RNA‑seq analyses of antibiotic resistance mechanisms in Serratia�marcescens. Molecular Medicine Reports, 2019, 20, 745-754.	1.1	6
1132	Characterization of a prognostic four‑gene methylation signature associated with radiotherapy for head and neck squamous cell carcinoma. Molecular Medicine Reports, 2019, 20, 622-632.	1.1	17
1133	AXL knockdown gene signature reveals a drug repurposing opportunity for a class of antipsychotics to reduce growth and metastasis of triple-negative breast cancer. Oncotarget, 2019, 10, 2055-2067.	0.8	32

#	Article	IF	CITATIONS
1134	Literature-Based Enrichment Insights into Redox Control of Vascular Biology. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-16.	1.9	8
1135	Unprecedented reorganization of holocentric chromosomes provides insights into the enigma of lepidopteran chromosome evolution. Science Advances, 2019, 5, eaau3648.	4.7	66
1136	Metabolic Remodeling during Biofilm Development of Bacillus subtilis. MBio, 2019, 10, .	1.8	93
1137	Sub-cytotoxic doses of pharmaceutical silica nanoparticles show significant impact on the proteome of HepG2 cells. Journal of Controlled Release, 2019, 306, 1-14.	4.8	3
1138	Return to the Sea, Get Huge, Beat Cancer: An Analysis of Cetacean Genomes Including an Assembly for the Humpback Whale (Megaptera novaeangliae). Molecular Biology and Evolution, 2019, 36, 1746-1763.	3.5	75
1139	What Changed on the Folliculogenesis in the Process of Mouse Ovarian Aging?. BioMed Research International, 2019, 2019, 1-10.	0.9	5
1140	lce-Age Climate Adaptations Trap the Alpine Marmot in a State of Low Genetic Diversity. Current Biology, 2019, 29, 1712-1720.e7.	1.8	27
1141	Genetic mechanism underlying sexual plasticity and its association with colour patterning in zebrafish (Danio rerio). BMC Genomics, 2019, 20, 341.	1.2	15
1142	A novel long noncoding RNA FAF inhibits apoptosis via upregulating FGF9 through PI3K/AKT signaling pathway in ischemia–hypoxia cardiomyocytes. Journal of Cellular Physiology, 2019, 234, 21973-21987.	2.0	25
1143	In silico analysis revealed Zika virus miRNAs associated with viral pathogenesis through alteration of host genes involved in immune response and neurological functions. Journal of Medical Virology, 2019, 91, 1584-1594.	2.5	28
1144	Identification of novel blood-based HCC-specific diagnostic biomarkers for human hepatocellular carcinoma. Artificial Cells, Nanomedicine and Biotechnology, 2019, 47, 1908-1916.	1.9	34
1145	Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. Cell Systems, 2019, 8, 427-445.e10.	2.9	111
1146	SBOL-OWL: An Ontological Approach for Formal and Semantic Representation of Synthetic Biology Information. ACS Synthetic Biology, 2019, 8, 1498-1514.	1.9	12
1147	Preeclampsia-Associated Alteration of DNA Methylation in Fetal Endothelial Progenitor Cells. Frontiers in Cell and Developmental Biology, 2019, 7, 32.	1.8	17
1148	GScluster: network-weighted gene-set clustering analysis. BMC Genomics, 2019, 20, 352.	1.2	12
1149	Immunological Molecular Responses of Human Retinal Pigment Epithelial Cells to Infection With Toxoplasma gondii. Frontiers in Immunology, 2019, 10, 708.	2.2	17
1150	Cross-Regulation between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. Molecular Cell, 2019, 74, 951-965.e13.	4.5	85
1151	Postovulatory maternal transcriptome in Atlantic salmon and its relation to developmental potential of embryos. BMC Genomics, 2019, 20, 315.	1.2	10

#	Article	IF	CITATIONS
1152	Genome sequence analysis of the fairy ring-forming fungus Lepista sordida and gene candidates for interaction with plants. Scientific Reports, 2019, 9, 5888.	1.6	15
1153	Integration of Multiple Data Sources for Gene Network Inference Using Genetic Perturbation Data. Journal of Computational Biology, 2019, 26, 1113-1129.	0.8	7
1154	Prediction of seed gene function in progressive diabetic neuropathy by a network‑based inference method. Experimental and Therapeutic Medicine, 2019, 17, 4176-4182.	0.8	1
1155	Autism risk genes are evolutionarily ancient and maintain a unique feature landscape that echoes their function. Autism Research, 2019, 12, 860-869.	2.1	10
1157	Transcriptome-wide analysis of the difference of alternative splicing in susceptible and resistant silkworm strains after BmNPV infection. 3 Biotech, 2019, 9, 152.	1.1	16
1158	PRISMA: Protein Interaction Screen on Peptide Matrix Reveals Interaction Footprints and Modifications- Dependent Interactome of Intrinsically Disordered C/EBPβ. IScience, 2019, 13, 351-370.	1.9	31
1159	Bioinformatic analysis to explore key genes associated with brain ischemia–reperfusion injury in rats. International Journal of Neuroscience, 2019, 129, 945-954.	0.8	9
1160	Biomolecular Databases and Subnetwork Identification Approaches of Interest to Big Data Community: An Expert Review. OMICS A Journal of Integrative Biology, 2019, 23, 138-151.	1.0	12
1161	Identification of Candidate Genes and MicroRNAs for Acute Myocardial Infarction by Weighted Gene Coexpression Network Analysis. BioMed Research International, 2019, 2019, 1-11.	0.9	23
1162	RNAi-based small molecule repositioning reveals clinically approved urea-based kinase inhibitors as broadly active antivirals. PLoS Pathogens, 2019, 15, e1007601.	2.1	26
1163	Identification of Essential Proteins Based on Improved HITS Algorithm. Genes, 2019, 10, 177.	1.0	14
1164	Regulation of Intronic Polyadenylation by PCF11 Impacts mRNA Expression of Long Genes. Cell Reports, 2019, 26, 2766-2778.e6.	2.9	77
1165	Repository of Enriched Structures of Proteins Involved in the Red Blood Cell Environment (RESPIRE). PLoS ONE, 2019, 14, e0211043.	1.1	5
1166	Conserved regulation of RNA processing in somatic cell reprogramming. BMC Genomics, 2019, 20, 100.	1.2	4
1167	JNK modifies neuronal metabolism to promote proteostasis and longevity. Aging Cell, 2019, 18, e12849.	3.0	18
1168	The transcriptome landscape of the carcinogenic treatment response in the blind mole rat: insights into cancer resistance mechanisms. BMC Genomics, 2019, 20, 17.	1.2	14
1169	Differential long noncoding RNAs expression in cancer-associated fibroblasts of non-small-cell lung cancer. Pharmacogenomics, 2019, 20, 143-153.	0.6	9
1170	lsoform-specific GSK3A activity is negatively correlated with human sperm motility. Molecular Human Reproduction, 2019, 25, 171-183.	1.3	18

#	Article	IF	CITATIONS
1171	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	9.4	154
1172	Prediction of key gene function in spinal muscular atrophy using guilt by association method based on network and gene ontology. Experimental and Therapeutic Medicine, 2019, 17, 2561-2566.	0.8	4
1173	Identification of co-expression modules and pathways correlated with osteosarcoma and its metastasis. World Journal of Surgical Oncology, 2019, 17, 46.	0.8	12
1174	Investigating the role of <i>Osiris </i> genes in <i>Drosophila sechellia </i> larval resistance to a host plant toxin. Ecology and Evolution, 2019, 9, 1922-1933.	0.8	21
1175	SuCComBase: a manually curated repository of plant sulfur-containing compounds. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	10
1176	Dosage Compensation of the X Chromosomes in Bovine Germline, Early Embryos, and Somatic Tissues. Genome Biology and Evolution, 2019, 11, 242-252.	1.1	7
1177	Handling Big Data Scalability in Biological Domain Using Parallel and Distributed Processing: A Case of Three Biological Semantic Similarity Measures. BioMed Research International, 2019, 2019, 1-20.	0.9	3
1178	CSgator: an integrated web platform for compound set analysis. Journal of Cheminformatics, 2019, 11, 17.	2.8	7
1179	How to Develop a Drug Target Ontology: KNowledge Acquisition and Representation Methodology (KNARM). Methods in Molecular Biology, 2019, 1939, 49-69.	0.4	2
1180	New Zealand Tree and Giant Wētĕ(Orthoptera) Transcriptomics Reveal Divergent Selection Patterns in Metabolic Loci. Genome Biology and Evolution, 2019, 11, 1293-1306.	1.1	6
1181	Horizontal gene transfer in human-associated microorganisms inferred by phylogenetic reconstruction and reconciliation. Scientific Reports, 2019, 9, 5953.	1.6	55
1182	In silico Characterization of Human Prion-Like Proteins: Beyond Neurological Diseases. Frontiers in Physiology, 2019, 10, 314.	1.3	17
1183	miRâ€ʿ146aâ€ʿ5p expression is upregulated by the CXCR4 antagonist TN14003 and attenuates SDFâ€ʿ1â€ʻinduce cartilage degradation. Molecular Medicine Reports, 2019, 19, 4388-4400.	ed 1.1	16
1184	GO functional similarity clustering depends on similarity measure, clustering method, and annotation completeness. BMC Bioinformatics, 2019, 20, 155.	1.2	19
1185	Candidate gene prioritization for non-communicable diseases based on functional information: Case studies. Journal of Biomedical Informatics, 2019, 93, 103155.	2.5	2
1186	A Network Module for the Perseus Software for Computational Proteomics Facilitates Proteome Interaction Graph Analysis. Journal of Proteome Research, 2019, 18, 2052-2064.	1.8	60
1187	Genomic Variants Among Threatened <i>Acropora</i> Corals. G3: Genes, Genomes, Genetics, 2019, 9, 1633-1646.	0.8	31
1188	Identification of SERPINE1, PLAU and ACTA1 as biomarkers of head and neck squamous cell carcinoma based on integrated bioinformatics analysis. International Journal of Clinical Oncology, 2019, 24, 1030-1041.	1.0	56

			2
#	ARTICLE	IF	CITATIONS
1189	MSTD: an efficient method for detecting multi-scale topological domains from symmetric and asymmetric 3D genomic maps. Nucleic Acids Research, 2019, 47, e65-e65.	6.5	15
1190	The Kinome of Human Alveolar Type II and Basal Cells, and Its Reprogramming in Lung Cancer. American Journal of Respiratory Cell and Molecular Biology, 2019, 61, 481-491.	1.4	1
1191	Identification of Potential Key Genes and Pathways in Early-Onset Colorectal Cancer Through Bioinformatics Analysis. Cancer Control, 2019, 26, 107327481983126.	0.7	46
1192	Computational translation of genomic responses from experimental model systems to humans. PLoS Computational Biology, 2019, 15, e1006286.	1.5	37
1193	iTRAQ-based analysis of leaf proteome identifies important proteins in secondary metabolite biosynthesis and defence pathways crucial to cross-protection against TMV. Journal of Proteomics, 2019, 196, 42-56.	1.2	18
1194	CircFunBase: a database for functional circular RNAs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	108
1195	The y-ome defines the 35% of <i>Escherichia coli</i> genes that lack experimental evidence of function. Nucleic Acids Research, 2019, 47, 2446-2454.	6.5	117
1196	Longitudinal investigation of DNA methylation changes preceding adolescent psychotic experiences. Translational Psychiatry, 2019, 9, 69.	2.4	13
1197	Indoxyl Sulfate Induces Apoptosis Through Oxidative Stress and Mitogen-Activated Protein Kinase Signaling Pathway Inhibition in Human Astrocytes. Journal of Clinical Medicine, 2019, 8, 191.	1.0	30
1198	Distinct Cancer-Promoting Stromal Gene Expression Depending on Lung Function. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 348-358.	2.5	20
1199	Identification of the targets of hematoporphyrin derivative in lung adenocarcinoma using integrated network analysis. Biological Research, 2019, 52, 4.	1.5	8
1200	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
1201	Kids' Smart Campus Ontology to Retrieve Interest. , 2019, , .		3
1202	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates Aβ, tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	9.4	1,962
1203	The evolution of gene regulatory networks controlling Arabidopsis thaliana L. trichome development. BMC Plant Biology, 2019, 19, 53.	1.6	40
1204	Enhanced Growth of Pilin-Deficient Geobacter sulfurreducens Mutants in Carbon Poor and Electron Donor Limiting Conditions. Microbial Ecology, 2019, 78, 618-630.	1.4	1
1205	Transcriptional regulation of the genes involved in protein metabolism and processing in <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2019, 19, .	1.1	1
1206	Genomics Analysis of L-DOPA Exposure in <i>Drosophila sechellia</i> . G3: Genes, Genomes, Genetics, 2019, 9, 3973-3980.	0.8	8

#	Article	IF	CITATIONS
1207	Changing expression profiles of lncRNAs, circRNAs and mRNAs in esophageal squamous carcinoma. Oncology Letters, 2019, 18, 5363-5373.	0.8	10
1208	Quantitative Proteomics of Uukuniemi Virus-host Cell Interactions Reveals GBF1 as Proviral Host Factor for Phleboviruses. Molecular and Cellular Proteomics, 2019, 18, 2401-2417.	2.5	12
1209	Using Taxonomy Tree to Generalize a Fuzzy Thematic Cluster. , 2019, , .		2
1210	Tumorigenic effects of TLX overexpression in HEK 293T cells. Cancer Reports, 2019, 2, e1204.	0.6	2
1211	Metabolic gene alterations impact the clinical aggressiveness and drug responses of 32 human cancers. Communications Biology, 2019, 2, 414.	2.0	55
1212	A network-based approach reveals novel invasion and Maurer's clefts-related proteins in Plasmodium falciparum. Molecular Omics, 2019, 15, 431-441.	1.4	4
1213	Acute pancreatitis promotes the generation of two different exosome populations. Scientific Reports, 2019, 9, 19887.	1.6	31
1214	Local adaptation of a dominant coastal tree to freshwater availability and solar radiation suggested by genomic and ecophysiological approaches. Scientific Reports, 2019, 9, 19936.	1.6	19
1215	Towards Reproducible Bioinformatics: The OpenBio-C Scientific Workflow Environment. , 2019, , .		7
1216	TS-GOEA: a web tool for tissue-specific gene set enrichment analysis based on gene ontology. BMC Bioinformatics, 2019, 20, 572.	1.2	7
1217	Phylostratigraphic Analysis Shows the Earliest Origination of the Abiotic Stress Associated Genes in A. thaliana. Genes, 2019, 10, 963.	1.0	11
1218	NNTox: Gene Ontology-Based Protein Toxicity Prediction Using Neural Network. Scientific Reports, 2019, 9, 17923.	1.6	10
1219	Multivariable regulation of gene expression plasticity in metazoans. Open Biology, 2019, 9, 190150.	1.5	11
1220	Analysis of master transcription factors related to Parkinson's disease through the gene transcription regulatory network. Archives of Medical Science, 2021, 17, 1184-1190.	0.4	2
1221	LePrimAlign: local entropy-based alignment of PPI networks to predict conserved modules. BMC Genomics, 2019, 20, 964.	1.2	4
1222	A novel algorithm for alignment of multiple PPI networks based on simulated annealing. BMC Genomics, 2019, 20, 932.	1.2	3
1223	Comparative analysis of squamate brains unveils multi-level variation in cerebellar architecture associated with locomotor specialization. Nature Communications, 2019, 10, 5560.	5.8	36
1224	Epigenome-wide association of father's smoking with offspring DNA methylation: a hypothesis-generating study. Environmental Epigenetics, 2019, 5, dvz023.	0.9	28

#	Article	IF	CITATIONS
1225	Genetic pathway analysis reveals a major role for extracellular matrix organization in inflammatory and neuropathic pain. Pain, 2019, 160, 932-944.	2.0	53
1226	The Biology of mRNA: Structure and Function. Advances in Experimental Medicine and Biology, 2019, , .	0.8	3
1227	Identification of Yeast's Interactome Using Neural Networks. IEEE Access, 2019, 7, 179634-179645.	2.6	0
1228	OntoPlot: A Novel Visualisation for Non-hierarchical Associations in Large Ontologies. IEEE Transactions on Visualization and Computer Graphics, 2019, 26, 1-1.	2.9	0
1229	The role of TCF3 as potential master regulator in blastemal Wilms tumors. International Journal of Cancer, 2019, 144, 1432-1443.	2.3	4
1230	Tomato stigma exsertion induced by high temperature is associated with the jasmonate signalling pathway. Plant, Cell and Environment, 2019, 42, 1205-1221.	2.8	47
1231	Curse: building expression atlases and co-expression networks from public RNA-Seq data. Bioinformatics, 2019, 35, 2880-2881.	1.8	25
1232	Classification of Widely and Rarely Expressed Genes with Recurrent Neural Network. Computational and Structural Biotechnology Journal, 2019, 17, 49-60.	1.9	49
1233	Identification of genes associated with cancer progression and prognosis in lung adenocarcinoma: Analyses based on microarray from Oncomine and The Cancer Genome Atlas databases. Molecular Genetics & Genomic Medicine, 2019, 7, e00528.	0.6	42
1234	MiRNA–target interactions in osteogenic signaling pathways involving zinc via the metal regulatory element. BioMetals, 2019, 32, 111-121.	1.8	6
1235	Cold Acclimation of the Thermoacidophilic Red Alga Galdieria sulphuraria: Changes in Gene Expression and Involvement of Horizontally Acquired Genes. Plant and Cell Physiology, 2019, 60, 702-712.	1.5	15
1236	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
1237	Modelling of zero-inflation improves inference of metagenomic gene count data. Statistical Methods in Medical Research, 2019, 28, 3712-3728.	0.7	10
1238	Human Disease Ontology 2018 update: classification, content and workflow expansion. Nucleic Acids Research, 2019, 47, D955-D962.	6.5	383
1239	Elevation in Cell Cycle and Protein Metabolism Gene Transcription in Inactive Colonic Tissue From Icelandic Patients With Ulcerative Colitis. Inflammatory Bowel Diseases, 2019, 25, 317-327.	0.9	5
1240	Assembly of a parts list of the human mitotic cell cycle machinery. Journal of Molecular Cell Biology, 2019, 11, 703-718.	1.5	80
1241	Low Expression of the Androgen-Induced Tumor Suppressor Gene <i>PLZF</i> and Lethal Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 707-714.	1.1	11
1242	Ethnicity-Specific Skeletal Muscle Transcriptional Signatures and Their Relevance to Insulin Resistance in Singapore. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 465-486.	1.8	4

#	Article	IF	CITATIONS
1243	Quantitative Proteomics of Potato Leaves Infected with Phytophthora infestans Provides Insights into Coordinated and Altered Protein Expression during Early and Late Disease Stages. International Journal of Molecular Sciences, 2019, 20, 136.	1.8	20
1244	Variation in the transcriptome of different ecotypes of <i>Arabidopsis thaliana</i> reveals signatures of oxidative stress in plant responses to spaceflight. American Journal of Botany, 2019, 106, 123-136.	0.8	57
1245	Expression profile of long non-coding RNAs in cervical spondylotic myelopathy of rats by microarray and bioinformatics analysis. Genomics, 2019, 111, 1192-1200.	1.3	5
1246	ETCM: an encyclopaedia of traditional Chinese medicine. Nucleic Acids Research, 2019, 47, D976-D982.	6.5	507
1247	OrthoInspector 3.0: open portal for comparative genomics. Nucleic Acids Research, 2019, 47, D411-D418.	6.5	46
1248	CCM111 prevents hepatic fibrosis via cooperative inhibition of TGF-β, Wnt and STAT3 signaling pathways. Journal of Food and Drug Analysis, 2019, 27, 184-194.	0.9	13
1249	Fusarium oxysporum cultured with complex nitrogen sources can degrade agricultural residues: Evidence from analysis of secreted enzymes and intracellular proteome. Renewable Energy, 2019, 133, 941-950.	4.3	12
1251	In Silico Oncology Drug Repositioning and Polypharmacology. Methods in Molecular Biology, 2019, 1878, 243-261.	0.4	48
1252	Hippocampal transcriptome profiling combined with protein-protein interaction analysis elucidates Alzheimer's disease pathways and genes. Neurobiology of Aging, 2019, 74, 225-233.	1.5	30
1253	Sequence Alterations of Cortical Genes Linked to Individual Connectivity of the Human Brain. Cerebral Cortex, 2019, 29, 3828-3835.	1.6	10
1254	Targeting the endoplasmic reticulum-mitochondria interface sensitizes leukemia cells to cytostatics. Haematologica, 2019, 104, 546-555.	1.7	10
1255	EWASdb: epigenome-wide association study database. Nucleic Acids Research, 2019, 47, D989-D993.	6.5	39
1256	Gene ontology improves template selection in comparative protein docking. Proteins: Structure, Function and Bioinformatics, 2019, 87, 245-253.	1.5	2
1257	Comparative proteomics of Tobacco mosaic virus-infected Nicotiana tabacum plants identified major host proteins involved in photosystems and plant defence. Journal of Proteomics, 2019, 194, 191-199.	1.2	30
1258	In Silico Target Prediction for Small Molecules. Methods in Molecular Biology, 2019, 1888, 273-309.	0.4	19
1259	The subcellular organisation of Saccharomyces cerevisiae. Current Opinion in Chemical Biology, 2019, 48, 86-95.	2.8	26
1260	Draft genome analysis of lignocellulolytic enzymes producing Aspergillus terreus with structural insight of β-glucosidases through molecular docking approach. International Journal of Biological Macromolecules, 2019, 125, 181-190.	3.6	28
1261	Identification of key genes and pathways in diabetic nephropathy by bioinformatics analysis. Journal of Diabetes Investigation, 2019, 10, 972-984.	1.1	52

#	Article	IF	CITATIONS
1264	The jPOST environment: an integrated proteomics data repository and database. Nucleic Acids Research, 2019, 47, D1218-D1224.	6.5	94
1265	The Use of Proteomics Studies in Identifying Moonlighting Proteins. Methods in Molecular Biology, 2019, 1871, 437-443.	0.4	5
1266	Identification of a 3′â€Untranslated Genetic Variant of <i><scp>RARB</scp></i> Associated With Carotid Intimaâ€Media Thickness in Rheumatoid Arthritis: A Genomeâ€Wide Association Study. Arthritis and Rheumatology, 2019, 71, 351-360.	2.9	26
1267	Symposium review: Omics in dairy and animal science—Promise, potential, and pitfalls. Journal of Dairy Science, 2019, 102, 4741-4754.	1.4	9
1268	Genomic Profiling of BDE-47 Effects on Human Placental Cytotrophoblasts. Toxicological Sciences, 2019, 167, 211-226.	1.4	32
1269	Protease target prediction via matrix factorization. Bioinformatics, 2019, 35, 923-929.	1.8	14
1270	The BioCyc collection of microbial genomes and metabolic pathways. Briefings in Bioinformatics, 2019, 20, 1085-1093.	3.2	582
1271	It is time to apply biclustering: a comprehensive review of biclustering applications in biological and biomedical data. Briefings in Bioinformatics, 2019, 20, 1450-1465.	3.2	42
1272	GPS: Identification of disease genes by rank aggregation of multi-genomic scoring schemes. Genomics, 2019, 111, 612-618.	1.3	5
1273	Drug knowledge bases and their applications in biomedical informatics research. Briefings in Bioinformatics, 2019, 20, 1308-1321.	3.2	29
1274	GESgnExt: Gene Expression Signature Extraction and Meta-Analysis on Gene Expression Omnibus. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 311-318.	3.9	4
1275	Microhomology-mediated end joining drives complex rearrangements and overexpression of <i>MYC</i> and <i>PVT1</i> in multiple myeloma. Haematologica, 2020, 105, 1055-1066.	1.7	42
1276	Detection of Driver Modules with Rarely Mutated Genes in Cancers. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 390-401.	1.9	9
1277	Developmental effects of maternal smoking during pregnancy on the human frontal cortex transcriptome. Molecular Psychiatry, 2020, 25, 3267-3277.	4.1	16
1278	Examination of the shared genetic basis of anorexia nervosa and obsessive–compulsive disorder. Molecular Psychiatry, 2020, 25, 2036-2046.	4.1	83
1279	Parsimonious generalization of fuzzy thematic sets in taxonomies applied to the analysis of tendencies of research in data science. Information Sciences, 2020, 512, 595-615.	4.0	10
1280	KCNH2-3.1 mediates aberrant complement activation and impaired hippocampal-medial prefrontal circuitry associated with working memory deficits. Molecular Psychiatry, 2020, 25, 206-229.	4.1	13
1281	An <i>in silico</i> Approach for Integrating Phenotypic and Targetâ€based Approaches in Drug Discovery. Molecular Informatics, 2020, 39, e1900096.	1.4	8

#	Article	IF	CITATIONS
1282	A sevenâ€ÐNA methylation signature as a novel prognostic biomarker in breast cancer. Journal of Cellular Biochemistry, 2020, 121, 2385-2393.	1.2	31
1283	KnockTF: a comprehensive human gene expression profile database with knockdown/knockout of transcription factors. Nucleic Acids Research, 2020, 48, D93-D100.	6.5	72
1284	Tensor-based mathematical framework and new centralities for temporal multilayer networks. Information Sciences, 2020, 512, 563-580.	4.0	13
1285	Simultaneous Enrichment Analysis of all Possible Gene-sets: Unifying Self-Contained and Competitive Methods. Briefings in Bioinformatics, 2020, 21, 1302-1312.	3.2	13
1286	Investigating Maize Yield-Related Genes in Multiple Omics Interaction Network Data. IEEE Transactions on Nanobioscience, 2020, 19, 142-151.	2.2	3
1287	Exosomal miR-1246 in serum as a potential biomarker for early diagnosis of gastric cancer. International Journal of Clinical Oncology, 2020, 25, 89-99.	1.0	79
1288	Melittin inhibits proliferation, migration and invasion of bladder cancer cells by regulating key genes based on bioinformatics and experimental assays. Journal of Cellular and Molecular Medicine, 2020, 24, 655-670.	1.6	19
1289	A transcriptome-wide association study implicates specific pre- and post-synaptic abnormalities in schizophrenia. Human Molecular Genetics, 2020, 29, 159-167.	1.4	54
1290	Matching whole genomes to rare genetic disorders: Identification of potential causative variants using phenotypeâ€weighted knowledge in the CAGI SickKids5 clinical genomes challenge. Human Mutation, 2020, 41, 347-362.	1.1	4
1291	Impact of left ventricular assist device therapy on the cardiac proteome and metabolome composition in ischemic cardiomyopathy. Artificial Organs, 2020, 44, 257-267.	1.0	6
1292	RCSB Protein Data Bank: Enabling biomedical research and drug discovery. Protein Science, 2020, 29, 52-65.	3.1	223
1293	miR-149 Suppresses Breast Cancer Metastasis by Blocking Paracrine Interactions with Macrophages. Cancer Research, 2020, 80, 1330-1341.	0.4	41
1294	Translational Knowledge Discovery Between Drug Interactions and Pharmacogenetics. Clinical Pharmacology and Therapeutics, 2020, 107, 886-902.	2.3	11
1295	\$\$varvec{extsc {Orpheus}}\$\$DB: bolt-on versioning for relational databases (extended version). VLDB Journal, 2020, 29, 509-538.	2.7	3
1296	Shotgun proteomics of Strongyloides venezuelensis infective third stage larvae: Insights into host–parasite interaction and novel targets for diagnostics. Molecular and Biochemical Parasitology, 2020, 235, 111249.	0.5	5
1297	Identification of Regulatory Modules That Stratify Lupus Disease Mechanism through Integrating Multi-Omics Data. Molecular Therapy - Nucleic Acids, 2020, 19, 318-329.	2.3	10
1299	Gene Regulatory Network of Dorsolateral Prefrontal Cortex: a Master Regulator Analysis of Major Psychiatric Disorders. Molecular Neurobiology, 2020, 57, 1305-1316.	1.9	6
1300	pH Gradient Mitigation in the Leaf Cell Secretory Pathway Attenuates the Defense Response of <i>Nicotiana benthamiana</i> to Agroinfiltration. Journal of Proteome Research, 2020, 19, 106-118.	1.8	2

#	Article	IF	CITATIONS
1301	Next-generation hypomethylating agent SGI-110 primes acute myeloid leukemia cells to IAP antagonist by activating extrinsic and intrinsic apoptosis pathways. Cell Death and Differentiation, 2020, 27, 1878-1895.	5.0	8
1302	Molecular responses to freshwater limitation in the mangrove tree <i>Avicennia germinans</i> (Acanthaceae). Molecular Ecology, 2020, 29, 344-362.	2.0	12
1303	An ectomycorrhizal fungus alters sensitivity to jasmonate, salicylate, gibberellin, and ethylene in host roots. Plant, Cell and Environment, 2020, 43, 1047-1068.	2.8	30
1304	Identification of distinct blood-based biomarkers in early stage of Parkinson's disease. Neurological Sciences, 2020, 41, 893-901.	0.9	17
1305	Analysis of topology properties in different tissues of poplar based on gene co-expression networks. Tree Genetics and Genomes, 2020, 16, 1.	0.6	4
1306	Fungal functional ecology: bringing a traitâ€based approach to plantâ€associated fungi. Biological Reviews, 2020, 95, 409-433.	4.7	171
1307	Transcriptional network dynamics during the progression of pluripotency revealed by integrative statistical learning. Nucleic Acids Research, 2020, 48, 1828-1842.	6.5	14
1308	IncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. Scientific Data, 2020, 7, 326.	2.4	40
1309	Single-Cell Transcriptome Analysis of Colon Cancer Cell Response to 5-Fluorouracil-Induced DNA Damage. Cell Reports, 2020, 32, 108077.	2.9	40
1310	The similarity of inherited diseases (II): clinical and biological similarity between the phenotypic series. BMC Medical Genomics, 2020, 13, 139.	0.7	2
1311	Predicted functional interactome of Caenorhabditis elegans and a web tool for the functional interpretation of differentially expressed genes. Biology Direct, 2020, 15, 20.	1.9	3
1312	GeneSetCluster: a tool for summarizing and integrating gene-set analysis results. BMC Bioinformatics, 2020, 21, 443.	1.2	13
1313	Identification of putative master regulators in rheumatoid arthritis synovial fibroblasts using gene expression data and network inference. Scientific Reports, 2020, 10, 16236.	1.6	12
1314	Identification of COVID-19 Infection-Related Human Genes Based on a Random Walk Model in a Virus–Human Protein Interaction Network. BioMed Research International, 2020, 2020, 1-7.	0.9	16
1315	Genomic characterization of Parengyodontium americanum sp. nov. Fungal Genetics and Biology, 2020, 138, 103351.	0.9	4
1316	Genomic adaptations of the green alga Dunaliella salina to life under high salinity. Algal Research, 2020, 50, 101990.	2.4	18
1317	GADL1 is a multifunctional decarboxylase with tissue-specific roles in Î <sup>2</sup> -alanine and carnosine production. Science Advances, 2020, 6, eabb3713.	4.7	27
1318	Bile acids regulate intestinal antigen presentation and reduce graft-versus-host disease without impairing the graft-versus-leukemia effect. Haematologica, 2021, 106, 2131-2146.	1.7	26

#	Article	IF	CITATIONS
1319	Proteome analysis revealed the essential functions of protein phosphatase PP2A in the induction of Th9 cells. Scientific Reports, 2020, 10, 10992.	1.6	6
1320	Next Generation Sequencing Identify Rare Copy Number Variants in Non-syndromic Patent Ductus Arteriosus. Frontiers in Genetics, 2020, 11, 600787.	1.1	5
1321	The Broad Transcription Factor Links Hormonal Signaling, Gene Expression, and Cellular Morphogenesis Events During <i>Drosophila</i> Imaginal Disc Development. Genetics, 2020, 216, 1137-1152.	1.2	2
1322	Transcriptional Remodeling Patterns in Murine Dendritic Cells Infected with Paracoccidioides brasiliensis: More Is Not Necessarily Better. Journal of Fungi (Basel, Switzerland), 2020, 6, 311.	1.5	2
1323	Transcriptomic analysis of peripheral leukocytes in dairy cows with and without evidence of metritis and associated early postpartum disease. Applied Animal Science, 2020, 36, 784-798.	0.4	2
1324	A six-amino-acid motif is a major determinant in functional evolution of HOX1 proteins. Genes and Development, 2020, 34, 1680-1696.	2.7	16
1325	Identification and quantification of target metabolites combined with transcriptome of two rheum species focused on anthraquinone and flavonoids biosynthesis. Scientific Reports, 2020, 10, 20241.	1.6	17
1326	Recent advances in network-based methods for disease gene prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	42
1327	Genetic profiling for diffuse type and genomically stable subtypes in gastric cancer. Computational and Structural Biotechnology Journal, 2020, 18, 3301-3308.	1.9	12
1328	GelFAP: Gene Functional Analysis Platform for Gastrodia elata. Frontiers in Plant Science, 2020, 11, 563237.	1.7	7
1329	Characterization and validation of long noncoding RNAs as new candidates in prostate cancer. Cancer Cell International, 2020, 20, 531.	1.8	7
1330	Molecular Signatures and Networks of Cardiomyocyte Differentiation in Humans and Mice. Molecular Therapy - Nucleic Acids, 2020, 21, 696-711.	2.3	11
1331	Drug discovery strategies for modulating oxidative stress in gastrointestinal disorders. Expert Opinion on Drug Discovery, 2020, 15, 1309-1341.	2.5	18
1332	An interspecies translation model implicates integrin signaling in infliximab-resistant inflammatory bowel disease. Science Signaling, 2020, 13, .	1.6	19
1333	Gene Set Analysis: Challenges, Opportunities, and Future Research. Frontiers in Genetics, 2020, 11, 654.	1.1	120
1334	Single-Cell Transcriptomic Profiling of Vascular Smooth Muscle Cell Phenotype Modulation in Marfan Syndrome Aortic Aneurysm. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 40, 2195-2211.	1.1	126
1335	Salt stress induces endoplasmic reticulum stress-responsive genes in a grapevine rootstock. PLoS ONE, 2020, 15, e0236424.	1.1	28
1336	Formal axioms in biomedical ontologies improve analysis and interpretation of associated data. Bioinformatics, 2020, 36, 2229-2236.	1.8	13

#	Article	IF	CITATIONS
1337	Network Pharmacology-Based Analysis of the Pharmacological Mechanisms of Aloperine on Cardiovascular Disease. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-8.	0.5	7
1338	Genomeâ€wide effect of tetracycline, doxycycline and 4â€epidoxycycline on gene expression inSaccharomyces cerevisiae. Yeast, 2020, 37, 389-396.	0.8	8
1339	Comparative proteomic analysis of human mesenchymal stromal cell behavior on calcium phosphate ceramics with different osteoinductive potential. Materials Today Bio, 2020, 7, 100066.	2.6	13
1340	Predicted yeast interactome and networkâ€based interpretation of transcriptionally changed genes. Yeast, 2020, 37, 573-583.	0.8	1
1341	Evaluation of immune infiltrating of thyroid cancer based on the intrinsic correlation between pair-wise immune genes. Life Sciences, 2020, 259, 118248.	2.0	9
1343	Proximity labeling in mammalian cells with TurboID and split-TurboID. Nature Protocols, 2020, 15, 3971-3999.	5.5	171
1344	Ancient RNA virus epidemics through the lens of recent adaptation in human genomes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190575.	1.8	37
1345	Identification of Key Genes and Potential New Biomarkers for Ovarian Aging: A Study Based on RNA-Sequencing Data. Frontiers in Genetics, 2020, 11, 590660.	1.1	21
1346	Interferon-Mediated Long Non-Coding RNA Response in Macrophages in the Context of HIV. International Journal of Molecular Sciences, 2020, 21, 7741.	1.8	12
1347	Preclinical validation of therapeutic targets predicted by tensor factorization on heterogeneous graphs. Scientific Reports, 2020, 10, 18250.	1.6	30
1348	Stromal microenvironment promoted infiltration in esophageal adenocarcinoma and squamous cell carcinoma: a multi-cohort gene-based analysis. Scientific Reports, 2020, 10, 18589.	1.6	6
1349	Correlations Between Phenotypes and Biological Process Ontologies in Monogenic Human Diseases. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 547-554.	2.2	1
1350	Sex-Specific Transcriptome Differences in Human Adipose Mesenchymal Stem Cells. Genes, 2020, 11, 909.	1.0	24
1351	Transcriptome sequencing and metabolite profiling analyses provide comprehensive insight into molecular mechanisms of flower development in Dendrobium officinale (Orchidaceae). Plant Molecular Biology, 2020, 104, 529-548.	2.0	23
1352	Dissecting Transcription Factor-Target Interaction in Bovine Coronavirus Infection. Microorganisms, 2020, 8, 1323.	1.6	5
1353	Mass spectrometry-based analysis of formalin-fixed, paraffin-embedded distal cholangiocarcinoma identifies stromal thrombospondin-2 as a potential prognostic marker. Journal of Translational Medicine, 2020, 18, 343.	1.8	10
1354	Review on the Computational Genome Annotation of Sequences Obtained by Next-Generation Sequencing. Biology, 2020, 9, 295.	1.3	45
1355	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	13.5	243

#	Article	IF	CITATIONS
1356	DNA methylation study of Huntington's disease and motor progression in patients and in animal models. Nature Communications, 2020, 11, 4529.	5.8	45
1357	Ontological approach to the knowledge systematization of a toxic process and toxic course representation framework for early drug risk management. Scientific Reports, 2020, 10, 14581.	1.6	2
1358	Disease Cluster Detection and Functional Characterization. IEEE Access, 2020, 8, 141958-141966.	2.6	5
1359	Computational Analysis of the Global Effects of Ly6E in the Immune Response to Coronavirus Infection Using Gene Networks. Genes, 2020, 11, 831.	1.0	6
1360	A new strategy of studying protein–protein interactions: Integrated strong anion exchange/reversedâ€phase chromatography/immunoprecipitation coupled with mass spectrometry for largeâ€scale identification of proteins interact with immunoglobulin G in HeLa cells. Journal of Separation Science, 2020, 43, 3913-3920.	1.3	2
1361	Matrix Metallopeptidase 14: A Candidate Prognostic Biomarker for Diffuse Large B-Cell Lymphoma. Frontiers in Oncology, 2020, 10, 1520.	1.3	5
1362	Mito-oncology agent: fermented extract suppresses the Warburg effect, restores oxidative mitochondrial activity, and inhibits in vivo tumor growth. Scientific Reports, 2020, 10, 14174.	1.6	8
1363	Construction and analysis of the protein–protein interaction network for the olfactory system of the silkworm <i>Bombyx mori</i> . Archives of Insect Biochemistry and Physiology, 2020, 105, e21737.	0.6	9
1364	A Novel Graph Topology based GO-Similarity Measure for Signature Detection from Multi-Omics Data and its Application to Other Problems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	1.9	5
1365	PCOSKBR2: a database of genes, diseases, pathways, and networks associated with polycystic ovary syndrome. Scientific Reports, 2020, 10, 14738.	1.6	16
1366	DEAD-Box Helicase 4 (Ddx4)+ Stem Cells Sustain Tumor Progression in Non-Serous Ovarian Cancers. International Journal of Molecular Sciences, 2020, 21, 6096.	1.8	2
1367	Ontologies and Artificial Intelligence Systems for the Cooperative Smart Farming Ecosystem. IEEE Access, 2020, 8, 164045-164064.	2.6	52
1368	Multi-View Gene Clustering using Gene Ontology and Expression-based Similarities. , 2020, , .		2
1369	HIF-1α and HIF-2α differently regulate tumour development and inflammation of clear cell renal cell carcinoma in mice. Nature Communications, 2020, 11, 4111.	5.8	141
1370	Deciphering serous ovarian carcinoma histopathology and platinum response by convolutional neural networks. BMC Medicine, 2020, 18, 236.	2.3	33
1371	A Clinical Extensively-Drug Resistant (XDR) Escherichia coli and Role of Its β-Lactamase Genes. Frontiers in Microbiology, 2020, 11, 590357.	1.5	8
1372	A methodology for predicting tissue-specific metabolic roles of receptors applied to subcutaneous adipose. Scientific Reports, 2020, 10, 19535.	1.6	2
1373	Identify and Validate the Transcriptomic, Functional Network, and Predictive Validity of FBXL19-AS1 in Hepatocellular Carcinoma. Frontiers in Oncology, 2020, 10, 609601.	1.3	4

# 1374	ARTICLE Automated Extraction of Information From Texts of Scientific Publications: Insights Into HIV Treatment Strategies. Frontiers in Genetics, 2020, 11, 618862.	IF 1.1	CITATIONS
1375	Platelet microparticles load a repertory of miRNAs programmed to drive osteogenic phenotype. Journal of Biomedical Materials Research - Part A, 2021, 109, 1502-1511.	2.1	6
1376	scREAD: A Single-Cell RNA-Seq Database for Alzheimer's Disease. IScience, 2020, 23, 101769.	1.9	77
1377	Immunogenetic and tolerance strategies against a novel parasitoid of wild field crickets. Ecology and Evolution, 2020, 10, 13312-13326.	0.8	0
1378	Comprehensive gene expression profiling of human astrocytes treated with a hepatic encephalopathy-inducible factor, alpha 1-antichymotripsin. Biochemistry and Biophysics Reports, 2020, 24, 100855.	0.7	0
1379	Proteomic Profiling Change and Its Implies in the Early Mycosis Fungoides (MF) Using Isobaric Tags for Relative and Absolute Quantification (iTRAQ). BioMed Research International, 2020, 2020, 1-13.	0.9	3
1380	multiGSEA: a GSEA-based pathway enrichment analysis for multi-omics data. BMC Bioinformatics, 2020, 21, 561.	1.2	70
1381	Comparative transcriptomic analysis of antimony resistant and susceptible Leishmania infantum lines. Parasites and Vectors, 2020, 13, 600.	1.0	22
1382	Integrative Analysis Reveals Common and Unique Roles of Tetraspanins in Fibrosis and Emphysema. Frontiers in Genetics, 2020, 11, 585998.	1.1	3
1383	Common Factors in Neurodegeneration: A Meta-Study Revealing Shared Patterns on a Multi-Omics Scale. Cells, 2020, 9, 2642.	1.8	32
1384	An Automated Functional Annotation Pipeline That Rapidly Prioritizes Clinically Relevant Genes for Autism Spectrum Disorder. International Journal of Molecular Sciences, 2020, 21, 9029.	1.8	1
1385	Genetic insights into the evolution of genera with the eastern Asia–eastern North America floristic disjunction: a transcriptomics analysis. American Journal of Botany, 2020, 107, 1736-1748.	0.8	6
1386	UPEFinder: A Bioinformatic Tool for the Study of Uncharacterized Proteins Based on Gene Expression Correlation and the PageRank Algorithm. Journal of Proteome Research, 2020, 19, 4795-4807.	1.8	3
1387	Identified plasma proteins related to vascular structure are associated with coarctation of the aorta in children. Italian Journal of Pediatrics, 2020, 46, 63.	1.0	0
1388	Prognostic Value of a Stemness Index-Associated Signature in Primary Lower-Grade Glioma. Frontiers in Genetics, 2020, 11, 441.	1.1	35
1389	Galectin-3 modulates epithelial cell adaptation to stress at the ER-mitochondria interface. Cell Death and Disease, 2020, 11, 360.	2.7	22
1390	Comprehensive analysis of mutations of renal cell carcinoma in an autosomal dominant polycystic kidney disease patient. Medicine (United States), 2020, 99, e20071.	0.4	3
1391	Mining the role of angiopoietinâ€like protein family in gastric cancer and seeking potential therapeutic targets by integrative bioinformatics analysis. Cancer Medicine, 2020, 9, 4850-4863.	1.3	12

#	Article	IF	CITATIONS
1392	Genomic competition for noise reduction shaped evolutionary landscape of mir-4673. Npj Systems Biology and Applications, 2020, 6, 12.	1.4	4
1393	Genome sequence of Kobresia littledalei, the first chromosome-level genome in the family Cyperaceae. Scientific Data, 2020, 7, 175.	2.4	20
1394	Genome-wide transcriptome architecture in a mouse model of Gulf War Illness. Brain, Behavior, and Immunity, 2020, 89, 209-223.	2.0	13
1395	Host-Virus Arms Races Drive Elevated Adaptive Evolution in Viral Receptors. Journal of Virology, 2020, 94, .	1.5	18
1396	The effect of baicalin on microRNA expression profiles in porcine aortic vascular endothelial cells infected by Haemophilus parasuis. Molecular and Cellular Biochemistry, 2020, 472, 45-56.	1.4	6
1397	Gut–Brain Axis and Neurodegeneration: State-of-the-Art of Meta-Omics Sciences for Microbiota Characterization. International Journal of Molecular Sciences, 2020, 21, 4045.	1.8	46
1398	Anti-infective nitazoxanide disrupts transcription of ribosome biogenesis-related genes in yeast. Genes and Genomics, 2020, 42, 915-926.	0.5	6
1399	Proteomics analysis of zebrafish larvae exposed to 3,4â€dichloroaniline using the fish embryo acute toxicity test. Environmental Toxicology, 2020, 35, 849-860.	2.1	16
1400	Effects of High-Dose Ionizing Radiation in Human Gene Expression: A Meta-Analysis. International Journal of Molecular Sciences, 2020, 21, 1938.	1.8	8
1401	Identification of small RNAs involved in nitrogen fixation in Anabaena sp. PCC 7120 based on RNA-seq under steady state conditions. Annals of Microbiology, 2020, 70, .	1.1	5
1402	Complexities in Genetics of Psoriatic Arthritis. Current Rheumatology Reports, 2020, 22, 10.	2.1	23
1404	LncRNAs Predicted to Interfere With the Gene Regulation Activity of miR-637 and miR-196a-5p in GBM. Frontiers in Oncology, 2020, 10, 303.	1.3	5
1405	Heterogeneity of chondrosarcomas response to irradiations with X-rays and carbon ions: A comparative study on five cell lines. Journal of Bone Oncology, 2020, 22, 100283.	1.0	10
1406	Functional colour genes and signals of selection in colourâ€polymorphic salamanders. Molecular Ecology, 2020, 29, 1284-1299.	2.0	15
1407	Loss of Cx43 in Murine Sertoli Cells Leads to Altered Prepubertal Sertoli Cell Maturation and Impairment of the Mitosis-Meiosis Switch. Cells, 2020, 9, 676.	1.8	11
1408	Polyhydroxyalkanoate (PHA) synthase genes and PHA-associated gene clusters in Pseudomonas spp. and Janthinobacterium spp. isolated from Antarctica. Journal of Biotechnology, 2020, 313, 18-28.	1.9	31
1409	Sustainable engineering technologies to promote activities of beneficial microbiome. , 2020, , 231-275.		1
1410	Exploring the mechanism of action Xianlingubao Prescription in the treatment of osteoporosis by network pharmacology. Computational Biology and Chemistry, 2020, 85, 107240.	1.1	50

#	Article	IF	CITATIONS
1411	Predicted Drosophila Interactome Resource and web tool for functional interpretation of differentially expressed genes. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	8
1412	Identification of Four Potential Biomarkers Associated With Coronary Artery Disease in Non-diabetic Patients by Gene Co-expression Network Analysis. Frontiers in Genetics, 2020, 11, 542.	1.1	13
1413	Differential DNA methylation profiles of peripheral blood mononuclear cells in allergic asthmatic children following dust mite immunotherapy. Journal of Microbiology, Immunology and Infection, 2020, 53, 986-995.	1.5	4
1414	Modulation of stress and immune response by Amblyomin-X results in tumor cell death in a horse melanoma model. Scientific Reports, 2020, 10, 6388.	1.6	12
1415	Adipose tissue in health and disease through the lens of its building blocks. Scientific Reports, 2020, 10, 10433.	1.6	40
1416	GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. PLoS ONE, 2020, 15, e0233311.	1.1	7
1417	A transcriptome-based approach to identify functional modules within and across primary human immune cells. PLoS ONE, 2020, 15, e0233543.	1.1	10
1418	Identification of potential key pathways, genes and circulating markers in the development of intracranial aneurysm based on weighted gene co-expression network analysis. Artificial Cells, Nanomedicine and Biotechnology, 2020, 48, 999-1007.	1.9	4
1419	Transcriptome profiling of venom gland from wasp species: de novo assembly, functional annotation, and discovery of molecular markers. BMC Genomics, 2020, 21, 427.	1.2	7
1420	Co-expression network analysis identifies a gene signature as a predictive biomarker for energy metabolism in osteosarcoma. Cancer Cell International, 2020, 20, 259.	1.8	24
1421	Unveiling ncRNA regulatory axes in atherosclerosis progression. Clinical and Translational Medicine, 2020, 9, 5.	1.7	24
1422	ncRPheno: a comprehensive database platform for identification and validation of disease related noncoding RNAs. RNA Biology, 2020, 17, 943-955.	1.5	23
1423	Genome sequence of the agarwood tree Aquilaria sinensis (Lour.) Spreng: the first chromosome-level draft genome in the Thymelaeceae family. GigaScience, 2020, 9, .	3.3	34
1424	Enhancing reproducibility of gene expression analysis with known protein functional relationships: The concept of well-associated protein. PLoS Computational Biology, 2020, 16, e1007684.	1.5	2
1425	Volatile Organic Compounds of Endophytic <i>Burkholderia pyrrocinia</i> Strain JK-SH007 Promote Disease Resistance in Poplar. Plant Disease, 2020, 104, 1610-1620.	0.7	19
1426	A New Scheme for Essential Protein Identification Based on Uncertain Networks. IEEE Access, 2020, 8, 33977-33989.	2.6	4
1427	Genome-wide meta-analysis associates GPSM1 with type 2 diabetes, a plausible gene involved in skeletal muscle function. Journal of Human Genetics, 2020, 65, 411-420.	1.1	6
1428	EcoToxModules: Custom Gene Sets to Organize and Analyze Toxicogenomics Data from Ecological Species. Environmental Science & amp; Technology, 2020, 54, 4376-4387.	4.6	16

		CITATION REPORT		
#	Article		IF	CITATIONS
1429	Domain-mediated interactions for protein subfamily identification. Scientific Reports, 2	2020, 10, 264.	1.6	2
1430	Transcriptome differences in adipose stromal cells derived from pre- and postmenopau Stem Cell Research and Therapy, 2020, 11, 92.	sal women.	2.4	2
1431	Stem Cell-Derived Endothelial Cell Model that Responds to Tobacco Smoke Like Prima Cells. Chemical Research in Toxicology, 2020, 33, 751-763.	y Endothelial	1.7	12
1432	NETGE-PLUS: Standard and Network-Based Gene Enrichment Analysis in Human and M Journal of Proteome Research, 2020, 19, 2873-2878.	odel Organisms.	1.8	3
1433	Variations and expression features of CYP2D6 contribute to schizophrenia risk. Molect 2021, 26, 2605-2615.	ılar Psychiatry,	4.1	8
1434	Recent trends and advances in identification and functional characterization of plant r Physiologiae Plantarum, 2020, 42, 1.	niRNAs. Acta	1.0	22
1435	Single-cell morphology encodes metastatic potential. Science Advances, 2020, 6, eaav	<i>v</i> 6938.	4.7	112
1436	A Circulating Bioreactor Reprograms Cancer Cells Toward a More Mesenchymal Niche. Biology, 2020, 4, 1900139.	Advanced	3.0	4
1437	Machine Learning and Network Analyses Reveal Disease Subtypes of Pancreatic Cance Molecular Characteristics. Scientific Reports, 2020, 10, 1212.	r and their	1.6	62
1438	Ontology engineering: Current state, challenges, and future directions. Semantic Web 125-138.	, 2020, 11,	1.1	26
1439	A framework towards data analytics on host–pathogen protein–protein interactio Ambient Intelligence and Humanized Computing, 2020, 11, 4667-4679.	ns. Journal of	3.3	7
1440	Systematic metadata analysis of brown rot fungi gene expression data reveals the gen Fenton's reaction and wood decay process. Mycology, 2020, 11, 22-37.	es involved in	2.0	9
1441	A multi-omic analysis of orange-spotted grouper larvae infected with nervous necrosis identifies increased adhesion molecules and collagen synthesis in the persistent state. Shellfish Immunology, 2020, 98, 595-604.	virus Fish and	1.6	15
1442	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.		13.7	280
1443	ORSO (Online Resource for Social Omics): A data-driven social network connecting sci genomics datasets. PLoS Computational Biology, 2020, 16, e1007571.	entists to	1.5	2
1444	Rewilding Nod2 and Atg16l1 Mutant Mice Uncovers Genetic and Environmental Contr Microbial Responses and Immune Cell Composition. Cell Host and Microbe, 2020, 27,		5.1	62
1445	The impact of rattlesnake venom on mice cerebellum proteomics points to synaptic in tissue damage. Journal of Proteomics, 2020, 221, 103779.	hibition and	1.2	8
1446	Extracting Explicable Rules for the Identification of Compound–Protein Interactions. 2020, 8, 70005-70012.	IEEE Access,	2.6	0

ARTICLE IF CITATIONS Identification of Pan-Cancer Prognostic Biomarkers Through Integration of Multi-Omics Data. 1447 2.0 21 Frontiers in Bioengineering and Biotechnology, 2020, 8, 268. Tissueâ€selective regulation of protein homeostasis and unfolded protein response signalling in 1448 1.6 sporadic ALS. Journal of Cellular and Molecular Medicine, 2020, 24, 6055-6069. Identification of HO-1 as a novel biomarker for graft acute cellular rejection and prognosis 1449 0.7 8 prediction after liver transplantation. Annals of Translational Medicine, 2020, 8, 221-221. DES-ROD: Exploring Literature to Develop New Links between RNA Oxidation and Human Diseases. 1450 1.9 Oxidative Medicine and Cellular Longevity, 2020, 2020, 1-13. Characterization of aerobic denitrification genome sequencing of Vibrio parahaemolyticus strain HA2 1451 1.7 13 from recirculating mariculture system in China. Aquaculture, 2020, 526, 735295. Interactions between Lactobacillus plantarum NCU116 and its environments based on extracellular 1.3 proteins and polysaccharides prediction by comparative analysis. Genomics, 2020, 112, 3579-3587. Investigation of miRNA and mRNA Co-expression Network in Ependymoma. Frontiers in Bioengineering 1453 2.0 13 and Biotechnology, 2020, 8, 177. Toward a gold standard for benchmarking gene set enrichment analysis. Briefings in Bioinformatics, 1454 3.2 2021, 22, 545-556. TMT-based proteomics analysis to screen potential biomarkers of acute-phase TBI in rats. Life Sciences, 1455 2.0 13 2021, 264, 118631. Genomeâ€wide analysis of acute traumatic spinal cord injuryâ€related RNA expression profiles and 1456 2.4 uncovering of a regulatory axis in spinal fibrotic scars. Cell Proliferation, 2021, 54, e12951. A novel method of highâ€purity extracellular vesicle enrichment from microliterâ€scale human serum 1457 1.3 18 for proteomic analysis. Electrophoresis, 2021, 42, 245-256. Neurogranin, Encoded by the Schizophrenia Risk Gene NRGN, Bidirectionally Modulates Synaptic Plasticity via Calmodulin-Dependent Regulation of the Neuronal Phosphoproteome. Biological Psychiatry, 2021, 89, 256-269. IDPology of the living cell: intrinsic disorder in the subcellular compartments of the human cell. 1459 2.4 15 Cellular and Molecular Life Sciences, 2021, 78, 2371-2385. From classical to new generation approaches: An excursus of -omics methods for investigation of 1460 1.2 protein-protein interaction networks. Journal of Proteomics, 2021, 230, 103990. Coronavirus: proteomics analysis of chicken kidney tissue infected with variant 2 (IS-1494)-like avian 1461 0.9 4 infectious bronchitis virus. Archives of Virology, 2021, 166, 101-113. A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. 1462 3.1 European Respiratory Journal, 2021, 57, 2002693. Identification and analysis of immune-related subtypes of hepatocellular carcinoma. Experimental 1463 1.1 1 Biology and Medicine, 2021, 246, 667-677. A fusion of CD63–BCAR4 identified in lung adenocarcinoma promotes tumorigenicity and metastasis. 1464 British Journal of Cancer, 2021, 124, 290-298.

#	Article	IF	CITATIONS
1465	Comparative proteomics of common allergenic tree pollens of birch, alder, and hazel. Allergy: European Journal of Allergy and Clinical Immunology, 2021, 76, 1743-1753.	2.7	5
1466	High gene space divergence contrasts with frozen vegetative architecture in the moss family Funariaceae. Molecular Phylogenetics and Evolution, 2021, 154, 106965.	1.2	5
1467	CNS genomic profiling in the mouse chronic social stress model implicates a novel category of candidate genes integrating affective pathogenesis. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2021, 105, 110086.	2.5	6
1468	Towards Integrating the Gene Ontology and the Hierarchical Bayesian Network Classification Model: An Empirical Case Study. Information Technology in Industry, 2019, 7, .	0.2	0
1470	The prognostic significance of tumor-infiltrating lymphocytes in cervical cancer. Journal of Gynecologic Oncology, 2021, 32, e32.	1.0	9
1471	The underlying molecular mechanism and identification of transcription factor markers for laryngeal squamous cell carcinoma. Bioengineered, 2021, 12, 208-224.	1.4	9
1472	Thromboangiitis obliterans plasma-derived exosomal miR-223-5p inhibits cell viability and promotes cell apoptosis of human vascular smooth muscle cells by targeting VCAM1. Annals of Medicine, 2021, 53, 1130-1142.	1.5	5
1473	Short loop functional commonality identified in leukaemia proteome highlights crucial protein sub-networks. NAR Genomics and Bioinformatics, 2021, 3, lqab010.	1.5	0
1474	Role of circular RNA expression in the pathological progression after spinal cord injury. Neural Regeneration Research, 2021, 16, 2048.	1.6	16
1475	Computational Genomics. , 2021, , 213-241.		0
1476	Gene expression and prognosis of x-ray repair cross-complementing family members in non-small cell lung cancer. Bioengineered, 2021, 12, 6210-6228.	1.4	4
1478	Database exploration: Selection and analysis of target protein structures. , 2021, , 89-106.		1
1479	Predicting and understanding synergistic pairwise compound combinations of Shexian Baoxin Pill (SBP) using network biology. Synergy, 2021, 11, 100073.	1.1	1
1480	Genome Recovery, Functional Profiling, and Taxonomic Classification from Metagenomes. Methods in Molecular Biology, 2021, 2242, 153-172.	0.4	2
1482	HIR V2: a human interactome resource for the biological interpretation of differentially expressed genes via gene set linkage analysis. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	3
1483	Wastewater Treatment for Bioenergy Purposes Using a Metaproteomic Approach. , 2021, , 253-278.		1
1484	A novel Foxp3-related immune prognostic signature for glioblastoma multiforme based on immunogenomic profiling. Aging, 2021, 13, 3501-3517.	1.4	11
1485	Bioinformatics analysis of miRNA and mRNA expression profiles to reveal the key miRNAs and genes in osteoarthritis. Journal of Orthopaedic Surgery and Research, 2021, 16, 63.	0.9	17

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#	Article	IF	CITATIONS
1486	Getting to know each other: PPIMem, a novel approach for predicting transmembrane protein-protein complexes. Computational and Structural Biotechnology Journal, 2021, 19, 5184-5197.	1.9	5
1487	Amino Acid Composition in Various Types of Nucleic Acid-Binding Proteins. International Journal of Molecular Sciences, 2021, 22, 922.	1.8	14
1488	Disease severity-specific neutrophil signatures in blood transcriptomes stratify COVID-19 patients. Genome Medicine, 2021, 13, 7.	3.6	193
1489	Prediction and collection of protein–metabolite interactions. Briefings in Bioinformatics, 2021, 22, .	3.2	52
1491	Ontology-guided segmentation and object identification for developmental mouse lung immunofluorescent images. BMC Bioinformatics, 2021, 22, 82.	1.2	2
1492	The Paradoxical Behavior of microRNA-211 in Melanomas and Other Human Cancers. Frontiers in Oncology, 2020, 10, 628367.	1.3	6
1493	Ferroptosisâ€related gene signature as a prognostic marker for lowerâ€grade gliomas. Journal of Cellular and Molecular Medicine, 2021, 25, 3080-3090.	1.6	29
1494	Network mapping of primary CD34+ cells by Ampliseq based whole transcriptome targeted resequencing identifies unexplored differentiation regulatory relationships. PLoS ONE, 2021, 16, e0246107.	1.1	0
1495	Size changes in miR‑21 knockout mice: Geometric morphometrics on teeth, alveolar bone and mandible. Molecular Medicine Reports, 2021, 23, .	1.1	3
1496	The glycoconjugate ontology (GlycoCoO) for standardizing the annotation of glycoconjugate data and its application. Glycobiology, 2021, 31, 741-750.	1.3	7
1497	Named Data Networking for Genomics Data Management and Integrated Workflows. Frontiers in Big Data, 2021, 4, 582468.	1.8	3
1499	Weight Loss Following Rouxâ€en‥ Gastric Bypass Causally Implicated with Serum Levels of ILâ€22: A Mendelian Randomization and Phenomeâ€Wide Association Study. Obesity, 2021, 29, 610-615.	1.5	1
1500	A Meta-Analysis of the Effects of High-LET Ionizing Radiations in Human Gene Expression. Life, 2021, 11, 115.	1.1	8
1501	Transcriptomic Analysis of the Anthocyanin Biosynthetic Pathway Reveals the Molecular Mechanism Associated with Purple Color Formation in Dendrobium Nestor. Life, 2021, 11, 113.	1.1	14
1502	Deep Protein Subcellular Localization Predictor Enhanced with Transfer Learning of GO Annotation. IEEJ Transactions on Electrical and Electronic Engineering, 2021, 16, 559-567.	0.8	3
1503	Putative Circulating MicroRNAs Are Able to Identify Patients with Mitral Valve Prolapse and Severe Regurgitation. International Journal of Molecular Sciences, 2021, 22, 2102.	1.8	6
1504	Cross-species RNA-seq for deciphering host–microbe interactions. Nature Reviews Genetics, 2021, 22, 361-378.	7.7	52
1505	Sialotranscriptomics of the argasid tick Ornithodoros moubata along the trophogonic cycle. PLoS Neglected Tropical Diseases, 2021, 15, e0009105.	1.3	16

#	Article	IF	CITATIONS
1506	GeneWalk identifies relevant gene functions for a biological context using network representation learning. Genome Biology, 2021, 22, 55.	3.8	28
1507	Analysing the yeast complexome—the Complex Portal rising to the challenge. Nucleic Acids Research, 2021, 49, 3156-3167.	6.5	5
1508	Immune gene expression networks in sepsis: A network biology approach. PLoS ONE, 2021, 16, e0247669.	1.1	17
1509	Structural and functional study ofLegionella pneumophilaeffector RavA. Protein Science, 2021, 30, 940-955.	3.1	6
1510	STATegra: Multi-Omics Data Integration – A Conceptual Scheme With a Bioinformatics Pipeline. Frontiers in Genetics, 2021, 12, 620453.	1.1	24
1511	The factors for the early and late development of midbrain dopaminergic neurons segregate into two distinct evolutionary clusters. Brain Disorders, 2021, 1, 100002.	1.1	3
1512	CRISPR-cas9 Screening Identified Lethal Genes Enriched in Cell Cycle Pathway and of Prognosis Significance in Breast Cancer. Frontiers in Cell and Developmental Biology, 2021, 9, 646774.	1.8	6
1513	Unveiling the long non-coding RNA profile of porcine reproductive and respiratory syndrome virus-infected porcine alveolar macrophages. BMC Genomics, 2021, 22, 177.	1.2	11
1514	RNA-seq analysis and gene expression dynamics in the salivary glands of the argasid tick Ornithodoros erraticus along the trophogonic cycle. Parasites and Vectors, 2021, 14, 170.	1.0	14
1515	Complete genome sequencing of Bacillus sp. TK-2, analysis of its cold evolution adaptability. Scientific Reports, 2021, 11, 4836.	1.6	11
1516	Gill microbiome structure and function in the chemosymbiotic coastal lucinid <i>Stewartia floridana</i> . FEMS Microbiology Ecology, 2021, 97, .	1.3	2
1519	A multi-omic characterization of temperature stress in a halotolerant Scenedesmus strain for algal biotechnology. Communications Biology, 2021, 4, 333.	2.0	22
1520	Research and Clinical Significance of the Differentially Expressed Genes TP63 and LMO4 in Human Immunodeficiency Virus-Related Penile Squamous Cell Carcinoma. American Journal of Men's Health, 2021, 15, 155798832110113.	0.7	0
1522	Genetic Polymorphism Drives Susceptibility Between Bacteria and Bacteriophages. Frontiers in Microbiology, 2021, 12, 627897.	1.5	5
1523	Comparative transcriptome profiling reveals differentially expressed genes involved in flavonoid biosynthesis between biennial and triennial Sophora flavescens. Industrial Crops and Products, 2021, 161, 113217.	2.5	6
1524	A Streamlined Approach to Pathway Analysis from RNA-Sequencing Data. Methods and Protocols, 2021, 4, 21.	0.9	0
1525	Tumor Microenvironment Proteomics: Lessons From Multiple Myeloma. Frontiers in Oncology, 2021, 11, 563384.	1.3	2
1526	KRAS, YWHAE, SP1 and MSRA as biomarkers in endometrial cancer. Translational Cancer Research, 2021, 10, 1295-1312.	0.4	7

#	Article	IF	CITATIONS
1527	Transcriptional regulation of alcohol induced liver fibrosis in a translational porcine hepatocellular carcinoma model. Biochimie, 2021, 182, 73-84.	1.3	7
1528	Genome-wide association meta-analysis identifies pleiotropic risk loci for aerodigestive squamous cell cancers. PLoS Genetics, 2021, 17, e1009254.	1.5	19
1529	Genomeâ€wide ancestry and introgression in a Zambian baboon hybrid zone. Molecular Ecology, 2021, 30, 1907-1920.	2.0	9
1530	Immunogenomic Profiling Demonstrate AC003092.1 as an Immune-Related eRNA in Glioblastoma Multiforme. Frontiers in Genetics, 2021, 12, 633812.	1.1	12
1531	Identification of Decrease in TRiC Proteins as Novel Targets of Alpha-Amanitin-Derived Hepatotoxicity by Comparative Proteomic Analysis In Vitro. Toxins, 2021, 13, 197.	1.5	5
1532	Identification of disease treatment mechanisms through the multiscale interactome. Nature Communications, 2021, 12, 1796.	5.8	72
1533	Network pharmacology and RNA-sequencing reveal the molecular mechanism of Xuebijing injection on COVID-19-induced cardiac dysfunction. Computers in Biology and Medicine, 2021, 131, 104293.	3.9	14
1534	AdaReg: data adaptive robust estimation in linear regression with application in GTEx gene expressions. Statistical Applications in Genetics and Molecular Biology, 2021, 20, 51-71.	0.2	1
1535	CXCL1 Clone Evolution Induced by the HDAC Inhibitor Belinostat Might Be a Favorable Prognostic Indicator in Triple-Negative Breast Cancer. BioMed Research International, 2021, 2021, 1-12.	0.9	4
1536	The tree of life describes a tripartite cellular world. BioEssays, 2021, 43, 2000343.	1.2	8
1537	Comparative transcriptome and histological analyses provide insights into the skin pigmentation in Minxian black fur sheep (Ovis aries). PeerJ, 2021, 9, e11122.	0.9	8
1538	An Overview of Biological and Computational Methods for Designing Mechanism-Informed Anti-biofilm Agents. Frontiers in Microbiology, 2021, 12, 640787.	1.5	25
1539	Assessment of <i>Erythrobacter</i> Species Diversity through Pan-Genome Analysis with Newly Isolated <i>Erythrobacter</i> sp. 3-20A1M. Journal of Microbiology and Biotechnology, 2021, 31, 601-609.	0.9	3
1540	A random walk-based method for detecting essential proteins by integrating the topological and biological features of PPI network. Soft Computing, 2021, 25, 8883-8903.	2.1	6
1541	On the Unfounded Enthusiasm for Soft Selective Sweeps III: The Supervised Machine Learning Algorithm That Isn't. Genes, 2021, 12, 527.	1.0	2
1542	Deciphering Pharmacological Mechanism of Buyang Huanwu Decoction for Spinal Cord Injury by Network Pharmacology Approach. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-20.	0.5	3
1543	Exploring the Pharmacological Mechanism of Duhuo Jisheng Decoction in Treating Osteoporosis Based on Network Pharmacology. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-21.	0.5	16
1544	Genome-wide association study of antipsychotic-induced sinus bradycardia in Chinese schizophrenia patients. PLoS ONE, 2021, 16, e0249997.	1.1	3

#	Article	IF	CITATIONS
1545	Expression analysis of progesterone‑regulated miRNAs in cells derived from human glioblastoma. Molecular Medicine Reports, 2021, 23, .	1.1	0
1549	Lantern: an integrative repository of functional annotations for IncRNAs in the human genome. BMC Bioinformatics, 2021, 22, 279.	1.2	2
1551	Circular RNA Plek promotes fibrogenic activation by regulating the miR-135b-5p/TGF-βR1 axis after spinal cord injury. Aging, 2021, 13, 13211-13224.	1.4	12
1552	Planococcus soli sp. nov., isolated from antarctic soil. Antonie Van Leeuwenhoek, 2021, 114, 1107-1115.	0.7	2
1553	Mining a stroke knowledge graph from literature. BMC Bioinformatics, 2021, 22, 387.	1.2	4
1554	Sporulation is dispensable for the vegetableâ€associated life cycle of the human pathogen <i>BacillusÂcereus</i> . Microbial Biotechnology, 2021, 14, 1550-1565.	2.0	13
1555	Gene and protein expression in human megakaryocytes derived from induced pluripotent stem cells. Journal of Thrombosis and Haemostasis, 2021, 19, 1783-1799.	1.9	6
1556	Bioinformatics-based Identification of Key Pathways and Hub Genes of Traumatic Brain Injury in a Rat Model. Current Medical Science, 2021, 41, 610-617.	0.7	2
1557	DNA methylation signatures associated with prognosis of gastric cancer. BMC Cancer, 2021, 21, 610.	1.1	9
1558	Establishment of a prognostic model of four genes in gastric cancer based on multiple data sets. Cancer Medicine, 2021, 10, 3309-3322.	1.3	13
1559	Differentially expressed genes induced by $\hat{l}^2$ -caryophyllene in a rat model of cerebral ischemia-reperfusion injury. Life Sciences, 2021, 273, 119293.	2.0	9
1560	MSCFS: inferring circRNA functional similarity based on multiple data sources. BMC Bioinformatics, 2021, 22, 371.	1.2	2
1561	Bibliometric Analysis on Bibliometric-based Ontology Research. Science and Technology Libraries, 0, , 1-19.	0.8	3
1562	An 8-gene DNA methylation signature predicts the recurrence risk of cervical cancer. Journal of International Medical Research, 2021, 49, 030006052110184.	0.4	6
1563	The Synergistic Effects of 5-Aminosalicylic Acid and Vorinostat in the Treatment of Ulcerative Colitis. Frontiers in Pharmacology, 2021, 12, 625543.	1.6	10
1564	MicroRNA Profiles of Maternal and Neonatal Endothelial Progenitor Cells in Preeclampsia. International Journal of Molecular Sciences, 2021, 22, 5320.	1.8	12
1565	System biology and bioinformatics pipeline to identify comorbidities risk association: Neurodegenerative disorder case study. PLoS ONE, 2021, 16, e0250660.	1.1	4
1567	Long-chain non-coding RNA n337374 relieves symptoms of respiratory syncytial virus-induced asthma by inhibiting dendritic cell maturation via the CD86 and ERK pathway. Allergologia Et Immunopathologia, 2021, 49, 100-107.	1.0	12

#	Article	IF	CITATIONS
1568	Identification of Ten Mitosis Genes Associated with Tamoxifen Resistance in Breast Cancer. OncoTargets and Therapy, 2021, Volume 14, 3611-3624.	1.0	1
1569	Model-based pathway enrichment analysis applied to the TGF-beta regulation of autophagy in autism. Journal of Biomedical Informatics, 2021, 118, 103781.	2.5	3
1571	RTP4 is a novel prognosis-related hub gene in cutaneous melanoma. Hereditas, 2021, 158, 22.	0.5	9
1572	Regulatory miRNA–mRNA Networks in Parkinson's Disease. Cells, 2021, 10, 1410.	1.8	12
1573	Determining protein–protein functional associations by functional rules based on gene ontology and KEGG pathway. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140621.	1.1	58
1574	Metabolomics and Network Pharmacology-Based Investigation into the Mechanisms Underlying the Therapeutic Effect of a New Chinese Traditional Medicine (Cui Nai Ling) on Bromocriptine-Induced Hypogalactia. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-17.	0.5	2
1575	Comprehensive Bioinformatics Analysis of mRNA Expression Profiles and Identification of a miRNA–mRNA Network Associated with the Pathogenesis of Low-Grade Gliomas. Cancer Management and Research, 2021, Volume 13, 5135-5147.	0.9	4
1576	Annotating the Insect Regulatory Genome. Insects, 2021, 12, 591.	1.0	4
1577	Association Analysis of Chromosome X to Identify Genetic Modifiers of Huntington's Disease. Journal of Huntington's Disease, 2021, 10, 367-375.	0.9	5
1578	Gene Expression Profiles Associated with Radio-Responsiveness in Locally Advanced Rectal Cancer. Biology, 2021, 10, 500.	1.3	9
1579	Screening and identification of potential biomarkers and therapeutic targets for systemic sclerosis-associated interstitial lung disease. Archives of Rheumatology, 2021, 36, 548-559.	0.3	0
1580	Tankyrase regulates epithelial lumen formation via suppression of Rab11 GEFs. Journal of Cell Biology, 2021, 220, .	2.3	6
1581	Computational analysis revealed miRNAs produced by Chikungunya virus target genes associated with antiviral immune responses and cell cycle regulation. Computational Biology and Chemistry, 2021, 92, 107462.	1.1	4
1582	LjaFGD: <i>Lonicera japonica</i> functional genomics database. Journal of Integrative Plant Biology, 2021, 63, 1422-1436.	4.1	12
1583	Genome-wide detection of copy number variations in Tharparkar cattle. Animal Biotechnology, 2023, 34, 448-455.	0.7	22
1584	Advances in protein-protein interaction network analysis for Parkinson's disease. Neurobiology of Disease, 2021, 155, 105395.	2.1	31
1585	Identification and Validation of Immune Molecular Subtypes in Pancreatic Ductal Adenocarcinoma: Implications for Prognosis and Immunotherapy. Frontiers in Immunology, 2021, 12, 690056.	2.2	13
1586	Seven key hub genes identified by gene co-expression network in cutaneous squamous cell carcinoma. BMC Cancer, 2021, 21, 852.	1.1	16

ARTICLE IF CITATIONS Correlation between targeted RNAseq signature of breast cancer CTCs and onset of bone-only 1587 2.9 10 metastases. British Journal of Cancer, 2022, 126, 419-429. Identification of differentially expressed genes in diabetic kidney disease by RNAâ€5eq analysis of venous 1.0 blood platelets. FEBS Open Bio, 2021, 11, 2095-2109. Identification of novel heavy metal detoxification proteins in Solanum tuberosum: Insights to improve 1589 3.9 22 food security protection from metal ion stress. Science of the Total Environment, 2021, 779, 146197. Uncovering Potential IncRNAs and mRNAs in the Progression From Acute Myocardial Infarction to 1590 1.1 Myocardial Fibrosis to Heart Failure. Frontiers in Cardiovascular Medicine, 2021, 8, 664044. Metatranscriptomics for the Human Microbiome and Microbial Community Functional Profiling. 1591 2.8 36 Annual Review of Biomedical Data Science, 2021, 4, 279-311. Gene expression analysis method integration and co-expression module detection applied to rare glucide metabolism disorders using ExpHunterSuite. Scientific Reports, 2021, 11, 15062. 1592 1.6 DES-Tcell is a knowledgebase for exploring immunology-related literature. Scientific Reports, 2021, 11, 1593 1.6 1 14344. An ancestral recombination graph of human, Neanderthal, and Denisovan genomes. Science Advances, 1594 4.7 47 2021, 7, . 1595 The Taxus genome provides insights into paclitaxel biosynthesis. Nature Plants, 2021, 7, 1026-1036. 103 4.7 Chaperone-like protein DAY plays critical roles in photomorphogenesis. Nature Communications, 2021, 1596 5.8 12, 4194. Gentamicin-induced hearing loss: A retrospective study using the Food and Drug Administration Adverse Event Reporting System and a toxicological study using druga "gene network analysis. Heliyon, 1597 2 1.4 2021, 7, e07429. Euzebya pacifica sp. nov., a novel member of the class Nitriliruptoria. International Journal of 1598 0.8 Systematic and Evolutionary Microbiology, 2021, 71, . Exploring the Pharmacological Mechanisms of Tripterygium wilfordii Hook F against Cardiovascular Disease Using Network Pharmacology and Molecular Docking. BioMed Research International, 2021, 1599 0.9 3 2021, 1-11. HiDRA: Hierarchical Network for Drug Response Prediction with Attention. Journal of Chemical Information and Modeling, 2021, 61, 3858-3867. 1600 2.5 Strategy for high-throughput identification of protein complexes by array-based multi-dimensional 1601 10 1.8 liquid chromatography-mass spectrometry. Journal of Chromatography A, 2021, 1652, 462351. Utilization of Transcriptome, Small RNA, and Degradome Sequencing to Provide Insights Into Drought Stress and Rewatering Treatment in Medicago ruthenica. Frontiers in Plant Science, 2021, 12, 675903. Identification of potential biomarkers in dengue via integrated bioinformatic analysis. PLoS Neglected 1603 1.35 Tropical Diseases, 2021, 15, e0009633. Circulating microRNAs in Early Breast Cancer Patients and Its Association With Lymph Node 1604 1.3 Metastases. Frontiers in Oncology, 2021, 11, 627811.

#	Article	IF	CITATIONS
1605	High glycosyltransferaseÂ8 domain containing two protein levels contribute to poor prognosis in urothelial carcinoma. International Journal of Urology, 2021, 28, 1178-1187.	0.5	0
1606	An ancient viral epidemic involving host coronavirus interacting genes more than 20,000 years ago in East Asia. Current Biology, 2021, 31, 3504-3514.e9.	1.8	71
1607	Identification of cytokeratin24 as a tumor suppressor for the management of head and neck cancer. Biological Chemistry, 2022, 403, 869-890.	1.2	9
1608	New Insights Into Mitochondrial Dysfunction at Disease Susceptibility Loci in the Development of Type 2 Diabetes. Frontiers in Endocrinology, 2021, 12, 694893.	1.5	6
1609	Establishment of an Immune-Related Gene Signature for Risk Stratification for Patients with Glioma. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-20.	0.7	2
1610	Protein function prediction with gene ontology: from traditional to deep learning models. PeerJ, 2021, 9, e12019.	0.9	8
1611	Identification and Validation of a Five-Gene Signature Associated With Overall Survival in Breast Cancer Patients. Frontiers in Oncology, 2021, 11, 660242.	1.3	7
1613	Exploring new targets for the treatment of hepatitis-B virus and hepatitis-B virus-associated hepatocellular carcinoma. Medicine (United States), 2021, 100, e26917.	0.4	5
1614	Experimental and computational investigation of enzyme functional annotations uncovers misannotation in the EC 1.1.3.15 enzyme class. PLoS Computational Biology, 2021, 17, e1009446.	1.5	21
1616	Genome-Wide DNA Methylation and Hydroxymethylation Changes Revealed Epigenetic Regulation of Neuromodulation and Myelination in Yak Hypothalamus. Frontiers in Genetics, 2021, 12, 592135.	1.1	2
1617	Exploring Diagnostic Biomarkers and Comorbid Pathogenesis for Osteoarthritis and Metabolic Syndrome via Bioinformatics Approach. International Journal of General Medicine, 2021, Volume 14, 6201-6213.	0.8	5
1618	Recurrence biomarkers of triple negative breast cancer treated with neoadjuvant chemotherapy and anti-EGFR antibodies. Npj Breast Cancer, 2021, 7, 124.	2.3	7
1619	A High-Throughput Method to Analyze the Interaction Proteins With p22 Protein of African Swine Fever Virus In Vitro. Frontiers in Veterinary Science, 2021, 8, 719859.	0.9	5
1620	Risk Prediction of Cardiovascular Events by Exploration of Molecular Data with Explainable Artificial Intelligence. International Journal of Molecular Sciences, 2021, 22, 10291.	1.8	21
1621	Transcriptomic profiling in canines and humans reveals cancer specific gene modules and biological mechanisms common to both species. PLoS Computational Biology, 2021, 17, e1009450.	1.5	11
1622	An Integrated Analysis of Network Pharmacology and Experimental Validation to Reveal the Mechanism of Chinese Medicine Formula Naotaifang in Treating Cerebral Ischemia-Reperfusion Injury. Drug Design, Development and Therapy, 2021, Volume 15, 3783-3808.	2.0	15
1623	Cannabinoid receptor 2 is necessary to induce tollâ€like receptorâ€mediated microglial activation. Glia, 2022, 70, 71-88.	2.5	24
1624	Evidenceâ€based complementary and alternative medicine bioinformatics approach through network pharmacology and molecular docking to determine the molecular mechanisms of Erjing pill in Alzheimer's disease. Experimental and Therapeutic Medicine, 2021, 22, 1252.	0.8	4

#	Article	IF	CITATIONS
1625	Elucidation of the Algicidal Mechanism of the Marine Bacterium Pseudoruegeria sp. M32A2M Against the Harmful Alga Alexandrium catenella Based on Time-Course Transcriptome Analysis. Frontiers in Marine Science, 2021, 8, .	1.2	4
1626	Cell-specific gene association network construction from single-cell RNA sequence. Cell Cycle, 2021, 20, 1-16.	1.3	3
1627	Immune Mechanism, Gene Module, and Molecular Subtype Identification of Astragalus Membranaceus in the Treatment of Dilated Cardiomyopathy: An Integrated Bioinformatics Study. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-29.	0.5	1
1628	Malignant Tumor Purity Reveals the Driven and Prognostic Role of CD3E in Low-Grade Glioma Microenvironment. Frontiers in Oncology, 2021, 11, 676124.	1.3	10
1629	Transcriptomic and Metabolomic Analyses Reveals That Exogenous Methyl Jasmonate Regulates Galanthamine Biosynthesis in Lycoris longituba Seedlings. Frontiers in Plant Science, 2021, 12, 713795.	1.7	9
1630	Coronary revascularization in acute coronary syndrome: does the choice of the conduit matter?. Journal of Cardiovascular Surgery, 2022, 62, .	0.3	0
1632	Recurrence-associated gene signature in patients with stage I non-small-cell lung cancer. Scientific Reports, 2021, 11, 19596.	1.6	5
1633	Identification of immune-associated gene signature and immune cell infiltration related to overall survival in progressive multiple sclerosis. Multiple Sclerosis and Related Disorders, 2021, 55, 103188.	0.9	2
1634	Gene Ontology representation for transcription factor functions. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194752.	0.9	17
1635	Testes morphology and the identification of transcripts of the hormonal pathways of the velvetbean caterpillar Anticarsia gemmatalis Hübner, 1818 (Lepidoptera: Erebidae). Arthropod Structure and Development, 2021, 65, 101111.	0.8	1
1636	Identification and expression analysis of miRNAs in germination and seedling growth of Tibetan hulless barley. Genomics, 2021, 113, 3735-3749.	1.3	9
1637	Integrative analysis of potential biomarkers and immune cell infiltration in Parkinson's disease. Brain Research Bulletin, 2021, 177, 53-63.	1.4	5
1638	The important role of RPS14, RPL5 and MDM2 in TP53-associated ribosome stress in mycophenolic acid-induced microtia. International Journal of Pediatric Otorhinolaryngology, 2021, 151, 110916.	0.4	1
1639	Down-regulating Circular RNA Prkcsh suppresses the inflammatory response after spinal cord injury. Neural Regeneration Research, 2022, 17, 144.	1.6	20
1640	RGS2-mediated translational control mediates cancer cell dormancy and tumor relapse. Journal of Clinical Investigation, 2021, 131, .	3.9	23
1641	Predicting Genotype Information Related to COVID-19 for Molecular Mechanism Based on Computational Methods. CMES - Computer Modeling in Engineering and Sciences, 2021, 129, 31-45.	0.8	2
1642	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	5
1643	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

#	Article	IF	CITATIONS
1644	Genomics Reveals the Origins of Historical Specimens. Molecular Biology and Evolution, 2021, 38, 2166-2176.	3.5	24
1645	Toward Data-Driven Radiation Oncology Using Standardized Terminology as a Starting Point: Cross-sectional Study. JMIR Formative Research, 2022, 6, e27550.	0.7	0
1646	Viral miRNAs confer survival in host cells by targeting apoptosis related host genes. Informatics in Medicine Unlocked, 2021, 22, 100501.	1.9	5
1647	Bioinformatics and machine learning methodologies to identify the effects of central nervous system disorders on glioblastoma progression. Briefings in Bioinformatics, 2021, 22, .	3.2	24
1648	Protein Bioinformatics Databases and Resources. Methods in Molecular Biology, 2017, 1558, 3-39.	0.4	154
1649	Bioinformatics Analysis of Protein Phosphorylation in Plant Systems Biology Using P3DB. Methods in Molecular Biology, 2017, 1558, 127-138.	0.4	12
1650	Bioinformatics Approaches to Gain Insights into cis-Regulatory Motifs Involved in mRNA Localization. Advances in Experimental Medicine and Biology, 2019, 1203, 165-194.	0.8	2
1651	The Product Guides the Process: Discovering Disease Mechanisms. Studies in Applied Philosophy, Epistemology and Rational Ethics, 2018, , 101-117.	0.2	4
1652	GARUM: A Semantic Similarity Measure Based on Machine Learning and Entity Characteristics. Lecture Notes in Computer Science, 2018, , 169-183.	1.0	3
1653	GlycoGene Database (GGDB) on the Semantic Web. , 2017, , 163-175.		10
1654	Predicting Protein-Protein Interaction in Multi-layer Blood Cell PPI Networks. Communications in Computer and Information Science, 2019, , 240-251.	0.4	3
1655	The constitutive protease release by primary human acute myeloid leukemia cells. Journal of Cancer Research and Clinical Oncology, 2017, 143, 1985-1998.	1.2	16
1656	CHARGE and Kabuki Syndromes: Gene-Specific DNA Methylation Signatures Identify Epigenetic Mechanisms Linking These Clinically Overlapping Conditions. American Journal of Human Genetics,		
	2017, 100, 773-788.	2.6	166
1657	Targeting XIAP and PPAR <sup>î</sup> <sup>3</sup> in Granulosa Cell Tumors Alters Metabolic Signaling. Journal of Proteome Research, 2019, 18, 1691-1702.	2.6 1.8	166 8
1657 1658	2017, 100, 773-788. Targeting XIAP and PPARÎ <sup>3</sup> in Granulosa Cell Tumors Alters Metabolic Signaling. Journal of Proteome		
	<ul> <li>2017, 100, 773-788.</li> <li>Targeting XIAP and PPARÎ<sup>3</sup> in Granulosa Cell Tumors Alters Metabolic Signaling. Journal of Proteome Research, 2019, 18, 1691-1702.</li> <li>Genetic variation in the exome: Associations with alcohol and tobacco co-use Psychology of</li> </ul>	1.8	8
1658	<ul> <li>2017, 100, 773-788.</li> <li>Targeting XIAP and PPARÎ<sup>3</sup> in Granulosa Cell Tumors Alters Metabolic Signaling. Journal of Proteome Research, 2019, 18, 1691-1702.</li> <li>Genetic variation in the exome: Associations with alcohol and tobacco co-use Psychology of Addictive Behaviors, 2017, 31, 354-366.</li> <li>Lymphatic endothelial cells prime naÃ<sup>-</sup>ve CD8+ T cells into memory cells under steady-state conditions.</li> </ul>	1.8 1.4	8

ARTICLE IF CITATIONS Transcriptomic Analysis of <i>Arabidopsis</i> Seedlings in Response to an <i>Agrobacterium</i>-Mediated Transformation Process. Molecular Plant-Microbe Interactions, 2018, 1662 16 1.4 31, 445-459. An assessment of genome annotation coverage across the bacterial tree of life. Microbial Genomics, 1.0 2020, 6, . GNG5 is an unfavourable independent prognostic indicator of gliomas. Journal of Cellular and 1743 1.6 12 Molecular Medicine, 2020, 24, 12873-12878. Emergence of pathway-level composite biomarkers from converging gene set signals of heterogeneous 1744 transcriptomic responses., 2018, , . Pediatric dilated cardiomyopathy hearts display a unique gene expression profile. JCI Insight, 2017, 2, . 1745 2.3 46 Cancer-associated fibroblast-derived annexin A6+ extracellular vesicles support pancreatic cancer 1746 169 aggressiveness. Journal of Clinical Investigation, 2016, 126, 4140-4156. Insulin resistance causes inflammation in adipose tissue. Journal of Clinical Investigation, 2018, 128, 1747 3.9 303 1538-1550. Proteomics and Bioinformatics Analysis of Cartilage in Post-Traumatic Osteoarthritis in a Mini-Pig 1748 Model of Anterior Cruciate Ligament Repair. Medical Science Monitor, 2020, 26, e920104. ELIXIR pilot action: Marine metagenomics  $\hat{a} \in \hat{}$  towards a domain specific set of sustainable services. 1749 0.8 8 F1000Research, 2017, 6, 70. An end to end workflow for differential gene expression using Affymetrix microarrays. 0.8 F1000Research, 2016, 5, 1384. An end to end workflow for differential gene expression using Affymetrix microarrays. 1751 31 0.8 F1000Research, 2016, 5, 1384. Identification of potential pathogenic genes associated with osteoporosis. Bone and Joint Research, 1.3 2017, 6, 640-648. Isofunctional Protein Subfamily Detection Using Data Integration and Spectral Clustering. PLoS 1753 1.5 7 Computational Biology, 2016, 12, e1005001. Bipartite Community Structure of eQTLs. PLoS Computational Biology, 2016, 12, e1005033. 1754 1.5 Utility and Limitations of Using Gene Expression Data to Identify Functional Associations. PLoS 1755 1.5 63 Computational Biology, 2016, 12, e1005244. Oncodomains: A protein domain-centric framework for analyzing rare variants in tumor samples. PLoS Computational Biology, 2017, 13, e1005428. Protein charge distribution in proteomes and its impact on translation. PLoS Computational Biology, 1757 1.556 2017, 13, e1005549. Predictive network modeling in human induced pluripotent stem cells identifies key driver genes for 1.5

CITATION REPORT

insulin responsiveness. PLoS Computational Biology, 2020, 16, e1008491.

#

# 1759	ARTICLE NUCLEAR FACTOR Y, Subunit C (NF-YC) Transcription Factors Are Positive Regulators of Photomorphogenesis in Arabidopsis thaliana. PLoS Genetics, 2016, 12, e1006333.	IF 1.5	CITATIONS
1760	Hereditary cancer genes are highly susceptible to splicing mutations. PLoS Genetics, 2018, 14, e1007231.	1.5	45
1761	High-Throughput Sequencing and De Novo Assembly of Red and Green Forms of the Perilla frutescens var. crispa Transcriptome. PLoS ONE, 2015, 10, e0129154.	1.1	40
1762	Bioinformatics Knowledge Map for Analysis of Beta-Catenin Function in Cancer. PLoS ONE, 2015, 10, e0141773.	1.1	12
1763	Union Exon Based Approach for RNA-Seq Gene Quantification: To Be or Not to Be?. PLoS ONE, 2015, 10, e0141910.	1.1	25
1764	Insight into the Salivary Gland Transcriptome of Lygus lineolaris (Palisot de Beauvois). PLoS ONE, 2016, 11, e0147197.	1.1	23
1765	Novel Biomarker Proteins in Chronic Lymphocytic Leukemia: Impact on Diagnosis, Prognosis and Treatment. PLoS ONE, 2016, 11, e0148500.	1.1	13
1766	Targeted Sequencing and Meta-Analysis of Preterm Birth. PLoS ONE, 2016, 11, e0155021.	1.1	13
1767	SVM-Prot 2016: A Web-Server for Machine Learning Prediction of Protein Functional Families from Sequence Irrespective of Similarity. PLoS ONE, 2016, 11, e0155290.	1.1	98
1768	Changes to the Aqueous Humor Proteome during Glaucoma. PLoS ONE, 2016, 11, e0165314.	1.1	53
1769	Integrity of Induced Pluripotent Stem Cell (iPSC) Derived Megakaryocytes as Assessed by Genetic and Transcriptomic Analysis. PLoS ONE, 2017, 12, e0167794.	1.1	9
1770	Human Lacrimal Gland Gene Expression. PLoS ONE, 2017, 12, e0169346.	1.1	12
1771	Metabox: A Toolbox for Metabolomic Data Analysis, Interpretation and Integrative Exploration. PLoS ONE, 2017, 12, e0171046.	1.1	85
1772	Large-scale bioactivity analysis of the small-molecule assayed proteome. PLoS ONE, 2017, 12, e0171413.	1.1	4
1773	A three-way approach for protein function classification. PLoS ONE, 2017, 12, e0171702.	1.1	11
1774	Splicing-related genes are alternatively spliced upon changes in ambient temperatures in plants. PLoS ONE, 2017, 12, e0172950.	1.1	75
1775	Epigenetic silencing of V(D)J recombination is a major determinant for selective differentiation of mucosal-associated invariant t cells from induced pluripotent stem cells. PLoS ONE, 2017, 12, e0174699.	1.1	8
1776	Identifying novel fruit-related genes in Arabidopsis thaliana based on the random walk with restart algorithm. PLoS ONE, 2017, 12, e0177017.	1.1	10

## # ARTICLE

IF CITATIONS

De novo assembly and annotation of the retinal transcriptome for the Nile grass rat (Arvicanthis) Tj ETQq000 rgBT<sub>1.1</sub> Overlock 10 Tf 50 7

1778	RBM10 promotes transformation-associated processes in small cell lung cancer and is directly regulated by RBM5. PLoS ONE, 2017, 12, e0180258.	1.1	25
1779	Proteomic comparison by iTRAQ combined with mass spectrometry of egg white proteins in laying hens (Gallus gallus) fed with soybean meal and cottonseed meal. PLoS ONE, 2017, 12, e0182886.	1.1	12
1780	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
1781	Restoration of type 1 iodothyronine deiodinase expression in renal cancer cells downregulates oncoproteins and affects key metabolic pathways as well as anti-oxidative system. PLoS ONE, 2017, 12, e0190179.	1.1	17
1782	Generalising better: Applying deep learning to integrate deleteriousness prediction scores for whole-exome SNV studies. PLoS ONE, 2018, 13, e0192829.	1.1	14
1783	Ebola virus glycoprotein directly triggers T lymphocyte death despite of the lack of infection. PLoS Pathogens, 2017, 13, e1006397.	2.1	58
1784	Regulation of Secondary Metabolism by the Velvet Complex Is Temperature-Responsive in <i>Aspergillus</i> . G3: Genes, Genomes, Genetics, 2016, 6, 4023-4033.	0.8	58
1785	Gene Ontology: A Resource for Analysis and Interpretation of Alzheimer's Disease Data. , 0, , 23-36.		9
1786	Construction and evaluation of yeast expression networks by database-guided predictions. Microbial Cell, 2016, 3, 236-247.	1.4	7
1787	Identification of differentially expressed metastatic genes and their signatures to predict the overall survival of uveal melanoma patients by bioinformatics analysis. International Journal of Ophthalmology, 2020, 13, 1046-1053.	0.5	20
1788	RNA-Seq-based analysis of differential gene expression associated with hepatitis C virus infection in cell culture. Acta Biochimica Polonica, 2017, 63, 789-798.	0.3	5
1789	From Protein Variations to Biological Processes and Pathways with NET-GE. Genomics and Computational Biology, 2017, 3, 45.	0.7	2
1790	Genetic variants determining survival and fertility in an adverse African environment: a population-based large-scale candidate gene association study. Aging, 2016, 8, 1364-1383.	1.4	1
1791	An intestinal microRNA modulates the homeostatic adaptation to chronic oxidative stress in C. elegans. Aging, 2016, 8, 1979-2005.	1.4	29
1792	Identification of noncoding RNA expression profiles and regulatory interaction networks following traumatic spinal cord injury by sequence analysis. Aging, 2019, 11, 2352-2368.	1.4	26
1793	Epidermal growth factor receptor inhibitors trigger a type I interferon response in human skin. Oncotarget, 2016, 7, 47777-47793.	0.8	33
1794	Identification of biomarkers for pseudo and true progression of GBM based on radiogenomics study. Oncotarget, 2016, 7, 55377-55394.	0.8	29

#	Article	IF	CITATIONS
1795	Somatic polyploidy is associated with the upregulation of c-MYC interacting genes and EMT-like signature. Oncotarget, 2016, 7, 75235-75260.	0.8	39
1796	DDX11-AS1 as potential therapy targets for human hepatocellular carcinoma. Oncotarget, 2017, 8, 44195-44202.	0.8	21
1797	GFAPÎ′/GFAPα ratio directs astrocytoma gene expression towards a more malignant profile. Oncotarget, 2017, 8, 88104-88121.	0.8	19
1798	Prioritizing chronic obstructive pulmonary disease (COPD) candidate genes in COPD-related networks. Oncotarget, 2017, 8, 103375-103384.	0.8	5
1799	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. Oncotarget, 2017, 8, 100066-100078.	0.8	13
1800	Proteomic analyses identify prognostic biomarkers for pancreatic ductal adenocarcinoma. Oncotarget, 2018, 9, 9789-9807.	0.8	38
1801	Cross-Regulation Between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. SSRN Electronic Journal, 0, , .	0.4	2
1802	Ligand- and Structure-Based Drug Design and Optimization using KNIME. Current Medicinal Chemistry, 2020, 27, 6458-6479.	1.2	14
1803	Analysis of Four Types of Leukemia Using Gene Ontology Term and Kyoto Encyclopedia of Genes and Genomes Pathway Enrichment Scores. Combinatorial Chemistry and High Throughput Screening, 2020, 23, 295-303.	0.6	2
1804	Constructing Networks of Organelle Functional Modules in Arabidopsis. Current Genomics, 2016, 17, 427-438.	0.7	16
1805	Systems Genomics Support for Immune and Inflammation Hypothesis of Depression. Current Neuropharmacology, 2016, 14, 749-758.	1.4	19
1806	Advances in the Prediction of Protein Subcellular Locations with Machine Learning. Current Bioinformatics, 2019, 14, 406-421.	0.7	13
1807	Trichostatin A Sensitizes Hepatocellular Carcinoma Cells to Enhanced NK Cell-mediated Killing by Regulating Immune-related Genes. Cancer Genomics and Proteomics, 2017, 14, 349-362.	1.0	22
1808	The Anatomy of the SARS-CoV-2 Biomedical Literature: Introducing the CovidX Network Algorithm for Drug Repurposing Recommendation. Journal of Medical Internet Research, 2020, 22, e21169.	2.1	16
1809	MyGeneFriends: A Social Network Linking Genes, Genetic Diseases, and Researchers. Journal of Medical Internet Research, 2017, 19, e212.	2.1	5
1810	An integrated information-based similarity measurement of gene ontology terms. Computer Science and Information Systems, 2015, 12, 1235-1253.	0.7	2
1811	miR-190, CDK1, MCM10 and NDC80 predict the prognosis of the patients with lung cancer. Romanian Journal of Laboratory Medicine, 2019, 27, 15-24.	0.1	3
1812	A Network-Based Bioinformatics Approach to Identify Molecular Biomarkers for Type 2 Diabetes that Are Linked to the Progression of Neurological Diseases. International Journal of Environmental Research and Public Health, 2020, 17, 1035.	1.2	52

#	Article	IF	CITATIONS
1813	Expression and potential prognostic value of histone family gene signature in breast cancer. Experimental and Therapeutic Medicine, 2019, 18, 4893-4903.	0.8	17
1814	Identification of potential markers for type 2 diabetes mellitus via bioinformatics analysis. Molecular Medicine Reports, 2020, 22, 1868-1882.	1.1	18
1815	Treatment of keloids through Runx2 siRNA‑induced inhibition of the PI3K/AKT signaling pathway. Molecular Medicine Reports, 2020, 23, .	1.1	13
1816	Prognostic genes of melanoma identified by weighted gene co‑expression network analysis and drug repositioning using a network‑based method. Oncology Letters, 2019, 18, 6066-6078.	0.8	9
1817	Comprehensive gene and pathway analysis of cervical cancer progression. Oncology Letters, 2020, 19, 3316-3332.	0.8	49
1818	Dendritic Cell-Mediated Mechanisms Triggered by LT-IIa-B5, a Mucosal Adjuvant Derived from a Type II Heat-Labile Enterotoxin of Escherichia coli. Journal of Microbiology and Biotechnology, 2017, 27, 709-717.	0.9	7
1819	Elucidation of the Biosynthetic Pathway of Vitamin B Groups and Potential Secondary Metabolite Gene Clusters Via Genome Analysis of a Marine Bacterium Pseudoruegeria sp. M32A2M. Journal of Microbiology and Biotechnology, 2020, 30, 505-514.	0.9	9
1820	Global Data Quality Assessment and the Situated Nature of "Best―Research Practices in Biology. Data Science Journal, 2017, 16, .	0.6	16
1821	Building accurate sequence-to-affinity models from high-throughput in vitro protein-DNA binding data using FeatureREDUCE. ELife, 2015, 4, .	2.8	32
1822	Egr-5 is a post-mitotic regulator of planarian epidermal differentiation. ELife, 2015, 4, e10501.	2.8	97
1823	Viruses are a dominant driver of protein adaptation in mammals. ELife, 2016, 5, .	2.8	267
1824	PDZD7-MYO7A complex identified in enriched stereocilia membranes. ELife, 2016, 5, .	2.8	40
1825	Suppression of C9orf72 RNA repeat-induced neurotoxicity by the ALS-associated RNA-binding protein Zfp106. ELife, 2017, 6, .	2.8	44
1826	Genetic evidence that Nkx2.2 acts primarily downstream of Neurog3 in pancreatic endocrine lineage development. ELife, 2017, 6, .	2.8	1,027
1827	Embryonic origin of adult stem cells required for tissue homeostasis and regeneration. ELife, 2017, 6, .	2.8	67
1828	Extensive cargo identification reveals distinct biological roles of the 12 importin pathways. ELife, 2017, 6, .	2.8	77
1829	The DREAM complex through its subunit Lin37 cooperates with Rb to initiate quiescence. ELife, 2017, 6, .	2.8	41
1830	Integrating images from multiple microscopy screens reveals diverse patterns of change in the subcellular localization of proteins. ELife, 2018, 7, .	2.8	24

#	Article	IF	CITATIONS
1831	Single cell functional genomics reveals the importance of mitochondria in cell-to-cell phenotypic variation. ELife, 2019, 8, .	2.8	28
1832	BioAssay Templates for the semantic web. PeerJ Computer Science, 0, 2, e61.	2.7	6
1833	Temporal dynamics of the developing lung transcriptome in three common inbred strains of laboratory mice reveals multiple stages of postnatal alveolar development. PeerJ, 2016, 4, e2318.	0.9	47
1834	GeNET: a web application to explore and share Gene Co-expression Network Analysis data. PeerJ, 2017, 5, e3678.	0.9	6
1835	Transcriptome dynamics along axolotl regenerative development are consistent with an extensive reduction in gene expression heterogeneity in dedifferentiated cells. PeerJ, 2017, 5, e4004.	0.9	3
1836	Codominant grasses differ in gene expression under experimental climate extremes in native tallgrass prairie. PeerJ, 2018, 6, e4394.	0.9	7
1837	An automated identification and analysis of ontological terms in gastrointestinal diseases and nutrition-related literature provides useful insights. PeerJ, 2018, 6, e5047.	0.9	2
1838	Comparison of gene expression profiles between human erythroid cells derived from fetal liver and adult peripheral blood. PeerJ, 2018, 6, e5527.	0.9	16
1839	T cell receptor signaling pathway and cytokine-cytokine receptor interaction affect the rehabilitation process after respiratory syncytial virus infection. PeerJ, 2019, 7, e7089.	0.9	41
1840	Screening and identification of critical biomarkers in erectile dysfunction: evidence from bioinformatic analysis. PeerJ, 2020, 8, e8653.	0.9	8
1841	Identification and validation of HELLS (Helicase, Lymphoid-Specific) and ICAM1 (Intercellular adhesion) Tj ETQqO	0 0 rgBT /	Overlock 10 T
1842	Proteomic analysis of human cervical adenocarcinoma mucus to identify potential protein biomarkers. PeerJ, 2020, 8, e9527.	0.9	9
1843	Overexpression of EWSR1 (Ewing sarcoma breakpoint region 1/EWS RNA binding protein 1) predicts poor survival in patients with hepatocellular carcinoma. Bioengineered, 2021, 12, 7941-7949.	1.4	6
1844	Identification of Conserved Pappalysin 1-Derived Circular RNA-Mediated Competing Endogenous RNA in Osteosarcoma. Evolutionary Bioinformatics, 2021, 17, 117693432110413.	0.6	0
1845	UbiBrowser 2.0: a comprehensive resource for proteome-wide known and predicted ubiquitin ligase/deubiquitinase–substrate interactions in eukaryotic species. Nucleic Acids Research, 2022, 50, D719-D728.	6.5	46
1846	Mouse Genome Informatics (MGI): latest news from MGD and GXD. Mammalian Genome, 2022, 33, 4-18.	1.0	30
1847	TPSC: a module detection method based on topology potential and spectral clustering in weighted networks and its application in gene co-expression module discovery. BMC Bioinformatics, 2021, 22, 111.	1.2	6
1848	The fungal root endophyte <i>Serendipita vermifera</i> displays inter-kingdom synergistic beneficial effects with the microbiota in <i>Arabidopsis thaliana</i> and barley. ISME Journal, 2022, 16, 876-889.	4.4	22

#	Article	IF	CITATIONS
1849	Melatonin Alleviates Cardiac Function in Sepsis-Caused Myocarditis via Maintenance of Mitochondrial Function. Frontiers in Nutrition, 2021, 8, 754235.	1.6	19
1851	Pleiotropic Effects of the P5-Type ATPase SpfA on Stress Response Networks Contribute to Virulence in the Pathogenic Mold Aspergillus fumigatus. MBio, 2021, 12, e0273521.	1.8	4
1852	Where to Publish and Find Ontologies? A Survey of Ontology Libraries. SSRN Electronic Journal, 0, , .	0.4	2
1858	Convergent evidence from systematic analysis of GWAS revealed genetic basis of esophageal cancer. Oncotarget, 2016, 7, 44621-44629.	0.8	2
1864	Characterization of TPP-binding proteins in Methanococci archaeal species. Bioinformation, 2016, 12, 359-367.	0.2	0
1872	Function Prediction of Proteins from their Sequences with BAR 3.0. , 2017, 1, 001-005.		0
1873	Finding Genes. , 2017, , 127-141.		0
1874	Tutorial on Protein Ontology Resources. Methods in Molecular Biology, 2017, 1558, 57-78.	0.4	2
1880	Ninjurin1 Is Up-regulated in Circulating Prostate Tumor Cells and Plays a Critical Role in Prostate Cancer Cell Motility. Anticancer Research, 2017, 37, 1687-1696.	0.5	7
1895	EXTRACT 2.0: interactive identification of biological entities mentioned in text to assist database curation and knowledge extraction. Biodiversity Information Science and Standards, 0, 1, e20152.	0.0	2
1896	Differential Gene Expression Analysis of Prostate Cancer for Biomarkers and Potential Drug Targets Identification. International Journal of Current Microbiology and Applied Sciences, 2017, 6, 185-193.	0.0	1
1904	Single subject transcriptome analysis to identify functionally signed gene set or pathway activity. , 2018, , .		0
1912	Polyploidy activates biological pathways related to morphogenesis in mammalian tissues. MOJ Immunology, 2018, 6, .	11.0	2
1913	SEMANTIC-ENABLED HYBRID GENETIC DISEASE DIAGNOSTICS IN NEXT-GENERATION SEQUENCED DATA. Computer Science, 2018, 19, 179.	0.4	0
1914	Application of Bioinformatics to Asthma. Translational Bioinformatics, 2018, , 349-359.	0.0	0
1915	The Response to Past Climate Perturbations Explains Extremely Low Genetic Diversity in the Genome of an Abundant Ice-Age Remnant, the Alpine Marmot. SSRN Electronic Journal, 0, , .	0.4	0
1917	Identifying the dynamic gene regulatory network during latent HIV-1 reactivation using high-dimensional ordinary differential equations. International Journal of Computational Biology and Drug Design, 2018, 11, 135.	0.3	0
1922	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. Kagaku To Seibutsu, 2018, 56, 353-363.	0.0	0

#	Article	IF	CITATIONS
1932	Precision drug repurposing via convergent eQTL-based molecules and pathway targeting independent disease-associated polymorphisms. , 2018, , .		3
1933	Linked Data Based Multi-omics Integration and Visualization for Cancer Decision Networks. Lecture Notes in Computer Science, 2019, , 164-181.	1.0	1
1937	An Approach for Semantic Data Integration in Cancer Studies. Lecture Notes in Computer Science, 2019, , 60-73.	1.0	2
1938	A Novel Conversion of Roots into Organs with Shoot Stem Characteristics by Inducing Two Transcription Factors. SSRN Electronic Journal, 0, , .	0.4	Ο
1939	Semantic Integration and Enrichment of Heterogeneous Biological Databases. Methods in Molecular Biology, 2019, 1910, 655-690.	0.4	10
1947	Identification of Gene Changes Induced by Dexamethasone in the Anterior Segment of the Human Eye Using Bioinformatics Analysis. Medical Science Monitor, 2019, 25, 5501-5509.	0.5	7
1957	Modern Education with a Computational Model of the Mind. , 2019, , .		1
1960	Dynamic gene regulatory network reconstruction and analysis based on clinical transcriptomic data of colorectal cancer. Mathematical Biosciences and Engineering, 2020, 17, 3224-3239.	1.0	1
1961	Structure prediction algorithm for protein complexes based on gene ontology. , 2020, 64, 150-158.	0.0	0
1962	The identification of gene ontologies and candidate genes for digital dermatitis in beef cattle from a genome-wide association study. International Journal of Veterinary Science and Research, 2020, 6, 027-037.	0.1	3
1963	Impaired Metabolic Pathways Related to Colorectal Cancer Progression and Therapeutic Implications. Iranian Journal of Public Health, 0, , .	0.3	1
1964	Integrative analysis of competitive endogenous RNA network reveals the regulatory role of non-coding RNAs in high-glucose-induced human retinal endothelial cells. PeerJ, 2020, 8, e9452.	0.9	6
1968	Identification of genes involved in flowering in Stevia rebaudiana using expressed sequence tags (ESTs). Asia-Pacific Journal of Molecular Biology and Biotechnology, 0, , 105-112.	0.2	0
1969	Bioinformatic screening and identification of downregulated hub genes in adrenocortical carcinoma. Experimental and Therapeutic Medicine, 2020, 20, 2730-2742.	0.8	2
1971	Overexpression of novel long intergenic non‑coding RNA LINC02454 is associated with a poor prognosis in papillary thyroid cancer. Oncology Reports, 2020, 44, 1489-1501.	1.2	9
1973	Study on the Mechanism of Liuwei Dihuang Pills in Treating Parkinson's Disease Based on Network Pharmacology. BioMed Research International, 2021, 2021, 1-12.	0.9	6
1974	HoSeIn: A Workflow for Integrating Various Homology Search Results from Metagenomic and Metatranscriptomic Sequence Datasets. Bio-protocol, 2020, 10, e3679.	0.2	0
1975	Integrated Analysis of Key Pathways and Drug Targets Associated With Vogt-Koyanagi-Harada Disease. Frontiers in Immunology, 2020, 11, 587443.	2.2	11

		15	0
#	ARTICLE	IF	CITATIONS
1976	A New Scheme for Essential Proteins Identification in Dynamic Weighted Protein-Protein Interaction Networks. Lecture Notes in Computer Science, 2020, , 195-206.	1.0	0
1977	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	1
1979	Decision Support System for Acupuncture Treatment of Ischemic Stroke. Lecture Notes in Computer Science, 2020, , 582-594.	1.0	1
1980	MSTD for Detecting Topological Domains from 3D Genomic Maps. Methods in Molecular Biology, 2020, 2117, 79-92.	0.4	0
1981	Oil Palm Genome: Strategies and Applications. Compendium of Plant Genomes, 2020, , 83-115.	0.3	2
1982	Construction of Chinese Pediatric Medical Knowledge Graph. Communications in Computer and Information Science, 2020, , 213-220.	0.4	1
1984	<b>Lrrc34  Is Highly Expressed in SSC and Is Necessary for SSCs Expansion <i>In Vitro</i></b> . Chinese Medical Sciences Journal, 2020, 35, 1.	0.2	1
1985	Identification of Biomarkers for Osteosarcoma Based on Integration Strategy. Medical Science Monitor, 2020, 26, e920803.	0.5	1
1988	Dictionary learning for transcriptomics data reveals type-specific gene modules in a multi-class setting. IT - Information Technology, 2020, 62, 119-134.	0.6	0
1989	Functional analysis and signaling pathway enrichment analysis of genes associated with Alzheimer's disease and Parkinson's disease. Bulletin of Siberian Medicine, 2020, 19, 108-113.	0.1	0
1990	Construction and analysis of the protein–protein interaction network for the detoxification enzymes of the silkworm, <i>Bombyx mori</i> . Archives of Insect Biochemistry and Physiology, 2021, 108, e21850.	0.6	4
1991	Predicting Human Protein Subcellular Locations by Using a Combination of Network and Function Features. Frontiers in Genetics, 2021, 12, 783128.	1.1	8
1992	Cigarette smoking-associated isoform switching and $3\hat{a}$ € <sup>2</sup> UTR lengthening via alternative polyadenylation. Genomics, 2021, 113, 4184-4195.	1.3	3
1993	Accumulating Knowledge in the Organizational Sciences. Annual Review of Organizational Psychology and Organizational Behavior, 2022, 9, 441-464.	5.6	1
1994	An ontology-based deep belief network model. Computing (Vienna/New York), 0, , 1.	3.2	1
1995	Multidimensional Single-Nuclei RNA-Seq Reconstruction of Adipose Tissue Reveals Adipocyte Plasticity Underlying Thermogenic Response. Cells, 2021, 10, 3073.	1.8	11
1996	Prediction of drug-related phenotypes based on the constructed phenotype-gene-drug heterogeneous network. , 2020, , .		0
1999	Features of functional annotation of rheumatoid arthritis susceptibility genes by Cytoscape. Bulletin of Siberian Medicine, 2020, 19, 101-104.	0.1	0

#	Article	IF	CITATIONS
2001	Functional Annotation of Genes of Predisposition to Schizophrenia and Celiac Disease. Russian Journal of Genetics, 2020, 56, 1246-1251.	0.2	1
2004	Construction of Protein Expression Network. Methods in Molecular Biology, 2021, 2189, 119-132.	0.4	1
2005	Upregulation of glutaminase 2 and neutrophil cytosolic factor 2 is associated with the poor prognosis of glioblastoma. Biomarkers in Medicine, 2020, 14, 1585-1597.	0.6	3
2006	Single subject transcriptome analysis to identify functionally signed gene set or pathway activity. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 400-411.	0.7	1
2007	Emergence of pathway-level composite biomarkers from converging gene set signals of heterogeneous transcriptomic responses. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 484-495.	0.7	7
2008	Chemical reaction vector embeddings: towards predicting drug metabolism in the human gut microbiome. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 56-67.	0.7	7
2009	Word-of-Mouth Innovation: Hypothesis Generation for Supplement Repurposing based on Consumer Reviews. AMIA Annual Symposium proceedings, 2017, 2017, 689-695.	0.2	1
2010	A Genome-Scale Co-Functional Network of Genes Can Accurately Reconstruct Regulatory Circuits Controlled by Two-Component Signaling Systems. Molecules and Cells, 2019, 42, 166-174.	1.0	7
2011	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
2012	Impaired Metabolic Pathways Related to Colorectal Cancer Progression and Therapeutic Implications. Iranian Journal of Public Health, 2020, 49, 56-67.	0.3	0
2013	Semantic Relations in Compound Nouns: Perspectives from Inter-Annotator Agreement. Studies in Health Technology and Informatics, 2017, 245, 644-648.	0.2	3
2014	Potential targets identified in adenoid cystic carcinoma point out new directions for further research. American Journal of Translational Research (discontinued), 2021, 13, 1085-1108.	0.0	0
2015	Information fusion as an integrative cross-cutting enabler to achieve robust, explainable, and trustworthy medical artificial intelligence. Information Fusion, 2022, 79, 263-278.	11.7	100
2016	Down-regulation of EPB41L4A-AS1 mediated the brain aging and neurodegenerative diseases via damaging synthesis of NAD+ and ATP. Cell and Bioscience, 2021, 11, 192.	2.1	8
2017	PangenomeNet: a pan-genome-based network reveals functional modules on antimicrobial resistome for Escherichia coli strains. BMC Bioinformatics, 2021, 22, 548.	1.2	7
2018	An intelligent system for modeling and evaluation of domain ontologies for Crystallography as a prospective domain with a focus on their retrieval. Computers and Electrical Engineering, 2021, 96, 107604.	3.0	18
2019	EP300 Selectively Controls the Enhancer Landscape of <i>MYCN</i> -Amplified Neuroblastoma. Cancer Discovery, 2022, 12, 730-751.	7.7	64
2020	Comprehensive analysis of miRNA–mRNA regulatory network and potential drugs in chronic chagasic cardiomyopathy across human and mouse. BMC Medical Genomics, 2021, 14, 283.	0.7	13

#	Article	IF	CITATIONS
	Identification and Potential Mechanisms of a 7-MicroRNA Signature That Predicts Prognosis in		
2021	Patients with Lower-Grade Glioma. Journal of Healthcare Engineering, 2021, 2021, 1-11.	1.1	4
2022	Webâ€based transcriptome analysis determines a sixteenâ€gene signature and associated drugs on hearing loss patients: A bioinformatics approach. Journal of Clinical Laboratory Analysis, 2021, 35, e24065.	0.9	6
2023	Singleâ€Cell Transcriptome Profiling Reveals Multicellular Ecosystem of Nucleus Pulposus during Degeneration Progression. Advanced Science, 2022, 9, e2103631.	5.6	35
2024	Automatic consistency assurance for literature-based gene ontology annotation. BMC Bioinformatics, 2021, 22, 565.	1.2	2
2025	Gene expression analysis of human induced pluripotent stem cells cryopreserved by vitrification using StemCell Keep. Biochemistry and Biophysics Reports, 2021, 28, 101172.	0.7	3
2026	Multi-domain and Explainable Prediction of Changes in Web Vocabularies. , 2021, , .		1
2027	Author-sourced capture of pathway knowledge in computable form using Biofactoid. ELife, 2021, 10, .	2.8	11
2028	The GeneCards Suite. , 2021, , 27-56.		182
2029	Comparative Secretome Analyses of Trichoderma/Arabidopsis Co-cultures Identify Proteins for Salt Stress, Plant Growth Promotion, and Root Colonization. Frontiers in Ecology and Evolution, 2022, 9, .	1.1	4
2030	Searching for New Z-DNA/Z-RNA Binding Proteins Based on Structural Similarity to Experimentally Validated Zα Domain. International Journal of Molecular Sciences, 2022, 23, 768.	1.8	11
2031	Gene Ontology GAN (GOGAN): a novel architecture for protein function prediction. Soft Computing, 2022, 26, 7653-7667.	2.1	7
2032	Comprehensive analysis reveals novel gene signature in head and neck squamous cell carcinoma: predicting is associated with poor prognosis in patients. Translational Cancer Research, 2020, 9, 5882-5892.	0.4	5
2033	STIL Acts as an Oncogenetic Driver in a Primary Cilia-Dependent Manner in Human Cancer. Frontiers in Cell and Developmental Biology, 2022, 10, 804419.	1.8	5
2034	Identification of Novel Subtypes in Lung Adenocarcinoma: Evidence from Gene Set Variation Analysis in Tumor and Adjacent Nontumor Samples. Disease Markers, 2022, 2022, 1-10.	0.6	0
2035	Bioinformatic Analysis Combined With Experimental Validation Reveals Novel Hub Genes and Pathways Associated With Focal Segmental Glomerulosclerosis. Frontiers in Molecular Biosciences, 2021, 8, 691966.	1.6	4
2036	PBK/TOPK Inhibitor Suppresses the Progression of Prolactinomas. Frontiers in Endocrinology, 2021, 12, 706909.	1.5	1
2037	Plant Reactome and PubChem: The Plant Pathway and (Bio)Chemical Entity Knowledgebases. Methods in Molecular Biology, 2022, 2443, 511-525.	0.4	7
2038	Syntenin Regulated by miR-216b Promotes Cancer Progression in Pancreatic Cancer. Frontiers in Oncology, 2022, 12, 790788.	1.3	5

#	Article	IF	CITATIONS
2039	The association of genetic alterations with response rate in newly diagnosed chronic myeloid leukemia patients. Leukemia Research, 2022, 114, 106791.	0.4	0
2040	MicroRNA‑4722‑5p and microRNA‑615‑3p serve as potential biomarkers for Alzheimer's disease. Experimental and Therapeutic Medicine, 2022, 23, 241.	0.8	14
2041	De Novo Peptide and Protein Design Using Generative Adversarial Networks: An Update. Journal of Chemical Information and Modeling, 2022, 62, 761-774.	2.5	12
2042	Weighted Co-Expression Network Analysis Identifies RNF181 as a Causal Gene of Coronary Artery Disease. Frontiers in Genetics, 2021, 12, 818813.	1.1	2
2043	Construction and Verification of a Combined Hypoxia and Immune Index for Clear Cell Renal Cell Carcinoma. Frontiers in Genetics, 2022, 13, 711142.	1.1	0
2044	Systems-based approaches to study immunometabolism. Cellular and Molecular Immunology, 2022, 19, 409-420.	4.8	25
2045	Differential gene expression associated with a floral scent polymorphism in the evening primrose Oenothera harringtonii (Onagraceae). BMC Genomics, 2022, 23, 124.	1.2	2
2046	Zinc finger C3H1-type containing serves as a novel prognostic biomarker in human pan-cancer. Gene, 2022, 820, 146251.	1.0	3
2048	Transcriptome Profiling Reveals Features of Immune Response and Metabolism of Acutely Infected, Dead and Asymptomatic Infection of African Swine Fever Virus in Pigs. Frontiers in Immunology, 2021, 12, 808545.	2.2	14
2049	Amycolatopsis aidingensis sp. nov., a Halotolerant Actinobacterium, Produces New Secondary Metabolites. Frontiers in Microbiology, 2021, 12, 743116.	1.5	11
2050	Gene Expression Profiles Identify Biomarkers of Resistance to Decitabine in Myelodysplastic Syndromes. Cells, 2021, 10, 3494.	1.8	4
2051	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
2052	Identification of molecular signatures and pathways common to blood cells and brain tissue based RNA-Seq datasets of bipolar disorder: Insights from comprehensive bioinformatics approach. Informatics in Medicine Unlocked, 2022, 29, 100881.	1.9	6
2053	OmicsView: Omics data analysis through interactive visual analytics. Computational and Structural Biotechnology Journal, 2022, 20, 1277-1285.	1.9	2
2054	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
2055	TransformerGO: predicting protein–protein interactions by modelling the attention between sets of gene ontology terms. Bioinformatics, 2022, 38, 2269-2277.	1.8	25
2056	Multiomics Reveals the Effect of Root Rot on Polygonati Rhizome and Identifies Pathogens and Biocontrol Strain. Microbiology Spectrum, 2022, 10, e0238521.	1.2	16
2057	Comprehensive Analysis of the Effect of 20(R)-Ginsenoside Rg3 on Stroke Recovery in Rats via the Integrative miRNA–mRNA Regulatory Network. Molecules, 2022, 27, 1573.	1.7	6

#	Article	IF	CITATIONS
2058	Prognostication of Pancreatic Cancer Using The Cancer Genome Atlas Based Ferroptosis-Related Long Non-Coding RNAs. Frontiers in Genetics, 2022, 13, 838021.	1.1	6
2059	Natural variation in Glume Coverage 1 causes naked grains in sorghum. Nature Communications, 2022, 13, 1068.	5.8	15
2060	Inflammation and Brain Structure in Schizophrenia and Other Neuropsychiatric Disorders. JAMA Psychiatry, 2022, 79, 498.	6.0	99
2062	Transcriptome sequencing and IncRNA-miRNA-mRNA network construction in cardiac fibrosis and heart failure. Bioengineered, 2022, 13, 7118-7133.	1.4	8
2063	Computed Tomography Imaging-Based Radiogenomics Analysis Reveals Hypoxia Patterns and Immunological Characteristics in Ovarian Cancer. Frontiers in Immunology, 2022, 13, 868067.	2.2	31
2065	Genetics and Brain Transcriptomics of Completed Suicide. American Journal of Psychiatry, 2022, 179, 226-241.	4.0	17
2066	Genome Sequence and Description of Paracoccus denitrificans Strain R-1, Isolated from Activated Sludge. Microbiology Resource Announcements, 2022, 11, e0123621.	0.3	2
2067	PLUS: Predicting cancer metastasis potential based on positive and unlabeled learning. PLoS Computational Biology, 2022, 18, e1009956.	1.5	9
2068	Comprehensive Analysis of Pyroptosis-Related Genes and Tumor Microenvironment Infiltration Characterization in Papillary Renal Cell Carcinoma. Frontiers in Molecular Biosciences, 2022, 9, 871602.	1.6	1
2069	Cupuassu (Theobroma grandiflorum [Willd. ex Sprengel] Schumann) Fruit Development: Key Genes Involved in Primary Metabolism and Stress Response. Agronomy, 2022, 12, 763.	1.3	1
2070	A Computational Text Mining-Guided Meta-Analysis Approach to Identify Potential Xerostomia Drug Targets. Journal of Clinical Medicine, 2022, 11, 1442.	1.0	4
2071	Integrated Bioinformatics Analysis and Validation of the Prognostic Value of RBM10 Expression in Hepatocellular Carcinoma. Cancer Management and Research, 2022, Volume 14, 969-980.	0.9	2
2072	Investigation of the Effect of Curcumin on Protein Targets in NAFLD Using Bioinformatic Analysis. Nutrients, 2022, 14, 1331.	1.7	11
2073	Genomic signatures of high-altitude adaptation and chromosomal polymorphism in geladas. Nature Ecology and Evolution, 2022, 6, 630-643.	3.4	13
2074	Predicted mouse interactome and network-based interpretation of differentially expressed genes. PLoS ONE, 2022, 17, e0264174.	1.1	0
2075	Single-Cell RNA-Seq Analysis of Cells from Degenerating and Non-Degenerating Intervertebral Discs from the Same Individual Reveals New Biomarkers for Intervertebral Disc Degeneration. International Journal of Molecular Sciences, 2022, 23, 3993.	1.8	39
2076	Genetic variants associated with longitudinal changes in brain structure across the lifespan. Nature Neuroscience, 2022, 25, 421-432.	7.1	75
2077	A Survey of Biological Data in a Big Data Perspective. Big Data, 2022, 10, 279-297.	2.1	8

#	Article	IF	CITATIONS
2078	Topological ranks reveal functional knowledge encoded in biological networks: a comparative analysis. Briefings in Bioinformatics, 2022, 23, .	3.2	5
2079	Integrated Bioinformatics Algorithms and Experimental Validation to Explore Robust Biomarkers and Landscape of Immune Cell Infiltration in Dilated Cardiomyopathy. Frontiers in Cardiovascular Medicine, 2022, 9, 809470.	1.1	6
2080	Autophagy Induced by BCL2-Related ceRNA Network Participates in the Occurrence of COPD. International Journal of COPD, 2022, Volume 17, 791-808.	0.9	4
2081	Investigation of the mechanisms and experimental verification of Cuscuta-Salvia in the treatment of polycystic ovary syndrome (PCOS) via network pharmacology. Journal of Ovarian Research, 2022, 15, 40.	1.3	5
2082	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. Life Sciences, 2022, 297, 120483.	2.0	10
2083	Bioinformatics and network-based approaches for determining pathways, signature molecules, and drug substances connected to genetic basis of schizophrenia etiology. Brain Research, 2022, 1785, 147889.	1.1	5
2084	The effects of blunt snout bream (Megalobrama amblycephala) IL-6 trans-signaling on immunity and iron metabolism via JAK/STAT3 pathway. Developmental and Comparative Immunology, 2022, 131, 104372.	1.0	2
2085	Benchmark Evaluation of Protein–Protein Interaction Prediction Algorithms. Molecules, 2022, 27, 41.	1.7	22
2086	Halomonas populi sp. nov. isolated from Populus euphratica. Archives of Microbiology, 2022, 204, 86.	1.0	12
2087	Tissue-specific transcriptomics reveal functional differences in floral development. Plant Physiology, 2022, 188, 1158-1173.	2.3	12
2088	Single cell sequencing analysis identifies genetics-modulated ORMDL3+ cholangiocytes having higher metabolic effects on primary biliary cholangitis. Journal of Nanobiotechnology, 2021, 19, 406.	4.2	16
2089	Different Regulatory Modes of <i>Synechocystis</i> sp. PCC 6803 in Response to Photosynthesis Inhibitory Conditions. MSystems, 2021, 6, e0094321.	1.7	7
2090	Computational Prediction of Biomarkers, Pathways, and New Target Drugs in the Pathogenesis of Immune-Based Diseases Regarding Kidney Transplantation Rejection. Frontiers in Immunology, 2021, 12, 800968.	2.2	11
2091	EdClust: A heuristic sequence clustering method with higher sensitivity. Journal of Bioinformatics and Computational Biology, 2022, 20, 2150036.	0.3	1
2092	NonLoss: a novel analytical method for differential biological module identification from single-cell transcriptome. Annals of Translational Medicine, 2021, 9, 1788-1788.	0.7	0
2093	Toward Measuring the Resemblance of Embedding Models for Evolving Ontologies. , 2021, , .		2
2094	A Cancer Associated Fibroblasts-Related Six-Gene Panel for Anti-PD-1 Therapy in Melanoma Driven by Weighted Correlation Network Analysis and Supervised Machine Learning. Frontiers in Medicine, 2022, 9, 880326.	1.2	9
2095	miR-589-3p promoted osteogenic differentiation of periodontal ligament stem cells through targeting ATF1. Journal of Orthopaedic Surgery and Research, 2022, 17, 221.	0.9	1

#	Article	IF	CITATIONS
2097	Analysis of the Molecular Mechanism of Evodia rutaecarpa Fruit in the Treatment of Nasopharyngeal Carcinoma Using Network Pharmacology and Molecular Docking. Journal of Healthcare Engineering, 2022, 2022, 1-15.	1,1	2
2098	Epigenetic Regulation of Immune and Inflammatory Responses in Rheumatoid Arthritis. Frontiers in Immunology, 2022, 13, 881191.	2.2	7
2255	Convergent evolution of polyploid genomes from across the eukaryotic tree of life. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	16
2256	SNARER: new molecular descriptors for SNARE proteins classification. BMC Bioinformatics, 2022, 23, 148.	1.2	4
2257	Identification and validation of a tumor mutation burden-related signature combined with immune microenvironment infiltration in adrenocortical carcinoma. Mathematical Biosciences and Engineering, 2022, 19, 7055-7075.	1.0	1
2258	Proteomic and Antibody Profiles Reveal Antigenic Composition and Signatures of Bacterial Ghost Vaccine of Brucella abortus A19. Frontiers in Immunology, 2022, 13, 874871.	2.2	2
2259	Computational Analysis of the Immune Infiltration Pattern and Candidate Diagnostic Biomarkers in Lumbar Disc Herniation. Frontiers in Molecular Neuroscience, 2022, 15, 846554.	1.4	3
2260	Abnormalities of hsa-mir-16 and hsa-mir-124 Affect Mitochondrial Function and Fatty Acid Metabolism in Tetralogy of Fallot. Combinatorial Chemistry and High Throughput Screening, 2023, 26, 373-382.	0.6	2
2261	Discovering Common Pathophysiological Processes between COVID-19 and Cystic Fibrosis by Differential Gene Expression Pattern Analysis. BioMed Research International, 2022, 2022, 1-12.	0.9	2
2262	Identification and validation of prognosis-associated DNA repair gene signatures in colorectal cancer. Scientific Reports, 2022, 12, 6946.	1.6	10
2263	A game changer for bipolar disorder diagnosis using RNA editing-based biomarkers. Translational Psychiatry, 2022, 12, 182.	2.4	7
2264	Transcriptome Analysis Using RNA Sequencing for Finding Genes Related to Fiber in Cotton: A Review. , 0, , .		0
2265	LncMIR181A1HG is a novel chromatin-bound epigenetic suppressor of early stage osteogenic lineage commitment. Scientific Reports, 2022, 12, 7770.	1.6	4
2266	Carbamazepine-modified HLA-A*24:02-bound peptidome: Implication of CORO1A in skin rash. International Immunopharmacology, 2022, 109, 108804.	1.7	1
2267	Breaking the Immune Complexity of the Tumor Microenvironment Using Single-Cell Technologies. Frontiers in Genetics, 2022, 13, .	1.1	3
2268	Identification of AKIRIN2 as a potential biomarker and correlation with immunotherapy in gastric adenocarcinoma by integrated bioinformatics analysis. Scientific Reports, 2022, 12, 8400.	1.6	1
2270	Ontologies in bioinformatics. , 2022, , 119-128.		0
2271	Three-Dimensional Organotypic Cultures Reshape the microRNAs Transcriptional Program in Breast Cancer Cells. Cancers, 2022, 14, 2490.	1.7	6

#	Article	IF	CITATIONS
2272	AnthraxKP: a knowledge graph-based, Anthrax Knowledge Portal mined from biomedical literature. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	0
2273	Specific Microglial Subtypes and Inflammatory Mechanisms in Early Diabetic Retinopathy. SSRN Electronic Journal, 0, , .	0.4	Ο
2274	Isoforms of miR-148a and miR-203a are putative suppressors of colorectal cancer. Bulletin of Russian State Medical University, 2022, , .	0.3	0
2275	Identification of an Endoplasmic Reticulum Stress-Related Gene Signature to Evaluate the Immune Status and Predict the Prognosis of Hepatocellular Carcinoma. Frontiers in Genetics, 0, 13, .	1.1	4
2276	TRP Family Genes Are Differently Expressed and Correlated with Immune Response in Glioma. Brain Sciences, 2022, 12, 662.	1.1	2
2278	A global analysis of alternative splicing of Dichocarpum medicinal plants, Ranunculales. Current Genomics, 2022, 23, .	0.7	0
2279	An Integrative Pan-Cancer Analysis Revealing MLN4924 (Pevonedistat) as a Potential Therapeutic Agent Targeting Skp2 in YAP-Driven Cancers. Frontiers in Genetics, 0, 13, .	1.1	3
2280	Whole-genome resequencing of the wheat A subgenome progenitor Triticum urartu provides insights into its demographic history and geographic adaptation. Plant Communications, 2022, , 100345.	3.6	1
2281	Graphical Data Representation and Analytics to Link the Potential Interaction for Lung Cancer Genes. International Journal of Pharmaceutical Research and Allied Sciences, 2022, 11, 62-72.	0.1	2
2282	Identification of biomarkers for immunotherapy response in prostate cancer and potential drugs to alleviate immunosuppression. Aging, 2022, 14, 4839-4857.	1.4	3
2283	Prognosis and Tumour Immune Microenvironment of Patients With Hepatocellular Carcinoma by a Novel Pyroptosis-Related IncRNA Signature. Frontiers in Immunology, 0, 13, .	2.2	5
2284	Identification of Hub Genes and Immune-Related Pathways for Membranous Nephropathy by Bioinformatics Analysis. Frontiers in Physiology, 0, 13, .	1.3	4
2285	Transcriptome study digs out BMP2 involved in adipogenesis in sheep tails. BMC Genomics, 2022, 23, .	1.2	8
2286	Rare Variants in Novel Candidate Genes Associated With Nonsyndromic Patent Ductus Arteriosus Identified With Whole-Exome Sequencing. Frontiers in Genetics, 0, 13, .	1.1	4
2287	Transcriptome Analysis Reveals the Regulatory Networks of Cytokinin in Promoting Floral Feminization in Castanea henryi. International Journal of Molecular Sciences, 2022, 23, 6389.	1.8	6
2288	Updated List of Transport Proteins in Plasmodium falciparum. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	5
2289	Identification and characterization of virus-encoded circular RNAs in host cells. Microbial Genomics, 2022, 8, .	1.0	4
2291	hnRNP E1 Regulates HPV16 Oncogene Expression and Inhibits Cervical Cancerization. Frontiers in Oncology, 0, 12, .	1.3	1

#	Article	IF	CITATIONS
2292	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 Tilletia caries and T. laevis. IMA Fungus, 2022, 13, .	1.7	5
2293	Post-modified porous hollow nanospheres incorporating multiple strategies for comprehensive phosphoproteomics analysis of serum of Alzheimer's disease. Microporous and Mesoporous Materials, 2022, 341, 112066.	2.2	5
2294	Fangchinoline inhibits non-small cell lung cancer metastasis by reversing epithelial-mesenchymal transition and suppressing the cytosolic ROS-related Akt-mTOR signaling pathway. Cancer Letters, 2022, 543, 215783.	3.2	24
2295	The Genome of the Marine Alga Ulva compressa (Chlorophyta) Reveals Protein-Coding Genes with Similarity to Plants and Green Microalgae, but Also to Animal, Bacterial, and Fungal Genes. International Journal of Molecular Sciences, 2022, 23, 7279.	1.8	8
2296	TTN mutations predict a poor prognosis in patients with thyroid cancer. Bioscience Reports, 2022, 42, .	1.1	13
2297	STAT3 and NTRK2 Genes Predicted by the Bioinformatics Approach May Play Important Roles in the Pathogenesis of Multiple Sclerosis and Obsessive–Compulsive Disorder. Journal of Personalized Medicine, 2022, 12, 1043.	1.1	3
2298	A Census of Human Methionine-Rich Prion-like Domain-Containing Proteins. Antioxidants, 2022, 11, 1289.	2.2	0
2299	Identification of TNFAIP6 as a hub gene associated with the progression of glioblastoma by weighted gene coâ€expression network analysis. IET Systems Biology, 2022, 16, 145-156.	0.8	6
2300	Analysis of Lymphoma-Related Genes with Gene Ontology and Kyoto Encyclopedia of Genes and Genomes Enrichment. BioMed Research International, 2022, 2022, 1-8.	0.9	0
2301	Transmembrane protein 121 as a novel inhibitor of cervical cancer metastasis. Experimental and Therapeutic Medicine, 2022, 24, .	0.8	1
2302	A novel signature derived from metabolism-related genes GPT and SMS to predict prognosis of laryngeal squamous cell carcinoma. Cancer Cell International, 2022, 22, .	1.8	3
2303	RNA-Seq Analysis Demonstrates Different Strategies Employed by Tiger Nuts (Cyperus esculentus L.) in Response to Drought Stress. Life, 2022, 12, 1051.	1.1	2
2304	Comparative Analysis of Gene Correlation Networks of Breast Cancer Patients Based on Mutations in TP53. Biomolecules, 2022, 12, 979.	1.8	1
2305	Seascape genomics of common dolphins (Delphinus delphis) reveals adaptive diversity linked to regional and local oceanography. Bmc Ecology and Evolution, 2022, 22, .	0.7	3
2306	Systemic approaches using single cell transcriptome reveal that C/EBPÎ <sup>3</sup> regulates autophagy under amino acid starved condition. Nucleic Acids Research, 2022, 50, 7298-7309.	6.5	3
2307	Orientation algorithm for PPI networks based on network propagation approach. Journal of Biosciences, 2022, 47, .	0.5	2
2308	Computational analysis of potential candidate genes involved in the cold stress response of ten Rosaceae members. BMC Genomics, 2022, 23, .	1.2	1
2309	Acute Myeloid Leukemia: New Multiomics Molecular Signatures and Implications for Systems Medicine Diagnostics and Therapeutics Innovation. OMICS A Journal of Integrative Biology, 2022, 26, 392-403.	1.0	5

#	Article	IF	CITATIONS
2310	Identifying RBBP7 as a Promising Diagnostic Biomarker for BK Virus-Associated Nephropathy. Journal of Immunology Research, 2022, 2022, 1-14.	0.9	0
2311	Bioinformatics Strategies to Identify Shared Molecular Biomarkers That Link Ischemic Stroke and Moyamoya Disease with Glioblastoma. Pharmaceutics, 2022, 14, 1573.	2.0	1
2312	Exploration of Potential Biomarkers and Immune Landscape for Hepatoblastoma: Evidence from Machine Learning Algorithm. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-10.	0.5	2
2313	DES-Amyloidoses "Amyloidoses through the looking-glassâ€₁ A knowledgebase developed for exploring and linking information related to human amyloid-related diseases. PLoS ONE, 2022, 17, e0271737.	1.1	0
2314	Construction and validation of a glioblastoma prognostic model based on immune-related genes. Frontiers in Neurology, 0, 13, .	1.1	3
2315	Multi-omics profiling of the cold tolerant Monoraphidium minutum 26B-AM in response to abiotic stress. Algal Research, 2022, 66, 102794.	2.4	3
2316	Screening and identification of immune-related genes for immunotherapy and prognostic assessment in colorectal cancer patients. BMC Medical Genomics, 2022, 15, .	0.7	2
2317	Interactome overlap between risk genes of epilepsy and targets of anti-epileptic drugs. PLoS ONE, 2022, 17, e0272428.	1.1	0
2318	Systematic review of gastric cancer-associated genetic variants, gene-based meta-analysis, and gene-level functional analysis to identify candidate genes for drug development. Frontiers in Genetics, 0, 13, .	1.1	4
2319	A signature constructed with mitophagy-related genes to predict the prognosis and therapy response for breast cancer. Aging, 2022, 14, 6169-6186.	1.4	9
2320	Liproxstatin‑1 induces cell cycle arrest, apoptosis, and caspase‑3/GSDME‑dependent secondary pyroptosis in K562 cells. International Journal of Oncology, 2022, 61, .	1.4	6
2321	Liver transcriptomics reveals features of the host response in a mouse model of dengue virus infection. Frontiers in Immunology, 0, 13, .	2.2	3
2322	Identification of key genes and immune cell infiltration in recurrent implantation failure: A study based on integrated analysis of multiple microarray studies. American Journal of Reproductive Immunology, 0, , .	1.2	8
2323	Transcriptomic signature associated with RNA-binding proteins for survival stratification of laryngeal cancer. Aging, 2022, 14, 6605-6625.	1.4	1
2324	Upregulation of key genes Eln and Tgfb3 were associated with the severity of cardiac hypertrophy. BMC Genomics, 2022, 23, .	1.2	2
2325	Brain-specific genes contribute to chronic but not to acute back pain. Pain Reports, 2022, 7, e1018.	1.4	14
2326	Identification and Validation in a Novel Classification of Helicase Patterns for the Prediction of Tumor Proliferation and Prognosis. Journal of Hepatocellular Carcinoma, 0, Volume 9, 885-900.	1.8	1
2328	Comprehensive Analysis of circRNA-Associated-ceRNA Networks in Human Corneal Endothelial Dysfunction. Cornea, 2022, 41, 1545-1552.	0.9	3

#	Article	IF	CITATIONS
2329	The successful use of -omic technologies to achieve the â€~One Health' concept in meat producing animals. Meat Science, 2022, 193, 108949.	2.7	3
2330	Construction and validation of a novel ten miRNA-pair based signature for the prognosis of clear cell renal cell carcinoma. Translational Oncology, 2022, 25, 101519.	1.7	0
2331	Sarcomatoid-associated gene risk index for clear cell renal cell carcinoma. Frontiers in Genetics, 0, 13, .	1.1	3
2332	Non-apoptotic activity of the mitochondrial protein SMAC/Diablo in lung cancer: Novel targetÂto disrupt survival, inflammation, and immunosuppression. Frontiers in Oncology, 0, 12, .	1.3	3
2333	Integrative analysis reveals histone demethylase LSD1 promotes RNA polymerase II pausing. IScience, 2022, 25, 105049.	1.9	4
2334	Deciphering the role of predicted miRNAs of polyomaviruses in carcinogenesis. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2022, 1868, 166537.	1.8	0
2335	Development and validation of novel inflammatory response-related gene signature to predict prostate cancer recurrence and response to immune checkpoint therapy. Mathematical Biosciences and Engineering, 2022, 19, 11345-11366.	1.0	0
2336	Bioinformatics Resources, Tools, and Strategies in Designing Therapeutic Proteins. , 2022, , 91-123.		0
2337	Predicting TF Proteins by Incorporating Evolution Information Through PSSM. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 1319-1326.	1.9	0
2339	Comprehensive bioinformatic analysis of key genes and signaling pathways in glioma. , 2022, 52, 3.		0
2340	Bioinformatics Analysis of Hub Genes Involved in Alcohol-Related Hemifacial Microsomia Pathogenesis. Journal of Craniofacial Surgery, 2022, 33, e607-e612.	0.3	1
2341	Discovering common pathogenetic processes between COVID-19 and sepsis by bioinformatics and system biology approach. Frontiers in Immunology, 0, 13, .	2.2	17
2342	Identification of protein–protein interaction associated functions based on gene ontology and KEGG pathway. Frontiers in Genetics, 0, 13, .	1.1	5
2343	Histidine kinase inhibitors impair shoot regeneration in Arabidopsis thaliana via cytokinin signaling and SAM patterning determinants. Frontiers in Plant Science, 0, 13, .	1.7	3
2344	Integrated bioinformatics analysis and screening of hub genes in polycystic ovary syndrome. Endocrine, 2022, 78, 615-627.	1.1	3
2345	A <scp>pyroptosisâ€related</scp> signature predicts prognosis and indicates immune microenvironment infiltration in glioma. Cancer Medicine, 0, , .	1.3	3
2346	Identification of kaempferol as an OSX upregulator by network pharmacology-based analysis of qianggu Capsule for osteoporosis. Frontiers in Pharmacology, 0, 13, .	1.6	4
2347	YAP/Smad3 promotes pathological extracellular matrix microenviromentâ€induced bladder smooth muscle proliferation in bladder fibrosis progression. MedComm, 2022, 3, .	3.1	8

#	Article	IF	CITATIONS
2348	Analysis and Validation of Differentially Expressed Ferroptosis-Related Genes in Regorafenib-Induced Cardiotoxicity. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-20.	1.9	2
2349	Screening and analysis of key genes in the biological behavior of bone mesenchymal stem cells seeded on gradient nanostructured titanium compared with native pure Ti. Journal of Biomaterials Applications, 0, , 088532822211250.	1.2	0
2350	Mutated processes predict immune checkpoint inhibitor therapy benefit in metastatic melanoma. Nature Communications, 2022, 13, .	5.8	16
2351	Systematic panâ€ʿcancer analysis identifies CDC45 as having an oncogenic role in human cancers. Oncology Reports, 2022, 48, .	1.2	4
2352	HSP90α induces immunosuppressive myeloid cells in melanoma via TLR4 signaling. , 2022, 10, e005551.		8
2353	Identification of Hub Genes and Potential Biomarkers for Childhood Asthma by Utilizing an Established Bioinformatic Analysis Approach. Biomedicines, 2022, 10, 2311.	1.4	2
2354	Golden 2-like transcription factor contributes to the major QTL against rice black-streaked dwarf virus disease. Theoretical and Applied Genetics, 2022, 135, 4233-4243.	1.8	4
2355	Identification and verification of hub genes associated with the progression of non-small cell lung cancer by integrated analysis. Frontiers in Pharmacology, 0, 13, .	1.6	1
2357	Identification of stage-associated exosome miRNAs in colorectal cancer by improved robust and corroborative approach embedded miRNA-target network. Frontiers in Medicine, 0, 9, .	1.2	1
2358	High DHCR7 Expression Predicts Poor Prognosis for Cervical Cancer. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-23.	0.7	4
2359	Crosstalk of necroptosis and pyroptosis defines tumor microenvironment characterization and predicts prognosis in clear cell renal carcinoma. Frontiers in Immunology, 0, 13, .	2.2	6
2360	Cuproptosis patterns in papillary renal cell carcinoma are characterized by distinct tumor microenvironment infiltration landscapes. Frontiers in Molecular Biosciences, 0, 9, .	1.6	2
2362	Exploring the protective mechanism of baicalin in treatment of atherosclerosis using endothelial cells deregulation model and network pharmacology. BMC Complementary Medicine and Therapies, 2022, 22, .	1.2	0
2363	Investigating the contributions of circadian pathway and insomnia risk genes to autism and sleep disturbances. Translational Psychiatry, 2022, 12, .	2.4	3
2364	Common and species-specific molecular signatures, networks, and regulators of influenza virus infection in mice, ferrets, and humans. Science Advances, 2022, 8, .	4.7	6
2365	AgeAnno: a knowledgebase of single-cell annotation of aging in human. Nucleic Acids Research, 2023, 51, D805-D815.	6.5	13
2366	Krüppel-like factor 7 influences translation and pathways involved in ribosomal biogenesis in breast cancer. Breast Cancer Research, 2022, 24, .	2.2	5
2367	Identification of candidate blood biomarkers for the diagnosis of septicaemic melioidosis based on WGCNA. Artificial Cells, Nanomedicine and Biotechnology, 2022, 50, 252-259.	1.9	3

#	Article	IF	CITATIONS
2368	Faithful Embeddings forÂ\$\$mathcal{E}mathcal{L}^{++}\$\$ Knowledge Bases. Lecture Notes in Computer Science, 2022, , 22-38.	1.0	4
2369	Zearalenone damages the male reproductive system of rats by destroying testicular focal adhesion. Environmental Toxicology, 2023, 38, 278-288.	2.1	3
2370	CTpathway: a CrossTalk-based pathway enrichment analysis method for cancer research. Genome Medicine, 2022, 14, .	3.6	10
2371	Sphingomicrobium nitratireducens sp. nov., isolated from a tidal flat in Guangxi. Archives of Microbiology, 2022, 204, .	1.0	1
2373	Deciphering the action mechanism of paeoniflorin in suppressing pancreatic cancer: A network pharmacology study and experimental validation. Frontiers in Pharmacology, 0, 13, .	1.6	5
2375	Identification of Specific Cervical Cancer Subtypes and Prognostic Gene Sets in Tumor and Nontumor Tissues Based on GSVA Analysis. Journal of Oncology, 2022, 2022, 1-17.	0.6	2
2376	miR-20b-5p is a novel biomarker for detecting prostate cancer. Oncology Letters, 2022, 24, .	0.8	2
2377	Downregulation of FXYD2 Is Associated with Poor Prognosis and Increased Regulatory T Cell Infiltration in Clear Cell Renal Cell Carcinoma. Journal of Immunology Research, 2022, 2022, 1-19.	0.9	1
2378	Shared Genetic Regulatory Networks Contribute to Neuropathic and Inflammatory Pain: Multi-Omics Systems Analysis. Biomolecules, 2022, 12, 1454.	1.8	3
2380	Traditional Chinese medicine for the treatment of diabetic kidney disease: A study-level pooled analysis of 44 randomized controlled trials. Frontiers in Pharmacology, 0, 13, .	1.6	2
2381	Constructed the ceRNA network and predicted a FEZF1-AS1/miR-92b-3p/ZIC5 axis in colon cancer. Molecular and Cellular Biochemistry, 0, , .	1.4	0
2382	Transcriptomic Profiling of Rectus Abdominis Muscle in Women with Gestational Diabetes-Induced Myopathy: Characterization of Pathophysiology and Potential Muscle Biomarkers of Pregnancy-Specific Urinary Incontinence. International Journal of Molecular Sciences, 2022, 23, 12864.	1.8	3
2383	Classification and Prognosis Analysis of Pancreatic Cancer Based on DNA Methylation Profile and Clinical Information. Genes, 2022, 13, 1913.	1.0	5
2384	The targets of aspirin in bladder cancer: bioinformatics analysis. BMC Urology, 2022, 22, .	0.6	0
2385	Expression Profiles, Prognosis and ceRNA Regulation of SOX Genes in Stomach Adenocarcinoma. Journal of Environmental Pathology, Toxicology and Oncology, 2022, , .	0.6	0
2387	Vaccination History, Body Mass Index, Age, and Baseline Gene Expression Predict Influenza Vaccination Outcomes. Viruses, 2022, 14, 2446.	1.5	5
2388	Integrated analysis identified prognostic microRNAs in breast cancer. BMC Cancer, 2022, 22, .	1.1	3
2389	HPV-Related Prognostic Signature Predicts Survival in Head and Neck Squamous Cell Carcinoma. Journal of Oncology, 2022, 2022, 1-10.	0.6	3

#	Article	IF	CITATIONS
2390	Identification of hub proteins in cerebrospinal fluid as potential biomarkers of Alzheimer's disease by integrated bioinformatics. Journal of Neurology, 2023, 270, 1487-1500.	1.8	7
2391	Whole-transcriptome sequencing revealed differentially expressed mRNAs and non-coding RNAs played crucial roles in NiONPs-induced liver fibrosis. Ecotoxicology and Environmental Safety, 2022, 248, 114308.	2.9	2
2392	Clustering Analysis Indicates Genes Involved inÂProgesterone-Induced Oxidative Stress inÂPancreatic Beta Cells: Insights toÂUnderstanding Gestational Diabetes. Lecture Notes in Computer Science, 2022, , 68-78.	1.0	0
2393	Identification and validation of key immune-related genes with promising diagnostic and predictive value in systemic sclerosis. Life Sciences, 2023, 312, 121238.	2.0	2
2394	Integrated analysis of transcriptomic and protein-protein interaction data reveals cadmium stress response in Geobacter sulfurreducens. Environmental Research, 2023, 218, 115063.	3.7	1
2395	Decoding Gene Expression Signatures Underlying Vegetative to Inflorescence Meristem Transition in the Common Bean. International Journal of Molecular Sciences, 2022, 23, 14783.	1.8	1
2396	Screening for Biomarkers for Progression from Oral Leukoplakia to Oral Squamous Cell Carcinoma and Evaluation of Diagnostic Efficacy by Multiple Machine Learning Algorithms. Cancers, 2022, 14, 5808.	1.7	3
2397	Construction and analysis of expression profile of exosomal <scp>lncRNAs</scp> in pleural effusion in lung adenocarcinoma. Journal of Clinical Laboratory Analysis, 2022, 36, .	0.9	3
2400	A vasculogenic mimicry prognostic signature associated with immune signature in human gastric cancer. Frontiers in Immunology, 0, 13, .	2.2	7
2401	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. Journal of Animal Science and Biotechnology, 2022, 13, .	2.1	2
2402	Plant Gene Expression Network. , 2022, , 137-150.		0
2403	Fatty acid metabolism-related signature predicts survival in patients with clear cell renal carcinoma. Aging, 2022, 14, 9969-9979.	1.4	6
2404	Prognosis and immune features of pyroptosis-related RNA patterns in low-grade glioma. Frontiers in Oncology, 0, 12, .	1.3	1
2405	Identification of cuproptosis-related long noncoding RNA signature for predicting prognosis and immunotherapy response in bladder cancer. Scientific Reports, 2022, 12, .	1.6	4
2406	Single-cell RNA sequencing reveals the Müller subtypes and inner blood–retinal barrier regulatory network in early diabetic retinopathy. Frontiers in Molecular Neuroscience, 0, 15, .	1.4	2
2408	Gastrodin improves neuroinflammation-induced cognitive dysfunction in rats by regulating NLRP3 inflammasome. BMC Anesthesiology, 2022, 22, .	0.7	5
2410	Morphometric dis-similarity between cortical and subcortical areas underlies cognitive function and psychiatric symptomatology: a preadolescence study from ABCD. Molecular Psychiatry, 2023, 28, 1146-1158.	4.1	9
2412	Weighted Gene Co-Expression Network Analysis of Immune Infiltration in Nonalcoholic Fatty Liver Disease. Endocrine, Metabolic and Immune Disorders - Drug Targets, 2022, 23, .	0.6	1

CITATION REPORT ARTICLE IF CITATIONS Metabolomics and transcriptomics provide insights into the flavonoid biosynthesis pathway in the 1.2 2 roots of developing Aster tataricus. Journal of Plant Research, 2023, 136, 139-156. Clinical identification of expressed proteins in adrenal medullary hyperplasia detected with 1.5 hypertension. Frontiers in Endocrinology, 0, 13, . Erythrobacter aurantius sp. nov., isolated from intertidal seawater in Taizhou. International Journal 0.8 4 of Systematic and Evolutionary Microbiology, 2022, 72, . Immune-related potential biomarkers and therapeutic targets in coronary artery disease. Frontiers in 1.1 Cardiovascular Medicine, 0, 9, . High-fiber-diet-related metabolites improve neurodegenerative symptoms in patients with obesity with diabetes mellitus by modulating the hippocampalâ€" hypothalamic endocrine axis. Frontiers in 0 1.1 Neurology, 0, 13, . Identification of two molecular subtypes and a novel prognostic model of lung adenocarcinoma based on a cuproptosis-associated gene signature. Frontiers in Genetics, 0, 13, . 1.1 Penetrating Exploration of Prognostic Correlations of the FKBP Gene Family with Lung 1.1 2 Adenocarcinoma. Journal of Personalized Medicine, 2023, 13, 49. Weighted gene co-expression network analysis combined with machine learning validation to identify 1.4 key hub biomarkers in colorectal cancer. Functional and Integrative Genomics, 2023, 23, . SMYD3 associates with the NuRD (MTA1/2) complex to regulate transcription and promote 2 1.7 proliferation and invasiveness in hepatocellular carcinoma cells. BMC Biology, 2022, 20, . hnRNP K induces HPV16 oncogene expression and promotes cervical cancerization. Journal of Cancer 1.2 Research and Clinical Oncology, 2023, 149, 6225-6237. Exploring the hub mechanisms of ischemic stroke based on protein-protein interaction networks 4 1.6 related to ischemic stroke and inflammatory bowel disease. Scientific Reports, 2023, 13, . Screening for diagnostic targets in tuberculosis and study on its pathogenic mechanism based on mRNA sequencing technology and miRNA-mRNA-pathway regulatory network. Frontiers in Immunology, 2.2 0, 14, . scDR: Predicting Drug Response at Single-Cell Resolution. Genes, 2023, 14, 268. 1.0 4 Identification and validation of a novel senescence-related biomarker for thyroid cancer to predict 2.2 the prognosis and immunotherapy. Frontiers in Immunology, 0, 14, . Integrative analysis of the expression profiles of whole coding and non-coding RNA transcriptomes and construction of the competing endogenous RNA networks for chronic obstructive pulmonary 4 1.1 disease. Frontiers in Genetics, 0, 14, . Network pharmacology integrated with experimental validation to explore the therapeutic role and 1.4 potential mechanism of Epimedium for spinal cord injury. Frontiers in Molecular Neuroscience, 0, 16, . Gut microbiota-derived ursodeoxycholic acid alleviates low birth weight-induced colonic 4.9 21 inflammation by enhancing M2 macrophage polarization. Microbiome, 2023, 11, .

2433	Genome-wide screening reveals the genetic basis of mammalian embryonic eye development. BMC Biology, 2023, 21, .	1.7	1	
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#	Article	IF	CITATIONS
2434	Comparison of methods for biological sequence clustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, , 1-24.	1.9	0
2435	Speciation Underpinned by Unexpected Molecular Diversity in the Mycorrhizal Fungal Genus <i>Pisolithus</i> . Molecular Biology and Evolution, 2023, 40, .	3.5	11
2437	ETCM v2.0: An update with comprehensive resource and rich annotations for traditional Chinese medicine. Acta Pharmaceutica Sinica B, 2023, 13, 2559-2571.	5.7	12
2438	Comprehensive analysis of cuproptosis-related immune biomarker signature to enhance prognostic accuracy in gastric cancer. Aging, 2023, 15, 2772-2796.	1.4	4
2439	GelFAP v2.0: an improved platform for Gene functional analysis in Gastrodia elata. BMC Genomics, 2023, 24, .	1.2	2
2440	DiDang decoction improves mitochondrial function and lipid metabolism via the HIF-1 signaling pathway to treat atherosclerosis and hyperlipidemia. Journal of Ethnopharmacology, 2023, 308, 116289.	2.0	9
2443	Citrus genomic resources unravel putative genetic determinants of Huanglongbing pathogenicity. IScience, 2023, 26, 106024.	1.9	6
2444	Comprehensive analysis of <i>ESR1</i> -related ceRNA axis as a novel prognostic biomarker in hepatocellular carcinoma. Epigenomics, 2022, 14, 1393-1409.	1.0	2
2446	Bioinformatics analysis identifies heparan sulfate proteoglycans acting as different progress subtypes of biliary atresia. Frontiers in Pediatrics, 0, 11, .	0.9	0
2447	Identifying miRNA biomarkers of polycystic ovary syndrome through text mining. Reproductive and Developmental Medicine, 2023, 7, 96-101.	0.2	0
2448	SLFN5 promotes reversible epithelial and mesenchymal transformation in ovarian cancer. Journal of Ovarian Research, 2023, 16, .	1.3	3
2450	Homologous repair deficiency-associated genes in invasive breast cancer revealed by WGCNA co-expression network analysis and genetic perturbation similarity analysis. Cell Cycle, 2023, 22, 1077-1100.	1.3	2
2451	MicroRNAs in mouse and rat models of experimental epilepsy and potential therapeutic targets. Neural Regeneration Research, 2023, 18, 2108.	1.6	2
2452	Repurposing ketamine to treat cocaine use disorder: integration of artificial intelligenceâ€based prediction, expert evaluation, clinical corroboration and mechanism of action analyses. Addiction, 2023, 118, 1307-1319.	1.7	12
2453	DZIP1 expressed in fibroblasts and tumor cells may affect immunosuppression and metastatic potential in gastric cancer. International Immunopharmacology, 2023, 117, 109886.	1.7	4
2455	Advanced Situation with Recombinant Toxins: Diversity, Production and Application Purposes. International Journal of Molecular Sciences, 2023, 24, 4630.	1.8	6
2457	Identification of autophagy-related genes in neuropathic pain through bioinformatic analysis. Hereditas, 2023, 160, .	0.5	1
2458	Exploration of the Shared Molecular Mechanisms between COVID-19 and Neurodegenerative Diseases through Bioinformatic Analysis. International Journal of Molecular Sciences, 2023, 24, 4839.	1.8	1

ARTICLE IF CITATIONS Nidogen-2 (NID2) is a Key Factor in Collagen Causing Poor Response to Immunotherapy in Melanoma. 2459 0.4 0 Pharmacogenomics and Personalized Medicine, 0, Volume 16, 153-172. Special transcriptome landscape and molecular prognostic signature of non-smoking head and neck 2460 1.4 cancer patients. Functional and Integrative Genomics, 2023, 23, . Predicting Key Genes and Therapeutic Molecular Modelling to Explain the Association between Porphyromonas gingivalis (P. gingivalis) and Alzheimer's Disease (AD). International Journal of Molecular Sciences, 2023, 24, 5432. 2461 2 1.8 Spatiotemporal expression patterns of genes coding for plasmalemmal chloride transporters and 2464 1.3 channels in neurological diseases. Molecular Brain, 2023, 16, . Transposable elements in the transcriptome of the velvetbean caterpillar <i>Anticarsia gemmatalis</i> 2466 0.9 0 HÃ1/4 bner, 1818 (Lepidoptera: Erebidae). Genome, 0, , . An Analysis Regarding the Association Between Proteasome (PSM) and Hepatocellular Carcinoma (HCC). Journal of Hepatocellular Carcinoma, 0, Volume 10, 497-515. 2468 1.8 Exploring the bi-directional relationship and shared genes between depression and stroke via NHANES 2469 1.1 0 and bioinformatic analysis. Frontiers in Genetics, 0, 14, . mIR-99a-5p and mIR-148a-3p as Candidate Molecular Biomarkers for the Survival of Lung Cancer Patients. , 2023, 52, 87-100. Hypoxia-inducible factor stabilisation-related lncRNAs in retinopathy of prematurity. Journal of 2471 0.4 0 Obstetrics and Gynaecology, 2023, 43, . Identification of differentially methylated genes for severe acne by genome-wide DNA methylation and 2472 1.3 gene expression analysis. Epigenetics, 2023, 18, . MicroRNA expression in osteoarthritis: a meta-analysis. Clinical and Experimental Medicine, 2023, 23, 2474 4 1.9 3737-3749. Identification the genetic influence of SARS-CoV-2 infections on IgA nephropathy based on 0.9 bioinformatics method.. Kidney and Blood Pressure Research, 0, , . Identification of diagnostic biomarks and immune cell infiltration in ulcerative colitis. Scientific 2476 1.6 2 Reports, 2023, 13, . Identification of coagulation-associated subtypes of lung adenocarcinoma and establishment of 2477 1.0 prognostic models. Mathematical Biosciences and Engineering, 2023, 20, 10626-10658. Integrated analysis of endoplasmic reticulum stress regulators' expression identifies distinct 2478 0 1.3 subtypes of autism spectrum disorder. Frontiers in Psychiatry, 0, 14, . Integrating genetics and transcriptomics to study major depressive disorder: a conceptual 2479 2.4 framework, bioinformatic approaches, and recent findings. Translational Psychiatry, 2023, 13, . Identification and validation of autophagy-related genes in Kawasaki disease. Hereditas, 2023, 160, . 2481 0.5 1 The Metal-binding Protein Atlas (MbPA): An Integrated Database for Curating Metalloproteins in All 2482 Aspects. Journal of Molecular Biology, 2023, 435, 168117.

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#	Article	IF	CITATIONS
2507	Gene editing for stem cells by CRISPR-Cas9. , 2023, , 153-175.		0
2558	A Workflow Guide to RNA-Seq Analysis of Chaperone Function and Beyond. Methods in Molecular Biology, 2023, , 39-60.	0.4	0
2599	Molecular Investigation of Protein–Protein Interaction Candidates Related to the Mammalian Brain. , 2023, , 81-107.		0
2613	Ontology and Machine Learning: A Two-Way Street to Improved Knowledge Representation and Algorithm Accuracy. Algorithms for Intelligent Systems, 2023, , 181-189.	0.5	Ο
2619	Parerythrobacter aestuarii sp. nov., Isolated from Seawater in the Tidal Region of Taizhou. Current Microbiology, 2023, 80, .	1.0	0