

PANTHER version 7: improved phylogenetic trees, orthology
Gene Ontology Consortium

Nucleic Acids Research

38, D204-D210

DOI: [10.1093/nar/gkp1019](https://doi.org/10.1093/nar/gkp1019)

Citation Report

#	ARTICLE	IF	CITATIONS
2	GIGA: a simple, efficient algorithm for gene tree inference in the genomic age. BMC Bioinformatics, 2010, 11, 312.	1.2	34
3	Formalization of taxon-based constraints to detect inconsistencies in annotation and ontology development. BMC Bioinformatics, 2010, 11, 530.	1.2	48
5	SPOT: a web-based tool for using biological databases to prioritize SNPs after a genome-wide association study. Nucleic Acids Research, 2010, 38, W201-W209.	6.5	57
6	Variability of the melanocortin 1 receptor (MC1R) gene explains the segregation of the bronze locus in turkey (<i>Meleagris gallopavo</i>). Poultry Science, 2010, 89, 1599-1602.	1.5	10
7	The Gene Ontology in 2010: extensions and refinements. Nucleic Acids Research, 2010, 38, D331-D335.	6.5	450
8	CellPublisher: a web platform for the intuitive visualization and sharing of metabolic, signalling and regulatory pathways: Fig. 1.. Bioinformatics, 2010, 26, 2997-2999.	1.8	19
9	Bioinformatics approach to identifying molecular biomarkers and networks in multiple sclerosis. Clinical and Experimental Neuroimmunology, 2010, 1, 127-140.	0.5	15
10	Statistical Methods for Pathway Analysis of Genome-Wide Data for Association with Complex Genetic Traits. Advances in Genetics, 2010, 72, 141-179.	0.8	86
11	Cardiac proteomic responses to ischemiaâ€“reperfusion injury and ischemic preconditioning. Expert Review of Proteomics, 2011, 8, 241-261.	1.3	32
12	HMMER web server: interactive sequence similarity searching. Nucleic Acids Research, 2011, 39, W29-W37.	6.5	4,492
13	Protein Structural Domains: Definition and Prediction. Current Protocols in Protein Science, 2011, 66, Unit2.14.	2.8	2
14	Reactome: a database of reactions, pathways and biological processes. Nucleic Acids Research, 2011, 39, D691-D697.	6.5	1,391
15	Integrative genomic analysis of human ribosomal DNA. Nucleic Acids Research, 2011, 39, 4949-4960.	6.5	141
16	Comparative genomics of the pathogenic ciliate <i>Ichthyophthirius multifiliis</i> , its free-living relatives and a host species provide insights into adoption of a parasitic lifestyle and prospects for disease control. Genome Biology, 2011, 12, R100.	13.9	102
17	Inferring Protein Function from Homology Using the Princeton Protein Orthology Database (Pâ€“POD). Current Protocols in Bioinformatics, 2011, 33, Unit 6.11.	25.8	4
18	Progranulin Is a Chemoattractant for Microglia and Stimulates Their Endocytic Activity. American Journal of Pathology, 2011, 178, 284-295.	1.9	103
19	BioPAX support in CellDesigner. Bioinformatics, 2011, 27, 3437-3438.	1.8	18
20	TIP: A probabilistic method for identifying transcription factor target genes from ChIP-seq binding profiles. Bioinformatics, 2011, 27, 3221-3227.	1.8	52

#	ARTICLE	IF	CITATIONS
21	Proteomic Profiling of Human Plasma by iTRAQ Reveals Down-Regulation of ITI-HC3 and VDBP by Cigarette Smoking. <i>Journal of Proteome Research</i> , 2011, 10, 1151-1159.	1.8	60
22	A differential proteomic approach identifies structural and functional components that contribute to the differentiation of brain capillary endothelial cells. <i>Journal of Proteomics</i> , 2011, 75, 628-641.	1.2	25
23	Data-driven approach to detect common copy-number variations and frequency profiles in a population-based Korean cohort. <i>European Journal of Human Genetics</i> , 2011, 19, 1167-1172.	1.4	7
24	The representation of heart development in the gene ontology. <i>Developmental Biology</i> , 2011, 354, 9-17.	0.9	35
25	Gene set analysis of genome-wide association studies: Methodological issues and perspectives. <i>Genomics</i> , 2011, 98, 1-8.	1.3	180
26	Plant protein-coding gene families: emerging bioinformatics approaches. <i>Trends in Plant Science</i> , 2011, 16, 558-567.	4.3	31
27	Ontologies and Standards in Bioscience Research: For Machine or for Human. <i>Frontiers in Physiology</i> , 2011, 2, 5.	1.3	7
28	Cranberry Proanthocyanidins Mediate Growth Arrest of Lung Cancer Cells through Modulation of Gene Expression and Rapid Induction of Apoptosis. <i>Molecules</i> , 2011, 16, 2375-2390.	1.7	38
29	Massive-Scale RNA-Seq Analysis of Non Ribosomal Transcriptome in Human Trisomy 21. <i>PLoS ONE</i> , 2011, 6, e18493.	1.1	62
30	Determining Signalling Nodes for Apoptosis by a Genetic High-Throughput Screen. <i>PLoS ONE</i> , 2011, 6, e25023.	1.1	5
31	Epigenetic Mechanism Underlying the Development of Polycystic Ovary Syndrome (PCOS)-Like Phenotypes in Prenatally Androgenized Rhesus Monkeys. <i>PLoS ONE</i> , 2011, 6, e27286.	1.1	128
32	Genome-Wide Signatures of "Rearrangement Hotspots"™ within Segmental Duplications in Humans. <i>PLoS ONE</i> , 2011, 6, e28853.	1.1	14
33	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. <i>Nature Genetics</i> , 2011, 43, 246-252.	9.4	1,201
34	Remote Thioredoxin Recognition Using Evolutionary Conservation and Structural Dynamics. <i>Structure</i> , 2011, 19, 461-470.	1.6	14
35	Characterization of the Secretome of Chickpea Suspension Culture Reveals Pathway Abundance and the Expected and Unexpected Secreted Proteins. <i>Journal of Proteome Research</i> , 2011, 10, 5006-5015.	1.8	26
36	Comparison of human glomerulus proteomic profiles obtained from low quantities of samples by different mass spectrometry with the comprehensive database. <i>Proteome Science</i> , 2011, 9, 47.	0.7	14
37	Combination of hydrogel nanoparticles and proteomics to reveal secreted proteins associated with decidualization of human uterine stromal cells. <i>Proteome Science</i> , 2011, 9, 50.	0.7	6
38	Proteomic and biochemical analyses reveal the activation of unfolded protein response, ERK-1/2 and ribosomal protein S6 signaling in experimental autoimmune myocarditis rat model. <i>BMC Genomics</i> , 2011, 12, 520.	1.2	15

#	ARTICLE	IF	CITATIONS
39	Changes in predicted protein disorder tendency may contribute to disease risk. BMC Genomics, 2011, 12, S2.	1.2	15
40	Phylogenetic and in silico structural analysis of the Parkinson disease-related kinase PINK1. Human Mutation, 2011, 32, 369-378.	1.1	32
41	Network-based function prediction and interactomics: The case for metabolic enzymes. Metabolic Engineering, 2011, 13, 1-10.	3.6	43
42	Conceptual framework and pilot study to benchmark phylogenomic databases based on reference gene trees. Briefings in Bioinformatics, 2011, 12, 423-435.	3.2	33
43	CIPRO 2.5: Ciona intestinalis protein database, a unique integrated repository of large-scale omics data, bioinformatic analyses and curated annotation, with user rating and reviewing functionality. Nucleic Acids Research, 2011, 39, D807-D814.	6.5	24
44	Comparative Gene Expression Analysis of Somatic Cell Nuclear Transfer-Derived Cloned Pigs with Normal and Abnormal Umbilical Cords1. Biology of Reproduction, 2011, 84, 189-199.	1.2	8
45	Genomic signatures of diet-related shifts during human origins. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 961-969.	1.2	48
46	OrthoDB: the hierarchical catalog of eukaryotic orthologs in 2011. Nucleic Acids Research, 2011, 39, D283-D288.	6.5	128
47	ICSNPathway: identify candidate causal SNPs and pathways from genome-wide association study by one analytical framework. Nucleic Acids Research, 2011, 39, W437-W443.	6.5	69
48	The Protein Ontology: a structured representation of protein forms and complexes. Nucleic Acids Research, 2011, 39, D539-D545.	6.5	102
49	Phylogenetic-based propagation of functional annotations within the Gene Ontology consortium. Briefings in Bioinformatics, 2011, 12, 449-462.	3.2	723
50	State-of-the-art bioinformatics protein structure prediction tools (Review). International Journal of Molecular Medicine, 2011, 28, 295-310.	1.8	25
51	Human leucine-rich repeat proteins: a genome-wide bioinformatic categorization and functional analysis in innate immunity. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4631-4638.	3.3	173
52	MicroRNA Expression and Regulation in Human, Chimpanzee, and Macaque Brains. PLoS Genetics, 2011, 7, e1002327.	1.5	126
53	The Arabidopsis HEI10 Is a New ZMM Protein Related to Zip3. PLoS Genetics, 2012, 8, e1002799.	1.5	208
54	Visual Analysis of Transcriptome Data in the Context of Anatomical Structures and Biological Networks. Frontiers in Plant Science, 2012, 3, 252.	1.7	6
55	Efficient algorithms for the reconciliation problem with gene duplication, horizontal transfer and loss. Bioinformatics, 2012, 28, i283-i291.	1.8	188
56	WormBase. Worm, 2012, 1, 15-21.	1.0	14

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57	MOPED: Model Organism Protein Expression Database. <i>Nucleic Acids Research</i> , 2012, 40, D1093-D1099.	6.5	106
58	ProtoNet 6.0: organizing 10 million protein sequences in a compact hierarchical family tree. <i>Nucleic Acids Research</i> , 2012, 40, D313-D320.	6.5	46
59	Common Structural and Epigenetic Changes in the Genome of Castration-Resistant Prostate Cancer. <i>Cancer Research</i> , 2012, 72, 616-625.	0.4	111
60	Heuristic Methods for Finding Pathogenic Variants in Gene Coding Sequences. <i>Journal of the American Heart Association</i> , 2012, 1, e002642.	1.6	12
61	Influenza infection and therapy: a systems approach. <i>Future Virology</i> , 2012, 7, 973-988.	0.9	1
62	The PRINTS database: a fine-grained protein sequence annotation and analysis resource—its status in 2012. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas019-bas019.	1.4	138
63	Manual GO annotation of predictive protein signatures: the InterPro approach to GO curation. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bar068-bar068.	1.4	108
64	Vesicular signalling and immune modulation as hedonic fingerprints: proteomic profiling in the chronic mild stress depression model. <i>Journal of Psychopharmacology</i> , 2012, 26, 1569-1583.	2.0	24
65	Unified modeling of gene duplication, loss, and coalescence using a locus tree. <i>Genome Research</i> , 2012, 22, 755-765.	2.4	153
66	Investigating the Contribution of Common Genetic Variants to the Risk and Pathogenesis of ADHD. <i>American Journal of Psychiatry</i> , 2012, 169, 186-194.	4.0	174
67	Genome-wide aberrant DNA methylation of microRNA host genes in hepatocellular carcinoma. <i>Epigenetics</i> , 2012, 7, 1230-1237.	1.3	59
68	Gene Ontology Annotations and Resources. <i>Nucleic Acids Research</i> , 2012, 41, D530-D535.	6.5	456
69	GeneCodis3: a non-redundant and modular enrichment analysis tool for functional genomics. <i>Nucleic Acids Research</i> , 2012, 40, W478-W483.	6.5	515
70	Genome-wide association analysis of coffee drinking suggests association with CYP1A1/CYP1A2 and NRCAM. <i>Molecular Psychiatry</i> , 2012, 17, 1116-1129.	4.1	112
71	A novel P66S mutation in exon 3 of the SOD1 gene with early onset and rapid progression. <i>Amyotrophic Lateral Sclerosis and Other Motor Neuron Disorders</i> , 2012, 13, 237-240.	2.3	11
72	Annotating Cancer Variants and Anti-Cancer Therapeutics in Reactome. <i>Cancers</i> , 2012, 4, 1180-1211.	1.7	270
73	Mutual exclusivity analysis identifies oncogenic network modules. <i>Genome Research</i> , 2012, 22, 398-406.	2.4	597
74	PANTHER in 2013: modeling the evolution of gene function, and other gene attributes, in the context of phylogenetic trees. <i>Nucleic Acids Research</i> , 2012, 41, D377-D386.	6.5	1,536

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75	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	6.5	921
76	IPAVS: Integrated Pathway Resources, Analysis and Visualization System. <i>Nucleic Acids Research</i> , 2012, 40, D803-D808.	6.5	20
77	BMP9 regulates endoglin-dependent chemokine responses in endothelial cells. <i>Blood</i> , 2012, 120, 4263-4273.	0.6	66
78	TSLP Signaling Network Revealed by SILAC-Based Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M112.017764.	2.5	47
79	Transcriptome Analysis of Garlic-Induced Hepatoprotection against Alcoholic Fatty Liver. <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 11104-11119.	2.4	35
80	Salivary peptidome in type 1 diabetes mellitus. <i>Biomedical Chromatography</i> , 2012, 26, 571-582.	0.8	24
81	Correlation between TGF- β 1 expression and proteomic profiling induced by severe acute respiratory syndrome coronavirus papain-like protease. <i>Proteomics</i> , 2012, 12, 3193-3205.	1.3	25
82	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. <i>Cell Reports</i> , 2012, 2, 1207-1219.	2.9	102
83	Increased Expression of LDL Receptor-Related Protein 1 during Human Cytomegalovirus Infection Reduces Virion Cholesterol and Infectivity. <i>Cell Host and Microbe</i> , 2012, 12, 86-96.	5.1	70
84	Proteomics and gene expression analyses of squalene-supplemented mice identify microsomal thioredoxin domain-containing protein 5 changes associated with hepatic steatosis. <i>Journal of Proteomics</i> , 2012, 77, 27-39.	1.2	25
85	Selective enrichment of newly synthesized proteins for quantitative secretome analysis. <i>Nature Biotechnology</i> , 2012, 30, 984-990.	9.4	234
86	Functional dissection of lysine deacetylases reveals that HDAC1 and p300 regulate AMPK. <i>Nature</i> , 2012, 482, 251-255.	13.7	87
87	Proteomic profiling of ATM kinase proficient and deficient cell lines upon blockage of proteasome activity. <i>Journal of Proteomics</i> , 2012, 75, 4632-4646.	1.2	20
88	GFam: a platform for automatic annotation of gene families. <i>Nucleic Acids Research</i> , 2012, 40, e152-e152.	6.5	3
89	Dual Lineage-Specific Expression of Sox17 During Mouse Embryogenesis. <i>Stem Cells</i> , 2012, 30, 2297-2308.	1.4	47
90	Bio-crude transcriptomics: Gene discovery and metabolic network reconstruction for the biosynthesis of the terpenome of the hydrocarbon oil-producing green alga, <i>Botryococcus braunii</i> race B (Showa)*. <i>BMC Genomics</i> , 2012, 13, 576.	1.2	52
91	Analysis of the peroxisome proliferator-activated receptor- β (PPAR β) cistrome reveals novel co-regulatory role of ATF4. <i>BMC Genomics</i> , 2012, 13, 665.	1.2	40
92	Integrative genome-wide expression profiling identifies three distinct molecular subgroups of renal cell carcinoma with different patient outcome. <i>BMC Cancer</i> , 2012, 12, 310.	1.1	25

#	ARTICLE	IF	CITATIONS
93	Novel mithramycins abrogate the involvement of protein factors in the transcription of cell cycle control genes. <i>Biochemical Pharmacology</i> , 2012, 84, 1133-1142.	2.0	16
94	Proteomic analysis of podosome fractions from macrophages reveals similarities to spreading initiation centres. <i>European Journal of Cell Biology</i> , 2012, 91, 908-922.	1.6	62
95	Using the Reactome Database. <i>Current Protocols in Bioinformatics</i> , 2012, 38, Unit8.7.	25.8	33
96	Genome-wide association study identifies eight new risk loci for polycystic ovary syndrome. <i>Nature Genetics</i> , 2012, 44, 1020-1025.	9.4	505
97	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012, 22, 778-790.	2.4	259
98	Human giant congenital melanocytic nevus exhibits potential proteomic alterations leading to melanotumorigenesis. <i>Proteome Science</i> , 2012, 10, 50.	0.7	10
99	A network module-based method for identifying cancer prognostic signatures. <i>Genome Biology</i> , 2012, 13, R112.	13.9	141
100	Cubic time algorithms of amalgamating gene trees and building evolutionary scenarios. <i>Biology Direct</i> , 2012, 7, 48.	1.9	4
101	H3K4me3 inversely correlates with DNA methylation at a large class of non-CpG-island-containing start sites. <i>Genome Medicine</i> , 2012, 4, 47.	3.6	39
102	Tight regulation of wingless-type signaling in the articular cartilage - subchondral bone biomechanical unit: transcriptomics in <i>Frzb</i> -knockout mice. <i>Arthritis Research and Therapy</i> , 2012, 14, R16.	1.6	39
103	Gene-Based Analysis of Regionally Enriched Cortical Genes in GWAS Data Sets of Cognitive Traits and Psychiatric Disorders. <i>PLoS ONE</i> , 2012, 7, e31687.	1.1	40
104	Differences in Gene Expression between First and Third Trimester Human Placenta: A Microarray Study. <i>PLoS ONE</i> , 2012, 7, e33294.	1.1	81
105	TNAP and EHD1 Are Over-Expressed in Bovine Brain Capillary Endothelial Cells after the Re-Induction of Blood-Brain Barrier Properties. <i>PLoS ONE</i> , 2012, 7, e48428.	1.1	26
106	Global Identification of Prokaryotic Glycoproteins Based on an <i>Escherichia coli</i> Proteome Microarray. <i>PLoS ONE</i> , 2012, 7, e49080.	1.1	9
107	Proteomic Analysis of Plasma Membrane Proteins in an In Vitro Blood-Brain Barrier Model. , 2012, , .		2
108	The Investigation of Gene Regulation and Variation in Human Cancers and Other Diseases. , 2012, , .		0
109	Computational Methods to Work as First-Pass Filter in Deleterious SNP Analysis of Alkaptonuria. <i>Scientific World Journal</i> , The, 2012, 2012, 1-9.	0.8	10
110	Proteomic analysis of rat microglia establishes a high-confidence reference data set of over 3000 proteins. <i>Proteomics</i> , 2012, 12, 246-250.	1.3	14

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111	Genetic architectures of psychiatric disorders: the emerging picture and its implications. <i>Nature Reviews Genetics</i> , 2012, 13, 537-551.	7.7	1,025
112	Hepatocarcinogenesis in non-irradiated liver is associated with a reduced number of clonal hepatocellular patches in non-tumorous liver parenchyma. <i>Journal of Pathology</i> , 2012, 228, 333-340.	2.1	4
113	Genome-wide DNA methylation profiles in hepatocellular carcinoma. <i>Hepatology</i> , 2012, 55, 1799-1808.	3.6	178
114	Revealing Mammalian Evolutionary Relationships by Comparative Analysis of Gene Clusters. <i>Genome Biology and Evolution</i> , 2012, 4, 586-601.	1.1	9
115	Protein repertoire impact of Ubiquitin-Proteasome System impairment: Insight into the protective role of beta-estradiol. <i>Journal of Proteomics</i> , 2012, 75, 1440-1453.	1.2	11
116	Differential protein profiling of synovial fluid from rheumatoid arthritis and osteoarthritis patients using LC-MALDI TOF/TOF. <i>Journal of Proteomics</i> , 2012, 75, 2869-2878.	1.2	106
117	Proteomics and gene expression analyses of mitochondria from squalene-treated apoE-deficient mice identify short-chain specific acyl-CoA dehydrogenase changes associated with fatty liver amelioration. <i>Journal of Proteomics</i> , 2012, 75, 2563-2575.	1.2	14
118	In-depth mass spectrometric mapping of the human vitreous proteome. <i>Proteome Science</i> , 2013, 11, 22.	0.7	58
119	Profiling and annotation of human kidney glomerulus proteome. <i>Proteome Science</i> , 2013, 11, 13.	0.7	18
120	Exosomes secreted by human cells transport largely mRNA fragments that are enriched in the 3'-untranslated regions. <i>Biology Direct</i> , 2013, 8, 12.	1.9	223
121	Mass spectrometry identification of granins and other proteins secreted by neuroblastoma cells. <i>Tumor Biology</i> , 2013, 34, 1773-1781.	0.8	13
122	Proteomics as a tool to explore human milk in health and disease. <i>Journal of Proteomics</i> , 2013, 88, 47-57.	1.2	37
123	Induction of DREB2A pathway with repression of E2F, jasmonic acid biosynthetic and photosynthesis pathways in cold acclimation-specific freeze-resistant wheat crown. <i>Functional and Integrative Genomics</i> , 2013, 13, 57-65.	1.4	16
124	Transcription profile of soybean-root-knot nematode interaction reveals a key role of phytohormones in the resistance reaction. <i>BMC Genomics</i> , 2013, 14, 322.	1.2	56
125	Large-scale gene function analysis with the PANTHER classification system. <i>Nature Protocols</i> , 2013, 8, 1551-1566.	5.5	2,276
126	Hunting human disease genes: lessons from the past, challenges for the future. <i>Human Genetics</i> , 2013, 132, 603-617.	1.8	31
127	Application of Genome-Scale Metabolic Models in Metabolic Engineering. <i>Industrial Biotechnology</i> , 2013, 9, 203-214.	0.5	26
128	On Identifying and Analyzing Significant Nodes in Protein-Protein Interaction Networks. , 2013, , .		1

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129	Tissue damage in organic rainbow trout muscle investigated by proteomics and bioinformatics. <i>Proteomics</i> , 2013, 13, 2180-2190.	1.3	0
130	Modeling of the hypothalamic-pituitary-adrenal axis-mediated interaction between the serotonin regulation pathway and the stress response using a Boolean approximation: a novel study of depression. <i>Theoretical Biology and Medical Modelling</i> , 2013, 10, 59.	2.1	18
131	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. <i>BMC Genomics</i> , 2013, 14, 876.	1.2	142
132	A systems biology approach using metabolomic data reveals genes and pathways interacting to modulate divergent growth in cattle. <i>BMC Genomics</i> , 2013, 14, 798.	1.2	76
133	Reconciliation Revisited: Handling Multiple Optima when Reconciling with Duplication, Transfer, and Loss. <i>Journal of Computational Biology</i> , 2013, 20, 738-754.	0.8	55
134	Identification of proteins interacting with HSP70 mRNAs in <i>Leishmania braziliensis</i> . <i>Journal of Proteomics</i> , 2013, 94, 124-137.	1.2	21
135	Characterization of Multiple Myeloma Vesicles by Label-Free Relative Quantitation. <i>Proteomics</i> , 2013, 13, n/a-n/a.	1.3	32
136	Integrative variable selection via Bayesian model uncertainty. <i>Statistics in Medicine</i> , 2013, 32, 4938-4953.	0.8	31
137	The early transcriptomic response to interleukin 1 β and interleukin 33 in rat neonatal cardiomyocytes. <i>Cytokine</i> , 2013, 61, 340-344.	1.4	1
138	Structure-based Comparative Analysis and Prediction of N-linked Glycosylation Sites in Evolutionarily Distant Eukaryotes. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 96-104.	3.0	47
139	In Vivo T-Box Transcription Factor Profiling Reveals Joint Regulation of Embryonic Neuromesodermal Bipotency. <i>Cell Reports</i> , 2013, 4, 1185-1196.	2.9	97
140	SNVDis: A Proteome-wide Analysis Service for Evaluating nsSNVs in Protein Functional Sites and Pathways. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 122-126.	3.0	15
141	The effect of organelle discovery upon sub-cellular protein localisation. <i>Journal of Proteomics</i> , 2013, 88, 129-140.	1.2	62
142	Altered immune pathway activity under exercise challenge in Gulf War Illness: An exploratory analysis. <i>Brain, Behavior, and Immunity</i> , 2013, 28, 159-169.	2.0	70
143	In Vivo SILAC-Based Proteomics Reveals Phosphoproteome Changes during Mouse Skin Carcinogenesis. <i>Cell Reports</i> , 2013, 3, 552-566.	2.9	90
144	Proteomic Profiling and Interactome Analysis of ER-Positive/HER2-Negative Invasive Ductal Carcinoma of the Breast: Towards Proteomics Biomarkers. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 27-40.	1.0	13
145	Integration of software tools in patent analysis. <i>World Patent Information</i> , 2013, 35, 97-104.	0.7	26
146	Glycolytic enzymes PGK1 and PKM2 as novel transcriptional targets of PPAR β in breast cancer pathophysiology. <i>Journal of Drug Targeting</i> , 2013, 21, 161-174.	2.1	44

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147	In utero and lactational exposure to vinclozolin and genistein induces genomic changes in the rat mammary gland. <i>Journal of Endocrinology</i> , 2013, 216, 245-263.	1.2	20
150	Proteomic profiling of developing cotton fibers from wild and domesticated <i>Gossypium barbadense</i> . <i>New Phytologist</i> , 2013, 200, 570-582.	3.5	72
151	Early Cone Setting in <i>Picea abies</i> Is Associated with Increased Transcriptional Activity of a MADS Box Transcription Factor. <i>Plant Physiology</i> , 2013, 161, 813-823.	2.3	46
152	T2D@ZJU: a knowledgebase integrating heterogeneous connections associated with type 2 diabetes mellitus. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat052.	1.4	24
153	Integrated Enrichment Analysis of Variants and Pathways in Genome-Wide Association Studies Indicates Central Role for IL-2 Signaling Genes in Type 1 Diabetes, and Cytokine Signaling Genes in Crohn's Disease. <i>PLoS Genetics</i> , 2013, 9, e1003770.	1.5	67
154	Using Biological Pathway Data with Paxtools. <i>PLoS Computational Biology</i> , 2013, 9, e1003194.	1.5	57
155	Phosphoproteomic Analyses Reveal Signaling Pathways That Facilitate Lytic Gammaherpesvirus Replication. <i>PLoS Pathogens</i> , 2013, 9, e1003583.	2.1	24
156	SpermatogenesisOnline 1.0: a resource for spermatogenesis based on manual literature curation and genome-wide data mining. <i>Nucleic Acids Research</i> , 2013, 41, D1055-D1062.	6.5	35
157	Exploration of Genome-Wide Circulating MicroRNA in Hepatocellular Carcinoma: MiR-483-5p as a Potential Biomarker. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013, 22, 2364-2373.	1.1	97
158	TSGene: a web resource for tumor suppressor genes. <i>Nucleic Acids Research</i> , 2013, 41, D970-D976.	6.5	295
159	The Epstein-Barr virus nuclear antigen-1 reprograms transcription by mimicry of high mobility group A proteins. <i>Nucleic Acids Research</i> , 2013, 41, 2950-2962.	6.5	40
160	Characterization of an M28 metalloprotease family member residing in the yeast vacuole. <i>FEMS Yeast Research</i> , 2013, 13, 471-484.	1.1	9
161	OrthoDB: a hierarchical catalog of animal, fungal and bacterial orthologs. <i>Nucleic Acids Research</i> , 2013, 41, D358-D365.	6.5	333
162	BREEDING AND GENETICS SYMPOSIUM: Networks and pathways to guide genomic selection. <i>Journal of Animal Science</i> , 2013, 91, 537-552.	0.2	57
163	Development of an integrated transcript sequence database and a gene expression atlas for gene discovery and analysis in switchgrass (<i>Panicum virgatum</i> L.). <i>Plant Journal</i> , 2013, 74, 160-173.	2.8	70
164	Integrated Analysis of Transcriptomic and Proteomic Data. <i>Current Genomics</i> , 2013, 14, 91-110.	0.7	387
165	Horizontal Transfer of a Subtilisin Gene from Plants into an Ancestor of the Plant Pathogenic Fungal Genus <i>Colletotrichum</i> . <i>PLoS ONE</i> , 2013, 8, e59078.	1.1	28
166	Simultaneous Transcriptome Analysis of <i>Sorghum</i> and <i>Bipolaris sorghicola</i> by Using RNA-seq in Combination with De Novo Transcriptome Assembly. <i>PLoS ONE</i> , 2013, 8, e62460.	1.1	79

#	ARTICLE	IF	CITATIONS
167	Bioinformatics for spermatogenesis: annotation of male reproduction based on proteomics. <i>Asian Journal of Andrology</i> , 2013, 15, 594-602.	0.8	32
168	Genome-Wide Microarray Expression and Genomic Alterations by Array-CGH Analysis in Neuroblastoma Stem-Like Cells. <i>PLoS ONE</i> , 2014, 9, e113105.	1.1	5
169	Comparative Genomics RNAi Screen Identifies Eftud2 as a Novel Regulator of Innate Immunity. <i>Genetics</i> , 2014, 197, 485-496.	1.2	51
170	Epstein-Barr virus encoded microRNA target SUMO-regulated cellular functions. <i>FEBS Journal</i> , 2014, 281, 4935-4950.	2.2	15
171	A 3-biomarker-panel predicts renal outcome in patients with proteinuric renal diseases. <i>BMC Medical Genomics</i> , 2014, 7, 75.	0.7	4
172	Differential DNA methylation profiles of infants exposed to maternal asthma during pregnancy. <i>Pediatric Pulmonology</i> , 2014, 49, 852-862.	1.0	59
173	The effects of glial cell line-derived neurotrophic factor on the in vitro matured porcine oocyte transcriptome. <i>Molecular Reproduction and Development</i> , 2014, 81, 217-229.	1.0	10
174	Impact of routinely employed procedures for tissue processing on the proteomic analysis of formalin-fixed paraffin-embedded tissue. <i>Proteomics - Clinical Applications</i> , 2014, 8, 796-804.	0.8	34
175	Genome-Wide Modulation of Gene Transcription in Ovarian Carcinoma Cells by a New Mithramycin Analogue. <i>PLoS ONE</i> , 2014, 9, e104687.	1.1	19
176	Reconciliation of Gene and Species Trees. <i>BioMed Research International</i> , 2014, 2014, 1-22.	0.9	17
177	WetA Is Required for Conidiogenesis and Conidium Maturation in the Ascomycete Fungus <i>Fusarium graminearum</i> . <i>Eukaryotic Cell</i> , 2014, 13, 87-98.	3.4	78
178	iPathCons and iPathDB: an improved insect pathway construction tool and the database. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	1.4	14
179	Genomics and bioinformatics resources for translational science in Rosaceae. <i>Plant Biotechnology Reports</i> , 2014, 8, 49-64.	0.9	18
180	Interleukin-1-induced changes in the glioblastoma secretome suggest its role in tumor progression. <i>Journal of Proteomics</i> , 2014, 99, 152-168.	1.2	65
181	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014, 15, 86.	1.2	375
182	Non-synonymous variations in cancer and their effects on the human proteome: workflow for NGS data biocuration and proteome-wide analysis of TCGA data. <i>BMC Bioinformatics</i> , 2014, 15, 28.	1.2	12
183	Detection and characterization of invasive circulating tumor cells derived from men with metastatic castration-resistant prostate cancer. <i>International Journal of Cancer</i> , 2014, 134, 2284-2293.	2.3	107
184	Differential Placental Gene Expression in Term Pregnancies Affected by Fetal Growth Restriction and Macrosomia. <i>Fetal Diagnosis and Therapy</i> , 2014, 36, 173-180.	0.6	25

#	ARTICLE	IF	CITATIONS
185	An Overview of the Challenges in Designing, Integrating, and Delivering BARD: A Public Chemical-Biology Resource and Query Portal for Multiple Organizations, Locations, and Disciplines. <i>Journal of Biomolecular Screening</i> , 2014, 19, 614-627.	2.6	22
186	Autoregulation of glypican-1 by intronic microRNA-149 fine-tunes the angiogenic response to fibroblast growth factor in human endothelial cells. <i>Journal of Cell Science</i> , 2014, 127, 1169-78.	1.2	61
187	Temperature threshold of isoprene emission from tropical trees, <i>Ficus virgata</i> and <i>Ficus septica</i> . <i>Chemosphere</i> , 2014, 95, 268-273.	4.2	25
188	Proteomics profiling of fiber development and domestication in upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq1 1 0.784314 rgBT /Ove	1.6	25
189	An evidence-based knowledgebase of pulmonary arterial hypertension to identify genes and pathways relevant to pathogenesis. <i>Molecular BioSystems</i> , 2014, 10, 732-740.	2.9	16
190	Proteomic analysis of human substantia nigra identifies novel candidates involved in Parkinson's disease pathogenesis. <i>Proteomics</i> , 2014, 14, 784-794.	1.3	85
191	Copy number variation in schizophrenia in Sweden. <i>Molecular Psychiatry</i> , 2014, 19, 762-773.	4.1	257
192	Transcriptomic microarray analysis of BoMac cells after infection with bovine foamy virus. <i>Archives of Virology</i> , 2014, 159, 1515-1519.	0.9	2
193	Robustness of birth-death and gain models for inferring evolutionary events. <i>BMC Genomics</i> , 2014, 15, S9.	1.2	2
194	Mouse Genome Database: From sequence to phenotypes and disease models. <i>Genesis</i> , 2015, 53, 458-473.	0.8	13
195	Phylotranscriptomic analysis uncovers a wealth of tissue inhibitor of metalloproteinases variants in echinoderms. <i>Royal Society Open Science</i> , 2015, 2, 150377.	1.1	21
196	NDEX, the Network Data Exchange. <i>Cell Systems</i> , 2015, 1, 302-305.	2.9	247
197	Antiphospholipid antibodies bind syncytiotrophoblast mitochondria and alter the proteome of extruded syncytial nuclear aggregates. <i>Placenta</i> , 2015, 36, 1463-1473.	0.7	26
198	Protein aggregation, structural disorder and RNA-binding ability: a new approach for physico-chemical and gene ontology classification of multiple datasets. <i>BMC Genomics</i> , 2015, 16, 1071.	1.2	14
199	MtiBase: a database for decoding microRNA target sites located within CDS and 5'UTR regions from CLIP-Seq and expression profile datasets. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav102.	1.4	23
200	The endogenous molecular clock orchestrates the temporal separation of substrate metabolism in skeletal muscle. <i>Skeletal Muscle</i> , 2015, 5, 17.	1.9	128
201	Study of phosphorylation events for cancer diagnoses and treatment. <i>Clinical and Translational Medicine</i> , 2015, 4, 59.	1.7	5
202	Gene expression profiling of <i>Mycobacterium tuberculosis</i> H37Rv-treated macrophages: A role of the <i>Bcl-2</i> family member <i>A1</i> in inhibition of apoptosis in mycobacteria-infected macrophages. <i>IUBMB Life</i> , 2015, 67, 726-736.	1.5	16

#	ARTICLE	IF	CITATIONS
203	DisGeNET: a discovery platform for the dynamical exploration of human diseases and their genes. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav028-bav028.	1.4	847
204	Role of Bioinformatic Tools and Databases in Cotton Research. Agronomy, 2015, , 303-337.	0.2	2
205	Identifying Highly Penetrant Disease Causal Mutations Using Next Generation Sequencing: Guide to Whole Process. BioMed Research International, 2015, 2015, 1-16.	0.9	7
206	Genome-Wide Gene Expression in relation to Age in Large Laboratory Cohorts of <i>Drosophila melanogaster</i> . Genetics Research International, 2015, 2015, 1-19.	2.0	30
207	Pathway Analysis and Its Applications. Advances in Bioinformatics and Biomedical Engineering Book Series, 2015, , 215-239.	0.2	0
208	Gene-Expression Novelty in Allopolyploid Cotton: A Proteomic Perspective. Genetics, 2015, 200, 91-104.	1.2	37
209	The language of the protein universe. Current Opinion in Genetics and Development, 2015, 35, 50-56.	1.5	27
210	Triple Negative Breast Cancer: A Multi-Omics Network Discovery Strategy for Candidate Targets and Driving Pathways. OMICS A Journal of Integrative Biology, 2015, 19, 115-130.	1.0	63
211	The InterPro protein families database: the classification resource after 15 years. Nucleic Acids Research, 2015, 43, D213-D221.	6.5	1,205
212	Application of comparative biology in GO functional annotation: the mouse model. Mammalian Genome, 2015, 26, 574-583.	1.0	11
213	Integrative Analysis Reveals Regulatory Programs in Endometriosis. Reproductive Sciences, 2015, 22, 1060-1072.	1.1	23
214	Emerging molecular networks common in ionizing radiation, immune and inflammatory responses by employing bioinformatics approaches. Cancer Letters, 2015, 368, 164-172.	3.2	60
215	Small-Scale duplication as a genomic signature for crop improvement. Journal of Crop Science and Biotechnology, 2015, 18, 45-51.	0.7	2
216	Visual Analytics of Signalling Pathways Using Time Profiles. Advances in Experimental Medicine and Biology, 2015, 823, 3-22.	0.8	0
217	Quantitative Proteomics Analysis Reveals Novel Insights into Mechanisms of Action of Long Noncoding RNA Hox Transcript Antisense Intergenic RNA (HOTAIR) in HeLa Cells*. Molecular and Cellular Proteomics, 2015, 14, 1447-1463.	2.5	44
218	Comprehensive protein profiling of synovial fluid in osteoarthritis following protein equalization. Osteoarthritis and Cartilage, 2015, 23, 1204-1213.	0.6	48
219	Computational Approach to Annotating Variants of Unknown Significance in Clinical Next Generation Sequencing. Laboratory Medicine, 2015, 46, 285-289.	0.8	28
220	The pathogenic human Torsin A in <i>Drosophila</i> activates the unfolded protein response and increases susceptibility to oxidative stress. BMC Genomics, 2015, 16, 338.	1.2	17

#	ARTICLE	IF	CITATIONS
221	Unraveling the evolution and regulation of the alternative oxidase gene family in plants. <i>Development Genes and Evolution</i> , 2015, 225, 331-339.	0.4	7
222	WetA and VosA are distinct regulators of conidiation capacity, conidial quality, and biological control potential of a fungal insect pathogen. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10069-10081.	1.7	68
223	Larger aggregates of mutant seipin in Celia's Encephalopathy, a new protein misfolding neurodegenerative disease. <i>Neurobiology of Disease</i> , 2015, 83, 44-53.	2.1	14
224	Presence of DNA methyltransferase activity and CpC methylation in <i>Drosophila melanogaster</i> . <i>Molecular Biology Reports</i> , 2015, 42, 1615-1621.	1.0	24
225	Human cells contain natural double-stranded RNAs with potential regulatory functions. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 89-97.	3.6	35
226	Norepinephrine transporter knock-out alters expression of the genes connected with antidepressant drugs action. <i>Brain Research</i> , 2015, 1594, 284-292.	1.1	5
227	Annexin A3 as a Potential Target for Immunotherapy of Liver Cancer Stem-Like Cells. <i>Stem Cells</i> , 2015, 33, 354-366.	1.4	54
228	A Beginners Guide to Estimating the Non-synonymous to Synonymous Rate Ratio of all Protein-Coding Genes in a Genome. <i>Methods in Molecular Biology</i> , 2015, 1201, 65-90.	0.4	105
229	<i>Drosophila</i> Torsin Protein Regulates Motor Control and Stress Sensitivity and Forms a Complex with Fragile-X Mental Retardation Protein. <i>Neural Plasticity</i> , 2016, 2016, 1-14.	1.0	2
230	Deciphering the Role of Emx1 in Neurogenesis: A Neuroproteomics Approach. <i>Frontiers in Molecular Neuroscience</i> , 2016, 9, 98.	1.4	18
231	Human Intervention Study to Assess the Effects of Supplementation with Olive Leaf Extract on Peripheral Blood Mononuclear Cell Gene Expression. <i>International Journal of Molecular Sciences</i> , 2016, 17, 2019.	1.8	24
232	WORMHOLE: Novel Least Diverged Ortholog Prediction through Machine Learning. <i>PLoS Computational Biology</i> , 2016, 12, e1005182.	1.5	21
233	Functional genetics-directed identification of novel pharmacological inhibitors of FAS- and TNF-dependent apoptosis that protect mice from acute liver failure. <i>Cell Death and Disease</i> , 2016, 7, e2145-e2145.	2.7	11
234	In-Depth Proteomic Quantification of Cell Secretome in Serum-Containing Conditioned Medium. <i>Analytical Chemistry</i> , 2016, 88, 4971-4978.	3.2	35
235	A dataset for assessing temporal changes in gene expression during the aging process of adult <i>Drosophila melanogaster</i> . <i>Data in Brief</i> , 2016, 7, 1652-1657.	0.5	0
236	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. <i>BMC Genomics</i> , 2016, 17, 267.	1.2	74
237	Characterization of the Translationally Controlled Tumor Protein (TCTP) Interactome Reveals Novel Binding Partners in Human Cancer Cells. <i>Journal of Proteome Research</i> , 2016, 15, 3741-3751.	1.8	21
238	Fast and reliable inference of semantic clusters. <i>Knowledge-Based Systems</i> , 2016, 111, 133-143.	4.0	3

#	ARTICLE	IF	CITATIONS
239	ModuleAlign: module-based global alignment of protein-protein interaction networks. <i>Bioinformatics</i> , 2016, 32, i658-i664.	1.8	34
240	A network-pathway based module identification for predicting the prognosis of ovarian cancer patients. <i>Journal of Ovarian Research</i> , 2016, 9, 73.	1.3	26
241	Tissue enrichment analysis for <i>C. elegans</i> genomics. <i>BMC Bioinformatics</i> , 2016, 17, 366.	1.2	155
242	Joint Alignment of Multiple Protein-Protein Interaction Networks via Convex Optimization. <i>Journal of Computational Biology</i> , 2016, 23, 903-911.	0.8	15
243	Genome-Wide Divergence in the West-African Malaria Vector <i>Anopheles melas</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2867-2879.	0.8	10
244	Systematic profiling of short tandem repeats in the cattle genome. <i>Genome Biology and Evolution</i> , 2016, 9, evw256.	1.1	20
245	RNA Sequencing Applied to Livestock Production. , 2016, , 63-94.		0
246	SYVN1, NEDD8, and FBXO2 Proteins Regulate F508 Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) Ubiquitin-mediated Proteasomal Degradation. <i>Journal of Biological Chemistry</i> , 2016, 291, 25489-25504.	1.6	27
247	Systems Biology in Animal Production and Health, Vol. 1. , 2016, , .		0
248	Population-genetic properties of differentiated copy number variations in cattle. <i>Scientific Reports</i> , 2016, 6, 23161.	1.6	91
249	GO annotation in InterPro: why stability does not indicate accuracy in a sea of changing annotations. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw027.	1.4	19
250	Reduced Expression of Histone Methyltransferases KMT2C and KMT2D Correlates with Improved Outcome in Pancreatic Ductal Adenocarcinoma. <i>Cancer Research</i> , 2016, 76, 4861-4871.	0.4	72
251	Emergence and Evolution of Hominidae-Specific Coding and Noncoding Genomic Sequences. <i>Genome Biology and Evolution</i> , 2016, 8, 2076-2092.	1.1	12
252	Proteomic characterization of circulating extracellular vesicles identifies novel serum myeloma associated markers. <i>Journal of Proteomics</i> , 2016, 136, 89-98.	1.2	68
253	Elucidating the Molecular Composition of Cartilage by Proteomics. <i>Journal of Proteome Research</i> , 2016, 15, 374-388.	1.8	57
254	Properties of human disease genes and the role of genes linked to Mendelian disorders in complex disease aetiology. <i>Human Molecular Genetics</i> , 2017, 26, ddw405.	1.4	38
255	La Deletion from Mouse Brain Alters Pre-tRNA Metabolism and Accumulation of Pre-5.8S rRNA, with Neuron Death and Reactive Astrocytosis. <i>Molecular and Cellular Biology</i> , 2017, 37, .	1.1	8
257	Human DDX21 binds and unwinds RNA guanine quadruplexes. <i>Nucleic Acids Research</i> , 2017, 45, 6656-6668.	6.5	79

#	ARTICLE	IF	CITATIONS
258	APRICOT: an integrated computational pipeline for the sequence-based identification and characterization of RNA-binding proteins. <i>Nucleic Acids Research</i> , 2017, 45, e96-e96.	6.5	22
259	Sequencing, de novo assembling, and annotating the genome of the endangered Chinese crocodile lizard <i>Shinisaurus crocodilurus</i> . <i>GigaScience</i> , 2017, 6, 1-6.	3.3	23
260	FlyRNAi.org—the database of the <i>Drosophila</i> RNAi screening center and transgenic RNAi project: 2017 update. <i>Nucleic Acids Research</i> , 2017, 45, D672-D678.	6.5	51
261	In-depth characterization of the tomato fruit pericarp proteome. <i>Proteomics</i> , 2017, 17, 1600406.	1.3	39
262	Porcine Esophageal Submucosal Gland Culture Model Shows Capacity for Proliferation and Differentiation. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2017, 4, 385-404.	2.3	32
263	Exploration of the bovine colostrum proteome and effects of heat treatment time on colostrum protein profile. <i>Journal of Dairy Science</i> , 2017, 100, 9392-9401.	1.4	26
264	Binding of PLD2-Generated Phosphatidic Acid to KIF5B Promotes MT1-MMP Surface Trafficking and Lung Metastasis of Mouse Breast Cancer Cells. <i>Developmental Cell</i> , 2017, 43, 186-197.e7.	3.1	63
265	CXCR3 Signaling Is Required for Restricted Homing of Parenteral Tuberculosis Vaccine-Induced T Cells to Both the Lung Parenchyma and Airway. <i>Journal of Immunology</i> , 2017, 199, 2555-2569.	0.4	54
266	Quantitative proteomic analysis of host responses triggered by <i>Mycobacterium tuberculosis</i> infection in human macrophage cells. <i>Acta Biochimica Et Biophysica Sinica</i> , 2017, 49, 835-844.	0.9	23
267	Tissue and time specific expression pattern of interferon regulated genes in the chicken. <i>BMC Genomics</i> , 2017, 18, 264.	1.2	19
268	Qualitative and Quantitative Analysis of Proteome and Peptidome of Human Follicular Fluid Using Multiple Samples from Single Donor with LC-MS and SWATH Methodology. <i>Journal of Proteome Research</i> , 2017, 16, 3053-3067.	1.8	26
269	Developing Human Radiation Biodosimetry Models: Testing Cross-Species Conversion Approaches Using an Ex Vivo Model System. <i>Radiation Research</i> , 2017, 187, 708.	0.7	38
271	Co-infection of Sweet Orange with Severe and Mild Strains of Citrus tristeza virus Is Overwhelmingly Dominated by the Severe Strain on Both the Transcriptional and Biological Levels. <i>Frontiers in Plant Science</i> , 2017, 8, 1419.	1.7	15
272	Differential Binding of Three Major Human ADAR Isoforms to Coding and Long Non-Coding Transcripts. <i>Genes</i> , 2017, 8, 68.	1.0	34
273	Identification of Key Candidate Genes and Pathways in Colorectal Cancer by Integrated Bioinformatical Analysis. <i>International Journal of Molecular Sciences</i> , 2017, 18, 722.	1.8	132
274	Pharmacological Stimulation of Phagocytosis Enhances Amyloid Plaque Clearance; Evidence from a Transgenic Mouse Model of ATTR Neuropathy. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 138.	1.4	7
275	WetA bridges cellular and chemical development in <i>Aspergillus flavus</i> . <i>PLoS ONE</i> , 2017, 12, e0179571.	1.1	48
276	Transcriptional analysis of sweet orange trees co-infected with <i>Candidatus Liberibacter asiaticus</i> ™ and mild or severe strains of Citrus tristeza virus. <i>BMC Genomics</i> , 2017, 18, 837.	1.2	10

#	ARTICLE	IF	CITATIONS
277	Feature selection and extraction from heterogeneous genomic characterizations. , 2017, , 45-81.		1
278	Genome-wide strategies identify downstream target genes of connective tissue-associated transcription factors. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	20
279	Gene Expression Analysis in Human Peripheral Blood Cells after 900 MHz RF-EMF Short-Term Exposure. <i>Radiation Research</i> , 2018, 189, 529-540.	0.7	6
280	QuantumClone: clonal assessment of functional mutations in cancer based on a genotype-aware method for clonal reconstruction. <i>Bioinformatics</i> , 2018, 34, 1808-1816.	1.8	20
281	Proteomic Analysis of Nucleus Pulposus Cell-derived Extracellular Matrix Niche and Its Effect on Phenotypic Alteration of Dermal Fibroblasts. <i>Scientific Reports</i> , 2018, 8, 1512.	1.6	14
282	Prognosis of ovarian cancer is associated with effector memory CD8 ⁺ T cell accumulation in ascites, CXCL9 levels and activation-triggered signal transduction in T cells. <i>Oncolmmunology</i> , 2018, 7, e1424672.	2.1	70
283	Proteotranscriptomics Reveal Signaling Networks in the Ovarian Cancer Microenvironment. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 270-289.	2.5	55
284	Prolonged Waking and Recovery Sleep Affect the Serum MicroRNA Expression Profile in Humans. <i>Clocks & Sleep</i> , 2018, 1, 75-87.	0.9	6
285	Spatiotemporal Control of CNS Myelination by Oligodendrocyte Programmed Cell Death through the TFEB-PUMA Axis. <i>Cell</i> , 2018, 175, 1811-1826.e21.	13.5	105
286	Large-Scale Analyses of Site-Specific Evolutionary Rates across Eukaryote Proteomes Reveal Confounding Interactions between Intrinsic Disorder, Secondary Structure, and Functional Domains. <i>Genes</i> , 2018, 9, 553.	1.0	10
287	Biomechanical Rigidity and Quantitative Proteomics Analysis of Segmental Regions of the Trabecular Meshwork at Physiologic and Elevated Pressures. , 2018, 59, 246.		54
288	The dilemma of bacterial expansins evolution. The unusual case of <i>Streptomyces acidiscabies</i> and <i>Kutzneria</i> sp. 744. <i>Communicative and Integrative Biology</i> , 2018, 11, e1539612.	0.6	2
289	The gut microbiome participates in transgenerational inheritance of low-temperature responses in <i>Drosophila melanogaster</i> . <i>FEBS Letters</i> , 2018, 592, 4078-4086.	1.3	23
290	Identification of Genes and Pathways Involved in Ovarian Epithelial Cancer by Bioinformatics Analysis. <i>Journal of Cancer</i> , 2018, 9, 3016-3022.	1.2	13
291	Insights on a putative aminoacyl-tRNA-protein transferase of <i>Leishmania major</i> . <i>PLoS ONE</i> , 2018, 13, e0203369.	1.1	0
292	Decane-1,2-diol derivatives as potential antitumor agents for the treatment of glioblastoma. <i>European Journal of Pharmacology</i> , 2018, 837, 105-116.	1.7	4
293	Survey of Human Chromosome 21 Gene Expression Effects on Early Development in <i>Danio rerio</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2215-2223.	0.8	37
294	Gene family innovation, conservation and loss on the animal stem lineage. <i>ELife</i> , 2018, 7, .	2.8	149

#	ARTICLE	IF	CITATIONS
295	IL-6 augments IL-4-induced polarization of primary human macrophages through synergy of STAT3, STAT6 and BATF transcription factors. <i>Oncolmmunology</i> , 2018, 7, e1494110.	2.1	37
296	Bioinformatics-based identification of potential microRNA biomarkers in frequent and non-frequent exacerbators of COPD. <i>International Journal of COPD</i> , 2018, Volume 13, 1217-1228.	0.9	24
297	Allopregnanolone Alters the Gene Expression Profile of Human Glioblastoma Cells. <i>International Journal of Molecular Sciences</i> , 2018, 19, 864.	1.8	9
298	Effect of ovarian cancer ascites on SKOV-3 cells proteome: new proteins associated with aggressive phenotype in epithelial ovarian cancer. <i>Proteome Science</i> , 2018, 16, 3.	0.7	5
299	Non-Coding Transcriptome Maps across Twenty Tissues of the Korean Black Chicken, Yeonsan Ogye. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2359.	1.8	6
300	Systematic Dissection of the Evolutionarily Conserved WetA Developmental Regulator across a Genus of Filamentous Fungi. <i>MBio</i> , 2018, 9, .	1.8	68
301	A<i>Cyclin E</i>-Centered Genetic Network Contributes to Alcohol-Induced Variation in <i>Drosophila</i> Development. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2643-2653.	0.8	14
302	Impact of Heat Shock Protein 90 Inhibition on the Proteomic Profile of Lung Adenocarcinoma as Measured by Two-Dimensional Electrophoresis Coupled with Mass Spectrometry. <i>Cells</i> , 2019, 8, 806.	1.8	3
303	Circular RNA Signature in Hepatocellular Carcinoma. <i>Journal of Cancer</i> , 2019, 10, 3361-3372.	1.2	57
304	m6A enhances the phase separation potential of mRNA. <i>Nature</i> , 2019, 571, 424-428.	13.7	460
305	Genome structure predicts modular transcriptome responses to genetic and environmental conditions. <i>Molecular Ecology</i> , 2019, 28, 3681-3697.	2.0	10
306	Ribosome profiling of selenoproteins in vivo reveals consequences of pathogenic Secisbp2 missense mutations. <i>Journal of Biological Chemistry</i> , 2019, 294, 14185-14200.	1.6	15
307	The Effects of Sindbis Viral Vectors on Neuronal Function. <i>Frontiers in Cellular Neuroscience</i> , 2019, 13, 362.	1.8	8
309	Research Article Genomic regions and genes associated with carcass quality in Nelore cattle. <i>Genetics and Molecular Research</i> , 2019, 18, .	0.3	15
310	Diagnostic potential of circulating micro RNA hsa-miR-320 in patients of high altitude induced deep vein thrombosis: An Indian study. <i>Gene Reports</i> , 2019, 17, 100550.	0.4	5
311	<sc>RNA</sc>â€seq analyses of <i>Arabidopsis thaliana</i> seedlings after exposure to blueâ€light phototropic stimuli in microgravity. <i>American Journal of Botany</i> , 2019, 106, 1466-1476.	0.8	53
312	An integrated genome-wide multi-omics analysis of gene expression dynamics in the preimplantation mouse embryo. <i>Scientific Reports</i> , 2019, 9, 13356.	1.6	39
313	Differential Gene Expression in Articular Cartilage and Subchondral Bone of Neonatal and Adult Horses. <i>Genes</i> , 2019, 10, 745.	1.0	4

#	ARTICLE	IF	CITATIONS
314	Genes for sexual body size dimorphism in hybrid tilapia (<i>Oreochromis sp. x Oreochromis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 Td (1.2	5
315	Therapy-Induced MHC I Ligands Shape Neo-Antitumor CD8 T Cell Responses during Oncolytic Virus-Based Cancer Immunotherapy. <i>Journal of Proteome Research</i> , 2019, 18, 2666-2675.	1.8	22
316	Analysis of cyclin E co-expression genes reveals nuclear transcription factor Y subunit alpha is an oncogene in gastric cancer. <i>Chronic Diseases and Translational Medicine</i> , 2019, 5, 44-52.	0.9	13
317	Quantitative proteomics identifies brain acid soluble protein 1 (BASP1) as a prognostic biomarker candidate in pancreatic cancer tissue. <i>EBioMedicine</i> , 2019, 43, 282-294.	2.7	43
318	The Pathway to Cancer Cachexia: MicroRNA-Regulated Networks in Muscle Wasting Based on Integrative Meta-Analysis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1962.	1.8	33
319	Decreased Protein Kinase C- β Type II Associated with the Prominent Endotoxin Exhaustion in the Macrophage of FcGR1b ^{+/+} / β ^{-/-} Lupus Prone Mice is Revealed by Phosphoproteomic Analysis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1354.	1.8	25
320	Identification of survival-associated key genes and long non-coding RNAs in glioblastoma multiforme by weighted gene co-expression network analysis. <i>International Journal of Molecular Medicine</i> , 2019, 43, 1709-1722.	1.8	13
321	Alkylaminophenol Induces G1/S Phase Cell Cycle Arrest in Glioblastoma Cells Through p53 and Cyclin-Dependent Kinase Signaling Pathway. <i>Frontiers in Pharmacology</i> , 2019, 10, 330.	1.6	42
322	Global host molecular perturbations upon in situ loss of bacterial endosymbionts in the deep-sea mussel <i>Bathymodiolus azoricus</i> assessed using proteomics and transcriptomics. <i>BMC Genomics</i> , 2019, 20, 109.	1.2	9
323	ABA-Induced Vegetative Diaspore Formation in <i>Physcomitrella patens</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 315.	1.7	30
324	Chromatin changes in <i>Anopheles gambiae</i> induced by <i>Plasmodium falciparum</i> infection. <i>Epigenetics and Chromatin</i> , 2019, 12, 5.	1.8	32
325	Dual-platform affinity proteomics identifies links between the recurrence of ovarian carcinoma and proteins released into the tumor microenvironment. <i>Theranostics</i> , 2019, 9, 6601-6617.	4.6	36
326	Multi-platform Affinity Proteomics Identify Proteins Linked to Metastasis and Immune Suppression in Ovarian Cancer Plasma. <i>Frontiers in Oncology</i> , 2019, 9, 1150.	1.3	47
327	JASPer controls interphase histone H3S10 phosphorylation by chromosomal kinase JIL-1 in <i>Drosophila</i> . <i>Nature Communications</i> , 2019, 10, 5343.	5.8	18
328	LTF, PRTN3, and MNDA in Synovial Fluid as Promising Biomarkers for Periprosthetic Joint Infection. <i>Journal of Bone and Joint Surgery - Series A</i> , 2019, 101, 2226-2234.	1.4	23
329	Cadmium accumulation capacity and resistance strategies of a cadmium-hypertolerant fern " <i>Microsorium fortunei</i> . <i>Science of the Total Environment</i> , 2019, 649, 1209-1223.	3.9	10
330	Interference between arsenic-induced toxicity and hypoxia. <i>Plant, Cell and Environment</i> , 2019, 42, 574-590.	2.8	34
331	Correlation of cell-surface CD 8 levels with function, phenotype and transcriptome of naive CD 8 T cells. <i>Immunology</i> , 2019, 156, 384-401.	2.0	6

#	ARTICLE	IF	CITATIONS
332	Developmental Heterogeneity of Microglia and Brain Myeloid Cells Revealed by Deep Single-Cell RNA Sequencing. <i>Neuron</i> , 2019, 101, 207-223.e10.	3.8	695
333	Elevated WBP2 Expression in HER2-positive Breast Cancers Correlates with Sensitivity to Trastuzumab-based Neoadjuvant Therapy: A Retrospective and Multicentric Study. <i>Clinical Cancer Research</i> , 2019, 25, 2588-2600.	3.2	11
334	Mixtures of Aluminum and Indium Induce More than Additive Phenotypic and Toxicogenomic Responses in <i>Daphnia magna</i> . <i>Environmental Science & Technology</i> , 2019, 53, 1639-1649.	4.6	19
335	Identification of key genes and pathways in diabetic nephropathy by bioinformatics analysis. <i>Journal of Diabetes Investigation</i> , 2019, 10, 972-984.	1.1	52
336	Dynamics of WNT signaling components in the human ovary from development to adulthood. <i>Histochemistry and Cell Biology</i> , 2019, 151, 115-123.	0.8	16
337	Human follicular fluid proteomic and peptidomic composition quantitative studies by SWATH-MS methodology. Applicability of high pH RP-HPLC fractionation. <i>Journal of Proteomics</i> , 2019, 191, 131-142.	1.2	18
338	Exploring mechanisms of increased cardiovascular disease risk with antipsychotic medications: Risperidone alters the cardiac proteomic signature in mice. <i>Pharmacological Research</i> , 2020, 152, 104589.	3.1	21
339	Variation under domestication in animal models: the case of the Mexican axolotl. <i>BMC Genomics</i> , 2020, 21, 827.	1.2	1
340	Design and Characterization of a Novel Tool for the Antigenic Enrichment of <i>Actinobacillus pleuropneumoniae</i> Outer Membrane. <i>Pathogens</i> , 2020, 9, 1014.	1.2	2
341	Differential gene expression analysis reveals pathways important in early post-traumatic osteoarthritis in an equine model. <i>BMC Genomics</i> , 2020, 21, 843.	1.2	7
342	Transcriptome-based design of antisense inhibitors potentiates carbapenem efficacy in CRE <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30699-30709.	3.3	20
343	The RNA-binding protein SERBP1 functions as a novel oncogenic factor in glioblastoma by bridging cancer metabolism and epigenetic regulation. <i>Genome Biology</i> , 2020, 21, 195.	3.8	55
344	Notch activation in the mouse mammary luminal lineage leads to ductal hyperplasia and altered partitioning of luminal cell subtypes. <i>Experimental Cell Research</i> , 2020, 395, 112156.	1.2	7
345	Immune network dysregulation precedes clinical diagnosis of asthma. <i>Scientific Reports</i> , 2020, 10, 12784.	1.6	3
346	Evolutionary Biology – A Transdisciplinary Approach. , 2020, , .		5
347	Mechanistic insights into toxicity pathways induced by nanomaterials in <i>Daphnia magna</i> from analysis of the composition of the acquired protein corona. <i>Environmental Science: Nano</i> , 2020, 7, 3343-3359.	2.2	19
348	Identification of zebrafish fumarate hydratase active site by molecular docking and simulation studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, , 1-13.	2.0	0
349	ZenoFishDb v1.1: A Database for Xenotransplantation Studies in Zebrafish. <i>Zebrafish</i> , 2020, 17, 305-318.	0.5	7

#	ARTICLE	IF	CITATIONS
350	Glucagon-like peptide-1 receptor and sarcoglycan delta genetic variants can affect cardiovascular risk in chronic kidney disease patients under hemodialysis. <i>CKJ: Clinical Kidney Journal</i> , 2020, 13, 666-673.	1.4	3
351	Poly(ADP-ribose) polymerase 1 in genome-wide expression control in <i>Drosophila</i> . <i>Scientific Reports</i> , 2020, 10, 21151.	1.6	9
352	Comparative analysis of metabolic and transcriptomic features of <i>Nothobranchius furzeri</i> . <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200217.	1.5	2
353	Identification of circular RNAs in porcine sperm and evaluation of their relation to sperm motility. <i>Scientific Reports</i> , 2020, 10, 7985.	1.6	27
354	Neurodevelopmental disorder risk gene <i>DYRK1A</i> is required for ciliogenesis and brain size in <i>Xenopus</i> embryos. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	27
355	CReP mediates selective translation initiation at the endoplasmic reticulum. <i>Science Advances</i> , 2020, 6, eaba0745.	4.7	15
356	Automated Hypothesis Generation to Identify Signals Relevant in the Development of Mammalian Cell and Tissue Bioprocesses, With Validation in a Retinal Culture System. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 534.	2.0	1
357	Population Genomics Advances and Opportunities in Conservation of Kiwi (<i>Apteryx</i> spp.). <i>Population Genomics</i> , 2020, , 493-521.	0.2	6
358	Targeting Pyruvate Carboxylase by a Small Molecule Suppresses Breast Cancer Progression. <i>Advanced Science</i> , 2020, 7, 1903483.	5.6	33
359	IL-6 blockade reverses bone marrow failure induced by human acute myeloid leukemia. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	52
360	Fulvic acid increases forage legume growth inducing preferential up-regulation of nodulation and signalling-related genes. <i>Journal of Experimental Botany</i> , 2020, 71, 5689-5704.	2.4	19
361	A Comprehensive Coexpression Network Analysis in <i>Vibrio cholerae</i> . <i>MSystems</i> , 2020, 5, .	1.7	5
362	Cell death and survival pathways in Alzheimer's disease: an integrative hypothesis testing approach utilizing -omic data sets. <i>Neurobiology of Aging</i> , 2020, 95, 15-25.	1.5	23
363	Phenotypic Convergence Is Not Mirrored at the Protein Level in a Lizard Adaptive Radiation. <i>Molecular Biology and Evolution</i> , 2020, 37, 1604-1614.	3.5	19
364	Embryonic Barcoding of Equipotent Mammary Progenitors Functionally Identifies Breast Cancer Drivers. <i>Cell Stem Cell</i> , 2020, 26, 403-419.e4.	5.2	15
365	Cellular Heterogeneity and Lineage Restriction during Mouse Digit Tip Regeneration at Single-Cell Resolution. <i>Developmental Cell</i> , 2020, 52, 525-540.e5.	3.1	56
366	Draft Genome of the Asian Buffalo Leech <i>Hirudinaria manillensis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1321.	1.1	11
367	Proteome alterations associated with the oleic acid and cis-9, trans-11 conjugated linoleic acid content in bovine skeletal muscle. <i>Journal of Proteomics</i> , 2020, 222, 103792.	1.2	2

#	ARTICLE	IF	CITATIONS
368	Modeling Basins of Attraction for Breast Cancer Using Hopfield Networks. <i>Frontiers in Genetics</i> , 2020, 11, 314.	1.1	14
369	A Strategic Target Rescues Trimethoprim Sensitivity in <i>Escherichia coli</i> . <i>IScience</i> , 2020, 23, 100986.	1.9	15
370	Human Hepatocyte Nuclear Factor 4 \hat{I} Encodes Isoforms with Distinct Transcriptional Functions. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 808-827.	2.5	31
371	Refinement of coding SNPs in the human aryl hydrocarbon receptor gene using ISNPPranker: An integrative-SNP ranking web-tool. <i>Computational Biology and Chemistry</i> , 2021, 90, 107416.	1.1	2
372	Parallel inÂvivo analysis of large-effect autism genes implicates cortical neurogenesis and estrogen in risk and resilience. <i>Neuron</i> , 2021, 109, 788-804.e8.	3.8	54
373	Whole-Genome Sequencing of Inbred Mouse Strains Selected for High and Low Open-Field Activity. <i>Behavior Genetics</i> , 2021, 51, 68-81.	1.4	7
374	Prediction, Analysis, Visualization, and Storage of Proteinâ€“Protein Interactions Using Computational Approaches. , 2021, , 265-346.		1
375	An altered secretome is an early marker of the pathogenesis of CLN6 Batten disease. <i>Journal of Neurochemistry</i> , 2021, 157, 764-780.	2.1	7
376	Computational modeling and bioinformatic analyses of functional mutations in drug target genes in <i>Mycobacterium tuberculosis</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2423-2446.	1.9	9
377	Generation of an isoform-level transcriptome atlas of macrophage activation. <i>Journal of Biological Chemistry</i> , 2021, 296, 100784.	1.6	18
378	Nuclear sensing of breaks in mitochondrial DNA enhances immune surveillance. <i>Nature</i> , 2021, 591, 477-481.	13.7	171
379	The histone demethylase KDM5 is required for synaptic structure and function at the <i>Drosophila</i> neuromuscular junction. <i>Cell Reports</i> , 2021, 34, 108753.	2.9	15
381	Dysregulated Provision of Oxidisable Substrates to the Mitochondria in ME/CFS Lymphoblasts. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2046.	1.8	24
382	SBGN Bricks Ontology as a tool to describe recurring concepts in molecular networks. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
383	Oncolytic virotherapy-mediated anti-tumor response: a single-cell perspective. <i>Cancer Cell</i> , 2021, 39, 394-406.e4.	7.7	63
384	Neuron-specific spinal cord translomes reveal a neuropeptide code for mouse dorsal horn excitatory neurons. <i>Scientific Reports</i> , 2021, 11, 5232.	1.6	15
385	Temperature-induced changes in the proteome of <i>Pseudomonas aeruginosa</i> during petroleum hydrocarbon degradation. <i>Archives of Microbiology</i> , 2021, 203, 2463-2473.	1.0	4
386	Disruption of Cxcr3 chemotactic signaling alters lysosomal function and renders macrophages more microbicidal. <i>Cell Reports</i> , 2021, 35, 109000.	2.9	3

#	ARTICLE	IF	CITATIONS
387	CDC20 and PTTG1 are Important Biomarkers and Potential Therapeutic Targets for Metastatic Prostate Cancer. <i>Advances in Therapy</i> , 2021, 38, 2973-2989.	1.3	18
388	Genome-Wide Mapping of Histone H3 Lysine 4 Trimethylation (H3K4me3) and Its Involvement in Fatty Acid Biosynthesis in Sunflower Developing Seeds. <i>Plants</i> , 2021, 10, 706.	1.6	10
389	Accelerated Evolution of Tissue-Specific Genes Mediates Divergence Amidst Gene Flow in European Green Lizards. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	1
390	Transcriptomic and metabolomic characterization of post-hatch metabolic reprogramming during hepatic development in the chicken. <i>BMC Genomics</i> , 2021, 22, 380.	1.2	7
391	Plasma proteomics analysis of adolescent idiopathic scoliosis patients revealed by Quadrupole-Orbitrap mass spectrometry. <i>Proteomics - Clinical Applications</i> , 2021, 15, e2100002.	0.8	5
392	A detailed map of coupled circadian clock and cell cycle with qualitative dynamics validation. <i>BMC Bioinformatics</i> , 2021, 22, 240.	1.2	4
394	Heat Stress-Dependent Association of Membrane Trafficking Proteins With mRNPs Is Selective. <i>Frontiers in Plant Science</i> , 2021, 12, 670499.	1.7	3
395	Rapid adaptation through genomic and epigenomic responses following translocations in an endangered salmonid. <i>Evolutionary Applications</i> , 2021, 14, 2470-2489.	1.5	10
396	Aberrantly methylated-differentially genes and pathways among Iranian patients with colorectal cancer. <i>Cancer Cell International</i> , 2021, 21, 346.	1.8	2
397	A forward genetics approach integrating genome-wide association study and expression quantitative trait locus mapping to dissect leaf development in maize (<i>Zea mays</i>). <i>Plant Journal</i> , 2021, 107, 1056-1071.	2.8	19
398	Changes to the identity of Endo- β H1 beta cells may be mediated by stress-induced depletion of HNRNPD. <i>Cell and Bioscience</i> , 2021, 11, 144.	2.1	0
399	Specific Endothelial Cells Govern Nanoparticle Entry into Solid Tumors. <i>ACS Nano</i> , 2021, 15, 14080-14094.	7.3	60
400	Transcriptomic analysis of endoplasmic reticulum stress in roots of grapevine rootstock. <i>Plant Biotechnology Reports</i> , 2021, 15, 683-706.	0.9	3
401	Genetic Analysis of Heterosis for Yield Influencing Traits in Brassica juncea Using a Doubled Haploid Population and Its Backcross Progenies. <i>Frontiers in Plant Science</i> , 2021, 12, 721631.	1.7	14
403	Panobinostat Effectively Increases Histone Acetylation and Alters Chromatin Accessibility Landscape in Canine Embryonic Fibroblasts but Does Not Enhance Cellular Reprogramming. <i>Frontiers in Veterinary Science</i> , 2021, 8, 716570.	0.9	3
404	Quantitative proteomics analysis reveals novel insights into mechanisms of action of disulfiram (DSF). <i>Proteomics - Clinical Applications</i> , 2022, 16, e2100031.	0.8	0
405	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale. <i>Molecular Biology and Evolution</i> , 2021, 38, 5825-5829.	3.5	1,174
406	<i>Aedes aegypti</i> post-emergence transcriptome: Unveiling the molecular basis for the hematophagic and gonotrophic capacitation. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0008915.	1.3	3

#	ARTICLE	IF	CITATIONS
407	Solving Biclustering with a GRASP-Like Metaheuristic: Two Case-Studies on Gene Expression Analysis. <i>Lecture Notes in Computer Science</i> , 2012, , 253-267.	1.0	1
408	An improved high-quality genome assembly and annotation of Tibetan hullless barley. <i>Scientific Data</i> , 2020, 7, 139.	2.4	27
409	DeepNOG: fast and accurate protein orthologous group assignment. <i>Bioinformatics</i> , 2021, 36, 5304-5312.	1.8	16
410	Repeated Evolution of Inactive Pseudonucleases in a Fungal Branch of the Dis3/RNase II Family of Nucleases. <i>Molecular Biology and Evolution</i> , 2021, 38, 1837-1846.	3.5	8
411	PANTHER version 16: a revised family classification, tree-based classification tool, enhancer regions and extensive API. <i>Nucleic Acids Research</i> , 2021, 49, D394-D403.	6.5	990
421	Bioinformatics Analysis of Macrophages Exposed to <i>Porphyromonas gingivalis</i> : Implications in Acute vs. Chronic Infections. <i>PLoS ONE</i> , 2010, 5, e15613.	1.1	14
422	Genomewide Analyses Define Different Modes of Transcriptional Regulation by Peroxisome Proliferator-Activated Receptor- γ (PPAR γ). <i>PLoS ONE</i> , 2011, 6, e16344.	1.1	72
423	Screening of MAMLD1 Mutations in 70 Children with 46,XY DSD: Identification and Functional Analysis of Two New Mutations. <i>PLoS ONE</i> , 2012, 7, e32505.	1.1	41
424	Global Effect of Inauhzin on Human p53-Responsive Transcriptome. <i>PLoS ONE</i> , 2012, 7, e52172.	1.1	18
425	High Throughput Gene Expression Analysis Identifies Reliable Expression Markers of Human Corneal Endothelial Cells. <i>PLoS ONE</i> , 2013, 8, e67546.	1.1	60
426	LABEL: Fast and Accurate Lineage Assignment with Assessment of H5N1 and H9N2 Influenza A Hemagglutinins. <i>PLoS ONE</i> , 2014, 9, e86921.	1.1	31
427	Protein Variants Form a System of Networks: Microdiversity of IMP Metallo-Beta-Lactamases. <i>PLoS ONE</i> , 2014, 9, e101813.	1.1	6
428	CardioGenBase: A Literature Based Multi-Omics Database for Major Cardiovascular Diseases. <i>PLoS ONE</i> , 2015, 10, e0143188.	1.1	23
429	Maternal Smoking during Pregnancy and DNA-Methylation in Children at Age 5.5 Years: Epigenome-Wide-Analysis in the European Childhood Obesity Project (CHOP)-Study. <i>PLoS ONE</i> , 2016, 11, e0155554.	1.1	82
430	Herpesvirus deconjugases inhibit the IFN response by promoting TRIM25 autoubiquitination and functional inactivation of the RIG-I signalosome. <i>PLoS Pathogens</i> , 2018, 14, e1006852.	2.1	56
431	Differentiating Total- or Partial-Body Irradiation in Baboons Using mRNA Expression Patterns: A Proof of Concept. <i>Radiation Research</i> , 2020, 194, 476-484.	0.7	7
432	Identification of microRNAs implicated in the late differentiation stages of normal B cells suggests a central role for miRNA targets ZEB1 and TP53. <i>Oncotarget</i> , 2017, 8, 11809-11826.	0.8	11
433	Profiling alterations in platelets induced by Amotosalen/UVA pathogen reduction and gamma irradiation—a LC-ESI-MS/MS-based proteomics approach. <i>Blood Transfusion</i> , 2012, 10 Suppl 2, s63-70.	0.3	14

#	ARTICLE	IF	CITATIONS
434	Characterization of the colostrum and transition milk proteomes from primiparous and multiparous Holstein dairy cows. <i>Journal of Dairy Science</i> , 2020, 103, 1993-2005.	1.4	25
435	MicroRNA alterations in Barrett's esophagus, esophageal adenocarcinoma, and esophageal adenocarcinoma cell lines following cranberry extract treatment: Insights for chemoprevention. <i>Journal of Carcinogenesis</i> , 2011, 10, 34.	2.5	24
436	Analysis of FOS, BTG2, and NR4A in the function of renal medullary hypertension. <i>Genetics and Molecular Research</i> , 2013, 12, 3735-3741.	0.3	5
437	Analysis of Global Gene Expression Profile of Human Adipose Tissue Derived Mesenchymal Stem Cell Cultured with Cancer Cells. <i>Journal of Life Science</i> , 2011, 21, 631-646.	0.2	2
438	K2P18.1 translates T cell receptor signals into thymic regulatory T cell development. <i>Cell Research</i> , 2022, 32, 72-88.	5.7	14
439	Arabidopsis bioinformatics: tools and strategies. <i>Plant Journal</i> , 2021, 108, 1585-1596.	2.8	9
441	Gene Expression Profiling and Pathway Analysis for Identification of Molecular Targets in MS. , 2013, , 229-255.		0
442	Putting It All Together: The Design of a Pipeline for Genome-Wide Functional Annotation of Fungi in the Modern Era of "Omics" Data and Systems Biology. <i>Lecture Notes in Computer Science</i> , 2013, , 113-127.	1.0	1
443	Studying Molecular Aspects of the Blood-Brain Barrier Using an in Vitro Model: Contribution of a Global Proteomics Strategy. <i>Journal of Biosciences and Medicines</i> , 2014, 02, 18-25.	0.1	2
446	Marine Informatics: A New Area of Research in Biology. , 2016, , 419-440.		0
452	Identificaci3n de prote3nas reguladoras de la expresi3n g3nica en tripanosom3tidos. <i>Revista De La Academia Colombiana De Ciencias Exactas, F3sicas Y Naturales</i> , 2018, 42, 306.	0.0	0
457	<scp>PANTHER</scp>: Making genome-scale phylogenetics accessible to all. <i>Protein Science</i> , 2022, 31, 8-22.	3.1	467
460	Automated Isoform Diversity Detector (AIDD): a pipeline for investigating transcriptome diversity of RNA-seq data. <i>BMC Bioinformatics</i> , 2020, 21, 578.	1.2	3
461	Orthology: Promises and Challenges. , 2020, , 203-228.		10
462	A Systems Biology Driven Approach to Map the EP300 Interactors Using Comprehensive Protein Interaction Network. <i>Lecture Notes in Computer Science</i> , 2020, , 204-214.	1.0	0
466	Bioinformatic Tools in Arabidopsis Research. <i>Methods in Molecular Biology</i> , 2021, 2200, 25-89.	0.4	4
467	Predicting the Radiation Sensitivity of Male and Female Rhesus Macaques Using Gene Expression. <i>Radiation Research</i> , 2020, 195, 25-37.	0.7	2
468	Ancient hybridization patterns between bighorn and thinhorn sheep. <i>Molecular Ecology</i> , 2021, 30, 6273-6288.	2.0	4

#	ARTICLE	IF	CITATIONS
469	Functional DNA annotation from a preliminary de novo genome assembly of Brycon orbignyanus, an endangered Neotropical migratory fish. <i>Latin American Data in Science</i> , 2021, 1, 42-48.	0.2	0
471	The novel anti-inflammatory activity of mclRBP from <i>Momordica charantia</i> is associated with the improvement of diabetic nephropathy. <i>Food and Function</i> , 2022, 13, 1268-1279.	2.1	6
472	Comparative proteomic analysis of nuclear and cytoplasmic compartments in human cardiac progenitor cells. <i>Scientific Reports</i> , 2022, 12, 146.	1.6	3
473	Genomic Diversity Profiling and Breed-Specific Evolutionary Signatures of Selection in Arunachali Yak. <i>Genes</i> , 2022, 13, 254.	1.0	11
474	The splicing factor DHX38/PRP16 is required for ovarian clear cell carcinoma tumorigenesis, as revealed by a CRISPR-Cas9 screen. <i>FEBS Open Bio</i> , 2021, , .	1.0	3
475	Genomic landscape, polymorphism and possible LINE-associated delivery of G-quadruplex motifs in the bovine genes. <i>Genomics</i> , 2022, 114, 110272.	1.3	5
476	Immune Checkpoint Blockade Augments Changes Within Oncolytic Virus-induced Cancer MHC-I Peptidome, Creating Novel Antitumor CD8 T Cell Reactivities. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100182.	2.5	3
477	Autosomal Recessive Cerebellar Atrophy and Spastic Ataxia in Patients With Pathogenic Biallelic Variants in GEMIN5. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 783762.	1.8	10
478	Tgfb2 in Dental Pulp Cells Guides Neurite Outgrowth in Developing Teeth. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 834815.	1.8	1
479	Genomic Resources for <i>Salminus brasiliensis</i> . <i>Frontiers in Genetics</i> , 2022, 13, 855718.	1.1	0
480	SHOOT: phylogenetic gene search and ortholog inference. <i>Genome Biology</i> , 2022, 23, 85.	3.8	28
482	Age-Related Changes of Gene Expression Profiles in <i>Drosophila</i> . <i>Genes</i> , 2021, 12, 1982.	1.0	8
483	iTRAQ based characterization of proteomic change in petroleum hydrocarbon-degrading <i>Pseudomonas aeruginosa</i> in different pH conditions. <i>Archives of Microbiology</i> , 2022, 204, 263.	1.0	2
516	Mining of Transcriptome Identified CD109 and LRP12 as Novel Biomarkers and Deregulation Mechanism of T Cell Receptor Pathway in Acute Myeloid Leukemia. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
518	Genome-wide DNA Methylation Differences in Nonfunctioning Pituitary Adenomas With and Without Postsurgical Progression. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, 2318-2328.	1.8	6
519	Epicardium-derived cells organize through tight junctions to replenish cardiac muscle in salamanders. <i>Nature Cell Biology</i> , 2022, 24, 645-658.	4.6	12
520	Modulation of GPCR receptors common to gut inflammatory diseases and neuronal disorders, Alzheimer's and Parkinson's diseases as druggable targets through <i>Withania somnifera</i> bioactives: an <i>in silico</i> study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 4485-4503.	2.0	5
521	Multi-Omics Analysis of Glioblastoma and Glioblastoma Cell Line: Molecular Insights Into the Functional Role of GPR56 and TG2 in Mesenchymal Transition. <i>Frontiers in Oncology</i> , 2022, 12, .	1.3	3

#	ARTICLE	IF	CITATIONS
522	Brucella activates the host RIDD pathway to subvert BLOS1-directed immune defense. <i>ELife</i> , 2022, 11, .	2.8	4
523	Dysregulated Gene Expression in Lymphoblasts from Parkinson's Disease. <i>Proteomes</i> , 2022, 10, 20.	1.7	3
524	In vitro ve in silico analizi ile metforminin meme t ^{1/4} m ^{1/4} r ^{1/4} h ^{1/4} crelelerinde protein profili ^{1/4} zerindeki etkinlii. <i>Ege Tıp Dergisi</i> , 0, , 215-224.	0.1	0
525	Exploring the expression patterns of palmitoylating and de-palmitoylating enzymes in the mouse brain using the curated RNA-seq database BrainPalmSeq. <i>ELife</i> , 0, 11, .	2.8	12
527	Panzootic chytrid fungus exploits diverse amphibian host environments through plastic infection strategies. <i>Molecular Ecology</i> , 2022, 31, 4558-4570.	2.0	6
529	Quantitative proteomic analytic approaches to identify metabolic changes in the medial prefrontal cortex of rats exposed to space radiation. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	3
530	Identifying the tumor location-associated candidate genes in development of new drugs for colorectal cancer using machine-learning-based approach. <i>Medical and Biological Engineering and Computing</i> , 0, , .	1.6	0
531	Gene Expression and DNA Methylation in Human Papillomavirus Positive and Negative Head and Neck Squamous Cell Carcinomas. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10967.	1.8	3
532	Cryptic lineages and standing genetic variation across independent cane toad introductions. <i>Molecular Ecology</i> , 2022, 31, 6440-6456.	2.0	9
533	Investigating Grapevine Red Blotch Virus Infection in <i>Vitis vinifera</i> L. cv. Cabernet Sauvignon Grapes: A Multi-Omics Approach. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13248.	1.8	2
534	Mining of transcriptome identifies CD109 and LRP12 as possible biomarkers and deregulation mechanism of T cell receptor pathway in Acute Myeloid Leukemia. <i>Heliyon</i> , 2022, 8, e11123.	1.4	2
535	Regio-Specific N-Glycome and N-Glycoproteome Map of the Elderly Human Brain With and Without Alzheimer's Disease. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100427.	2.5	4
536	Differential expression of immune-regulatory proteins C5AR1, CLEC4A and NLRP3 on peripheral blood mononuclear cells in early-stage non-small cell lung cancer patients. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
537	Lactate-mediated neural plasticity genes emerged during the evolution of memory systems. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
538	Bivariate GWAS reveals pleiotropic regions among feed efficiency and beef quality-related traits in Nelore cattle. <i>Mammalian Genome</i> , 2023, 34, 90-103.	1.0	6
539	Genome-wide analysis of annexin gene family in <i>Schrenkiella parvula</i> and <i>Eutrema salsugineum</i> suggests their roles in salt stress response. <i>PLoS ONE</i> , 2023, 18, e0280246.	1.1	4
540	517. Olfaction: a critical force driving adaptive evolution in yaks. , 2022, , .		0
541	lncRNA-miRNA-mRNA network in female offspring born from obese dams. <i>Experimental and Therapeutic Medicine</i> , 2023, 25, .	0.8	0

#	ARTICLE	IF	CITATIONS
542	Ovarian transcriptional response to <i>Wolbachia</i> infection in <i>D. melanogaster</i> in the context of between-genotype variation in gene expression. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	2
543	Genesâ€™ Pathways Species Conservation Analysis: Enabling the Exploration of Conservation of Biological Pathways and Processes Across Species. <i>Environmental Toxicology and Chemistry</i> , 2023, 42, 1152-1166.	2.2	4
544	Primate protein-ligand interfaces exhibit significant conservation and unveil human-specific evolutionary drivers. <i>PLoS Computational Biology</i> , 2023, 19, e1010966.	1.5	0
545	Genomic distribution and polymorphism of G-quadruplex motifs occupying ovine promoters and enhancers. <i>Mammalian Genome</i> , 2023, 34, 473-481.	1.0	1