

PANTHER version 10: expanded protein families and fu

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Citation Report

#	ARTICLE	IF	CITATIONS
3	Enhancer Sharing Promotes Neighborhoods of Transcriptional Regulation Across Eukaryotes. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 4167-4174.	0.8	39
4	XGSA: A statistical method for cross-species gene set analysis. <i>Bioinformatics</i> , 2016, 32, i620-i628.	1.8	18
5	Sea lampreys elicit strong transcriptomic responses in the lake trout liver during parasitism. <i>BMC Genomics</i> , 2016, 17, 675.	1.2	13
6	RGAugury: a pipeline for genome-wide prediction of resistance gene analogs (RGAs) in plants. <i>BMC Genomics</i> , 2016, 17, 852.	1.2	162
7	Comparative proteomic profiling of refractory/relapsed multiple myeloma reveals biomarkers involved in resistance to bortezomib-based therapy. <i>Oncotarget</i> , 2016, 7, 56726-56736.	0.8	58
8	Cluster Analysis of p53 Binding Site Sequences Reveals Subsets with Different Functions. <i>Cancer Informatics</i> , 2016, 15, CIN.S39968.	0.9	1
9	Meta-analysis of gene expression and integrin-associated signaling pathways in papillary renal cell carcinoma subtypes. <i>Oncotarget</i> , 2016, 7, 84178-84189.	0.8	4
10	Steric Clash in the SET Domain of Histone Methyltransferase NSD1 as a Cause of Sotos Syndrome and Its Genetic Heterogeneity in a Brazilian Cohort. <i>Genes</i> , 2016, 7, 96.	1.0	9
11	Multiple Sclerosis Biomarker Discovery via Bayesian Feature Selection. , 2016, , .		5
12	Genome and Transcriptome Sequences Reveal the Specific Parasitism of the Nematophagous <i>Purpureocillium lilacinum</i> 36-1. <i>Frontiers in Microbiology</i> , 2016, 7, 1084.	1.5	33
13	Whole-Transcriptome Analysis of Verocytotoxigenic <i>Escherichia coli</i> O157:H7 (Sakai) Suggests Plant-Species-Specific Metabolic Responses on Exposure to Spinach and Lettuce Extracts. <i>Frontiers in Microbiology</i> , 2016, 7, 1088.	1.5	34
14	Deciphering the Role of Emx1 in Neurogenesis: A Neuroproteomics Approach. <i>Frontiers in Molecular Neuroscience</i> , 2016, 9, 98.	1.4	18
15	Slitrk Missense Mutations Associated with Neuropsychiatric Disorders Distinctively Impair Slitrk Trafficking and Synapse Formation. <i>Frontiers in Molecular Neuroscience</i> , 2016, 9, 104.	1.4	31
16	Label-Free Quantitative Proteomics Reveals Differences in Molecular Mechanism of Atherosclerosis Related and Non-Related to Chronic Kidney Disease. <i>International Journal of Molecular Sciences</i> , 2016, 17, 631.	1.8	22
17	Deep Insight into the Phosphatomes of Parasitic Protozoa and a Web Resource ProtozPhosDB. <i>PLoS ONE</i> , 2016, 11, e0167594.	1.1	7
18	Time-Course Study of the Transcriptome of Peripheral Blood Mononuclear Cells (PBMCs) from Sheep Infected with <i>Fasciola hepatica</i> . <i>PLoS ONE</i> , 2016, 11, e0159194.	1.1	29
19	Transcriptome Profile of the Chicken Thrombocyte: New Implications as an Advanced Immune Effector Cell. <i>PLoS ONE</i> , 2016, 11, e0163890.	1.1	25
20	Stable Host Gene Expression in the Gut of Adult <i>Drosophila melanogaster</i> with Different Bacterial Mono-Associations. <i>PLoS ONE</i> , 2016, 11, e0167357.	1.1	23

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21	Two Subclasses of Differentially Expressed TPS1 Genes and Biochemically Active TPS1 Proteins May Contribute to Sugar Signalling in Kiwifruit <i>Actinidia chinensis</i> . <i>PLoS ONE</i> , 2016, 11, e0168075.	1.1	4
22	Comparative Transcriptomic Analysis of Two <i>Brassica napus</i> Near-Isogenic Lines Reveals a Network of Genes That Influences Seed Oil Accumulation. <i>Frontiers in Plant Science</i> , 2016, 7, 1498.	1.7	10
23	IRF5 governs liver macrophage activation that promotes hepatic fibrosis in mice and humans. <i>JCI Insight</i> , 2016, 1, e88689.	2.3	43
24	Hypoxia enhances the malignant nature of bladder cancer cells and concomitantly antagonizes protein O-glycosylation extension. <i>Oncotarget</i> , 2016, 7, 63138-63157.	0.8	58
25	Whole-Genome Sequencing of Native Sheep Provides Insights into Rapid Adaptations to Extreme Environments. <i>Molecular Biology and Evolution</i> , 2016, 33, 2576-2592.	3.5	271
26	Evidence of a broad histamine footprint on the human exercise transcriptome. <i>Journal of Physiology</i> , 2016, 594, 5009-5023.	1.3	35
27	Oncofetal Epigenetic Bivalency in Breast Cancer Cells: H3K4 and H3K27 Tri-Methylation as a Biomarker for Phenotypic Plasticity. <i>Journal of Cellular Physiology</i> , 2016, 231, 2474-2481.	2.0	25
28	Identification of learning-induced changes in protein networks in the hippocampi of a mouse model of Alzheimer's disease. <i>Translational Psychiatry</i> , 2016, 6, e849-e849.	2.4	14
29	Transcriptome analysis of trigeminal ganglia following masseter muscle inflammation in rats. <i>Molecular Pain</i> , 2016, 12, 174480691666852.	1.0	47
30	Alterations in the human proteome following administration of valproic acid. <i>Journal of Trauma and Acute Care Surgery</i> , 2016, 81, 1020-1027.	1.1	28
31	Impact of neonatal iron deficiency on hippocampal DNA methylation and gene transcription in a porcine biomedical model of cognitive development. <i>BMC Genomics</i> , 2016, 17, 856.	1.2	44
32	Identifying ultrasensitive HGF dose-response functions in a 3D mammalian system for synthetic morphogenesis. <i>Scientific Reports</i> , 2016, 6, 39178.	1.6	7
33	Phenotypic characterization and comparative transcriptomics of evolved <i>Saccharomyces cerevisiae</i> strains with improved tolerance to lignocellulosic derived inhibitors. <i>Biotechnology for Biofuels</i> , 2016, 9, 200.	6.2	37
34	De-novo protein function prediction using DNA binding and RNA binding proteins as a test case. <i>Nature Communications</i> , 2016, 7, 13424.	5.8	22
35	ThaleMine: A Warehouse for Arabidopsis Data Integration and Discovery. <i>Plant and Cell Physiology</i> , 2017, 58, pcw200.	1.5	39
36	Dissection of brassinosteroid-regulated proteins in rice embryos during germination by quantitative proteomics. <i>Scientific Reports</i> , 2016, 6, 34583.	1.6	20
37	The genome of the Gulf pipefish enables understanding of evolutionary innovations. <i>Genome Biology</i> , 2016, 17, 258.	3.8	76
38	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. <i>Scientific Reports</i> , 2016, 6, 34589.	1.6	47

#	ARTICLE	IF	CITATIONS
39	First insight into the proteome landscape of the porcine short posterior ciliary arteries: Key signalling pathways maintaining physiologic functions. <i>Scientific Reports</i> , 2016, 6, 38298.	1.6	10
40	Proteomic insight into the effects of the Salmonella ubiquitin ligase SlrP on host cells. <i>Biochemical and Biophysical Research Communications</i> , 2016, 472, 539-544.	1.0	7
41	Genes, dopamine pathways, and sociality in primates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6325-6327.	3.3	13
42	Mutational screening in patients with profound sensorineural hearing loss and neurodevelopmental delay: Description of a novel m.3861A>ÂC mitochondrial mutation in the MT-ND1 gene. <i>Biochemical and Biophysical Research Communications</i> , 2016, 474, 702-708.	1.0	4
43	Control of fluxes in metabolic networks. <i>Genome Research</i> , 2016, 26, 956-968.	2.4	40
44	High-Throughput LC-MS/MS Proteomic Analysis of a Mouse Model of Mesiotemporal Lobe Epilepsy Predicts Microglial Activation Underlying Disease Development. <i>Journal of Proteome Research</i> , 2016, 15, 1546-1562.	1.8	33
45	Freezing effects on the acute myeloid leukemia cell proteome and phosphoproteome revealed using optimal quantitative workflows. <i>Journal of Proteomics</i> , 2016, 145, 214-225.	1.2	35
46	Cell-free Determination of Binary Complexes That Comprise Extended Protein-Protein Interaction Networks of <i>Yersinia pestis</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3220-3232.	2.5	0
47	Born blonde: a recessive loss-of-function mutation in the melanocortin 1 receptor is associated with cream coat coloration in arctic fur seals. <i>Ecology and Evolution</i> , 2016, 6, 5705-5717.	0.8	16
48	Analysis of Body-wide Unfractionated Tissue Data to Identify a Core Human Endothelial Transcriptome. <i>Cell Systems</i> , 2016, 3, 287-301.e3.	2.9	44
49	TSHZ3 deletion causes an autism syndrome and defects in cortical projection neurons. <i>Nature Genetics</i> , 2016, 48, 1359-1369.	9.4	69
50	Transcriptomic response of <i>Drosophila melanogaster</i> pupae developed in hypergravity. <i>Genomics</i> , 2016, 108, 158-167.	1.3	11
51	Exploring the oviductal fluid proteome by a lectin-based affinity approach. <i>Proteomics</i> , 2016, 16, 2962-2966.	1.3	6
52	Genome-wide association studies of autoimmune vitiligo identify 23 new risk loci and highlight key pathways and regulatory variants. <i>Nature Genetics</i> , 2016, 48, 1418-1424.	9.4	225
53	Uncovering the liver's role in immunity through RNA co-expression networks. <i>Mammalian Genome</i> , 2016, 27, 469-484.	1.0	12
54	Metrics for the Human Proteome Project 2016: Progress on Identifying and Characterizing the Human Proteome, Including Post-Translational Modifications. <i>Journal of Proteome Research</i> , 2016, 15, 3951-3960.	1.8	72
55	Gene set analysis for interpreting genetic studies. <i>Human Molecular Genetics</i> , 2016, 25, R133-R140.	1.4	12
56	Model systems of DUX4 expression recapitulate the transcriptional profile of FSHD cells. <i>Human Molecular Genetics</i> , 2016, 25, ddw271.	1.4	75

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57	Reannotation of <i>Yersinia pestis</i> Strain 91001 Based on Omics Data. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 95, 562-570.	0.6	11
58	Genome-wide identification of potato long intergenic noncoding RNAs responsive to <i>Pectobacterium carotovorum</i> subspecies <i>brasiliense</i> infection. <i>BMC Genomics</i> , 2016, 17, 614.	1.2	48
59	Interferon response factor $\beta$ promotes the pro $\Theta$ 2 activity of mouse lung CD11b <sup>+</sup> conventional dendritic cells in response to house dust mite allergens. <i>European Journal of Immunology</i> , 2016, 46, 2614-2628.	1.6	12
60	EphA2 proteomics in human keratinocytes reveals a novel association with afadin and epidermal tight junctions. <i>Journal of Cell Science</i> , 2017, 130, 111-118.	1.2	21
61	Gene Expression Profiling in the Hibernating Primate, <i>Cheirogaleus Medius</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2413-2426.	1.1	23
62	Quantitative secretomic analysis of pancreatic cancer cells in serum-containing conditioned medium. <i>Scientific Reports</i> , 2016, 6, 37606.	1.6	39
63	On the saliva proteome of the Eastern European house mouse ( <i>Mus musculus musculus</i> ) focusing on sexual signalling and immunity. <i>Scientific Reports</i> , 2016, 6, 32481.	1.6	37
64	An association analysis between a missense polymorphism at the pig PCSK9 gene and serum lipid and meat quality traits in Duroc pigs. <i>Livestock Science</i> , 2016, 190, 27-30.	0.6	0
65	Exploring the neural mechanisms of finasteride: a proteomic analysis in the nucleus accumbens. <i>Psychoneuroendocrinology</i> , 2016, 74, 387-396.	1.3	14
66	Supplements of vitamins B9 and B12 affect hepatic and mammary gland gene expression profiles in lactating dairy cows. <i>BMC Genomics</i> , 2016, 17, 640.	1.2	19
67	Chromatin associated SETD3 negatively regulates VEGF expression. <i>Scientific Reports</i> , 2016, 6, 37115.	1.6	29
68	Large-Scale Gene Expression Profiling Platform for Identification of Context-Dependent Drug Responses in Multicellular Tumor Spheroids. <i>Cell Chemical Biology</i> , 2016, 23, 1428-1438.	2.5	32
69	Molecular Dissection of Seedling Salinity Tolerance in Rice ( <i>Oryza sativa</i> L.) Using a High-Density GBS-Based SNP Linkage Map. <i>Rice</i> , 2016, 9, 52.	1.7	125
70	Set of Novel Automated Quantitative Microproteomics Protocols for Small Sample Amounts and Its Application to Kidney Tissue Substructures. <i>Journal of Proteome Research</i> , 2016, 15, 4722-4730.	1.8	38
71	Genomic analysis reveals selection in Chinese native black pig. <i>Scientific Reports</i> , 2016, 6, 36354.	1.6	32
72	Horizontal gene transfer events reshape the global landscape of arm race between viruses and homo sapiens. <i>Scientific Reports</i> , 2016, 6, 26934.	1.6	14
73	Extensive transcriptome analysis correlates the plasticity of <i>Entamoeba histolytica</i> pathogenesis to rapid phenotype changes depending on the environment. <i>Scientific Reports</i> , 2016, 6, 35852.	1.6	49
74	The DPYSL2 gene connects mTOR and schizophrenia. <i>Translational Psychiatry</i> , 2016, 6, e933-e933.	2.4	39

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75	Incorporating topological information for predicting robust cancer subnetwork markers in human protein-protein interaction network. <i>BMC Bioinformatics</i> , 2016, 17, 351.	1.2	15
76	RNAi Screen Identifies Novel Regulators of RNP Granules in the <i>Caenorhabditis elegans</i> Germ Line. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2643-2654.	0.8	18
77	Protein profiles of hatchery egg shell membrane. <i>Proteome Science</i> , 2016, 15, 4.	0.7	11
78	Characterisation of the circulating acellular proteome of healthy sheep using LC-MS/MS-based proteomics analysis of serum. <i>Proteome Science</i> , 2016, 15, 11.	0.7	9
79	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
80	Characterization of Somatically Eliminated Genes During Development of the Sea Lamprey ( <i>Petromyzon marinus</i> ). <i>Molecular Biology and Evolution</i> , 2016, 33, 2337-2344.	3.5	40
81	Epigenetics and energetics in ventral hippocampus mediate rapid antidepressant action: Implications for treatment resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7906-7911.	3.3	75
82	Increased intramuscular fat induced by reduced dietary protein in finishing pigs: effects on the longissimus lumborum muscle proteome. <i>Molecular BioSystems</i> , 2016, 12, 2447-2457.	2.9	17
83	Pneumococcal Neuraminidase Substrates Identified through Comparative Proteomics Enabled by Chemoselective Labeling. <i>Bioconjugate Chemistry</i> , 2016, 27, 1013-1022.	1.8	15
84	De novo assembly of a tadpole shrimp ( <i>Triops newberryi</i> ) transcriptome and preliminary differential gene expression analysis. <i>Molecular Ecology Resources</i> , 2017, 17, 161-171.	2.2	28
85	Clonal hematopoiesis associated with TET2 deficiency accelerates atherosclerosis development in mice. <i>Science</i> , 2017, 355, 842-847.	6.0	999
86	Quantitative proteomic analysis of HIV-1 Tat-induced dysregulation in SH-SY5Y neuroblastoma cells. <i>Proteomics</i> , 2017, 17, 1600236.	1.3	8
87	Computational Methods for Annotation Transfers from Sequence. <i>Methods in Molecular Biology</i> , 2017, 1446, 55-67.	0.4	40
88	A Zip3-like protein plays a role in crossover formation in the SC-less meiosis of the protist <i>Tetrahymena</i> . <i>Molecular Biology of the Cell</i> , 2017, 28, 825-833.	0.9	16
89	WormBase ParaSite â” a comprehensive resource for helminth genomics. <i>Molecular and Biochemical Parasitology</i> , 2017, 215, 2-10.	0.5	527
90	Pharos: Collating protein information to shed light on the druggable genome. <i>Nucleic Acids Research</i> , 2017, 45, D995-D1002.	6.5	271
91	The 24th annual <i>Nucleic Acids Research</i> database issue: a look back and upcoming changes. <i>Nucleic Acids Research</i> , 2017, 45, D1-D11.	6.5	144
92	High density lipoproteins are modulators of protease activity: Implications in inflammation, complement activation, and atherothrombosis. <i>Atherosclerosis</i> , 2017, 259, 104-113.	0.4	48

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93	RNA sequencing of synaptic and cytoplasmic Upf1-bound transcripts supports contribution of nonsense-mediated decay to epileptogenesis. <i>Scientific Reports</i> , 2017, 7, 41517.	1.6	16
94	Biosynthesis of cabbage phytoalexins from indole glucosinolate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1910-1915.	3.3	72
95	Genome-wide DNA methylation reprogramming in response to inorganic arsenic links inhibition of CTCF binding, DNMT expression and cellular transformation. <i>Scientific Reports</i> , 2017, 7, 41474.	1.6	32
96	De novo assembly, annotation, and characterization of the whole brain transcriptome of male and female Syrian hamsters. <i>Scientific Reports</i> , 2017, 7, 40472.	1.6	18
97	Transcriptomic gene profiling of porcine muscle tissue depending on histological properties. <i>Animal Science Journal</i> , 2017, 88, 1178-1188.	0.6	13
98	Effector Regulatory T Cell Differentiation and Immune Homeostasis Depend on the Transcription Factor Myb. <i>Immunity</i> , 2017, 46, 78-91.	6.6	83
99	Tumour and host cell PD-L1 is required to mediate suppression of anti-tumour immunity in mice. <i>Nature Communications</i> , 2017, 8, 14572.	5.8	279
100	Dissection of Regulatory Elements During Direct Conversion of Somatic Cells Into Neurons. <i>Journal of Cellular Biochemistry</i> , 2017, 118, 3158-3170.	1.2	8
101	A pan-cancer analysis of secreted Frizzled-related proteins: re-examining their proposed tumour suppressive function. <i>Scientific Reports</i> , 2017, 7, 42719.	1.6	50
102	A Comprehensive Analysis of Metabolomics and Transcriptomics in Cervical Cancer. <i>Scientific Reports</i> , 2017, 7, 43353.	1.6	73
103	Quantitative changes in the protein and miRNA cargo of plasma exosome-like vesicles after exposure to ionizing radiation. <i>International Journal of Radiation Biology</i> , 2017, 93, 569-580.	1.0	63
104	Comprehensive Analysis of Interaction Networks of Telomerase Reverse Transcriptase with Multiple Bioinformatic Approaches: Deep Mining the Potential Functions of Telomere and Telomerase. <i>Rejuvenation Research</i> , 2017, 20, 320-333.	0.9	6
105	Integration of metabolic, regulatory and signaling networks towards analysis of perturbation and dynamic responses. <i>Current Opinion in Systems Biology</i> , 2017, 2, 59-66.	1.3	13
106	Bioinformatics analysis of the proteins interacting with LASP-1 and their association with HBV-related hepatocellular carcinoma. <i>Scientific Reports</i> , 2017, 7, 44017.	1.6	8
107	ENL links histone acetylation to oncogenic gene expression in acute myeloid leukaemia. <i>Nature</i> , 2017, 543, 265-269.	13.7	203
108	Targeted <i>glycoproteomics</i> explored increased sialylation and identified MUC16 as a poor prognosis biomarker in advanced-stage bladder tumours. <i>Molecular Oncology</i> , 2017, 11, 895-912.	2.1	50
109	Identifying Functional Cysteine Residues in the Mitochondria. <i>ACS Chemical Biology</i> , 2017, 12, 947-957.	1.6	65
110	Quantitative phosphoproteomic analysis reveals system-wide signaling pathways regulated by site-specific phosphorylation of Keratin $\epsilon$ 8 in skin squamous cell carcinoma derived cell line. <i>Proteomics</i> , 2017, 17, 1600254.	1.3	14

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111	Transposon insertional mutagenesis in mice identifies human breast cancer susceptibility genes and signatures for stratification. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2215-E2224.	3.3	34
112	A Systems Perspective of Signalling Networks in Host-Pathogen Interactions. Journal of the Indian Institute of Science, 2017, 97, 41-57.	0.9	0
113	Evolution of complexity in the zebrafish synapse proteome. Nature Communications, 2017, 8, 14613.	5.8	112
114	Phosphoproteins in extracellular vesicles as candidate markers for breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3175-3180.	3.3	328
115	Relative protein quantification and accessible biology in lung tumor proteomes from four LC-MS/MS discovery platforms. Proteomics, 2017, 17, 1600300.	1.3	15
116	Transcriptional Dependencies in Diffuse Intrinsic Pontine Glioma. Cancer Cell, 2017, 31, 635-652.e6.	7.7	290
117	Tip110 Deletion Impaired Embryonic and Stem Cell Development Involving Downregulation of Stem Cell Factors Nanog, Oct4, and Sox2. Stem Cells, 2017, 35, 1674-1686.	1.4	7
118	Altered protein expression pattern in colon tissue of mice upon supplementation with distinct selenium compounds. Proteomics, 2017, 17, 1600486.	1.3	6
119	Global exosome transcriptome profiling reveals biomarkers for multiple sclerosis. Annals of Neurology, 2017, 81, 703-717.	2.8	138
120	WebGestalt 2017: a more comprehensive, powerful, flexible and interactive gene set enrichment analysis toolkit. Nucleic Acids Research, 2017, 45, W130-W137.	6.5	1,071
121	Global Reprogramming of Host Kinase Signaling in Response to Fungal Infection. Cell Host and Microbe, 2017, 21, 637-649.e6.	5.1	44
122	Characterising the Influence of Rule-Based Knowledge Representations in Biological Knowledge Extraction from Transcriptomics Data. Lecture Notes in Computer Science, 2017, , 125-141.	1.0	2
123	Conservation and innovation in the DUX4-family gene network. Nature Genetics, 2017, 49, 935-940.	9.4	265
124	A translational approach from an animal model identifies CD80 as a candidate gene for the study of bone phenotypes in postmenopausal women. Osteoporosis International, 2017, 28, 2445-2455.	1.3	11
125	Insights into Ciliary Genes and Evolution from Multi-Level Phylogenetic Profiling. Molecular Biology and Evolution, 2017, 34, 2016-2034.	3.5	54
126	Transcriptome profiling of Arabian horse blood during training regimens. BMC Genetics, 2017, 18, 31.	2.7	27
127	Little Cigars are More Toxic than Cigarettes and Uniquely Change the Airway Gene and Protein Expression. Scientific Reports, 2017, 7, 46239.	1.6	29
128	Circular RNAs of human blood cells, plasma, and plasma subfractions. Russian Journal of Bioorganic Chemistry, 2017, 43, 115-125.	0.3	3



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129	The Chaperone Activity and Substrate Spectrum of Human Small Heat Shock Proteins. <i>Journal of Biological Chemistry</i> , 2017, 292, 672-684.	1.6	121
130	Toxicogenomics of iron oxide nanoparticles in the nematode <i>C. elegans</i> . <i>Nanotoxicology</i> , 2017, 11, 647-657.	1.6	40
131	Cerebrospinal fluid microRNAs are potential biomarkers of temporal lobe epilepsy and status epilepticus. <i>Scientific Reports</i> , 2017, 7, 3328.	1.6	93
132	Gene Expression Profiling of Large Cell Lung Cancer Links Transcriptional Phenotypes to the New Histological WHO 2015 Classification. <i>Journal of Thoracic Oncology</i> , 2017, 12, 1257-1267.	0.5	43
133	Reading LINEs within the cocaine addicted brain. <i>Brain and Behavior</i> , 2017, 7, e00678.	1.0	11
134	The islet-resident macrophage is in an inflammatory state and senses microbial products in blood. <i>Journal of Experimental Medicine</i> , 2017, 214, 2369-2385.	4.2	89
135	Quantitative Chemical Proteomic Profiling of the <i>In Vivo</i> Targets of Reactive Drug Metabolites. <i>ACS Chemical Biology</i> , 2017, 12, 2040-2050.	1.6	34
136	Confirmation of five novel susceptibility loci for Systemic Lupus Erythematosus (SLE) and integrated network analysis of 82 SLE susceptibility loci. <i>Human Molecular Genetics</i> , 2017, 26, ddx026.	1.4	47
137	DNA methylation changes in endometrium and correlation with gene expression during the transition from pre-receptive to receptive phase. <i>Scientific Reports</i> , 2017, 7, 3916.	1.6	37
138	Amplification and quantification of cold-associated microRNAs in the Colorado potato beetle ( <i>Leptinotarsa decemlineata</i> ) agricultural pest. <i>Insect Molecular Biology</i> , 2017, 26, 574-583.	1.0	18
139	THAP1: Role in Mouse Embryonic Stem Cell Survival and Differentiation. <i>Stem Cell Reports</i> , 2017, 9, 92-107.	2.3	27
141	Microproteome of dentoalveolar tissues. <i>Bone</i> , 2017, 101, 219-229.	1.4	26
142	Early transcriptome responses of the bovine midcycle corpus luteum to prostaglandin F <sub>2</sub> ± includes cytokine signaling. <i>Molecular and Cellular Endocrinology</i> , 2017, 452, 93-109.	1.6	29
143	Major hnRNP proteins act as general TDP-43 functional modifiers both in <i>Drosophila</i> and human neuronal cells. <i>Nucleic Acids Research</i> , 2017, 45, 8026-8045.	6.5	62
144	Bacterial and Viral Products Affect Differential Pattern Recognition Receptor Activation of Chicken Thrombocytes Evidenced through RNA Sequencing. <i>Journal of Immunology</i> , 2017, 199, 774-781.	0.4	13
145	Ocoxin oral solution® as a complement to irinotecan chemotherapy in the metastatic progression of colorectal cancer to the liver. <i>Oncology Letters</i> , 2017, 13, 4002-4012.	0.8	16
146	Biocuration in the structure–function linkage database: the anatomy of a superfamily. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	6
147	Cardiac Med1 deletion promotes early lethality, cardiac remodeling, and transcriptional reprogramming. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2017, 312, H768-H780.	1.5	22

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148	Nonreciprocal homeostatic compensation in <i>Drosophila</i> potassium channel mutants. <i>Journal of Neurophysiology</i> , 2017, 117, 2125-2136.	0.9	16
149	Mapping of SnTox3 as a major determinant of field susceptibility to <i>Septoria nodorum</i> leaf blotch in the SHA3/CBRD A— Naxos population. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1361-1374.	1.8	52
150	Data resources for the identification and interpretation of actionable mutations by clinicians. <i>Annals of Oncology</i> , 2017, 28, 946-957.	0.6	20
151	InterPro in 2017—beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
152	Astrocyte-shed extracellular vesicles regulate the peripheral leukocyte response to inflammatory brain lesions. <i>Science Signaling</i> , 2017, 10, .	1.6	199
153	Whole transcriptome profiling of the human hippocampus suggests an involvement of the KIBRA rs17070145 polymorphism in differential activation of the MAPK signaling pathway. <i>Hippocampus</i> , 2017, 27, 784-793.	0.9	19
154	Widespread pre-translational regulation of the inclusion of signal peptides in human proteins. <i>Genomics</i> , 2017, 109, 113-122.	1.3	2
155	An in silico functional annotation and screening of potential drug targets derived from <i>Leishmania</i> spp. hypothetical proteins identified by immunoproteomics. <i>Experimental Parasitology</i> , 2017, 176, 66-74.	0.5	15
156	Assessing the miRNA sponge potential of RUNX1T1 in t(8;21) acute myeloid leukemia. <i>Gene</i> , 2017, 615, 35-40.	1.0	12
157	Large-scale gene network analysis reveals the significance of extracellular matrix pathway and homeobox genes in acute myeloid leukemia: an introduction to the Pigengene package and its applications. <i>BMC Medical Genomics</i> , 2017, 10, 16.	0.7	34
158	Derivation of Functional Human Astrocytes from Cerebral Organoids. <i>Scientific Reports</i> , 2017, 7, 45091.	1.6	75
159	The Rhomboid Protease GlpG Promotes the Persistence of Extraintestinal Pathogenic <i>Escherichia coli</i> within the Gut. <i>Infection and Immunity</i> , 2017, 85, .	1.0	19
160	EXPath tool—a system for comprehensively analyzing regulatory pathways and coexpression networks from high-throughput transcriptome data. <i>DNA Research</i> , 2017, 24, 371-375.	1.5	12
161	Yeast Sub1 and human PC4 are G-quadruplex binding proteins that suppress genome instability at co-transcriptionally formed G4 DNA. <i>Nucleic Acids Research</i> , 2017, 45, 5850-5862.	6.5	41
162	CLK-dependent exon recognition and conjoined gene formation revealed with a novel small molecule inhibitor. <i>Nature Communications</i> , 2017, 8, 7.	5.8	108
163	Planarian Epidermal Stem Cells Respond to Positional Cues to Promote Cell-Type Diversity. <i>Developmental Cell</i> , 2017, 40, 491-504.e5.	3.1	72
164	Computational Modeling of complete HOXB13 protein for predicting the functional effect of SNPs and the associated role in hereditary prostate cancer. <i>Scientific Reports</i> , 2017, 7, 43830.	1.6	36
165	GFD-Net: A novel semantic similarity methodology for the analysis of gene networks. <i>Journal of Biomedical Informatics</i> , 2017, 68, 71-82.	2.5	7

#	ARTICLE	IF	CITATIONS
166	In silico analysis of nonsynonymous single nucleotide polymorphisms of the human adiponectin receptor 2 ( ADIPOR2 ) gene. Computational Biology and Chemistry, 2017, 68, 175-185.	1.1	20
167	Genetic diversity and signatures of selection in various goat breeds revealed by genome-wide SNP markers. BMC Genomics, 2017, 18, 229.	1.2	141
168	Identification of novel chemotherapeutic strategies for metastatic uveal melanoma. Scientific Reports, 2017, 7, 44564.	1.6	44
169	Network Reconstruction Reveals that Valproic Acid Activates Neurogenic Transcriptional Programs in Adult Brain Following Traumatic Injury. Pharmaceutical Research, 2017, 34, 1658-1672.	1.7	22
170	Fine-scale genetic structure due to adaptive divergence among microhabitats. Heredity, 2017, 118, 594-604.	1.2	24
171	Antigen presentation profiling reveals recognition of lymphoma immunoglobulin neoantigens. Nature, 2017, 543, 723-727.	13.7	232
172	Changes in protein expression profiles in bovine endometrial epithelial cells exposed to E. coli LPS challenge. Molecular BioSystems, 2017, 13, 392-405.	2.9	38
173	Modulation of MHC class I surface expression in B16F10 melanoma cells by methylseleninic acid. OncoImmunology, 2017, 6, e1259049.	2.1	20
174	The comparative landscape of duplications in Heliconius melpomene and Heliconius cydno. Heredity, 2017, 118, 78-87.	1.2	15
175	An optimised version of the secretome protein enrichment with click sugars (SPECS) method leads to enhanced coverage of the secretome. Proteomics, 2017, 17, 1600423.	1.3	12
176	Transcriptomic analysis displays the effect of (-)-roemerine on the motility and nutrient uptake in Escherichia coli. Current Genetics, 2017, 63, 709-722.	0.8	9
177	The Chlamydia trachomatis Inclusion Membrane Protein CpoS Counteracts STING-Mediated Cellular Surveillance and Suicide Programs. Cell Host and Microbe, 2017, 21, 113-121.	5.1	115
178	HIPPIE v2.0: enhancing meaningfulness and reliability of protein-protein interaction networks. Nucleic Acids Research, 2017, 45, D408-D414.	6.5	401
179	Evolution-informed modeling improves outcome prediction for cancers. Evolutionary Applications, 2017, 10, 68-76.	1.5	13
180	A Multi-step Transcriptional and Chromatin State Cascade Underlies Motor Neuron Programming from Embryonic Stem Cells. Cell Stem Cell, 2017, 20, 205-217.e8.	5.2	86
181	Proteomic Identification and Analysis of Arginine-Methylated Proteins of Plasmodium falciparum at Asexual Blood Stages. Journal of Proteome Research, 2017, 16, 368-383.	1.8	35
182	Salmonella Persistence in Tomatoes Requires a Distinct Set of Metabolic Functions Identified by Transposon Insertion Sequencing. Applied and Environmental Microbiology, 2017, 83, .	1.4	78
183	Mass Defect-Based <sup>15</sup> N, <sup>13</sup> C-Dimethyl Leucine Labels for Quantitative Proteomics and Amine Metabolomics of Pancreatic Cancer Cells. Analytical Chemistry, 2017, 89, 1138-1146.	3.2	49

#	ARTICLE	IF	CITATIONS
184	Plant genome and transcriptome annotations: from misconceptions to simple solutions. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw135.	3.2	62
185	DisGeNET: a comprehensive platform integrating information on human disease-associated genes and variants. <i>Nucleic Acids Research</i> , 2017, 45, D833-D839.	6.5	1,865
186	Enrichment of deleterious variants of mitochondrial DNA polymerase gene ( <i>POLG1</i> ) in bipolar disorder. <i>Psychiatry and Clinical Neurosciences</i> , 2017, 71, 518-529.	1.0	29
187	Transcriptomic information from Pacific white shrimp ( <i>Litopenaeus vannamei</i> ) ovary and eyestalk, and expression patterns for genes putatively involved in the reproductive process. <i>General and Comparative Endocrinology</i> , 2017, 246, 164-182.	0.8	18
188	Proteome Bioinformatics. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	5
189	The Monarch Initiative: an integrative data and analytic platform connecting phenotypes to genotypes across species. <i>Nucleic Acids Research</i> , 2017, 45, D712-D722.	6.5	306
190	Inference and interrogation of a coregulatory network in the context of lipid accumulation in <i>Yarrowia lipolytica</i> . <i>Npj Systems Biology and Applications</i> , 2017, 3, 21.	1.4	15
191	Transcriptomic and bioinformatics analysis of the early time-course of the response to prostaglandin F2 alpha in the bovine corpus luteum. <i>Data in Brief</i> , 2017, 14, 695-706.	0.5	6
192	Host mechanisms involved in cattle <i>Escherichia coli</i> O157 shedding: a fundamental understanding for reducing foodborne pathogen in food animal production. <i>Scientific Reports</i> , 2017, 7, 7630.	1.6	15
193	Quantitative proteome analysis of bovine mammary gland reveals protein dynamic changes involved in peak and late lactation stages. <i>Biochemical and Biophysical Research Communications</i> , 2017, 494, 292-297.	1.0	16
194	The Protein Corona of PEGylated PGMA-Based Nanoparticles is Preferentially Enriched with Specific Serum Proteins of Varied Biological Function. <i>Langmuir</i> , 2017, 33, 12926-12933.	1.6	16
195	A Problem-Driven Approach for Building a Bioinformatics GraphDB. <i>Lecture Notes in Computer Science</i> , 2017, , 134-144.	1.0	0
196	A hyperdynamic H3.3 nucleosome marks promoter regions in pluripotent embryonic stem cells. <i>Nucleic Acids Research</i> , 2017, 45, 12181-12194.	6.5	28
197	Pervasive coexpression of spatially proximal genes is buffered at the protein level. <i>Molecular Systems Biology</i> , 2017, 13, 937.	3.2	90
198	Genome-wide expression datasets of anti-VEGF and dexamethasone treatment of angiogenesis in the rat cornea. <i>Scientific Data</i> , 2017, 4, 170111.	2.4	4
199	Proteomic Analysis of the Human Olfactory Bulb. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 440-453.	1.0	12
200	Excretory/secretory products from two <i>Fasciola hepatica</i> isolates induce different transcriptional changes and IL-10 release in LPS-activated bovine $\alpha$ BOMA $\beta$ -macrophages. <i>Parasitology Research</i> , 2017, 116, 2775-2782.	0.6	17
201	$\hat{\pm}7$ nicotinic acetylcholine receptor signaling modulates the inflammatory phenotype of fetal brain microglia: first evidence of interference by iron homeostasis. <i>Scientific Reports</i> , 2017, 7, 10645.	1.6	24

#	ARTICLE	IF	CITATIONS
202	Retriever is a multiprotein complex for retromer-independent endosomal cargo recycling. <i>Nature Cell Biology</i> , 2017, 19, 1214-1225.	4.6	243
203	Small-Molecule Screens: A Gateway to Cancer Therapeutic Agents with Case Studies of Food and Drug Administration-Approved Drugs. <i>Pharmacological Reviews</i> , 2017, 69, 479-496.	7.1	58
204	A novel method for genome-wide profiling of dynamic host-pathogen interactions using 3 <sup>â€²</sup> end enriched RNA-seq. <i>Scientific Reports</i> , 2017, 7, 8681.	1.6	3
205	Proteomic Analysis of Secreted Proteins from Cell Microenvironment. <i>Methods in Molecular Biology</i> , 2017, 1662, 45-58.	0.4	4
206	Treating the placenta to prevent adverse effects of gestational hypoxia on fetal brain development. <i>Scientific Reports</i> , 2017, 7, 9079.	1.6	76
207	The role of the immunoproteasome in interferon-Î³-mediated microglial activation. <i>Scientific Reports</i> , 2017, 7, 9365.	1.6	39
208	Genome reconstruction in <i>Cynara cardunculus</i> taxa gains access to chromosome-scale DNA variation. <i>Scientific Reports</i> , 2017, 7, 5617.	1.6	30
209	Microarray analysis of bone marrow lesions in osteoarthritis demonstrates upregulation of genes implicated in osteochondral turnover, neurogenesis and inflammation. <i>Annals of the Rheumatic Diseases</i> , 2017, 76, 1764-1773.	0.5	99
210	Oxidative stress enhances and modulates protein S-nitrosation in smooth muscle cells exposed to S-nitrosoglutathione. <i>Nitric Oxide - Biology and Chemistry</i> , 2017, 69, 10-21.	1.2	24
211	Defining a Cancer Dependency Map. <i>Cell</i> , 2017, 170, 564-576.e16.	13.5	1,794
212	Robust feature selection for block covariance Bayesian models. , 2017, , .		8
213	Residual urinary extracellular vesicles in ultracentrifugation supernatants after hydrostatic filtration dialysis enrichment. <i>Journal of Extracellular Vesicles</i> , 2017, 6, 1267896.	5.5	30
214	A survey of single nucleotide polymorphisms identified from whole-genome sequencing and their functional effect in the porcine genome. <i>Animal Genetics</i> , 2017, 48, 404-411.	0.6	39
215	Positive and relaxed selection associated with flight evolution and loss in insect transcriptomes. <i>GigaScience</i> , 2017, 6, 1-14.	3.3	40
216	Model-based genome-wide determination of RNA chain elongation rates in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2017, 7, 17213.	1.6	6
217	Exposure to cigarette smoke extract and lipopolysaccharide modifies cytoskeleton organization in bronchial epithelial cells. <i>Experimental Lung Research</i> , 2017, 43, 347-358.	0.5	21
218	Path toward Precision Oncology: Review of Targeted Therapy Studies and Tools to Aid in Defining "Actionability" of a Molecular Lesion and Patient Management Support. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 2645-2655.	1.9	59
219	Glut3 Addiction Is a Druggable Vulnerability for a Molecularly Defined Subpopulation of Glioblastoma. <i>Cancer Cell</i> , 2017, 32, 856-868.e5.	7.7	121

#	ARTICLE	IF	CITATIONS
220	Resetting the Yeast Epigenome with Human Nucleosomes. <i>Cell</i> , 2017, 171, 1508-1519.e13.	13.5	53
221	Tumor-Suppressor Inactivation of GDF11 Occurs by Precursor Sequestration in Triple-Negative Breast Cancer. <i>Developmental Cell</i> , 2017, 43, 418-435.e13.	3.1	62
222	Comprehensive analysis of gene expression patterns in Friedreich's ataxia fibroblasts by RNA sequencing reveals altered levels of protein synthesis factors and solute carriers. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 1353-1369.	1.2	38
223	Variability of genome-wide DNA methylation and mRNA expression profiles in reproductive and endocrine disease related tissues. <i>Epigenetics</i> , 2017, 12, 897-908.	1.3	33
224	Secretoneurin A regulates neurogenic and inflammatory transcriptional networks in goldfish ( <i>Carassius auratus</i> ) radial glia. <i>Scientific Reports</i> , 2017, 7, 14930.	1.6	12
225	Quantitative Proteomics Analysis Reveals Novel Targets of miR-21 in Zebrafish Embryos. <i>Scientific Reports</i> , 2017, 7, 4022.	1.6	9
226	Transcriptional consequences of XPA disruption in human cell lines. <i>DNA Repair</i> , 2017, 57, 76-90.	1.3	19
227	Obesity-induces Organ and Tissue Specific Tight Junction Restructuring and Barrier Deregulation by Claudin Switching. <i>Scientific Reports</i> , 2017, 7, 5125.	1.6	94
228	Profiling conserved biological pathways in Autosomal Dominant Polycystic Kidney Disorder (ADPKD) to elucidate key transcriptomic alterations regulating cystogenesis: A cross-species meta-analysis approach. <i>Gene</i> , 2017, 627, 434-450.	1.0	11
229	A Human Tyrosine Phosphatase Interactome Mapped by Proteomic Profiling. <i>Journal of Proteome Research</i> , 2017, 16, 2789-2801.	1.8	14
230	LRRK2(I2020T) functional genetic interactors that modify eye degeneration and dopaminergic cell loss in <i>Drosophila</i> . <i>Human Molecular Genetics</i> , 2017, 26, 1247-1257.	1.4	17
231	PANTHER version 11: expanded annotation data from Gene Ontology and Reactome pathways, and data analysis tool enhancements. <i>Nucleic Acids Research</i> , 2017, 45, D183-D189.	6.5	2,113
232	Proteomic profiling of archaeological human bone. <i>Royal Society Open Science</i> , 2017, 4, 161004.	1.1	76
233	Expression profiling indicating low selenium-sensitive microRNA levels linked to cell cycle and cell stress response pathways in the CaCo-2 cell line. <i>British Journal of Nutrition</i> , 2017, 117, 1212-1221.	1.2	17
234	Dynamic changes in murine forebrain miR-211 expression associate with cholinergic imbalances and epileptiform activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4996-E5005.	3.3	45
235	Reactome pathway analysis: a high-performance in-memory approach. <i>BMC Bioinformatics</i> , 2017, 18, 142.	1.2	600
236	NFPscanner: a webtool for knowledge-based deciphering of biomedical networks. <i>BMC Bioinformatics</i> , 2017, 18, 262.	1.2	0
237	Genome-wide standing variation facilitates long-term response to bidirectional selection for antibody response in chickens. <i>BMC Genomics</i> , 2017, 18, 99.	1.2	23

#	ARTICLE	IF	CITATIONS
238	Membrane-enriched proteome changes and prion protein expression during neural differentiation and in neuroblastoma cells. <i>BMC Genomics</i> , 2017, 18, 319.	1.2	2
239	Response of turkey muscle satellite cells to thermal challenge. I. transcriptome effects in proliferating cells. <i>BMC Genomics</i> , 2017, 18, 352.	1.2	14
240	Transcriptomic analysis of maternally provisioned cues for phenotypic plasticity in the annual killifish, <i>Austrofundulus limnaeus</i> . <i>EvoDevo</i> , 2017, 8, 6.	1.3	50
241	Cestode parasites release extracellular vesicles with microRNAs and immunodiagnostic protein cargo. <i>International Journal for Parasitology</i> , 2017, 47, 675-686.	1.3	69
242	Deregulation of focal adhesion formation and cytoskeletal tension due to loss of A-type lamins. <i>Cell Adhesion and Migration</i> , 2017, 11, 447-463.	1.1	23
243	RNAseq profiling of primary microglia and astrocyte cultures in near-term ovine fetus: A glial in vivo-in vitro multi-hit paradigm in large mammalian brain. <i>Journal of Neuroscience Methods</i> , 2017, 276, 23-32.	1.3	11
244	Multiplexed MRMA <sup>2</sup> -based assays for the quantitation of proteins in mouse plasma and heart tissue. <i>Proteomics</i> , 2017, 17, 1600097.	1.3	22
245	AAGAtlas 1.0: a human autoantigen database. <i>Nucleic Acids Research</i> , 2017, 45, D769-D776.	6.5	48
246	Transcriptome analysis of equine sarcoids. <i>Veterinary and Comparative Oncology</i> , 2017, 15, 1370-1381.	0.8	11
247	Selection for higher fertility reflects in the seminal fluid proteome of modern domestic chicken. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 21, 27-40.	0.4	14
248	The longissimus thoracis muscle proteome in Alentejana bulls as affected by growth path. <i>Journal of Proteomics</i> , 2017, 152, 206-215.	1.2	22
249	Defining Trends in Global Gene Expression in Arabian Horses with Cerebellar Abiotrophy. <i>Cerebellum</i> , 2017, 16, 462-472.	1.4	7
250	Proteomic and Bioinformatic Characterization of Extracellular Vesicles Released from Human Macrophages upon Influenza A Virus Infection. <i>Journal of Proteome Research</i> , 2017, 16, 217-227.	1.8	55
251	Cargo selectivity of yeast sorting nexins. <i>Traffic</i> , 2017, 18, 110-122.	1.3	43
252	NanoLC-MS coupling of liquid microjunction microextraction for on-tissue proteomic analysis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 891-900.	1.1	25
253	Genome-wide genetic analyses highlight mitogen-activated protein kinase (MAPK) signaling in the pathogenesis of endometriosis. <i>Human Reproduction</i> , 2017, 32, 780-793.	0.4	81
254	Systems analysis identifies melanoma-enriched pro-oncogenic networks controlled by the RNA binding protein CELF1. <i>Nature Communications</i> , 2017, 8, 2249.	5.8	22
255	RNA-seq of serial kidney biopsies obtained during progression of chronic kidney disease from dogs with X-linked hereditary nephropathy. <i>Scientific Reports</i> , 2017, 7, 16776.	1.6	12

#	ARTICLE	IF	CITATIONS
256	Characterization of exosomes from body fluids of dairy cows <sup>1</sup> . <i>Journal of Animal Science</i> , 2017, 95, 3893-3904.	0.2	15
257	Membranome: a database for proteome-wide analysis of single-pass membrane proteins. <i>Nucleic Acids Research</i> , 2017, 45, D250-D255.	6.5	52
258	Sparse Learning of the Disease Severity Score for High-Dimensional Data. <i>Complexity</i> , 2017, 2017, 1-11.	0.9	2
259	Dynamic Editome of Zebrafish under Aminoglycosides Treatment and Its Potential Involvement in Ototoxicity. <i>Frontiers in Pharmacology</i> , 2017, 8, 854.	1.6	2
260	Expression, Localization of SUMO-1, and Analyses of Potential SUMOylated Proteins in <i>Bubalus bubalis</i> Spermatozoa. <i>Frontiers in Physiology</i> , 2017, 8, 354.	1.3	4
261	Key Components of Different Plant Defense Pathways Are Dispensable for Powdery Mildew Resistance of the <i>Arabidopsis mlo2 mlo6 mlo12</i> Triple Mutant. <i>Frontiers in Plant Science</i> , 2017, 8, 1006.	1.7	45
262	Antarctic Moss Multiprotein Bridging Factor 1c Overexpression in <i>Arabidopsis</i> Resulted in Enhanced Tolerance to Salt Stress. <i>Frontiers in Plant Science</i> , 2017, 8, 1206.	1.7	32
263	Application of Proteomics to Medical Diagnostics. , 2017, , 233-248.		0
264	Identification of key pathways and genes with aberrant methylation in prostate cancer using bioinformatics analysis. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 4925-4933.	1.0	11
265	TSC1 Mutations in Keratoconus Patients With or Without Tuberous Sclerosis. , 2017, 58, 6462.		10
266	HsigAtlas 1.0: a human immunosuppression gene database. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	44
267	pathDIP: an annotated resource for known and predicted human gene-pathway associations and pathway enrichment analysis. <i>Nucleic Acids Research</i> , 2017, 45, D419-D426.	6.5	105
268	Haustorium initiation in the obligate parasitic plant <i>Phelipanche ramosa</i> involves a host-exudated cytokinin signal. <i>Journal of Experimental Botany</i> , 2017, 68, 5539-5552.	2.4	40
269	Integrated proteomic and N-glycoproteomic analyses of doxorubicin sensitive and resistant ovarian cancer cells reveal glycoprotein alteration in protein abundance and glycosylation. <i>Oncotarget</i> , 2017, 8, 13413-13427.	0.8	18
270	Non-Coding RNAs in Lung Cancer: Contribution of Bioinformatics Analysis to the Development of Non-Invasive Diagnostic Tools. <i>Genes</i> , 2017, 8, 8.	1.0	28
271	Systematic Identification and Assessment of Therapeutic Targets for Breast Cancer Based on Genome-Wide RNA Interference Transcriptomes. <i>Genes</i> , 2017, 8, 86.	1.0	12
272	An Integrative Analysis Reveals a Central Role of P53 Activation via MDM2 in Zika Virus Infection Induced Cell Death. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 327.	1.8	23
273	Marine Animal Microbiomes: Toward Understanding Host-Microbiome Interactions in a Changing Ocean. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	142



#	ARTICLE	IF	CITATIONS
274	Outer Membrane Proteome of <i>Veillonella parvula</i> : A Diderm Firmicute of the Human Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 1215.	1.5	55
275	Variety of RNAs in Peripheral Blood Cells, Plasma, and Plasma Fractions. <i>BioMed Research International</i> , 2017, 2017, 1-10.	0.9	52
276	Serum Proteome Alterations in Patients with Cognitive Impairment after Traumatic Brain Injury Revealed by iTRAQ-Based Quantitative Proteomics. <i>BioMed Research International</i> , 2017, 2017, 1-13.	0.9	8
277	LPS-induced modules of co-expressed genes in equine peripheral blood mononuclear cells. <i>BMC Genomics</i> , 2017, 18, 34.	1.2	12
278	Pre-Exposure Gene Expression in Baboons with and without Pancytopenia after Radiation Exposure. <i>International Journal of Molecular Sciences</i> , 2017, 18, 541.	1.8	19
279	Î²1-Integrin Deletion From the Lens Activates Cellular Stress Responses Leading to Apoptosis and Fibrosis. , 2017, 58, 3896.		19
280	Underexpression of Specific Interferon Genes Is Associated with Poor Prognosis of Melanoma. <i>PLoS ONE</i> , 2017, 12, e0170025.	1.1	12
281	Transcriptome and proteome responses in RNAlater preserved tissue of <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2017, 12, e0175943.	1.1	38
282	A sorghum ( <i>Sorghum bicolor</i> ) mutant with altered carbon isotope ratio. <i>PLoS ONE</i> , 2017, 12, e0179567.	1.1	5
283	Tumor Necrosis Factor dynamically regulates the mRNA stabilome in rheumatoid arthritis fibroblast-like synoviocytes. <i>PLoS ONE</i> , 2017, 12, e0179762.	1.1	21
284	Challenges and advances for transcriptome assembly in non-model species. <i>PLoS ONE</i> , 2017, 12, e0185020.	1.1	38
285	Scrambled eggs: Proteomic portraits and novel biomarkers of egg quality in zebrafish ( <i>Danio rerio</i> ). <i>PLoS ONE</i> , 2017, 12, e0188084.	1.1	34
286	Parkinson's disease-associated genetic variation is linked to quantitative expression of inflammatory genes. <i>PLoS ONE</i> , 2017, 12, e0175882.	1.1	45
287	Whole transcriptome RNA-Seq analysis reveals extensive cell type-specific compartmentalization in <i>Volvox carteri</i> . <i>BMC Biology</i> , 2017, 15, 111.	1.7	19
288	Differential expression of genes related to gain and intake in the liver of beef cattle. <i>BMC Research Notes</i> , 2017, 10, 1.	0.6	268
289	Drug target ontology to classify and integrate drug discovery data. <i>Journal of Biomedical Semantics</i> , 2017, 8, 50.	0.9	63
290	Incorporating biological information in sparse principal component analysis with application to genomic data. <i>BMC Bioinformatics</i> , 2017, 18, 332.	1.2	15
291	Transcriptomic Profiling of Posterior Polymorphous Corneal Dystrophy. , 2017, 58, 3202.		24

#	ARTICLE	IF	CITATIONS
292	Protein Ontology (PRO): enhancing and scaling up the representation of protein entities. <i>Nucleic Acids Research</i> , 2017, 45, D339-D346.	6.5	73
293	Trinucleotide Repeat Expansion in the Transcription Factor 4 ( <i>TCF4</i> ) Gene Leads to Widespread mRNA Splicing Changes in Fuchs' Endothelial Corneal Dystrophy. , 2017, 58, 343.		59
294	Draft de novo transcriptome assembly and proteome characterization of the electric lobe of <i>Tetronarce californica</i> : a molecular tool for the study of cholinergic neurotransmission in the electric organ. <i>BMC Genomics</i> , 2017, 18, 611.	1.2	7
295	A TBX5 NONSENSE MUTATION IN SIBLINGS WITH DIVERGENT PHENOTYPES ASSOCIATED WITH ISOLATED SEPTAL DEFECTS. <i>Asian Journal of Pharmaceutical and Clinical Research</i> , 2017, 10, 126.	0.3	0
296	Temporally distinct transcriptional regulation of myocyte dedifferentiation and Myofiber growth during muscle regeneration. <i>BMC Genomics</i> , 2017, 18, 854.	1.2	9
297	Artificial selection for odor-guided behavior in <i>Drosophila</i> reveals changes in food consumption. <i>BMC Genomics</i> , 2017, 18, 867.	1.2	6
298	Exploring targeted therapy of osteosarcoma using proteomics data. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 565-577.	1.0	22
299	Suppression of dsRNA response genes and innate immunity following Oct4, Stella, and Nanos2 overexpression in mouse embryonic fibroblasts. <i>Cytokine</i> , 2018, 106, 1-11.	1.4	7
300	In Vivo Phosphoproteome Analysis Reveals Kinome Reprogramming in Hepatocellular Carcinoma. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1067-1083.	2.5	27
301	Challenges and emergent solutions for LC-MS/MS based untargeted metabolomics in diseases. <i>Mass Spectrometry Reviews</i> , 2018, 37, 772-792.	2.8	219
302	Functional analysis of cell-free RNA using mid-trimester amniotic fluid supernatant in pregnancy with the fetal growth restriction. <i>Medicine (United States)</i> , 2018, 97, e9572.	0.4	7
303	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
304	Comparative qualitative phosphoproteomics analysis identifies shared phosphorylation motifs and associated biological processes in evolutionary divergent plants. <i>Journal of Proteomics</i> , 2018, 181, 152-159.	1.2	20
305	The Egyptian Roussette Genome Reveals Unexpected Features of Bat Antiviral Immunity. <i>Cell</i> , 2018, 173, 1098-1110.e18.	13.5	220
306	Host serum microRNA profiling during the early stage of foot-and-mouth disease virus infection. <i>Archives of Virology</i> , 2018, 163, 2055-2063.	0.9	16
307	Cri-du-Chat Syndrome interactome network: Correlating genotypic variations to associated phenotypes. <i>Gene Reports</i> , 2018, 11, 179-187.	0.4	2
308	The Rheumatoid Arthritis-Associated Citrullinome. <i>Cell Chemical Biology</i> , 2018, 25, 691-704.e6.	2.5	158
309	De-novo assembly and transcriptome analysis of <i>Odontesthes argentinensis</i> gill tissue, with development of single sequence repeat markers. <i>Gene Reports</i> , 2018, 11, 220-228.	0.4	3

#	ARTICLE	IF	CITATIONS
310	Cancer-Germline Antigen Expression Discriminates Clinical Outcome to CTLA-4 Blockade. <i>Cell</i> , 2018, 173, 624-633.e8.	13.5	113
311	Initiating Events in Direct Cardiomyocyte Reprogramming. <i>Cell Reports</i> , 2018, 22, 1913-1922.	2.9	23
312	High-resolution spatiotemporal transcriptome mapping of tomato fruit development and ripening. <i>Nature Communications</i> , 2018, 9, 364.	5.8	255
313	BRCA1 and BRCA2 germline variants in breast cancer patients from the Republic of Macedonia. <i>Breast Cancer Research and Treatment</i> , 2018, 168, 745-753.	1.1	8
314	Regeneration in distantly related species: common strategies and pathways. <i>Npj Systems Biology and Applications</i> , 2018, 4, 5.	1.4	23
315	Kinome and phosphoproteome of high-grade meningiomas reveal AKAP12 as a central regulator of aggressiveness and its possible role in progression. <i>Scientific Reports</i> , 2018, 8, 2098.	1.6	42
316	Overexpression of PGC-1 $\alpha$ in aging muscle enhances a subset of young-like molecular patterns. <i>Aging Cell</i> , 2018, 17, e12707.	3.0	57
317	Differential Expression of MicroRNAs in Uterine Cervical Cancer and Its Implications in Carcinogenesis; An Integrative Approach. <i>International Journal of Gynecological Cancer</i> , 2018, 28, 553-562.	1.2	11
318	Proteomics of the Human Olfactory Tract. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 77-87.	1.0	6
319	Interactome analysis reveals ZNF804A, a schizophrenia risk gene, as a novel component of protein translational machinery critical for embryonic neurodevelopment. <i>Molecular Psychiatry</i> , 2018, 23, 952-962.	4.1	40
320	A KDM5 Inhibitor Increases Global H3K4 Trimethylation Occupancy and Enhances the Biological Efficacy of 5-Aza-2-Deoxycytidine. <i>Cancer Research</i> , 2018, 78, 1127-1139.	0.4	41
321	The Y Chromosome Modulates Splicing and Sex-Biased Intron Retention Rates in <i>Drosophila</i> . <i>Genetics</i> , 2018, 208, 1057-1067.	1.2	16
322	Genetic profile of patients with early onset inflammatory bowel disease. <i>Gene</i> , 2018, 645, 18-29.	1.0	29
323	Evolutionary expansion of DNA hypomethylation in the mammalian germline genome. <i>Genome Research</i> , 2018, 28, 145-158.	2.4	30
324	Paternal chromosome loss and metabolic crisis contribute to hybrid inviability in <i>Xenopus</i> . <i>Nature</i> , 2018, 553, 337-341.	13.7	69
325	The 2018 Nucleic Acids Research database issue and the online molecular biology database collection. <i>Nucleic Acids Research</i> , 2018, 46, D1-D7.	6.5	106
326	Characterization of a FOXP1:TLE1 transcriptional network in glioblastoma-initiating cells. <i>Molecular Oncology</i> , 2018, 12, 775-787.	2.1	23
327	O-GlcNAcylation of the Tumor Suppressor FOXO3 Triggers Aberrant Cancer Cell Growth. <i>Cancer Research</i> , 2018, 78, 1214-1224.	0.4	34

#	ARTICLE	IF	CITATIONS
328	Label free quantitative proteomics reveals the role of miR-200b in androgen-independent prostate cancer cells. <i>Clinical Proteomics</i> , 2018, 15, .	1.1	4
329	Characterization of Blimp-1 function in effector regulatory T cells. <i>Journal of Autoimmunity</i> , 2018, 91, 73-82.	3.0	36
330	Reconstruction of the ancestral metazoan genome reveals an increase in genomic novelty. <i>Nature Communications</i> , 2018, 9, 1730.	5.8	101
331	Identification of diverse target RNAs that are functionally regulated by human Pumilio proteins. <i>Nucleic Acids Research</i> , 2018, 46, 362-386.	6.5	80
332	Proteome profiling of exosomes derived from plasma of heifers with divergent genetic merit for fertility. <i>Journal of Dairy Science</i> , 2018, 101, 6462-6473.	1.4	23
333	Assessment of DNA repair susceptibility genes identified by whole exome sequencing in head and neck cancer. <i>DNA Repair</i> , 2018, 66-67, 50-63.	1.3	20
335	Integrated analysis of methylome, transcriptome and miRNAome of three pig breeds. <i>Epigenomics</i> , 2018, 10, 597-612.	1.0	11
336	Rapid regulatory evolution of a nonrecombining autosome linked to divergent behavioral phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2794-2799.	3.3	28
337	Proteomic content of circulating exosomes in dairy cows with or without uterine infection. <i>Theriogenology</i> , 2018, 114, 173-179.	0.9	19
338	Transcriptome Analysis Identifies Multifaceted Regulatory Mechanisms Dictating a Genetic Switch from Neuronal Network Establishment to Maintenance During Postnatal Prefrontal Cortex Development. <i>Cerebral Cortex</i> , 2018, 28, 833-851.	1.6	15
339	Transcriptome analysis of root-knot nematode ( <i>Meloidogyne incognita</i> )-infected tomato ( <i>Solanum lycopersicum</i> ) roots reveals complex gene expression profiles and metabolic networks of both host and nematode during susceptible and resistance responses. <i>Molecular Plant Pathology</i> , 2018, 19, 615-633.	2.0	127
340	Comparative analysis of DNA methylation patterns of equine sarcoid and healthy skin samples. <i>Veterinary and Comparative Oncology</i> , 2018, 16, 37-46.	0.8	9
341	Identification and comparative analysis of aluminum-induced microRNAs conferring plant tolerance to aluminum stress in soybean. <i>Biologia Plantarum</i> , 2018, 62, 97-108.	1.9	19
342	Effect of Sweetened Dried Cranberry Consumption on Urinary Proteome and Fecal Microbiome in Healthy Human Subjects. <i>OMICS A Journal of Integrative Biology</i> , 2018, 22, 145-153.	1.0	34
343	Removal of Cell-Activating Substances Using Dialyzers With Various Permeability Profiles. <i>Artificial Organs</i> , 2018, 42, 78-87.	1.0	8
344	Evidence of positive selection towards Zebuine haplotypes in the BoLA region of Brangus cattle. <i>Animal</i> , 2018, 12, 215-223.	1.3	27
345	Complement Activation in Peritoneal Dialysis-Induced Arteriopathy. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 268-282.	3.0	45
346	Integrating splice-isoform expression into genome-scale models characterizes breast cancer metabolism. <i>Bioinformatics</i> , 2018, 34, 494-501.	1.8	23

#	ARTICLE	IF	CITATIONS
347	Illuminating the role of the G $\beta\gamma$ heterotrimeric G protein subunit, RGA1, in regulating photoprotection and photoavoidance in rice. <i>Plant, Cell and Environment</i> , 2018, 41, 451-468.	2.8	36
348	A s<scp>RNA</scp> in a reduced mutualistic symbiont genome regulates its own gene expression. <i>Molecular Ecology</i> , 2018, 27, 1766-1776.	2.0	24
349	Identification of Mature Atherosclerotic Plaque Proteome Signatures Using Data-Independent Acquisition Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 164-176.	1.8	24
350	Proteomic and metabolomic characterization of streptozotocin-induced diabetic nephropathy in TIMP3-deficient mice. <i>Acta Diabetologica</i> , 2018, 55, 121-129.	1.2	25
351	Thyroid follicular adenomas and carcinomas: molecular profiling provides evidence for a continuous evolution. <i>Oncotarget</i> , 2018, 9, 10343-10359.	0.8	29
352	Preeclamptic placenta release factors that damage neurons: implications for foetal programming of disease. <i>Neuronal Signaling</i> , 2018, 2, NS20180139.	1.7	14
353	Identification of Candidate Genes Responsible for Age-related Macular Degeneration using Microarray Data. <i>International Journal of Service Science, Management, Engineering, and Technology</i> , 2018, 9, 33-60.	0.7	4
354	iTRAQ-Based Analysis of Proteins Co-Regulated by Brassinosteroids and Gibberellins in Rice Embryos during Seed Germination. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3460.	1.8	11
355	Influence of Disease Duration on Circulating Levels of miRNAs in Children and Adolescents with New Onset Type 1 Diabetes. <i>Non-coding RNA</i> , 2018, 4, 35.	1.3	21
356	Interactome and Proteome Dynamics Uncover Immune Modulatory Associations of the Pathogen Sensing Factor cGAS. <i>Cell Systems</i> , 2018, 7, 627-642.e6.	2.9	34
357	Dual-center, dual-platform microRNA profiling identifies potential plasma biomarkers of adult temporal lobe epilepsy. <i>EBioMedicine</i> , 2018, 38, 127-141.	2.7	88
358	Identification of hub genes and outcome in colon cancer based on bioinformatics analysis. <i>Cancer Management and Research</i> , 2019, Volume 11, 323-338.	0.9	28
359	Identifying mouse developmental essential genes using machine learning. <i>DMM Disease Models and Mechanisms</i> , 2018, 11, .	1.2	18
360	Mass Spectrometry-Based Comprehensive Analysis of Pancreatic Cyst Fluids. <i>BioMed Research International</i> , 2018, 2018, 1-12.	0.9	9
361	Unveiling the Role of the Most Impactful Cardiovascular Risk Locus through Haplotype Editing. <i>Cell</i> , 2018, 175, 1796-1810.e20.	13.5	95
362	USA300 <i>Staphylococcus aureus</i> persists on multiple body sites following an infection. <i>BMC Microbiology</i> , 2018, 18, 206.	1.3	12
363	Proteome and Metabolome of Subretinal Fluid in Central Serous Chorioretinopathy and Rhegmatogenous Retinal Detachment: A Pilot Case Study. <i>Translational Vision Science and Technology</i> , 2018, 7, 3.	1.1	34
364	AllerGAtlas 1.0: a human allergy-related genes database. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	11

#	ARTICLE	IF	CITATIONS
365	Biomechanical Rigidity and Quantitative Proteomics Analysis of Segmental Regions of the Trabecular Meshwork at Physiologic and Elevated Pressures. , 2018, 59, 246.		54
366	DNA methylation and gene expression alterations in zebrafish early-life stages exposed to the antibacterial agent triclosan. <i>Environmental Pollution</i> , 2018, 243, 1867-1877.	3.7	36
367	Signatures of genetic adaptation to extremely varied Australian environments in introduced European house sparrows. <i>Molecular Ecology</i> , 2018, 27, 4542-4555.	2.0	16
368	The proteome of perilymph in patients with vestibular schwannoma. A possibility to identify biomarkers for tumor associated hearing loss?. <i>PLoS ONE</i> , 2018, 13, e0198442.	1.1	29
369	Fc $\gamma$ RIIb on B Cells and Myeloid Cells Modulates B Cell Activation and Autoantibody Responses via Different but Synergistic Pathways in Lupus-Prone Yaa Mice. <i>Journal of Immunology</i> , 2018, 201, 3199-3210.	0.4	5
370	Identification of key differentially expressed MicroRNAs in cancer patients through pan-cancer analysis. <i>Computers in Biology and Medicine</i> , 2018, 103, 183-197.	3.9	28
371	Acid bone lysate activates TGF $\beta$ <sup>2</sup> signalling in human oral fibroblasts. <i>Scientific Reports</i> , 2018, 8, 16065.	1.6	23
372	Improving Interpretation of Cardiac Phenotypes and Enhancing Discovery With Expanded Knowledge in the Gene Ontology. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e001813.	1.6	24
373	Alternative polyadenylation analysis in animals and plants: newly developed strategies for profiling, processing and validation. <i>International Journal of Biological Sciences</i> , 2018, 14, 1709-1714.	2.6	6
374	Shared Biological Pathways Between Alzheimer's Disease and Ischemic Stroke. <i>Frontiers in Neuroscience</i> , 2018, 12, 605.	1.4	13
375	Setting the stage for a role of the postsynaptic proteome in inherited neurometabolic disorders. <i>Journal of Inherited Metabolic Disease</i> , 2018, 41, 1093-1101.	1.7	3
376	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	1.8	36
378	OBSOLETE: <i>Bioinformatics Principles for Deciphering Cardiovascular Diseases.</i> , 2018, , .		1
379	Lso2 is a conserved ribosome-bound protein required for translational recovery in yeast. <i>PLoS Biology</i> , 2018, 16, e2005903.	2.6	31
380	Gene expression profile analysis of aortic vascular smooth muscle cells reveals upregulation of cadherin genes in myocardial infarction patients. <i>Physiological Genomics</i> , 2018, 50, 648-657.	1.0	18
381	Nanocellulose: A New Multifunctional Tool for RNA Systems Biology Research. <i>RNA Technologies</i> , 2018, , 373-401.	0.2	0
382	Patterns of variation in cis-regulatory regions: examining evidence of purifying selection. <i>BMC Genomics</i> , 2018, 19, 95.	1.2	8
383	Mapping the HLA Ligandome of Colorectal Cancer Reveals an Imprint of Malignant Cell Transformation. <i>Cancer Research</i> , 2018, 78, 4627-4641.	0.4	56

#	ARTICLE	IF	CITATIONS
384	Characterization of an activating R1353H insulin-like growth factor 1 receptor variant in a male with extreme tall height. <i>European Journal of Endocrinology</i> , 2018, 179, 85-95.	1.9	6
385	Whole Root Transcriptomic Analysis Suggests a Role for Auxin Pathways in Resistance to <i>Ralstonia solanacearum</i> in Tomato. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 432-444.	1.4	55
386	Sculpting the Sculptors: Methods for Studying the Fetal Cholinergic Signaling on Systems and Cellular Scales. <i>Methods in Molecular Biology</i> , 2018, 1781, 341-352.	0.4	9
387	NuRD and CAF-1-mediated silencing of the D4Z4 array is modulated by DUX4-induced MBD3L proteins. <i>ELife</i> , 2018, 7, .	2.8	47
388	Role of the visual experience-dependent nascent proteome in neuronal plasticity. <i>ELife</i> , 2018, 7, .	2.8	19
389	Bioinformatics Principles for Deciphering Cardiovascular Diseases. , 2018, , 273-292.		3
390	Pi-Pi contacts are an overlooked protein feature relevant to phase separation. <i>ELife</i> , 2018, 7, .	2.8	571
391	A Computational Approach Using Bioinformatics to Screening Drug Targets for <i>Leishmania infantum</i> Species. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-9.	0.5	13
392	Acute Complement Inhibition Potentiates Neurorehabilitation and Enhances tPA-Mediated Neuroprotection. <i>Journal of Neuroscience</i> , 2018, 38, 6527-6545.	1.7	20
393	Proteomic Analysis of Synaptoneurosomes Highlights the Relevant Role of Local Translation in the Hippocampus. <i>Proteomics</i> , 2018, 18, e1800005.	1.3	4
394	Ras-ERK-ETS inhibition alleviates neuronal mitochondrial dysfunction by reprogramming mitochondrial retrograde signaling. <i>PLoS Genetics</i> , 2018, 14, e1007567.	1.5	14
395	Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours. <i>Nature Ecology and Evolution</i> , 2018, 2, 1479-1491.	3.4	113
396	SWI/SNF regulates half of its targets without the need of ATP-driven nucleosome remodeling by Brahma. <i>BMC Genomics</i> , 2018, 19, 367.	1.2	20
397	RNA-Seq Meta-analysis identifies genes in skeletal muscle associated with gain and intake across a multi-season study of crossbred beef steers. <i>BMC Genomics</i> , 2018, 19, 430.	1.2	21
398	Molecular Profiling of Pierce's Disease Outlines the Response Circuitry of <i>Vitis vinifera</i> to <i>Xylella fastidiosa</i> Infection. <i>Frontiers in Plant Science</i> , 2018, 9, 771.	1.7	35
399	MinOmics, an Integrative and Immersive Tool for Multi-Omics Analysis. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	25
400	Pain-Associated Transcriptome Changes in Synovium of Knee Osteoarthritis Patients. <i>Genes</i> , 2018, 9, 338.	1.0	37
401	O-GlcNAcylation site mapping by (azide-alkyne) click chemistry and mass spectrometry following intensive fractionation of skeletal muscle cells proteins. <i>Journal of Proteomics</i> , 2018, 186, 83-97.	1.2	27

#	ARTICLE	IF	CITATIONS
402	Preliminary evaluation of neoblast-like stem cell factor and transcript expression profiles in <i>Schistosoma japonicum</i> . <i>Acta Tropica</i> , 2018, 187, 57-64.	0.9	3
403	Transcriptome response of human skeletal muscle to divergent exercise stimuli. <i>Journal of Applied Physiology</i> , 2018, 124, 1529-1540.	1.2	61
404	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. <i>BMC Genomics</i> , 2018, 19, 499.	1.2	51
405	Inorganic Polyphosphate Is Essential for <i>Salmonella Typhimurium</i> Virulence and Survival in <i>Dictyostelium discoideum</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 8.	1.8	32
406	Secretoneurin A Directly Regulates the Proteome of Goldfish Radial Glial Cells In Vitro. <i>Frontiers in Endocrinology</i> , 2018, 9, 68.	1.5	1
407	PU.1 Is Required for the Developmental Progression of Multipotent Progenitors to Common Lymphoid Progenitors. <i>Frontiers in Immunology</i> , 2018, 9, 1264.	2.2	30
408	Stability and Function of Hippocampal Mossy Fiber Synapses Depend on Bcl11b/Ctip2. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 103.	1.4	21
409	Direct control of somatic stem cell proliferation factors by the <i>Drosophila</i> testis stem cell niche. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	12
410	Computational analysis of deleterious SNPs of SLC45A2 involved in oculocutaneous albinism type 4. <i>Gene Reports</i> , 2018, 12, 248-254.	0.4	0
411	Developmental dynamics of gene expression and alternative polyadenylation in the <i>Caenorhabditis elegans</i> germline. <i>Genome Biology</i> , 2018, 19, 8.	3.8	31
412	Streamlined Tandem Mass Tag (SL-TMT) Protocol: An Efficient Strategy for Quantitative (Phospho)proteome Profiling Using Tandem Mass Tag-Synchronous Precursor Selection-MS3. <i>Journal of Proteome Research</i> , 2018, 17, 2226-2236.	1.8	245
413	Whole-genome sequencing reveals new insights into age-related hearing loss: cumulative effects, pleiotropy and the role of selection. <i>European Journal of Human Genetics</i> , 2018, 26, 1167-1179.	1.4	22
414	Small noncoding RNAs in FSHD2 muscle cells reveal both DUX4- and SMCHD1-specific signatures. <i>Human Molecular Genetics</i> , 2018, 27, 2644-2657.	1.4	6
415	Comparative Characterization of the Sindbis Virus Proteome from Mammalian and Invertebrate Hosts Identifies nsP2 as a Component of the Virion and Sorting Nexin 5 as a Significant Host Factor for Alphavirus Replication. <i>Journal of Virology</i> , 2018, 92, .	1.5	19
416	Interpretation of biological experiments changes with evolution of the Gene Ontology and its annotations. <i>Scientific Reports</i> , 2018, 8, 5115.	1.6	110
417	Diverse reprogramming codes for neuronal identity. <i>Nature</i> , 2018, 557, 375-380.	13.7	94
418	Metabolic oscillations on the circadian time scale in <i>Drosophila</i> cells lacking clock genes. <i>Molecular Systems Biology</i> , 2018, 14, e8376.	3.2	38
419	Turning omics data into therapeutic insights. <i>Current Opinion in Pharmacology</i> , 2018, 42, 95-101.	1.7	9



#	ARTICLE	IF	CITATIONS
420	ProMotE: an efficient algorithm for counting independent motifs in uncertain network topologies. <i>BMC Bioinformatics</i> , 2018, 19, 242.	1.2	4
421	Ancestry and genetic associations with bronchopulmonary dysplasia in preterm infants. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2018, 315, L858-L869.	1.3	24
422	Proteomics for blood biomarker exploration of severe mental illness: pitfalls of the past and potential for the future. <i>Translational Psychiatry</i> , 2018, 8, 160.	2.4	68
423	GILZ-dependent modulation of mTORC1 regulates spermatogonial maintenance. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	25
424	The effects of Capn1 gene inactivation on the differential expression of genes in skeletal muscle. <i>Gene</i> , 2018, 668, 54-58.	1.0	5
425	Analysis of Gene Expression Changes in PHA-M Stimulated Lymphocytes – Unraveling PHA Activity as Prerequisite for Dicentric Chromosome Analysis. <i>Radiation Research</i> , 2018, 189, 579.	0.7	3
426	Functional insights into the role of seminal plasma proteins on sperm motility of buffalo. <i>Animal Reproduction Science</i> , 2018, 195, 251-258.	0.5	18
427	Expression profiling of disease progression in canine model of Duchenne muscular dystrophy. <i>PLoS ONE</i> , 2018, 13, e0194485.	1.1	16
428	OmicsNet: A web-based tool for creation and visual analysis of biological networks in 3D space. <i>Nucleic Acids Research</i> , 2018, 46, W514-W522.	6.5	126
429	Probing seco-steroid inhibition of the hedgehog signaling pathway. <i>Molecular and Cellular Biochemistry</i> , 2019, 450, 75-85.	1.4	1
430	Evaluation of computational techniques for predicting non-synonymous single nucleotide variants pathogenicity. <i>Genomics</i> , 2019, 111, 869-882.	1.3	36
431	Comparative mRNA and miRNA expression in European mouflon ( <i>Ovis musimon</i> ) and sheep ( <i>Ovis aries</i> ) provides novel insights into the genetic mechanisms for female reproductive success. <i>Heredity</i> , 2019, 122, 172-186.	1.2	21
432	Immune gene expression in kidney biopsies of lupus nephritis patients at diagnosis and at renal flare. <i>Nephrology Dialysis Transplantation</i> , 2019, 34, 1197-1206.	0.4	24
433	Ocimum basilicum miRNOME revisited: A cross kingdom approach. <i>Genomics</i> , 2019, 111, 772-785.	1.3	12
434	Identification of Proteins From Proteomic Analysis. , 2019, , 855-870.		1
435	Quantification of Proteins From Proteomic Analysis. , 2019, , 871-890.		1
436	Two Decades of Biological Pathway Databases: Results and Challenges. , 2019, , 1071-1084.		5
437	Predicting Non-Synonymous Single Nucleotide Variants Pathogenic Effects in Human Diseases. , 2019, , 400-409.		1

#	ARTICLE	IF	CITATIONS
438	Functional Genomics. , 2019, , 118-133.		5
439	The Retinal Ganglion Cell Transportome Identifies Proteins Transported to Axons and Presynaptic Compartments in the Visual System In Vivo. Cell Reports, 2019, 28, 1935-1947.e5.	2.9	16
440	The Nutrient Response Transcriptional Regulome of Arabidopsis. IScience, 2019, 19, 358-368.	1.9	32
441	Effects of diethylcarbamazine and ivermectin treatment on Brugia malayi gene expression in infected gerbils (Meriones unguiculatus). Parasitology Open, 2019, 5, .	0.9	6
442	lncRNA expression predicts mRNA abundance. Epigenomics, 2019, 11, 1121-1128.	1.0	6
443	Intrinsically disordered proteins and structured proteins with intrinsically disordered regions have different functional roles in the cell. PLoS ONE, 2019, 14, e0217889.	1.1	84
444	Proteomic analysis of cortical neuronal cultures treated with poly-arginine peptide-18 (R18) and exposed to glutamic acid excitotoxicity. Molecular Brain, 2019, 12, 66.	1.3	6
445	Transcriptome Changes in the Alzheimer's Disease Middle Temporal Gyrus: Importance of RNA Metabolism and Mitochondria-Associated Membrane Genes. Journal of Alzheimer's Disease, 2019, 70, 691-713.	1.2	51
446	Proteomic Analysis of Endothelial Cells Exposed to Ultrasmall Nanoparticles Reveals Disruption in Paracellular and Transcellular Transport. Proteomics, 2019, 19, e1800228.	1.3	4
447	Transcriptomics-based screening of molecular signatures associated with patients overall survival and their key regulators in subtypes of breast cancer. Cancer Genetics, 2019, 239, 62-74.	0.2	8
448	A draft genome assembly of the solar-powered sea slug Elysia chlorotica. Scientific Data, 2019, 6, 190022.	2.4	48
449	A Systems-Based Map of Human Brain Cell-Type Enriched Genes and Malignancy-Associated Endothelial Changes. Cell Reports, 2019, 29, 1690-1706.e4.	2.9	22
450	A specific fungal transcription factor controls effector gene expression and orchestrates the establishment of the necrotrophic pathogen lifestyle on wheat. Scientific Reports, 2019, 9, 15884.	1.6	34
451	Human Cerebral Organoids and Fetal Brain Tissue Share Proteomic Similarities. Frontiers in Cell and Developmental Biology, 2019, 7, 303.	1.8	58
452	Effect of Age on the Protein Profile of Healthy Malay Adults and its Association with Cognitive Function Competency. Journal of Alzheimer's Disease, 2019, 70, S43-S62.	1.2	6
453	Insights into pathological mutations in insulin-like growth factor I through in silico screening and molecular dynamics simulation. Journal of Molecular Modeling, 2019, 25, 276.	0.8	1
454	Conservation and divergence of protein pathways in the vertebrate heart. PLoS Biology, 2019, 17, e3000437.	2.6	18
455	HADHA overexpression disrupts lipid metabolism and inhibits tumor growth in clear cell renal cell carcinoma. Experimental Cell Research, 2019, 384, 111558.	1.2	16

#	ARTICLE	IF	CITATIONS
456	DNA Sequencing Technologies. <i>ACM Computing Surveys</i> , 2020, 52, 1-30.	16.1	8
457	Prediction of lymphovascular space invasion in endometrial cancer using the 55-gene signature selected by DNA microarray analysis. <i>PLoS ONE</i> , 2019, 14, e0223178.	1.1	6
458	Lineage specific conservation of cis-regulatory elements in Cytokinin Response Factors. <i>Scientific Reports</i> , 2019, 9, 13387.	1.6	11
459	The Axial Organ and the Pharynx Are Sites of Hematopoiesis in the Sea Urchin. <i>Frontiers in Immunology</i> , 2019, 10, 870.	2.2	25
460	Exome sequencing in genomic regions related to racing performance of Quarter Horses. <i>Journal of Applied Genetics</i> , 2019, 60, 79-86.	1.0	9
461	Serum pyruvate dehydrogenase kinase as a prognostic marker for cholangiocarcinoma. <i>Oncology Letters</i> , 2019, 17, 5275-5282.	0.8	11
462	Investigating function roles of hypothetical proteins encoded by the <i>Mycobacterium tuberculosis</i> H37Rv genome. <i>BMC Genomics</i> , 2019, 20, 394.	1.2	62
463	Cross-linking Proteomics Indicates Effects of Simvastatin on the TLR2 Interactome and Reveals ACTR1A as a Novel Regulator of the TLR2 Signal Cascade. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1732-1744.	2.5	15
464	Computational and artificial neural network based study of functional SNPs of human LEPR protein associated with reproductive function. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 18910-18926.	1.2	5
465	Plasticity of intestinal gene expression profile signatures reflected by nutritional interventions in piglets. <i>BMC Genomics</i> , 2019, 20, 414.	1.2	1
466	Bioinformatics approaches for improving seminal plasma proteome analysis. <i>Theriogenology</i> , 2019, 137, 43-49.	0.9	2
467	Integrated proteomics and metabolomics analysis reveals differential lipid metabolism in human umbilical vein endothelial cells under high and low shear stress. <i>American Journal of Physiology - Cell Physiology</i> , 2019, 317, C326-C338.	2.1	21
468	A network pharmacology approach to investigate the pharmacological effect of curcumin and capsaicin targets in cancer angiogenesis by module-based PPI network analysis. <i>Journal of Proteins and Proteomics</i> , 2019, 10, 109-120.	1.0	5
469	Altered Expression and Localization of Tumor Suppressive E3 Ubiquitin Ligase SMURF2 in Human Prostate and Breast Cancer. <i>Cancers</i> , 2019, 11, 556.	1.7	19
470	<i>Arabidopsis mlo3</i> mutant plants exhibit spontaneous callose deposition and signs of early leaf senescence. <i>Plant Molecular Biology</i> , 2019, 101, 21-40.	2.0	16
471	Porcine Epidemic Diarrhea Virus (PEDV) ORF3 Interactome Reveals Inhibition of Virus Replication by Cellular VPS36 Protein. <i>Viruses</i> , 2019, 11, 382.	1.5	15
472	Sperm functional aspects and enriched proteomic pathways of seminal plasma of adult men with obesity. <i>Andrology</i> , 2019, 7, 341-349.	1.9	26
473	Shared Gene Expression Between Multiple Sclerosis and Ischemic Stroke. <i>Frontiers in Genetics</i> , 2018, 9, 598.	1.1	9

#	ARTICLE	IF	CITATIONS
474	Data Science Driven Drug Repurposing for Metabolic Disorders. , 2019, , 191-227.		7
475	Secreting oviduct epithelial cells of <i>Coturnix coturnix japonica</i> (QOEC) and changes to their proteome after nonviral transfection. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 12724-12739.	1.2	3
476	Exploring the genetics of trotting racing ability in horses using a unique Nordic horse model. <i>BMC Genomics</i> , 2019, 20, 104.	1.2	4
477	A Therapeutic Strategy for Chemotherapy-Resistant Gastric Cancer via Destabilization of Both $\beta$ -Catenin and RAS. <i>Cancers</i> , 2019, 11, 496.	1.7	9
478	A chromosome-scale genome assembly and dense genetic map for <i>Xenopus tropicalis</i> . <i>Developmental Biology</i> , 2019, 452, 8-20.	0.9	43
479	Invertebrate Models for Hyperthermia: What We Learned From <i>Caenorhabditis elegans</i> and <i>Hydra vulgaris</i> . , 2019, , 229-264.		2
480	Differential DNA Methylation and Network Analysis in Schizophrenia. , 2019, , 121-129.		2
481	Shedding Light on the Interaction of Human Anti-Apoptotic Bcl-2 Protein with Ligands through Biophysical and in Silico Studies. <i>International Journal of Molecular Sciences</i> , 2019, 20, 860.	1.8	25
482	Investigating skewness to understand gene expression heterogeneity in large patient cohorts. <i>BMC Bioinformatics</i> , 2019, 20, 668.	1.2	12
483	Quantitative Proteomics Reveal Peroxiredoxin Perturbation Upon Persistent Lymphocytic Choriomeningitis Virus Infection in Human Cells. <i>Frontiers in Microbiology</i> , 2019, 10, 2438.	1.5	7
484	Next generation sequencing and RNA-seq characterization of adipose tissue in the Nile crocodile ( <i>Crocodylus niloticus</i> ) in South Africa: Possible mechanism(s) of pathogenesis and pathophysiology of pansteatitis. <i>PLoS ONE</i> , 2019, 14, e0225073.	1.1	3
485	Abscisic Acid Represses Rice Lamina Joint Inclination by Antagonizing Brassinosteroid Biosynthesis and Signaling. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4908.	1.8	18
486	Systematic exploration of predicted destabilizing nonsynonymous single nucleotide polymorphisms (nsSNPs) of human aldehyde oxidase: A Bioinformatics study. <i>Pharmacology Research and Perspectives</i> , 2019, 7, e00538.	1.1	9
487	Muscle transcriptome resource for growth, lipid metabolism and immune system in Hilsa shad, <i>Tenualosa ilisha</i> . <i>Genes and Genomics</i> , 2019, 41, 1-15.	0.5	5
488	Transcriptomic Analysis Reveals Sex-Dependent Expression Patterns in the Basolateral Amygdala of Dominant and Subordinate Animals After Acute Social Conflict. <i>Molecular Neurobiology</i> , 2019, 56, 3768-3779.	1.9	17
489	Daily Regulation of Phototransduction, Circadian Clock, DNA Repair, and Immune Gene Expression by Heme Oxygenase in the Retina of <i>Drosophila</i> . <i>Genes</i> , 2019, 10, 6.	1.0	15
490	Using OmicsNet for Network Integration and 3D Visualization. <i>Current Protocols in Bioinformatics</i> , 2019, 65, e69.	25.8	44
491	Adaptation of Proteins to the Cold in Antarctic Fish: A Role for Methionine?. <i>Genome Biology and Evolution</i> , 2019, 11, 220-231.	1.1	25

#	ARTICLE	IF	CITATIONS
492	Formatting biological big data for modern machine learning in drug discovery. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2019, 9, e1408.	6.2	17
493	Identification and characterization of the zebra finch ( <i>Taeniopygia guttata</i> ) sperm proteome. <i>Journal of Proteomics</i> , 2019, 193, 192-204.	1.2	10
494	PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. <i>Nucleic Acids Research</i> , 2019, 47, D419-D426.	6.5	2,455
495	Combined proteomic and metabolomic analyses of cerebrospinal fluid from mice with ischemic stroke reveals the effects of a Buyang Huanwu decoction in neurodegenerative disease. <i>PLoS ONE</i> , 2019, 14, e0209184.	1.1	24
496	Functional pathways associated with human carotid atheroma: a proteomics analysis. <i>Hypertension Research</i> , 2019, 42, 362-373.	1.5	8
497	Unique Transcriptional Architecture in Airway Epithelial Cells and Macrophages Shapes Distinct Responses following Influenza Virus Infection Ex Vivo. <i>Journal of Virology</i> , 2019, 93, .	1.5	19
498	OrthoInspector 3.0: open portal for comparative genomics. <i>Nucleic Acids Research</i> , 2019, 47, D411-D418.	6.5	46
499	Ancestral Genomes: a resource for reconstructed ancestral genes and genomes across the tree of life. <i>Nucleic Acids Research</i> , 2019, 47, D271-D279.	6.5	17
500	SATrans: New Free Available Software for Annotation of Transcriptome and Functional Analysis of Differentially Expressed Genes. <i>Journal of Computational Biology</i> , 2019, 26, 117-123.	0.8	1
501	Genome-wide differential $\text{scp}$ DNA $\text{scp}$ methylation in tropically adapted Creole cattle and their Iberian ancestors. <i>Animal Genetics</i> , 2019, 50, 15-26.	0.6	32
502	Parallel evolution of gene classes, but not genes: Evidence from Hawai'ian honeycreeper populations exposed to avian malaria. <i>Molecular Ecology</i> , 2019, 28, 568-583.	2.0	26
503	New substrates and interactors of the mycobacterial Serine/Threonine protein kinase PknG identified by a tailored interactomic approach. <i>Journal of Proteomics</i> , 2019, 192, 321-333.	1.2	30
504	A review study: Computational techniques for expecting the impact of non-synonymous single nucleotide variants in human diseases. <i>Gene</i> , 2019, 680, 20-33.	1.0	47
505	Adipose tissue mitochondrial dysfunction in human obesity is linked to a specific DNA methylation signature in adipose-derived stem cells. <i>International Journal of Obesity</i> , 2019, 43, 1256-1268.	1.6	47
506	Critical period inhibition of NKCC1 rectifies synapse plasticity in the somatosensory cortex and restores adult tactile response maps in fragile X mice. <i>Molecular Psychiatry</i> , 2019, 24, 1732-1747.	4.1	46
507	Bayesian generalized biclustering analysis via adaptive structured shrinkage. <i>Biostatistics</i> , 2020, 21, 610-624.	0.9	10
508	Maternal choline supplementation ameliorates Alzheimer's disease pathology by reducing brain homocysteine levels across multiple generations. <i>Molecular Psychiatry</i> , 2020, 25, 2620-2629.	4.1	54
509	Advancing Pan-cancer Gene Expression Survival Analysis by Inclusion of Non-coding RNA. <i>RNA Biology</i> , 2020, 17, 1666-1673.	1.5	26

#	ARTICLE	IF	CITATIONS
510	Histidine Phosphorylation. <i>Methods in Molecular Biology</i> , 2020, , .	0.4	2
511	NBS-LRR genesâ€”Plant health sentinels: Structure, roles, evolution and biotechnological applications. , 2020, , 63-120.		9
512	Exploring the genetics underpinning dynamic laryngeal collapse associated with poll flexion in Norwegianâ€”Swedish Coldblooded Trotter racehorses. <i>Equine Veterinary Journal</i> , 2020, 52, 174-180.	0.9	3
513	Genes associated with body weight gain and feed intake identified by meta-analysis of the mesenteric fat from crossbred beef steers. <i>PLoS ONE</i> , 2020, 15, e0227154.	1.1	9
514	Are We Meeting the Promise of Endotypes and Precision Medicine in Asthma?. <i>Physiological Reviews</i> , 2020, 100, 983-1017.	13.1	62
515	Cross comparison of seminal plasma proteins from cattle and buffalo ( <i>Bubalus bubalis</i> ). <i>Reproduction in Domestic Animals</i> , 2020, 55, 81-92.	0.6	2
516	The hybrid protein interactome contributes to rice heterosis as epistatic effects. <i>Plant Journal</i> , 2020, 102, 116-128.	2.8	10
517	Interpretation of somatic <i>POLE</i> mutations in endometrial carcinoma. <i>Journal of Pathology</i> , 2020, 250, 323-335.	2.1	203
518	Lowâ€”Dose Aspirin Treatment Attenuates Male Rat Saltâ€”Sensitive Hypertension via Platelet Cyclooxygenase 1 and Complement Cascade Pathway. <i>Journal of the American Heart Association</i> , 2020, 9, e013470.	1.6	15
519	Expression correlation attenuates within and between key signaling pathways in chronic kidney disease. <i>BMC Medical Genomics</i> , 2020, 13, 134.	0.7	9
520	Genome-wide association study reveals novel genetic loci contributing to cold tolerance at the germination stage in indica rice. <i>Plant Science</i> , 2020, 301, 110669.	1.7	11
521	Quantitative proteomic dataset from oro- and naso-pharyngeal swabs used for COVID-19 diagnosis: Detection of viral proteins and host's biological processes altered by the infection. <i>Data in Brief</i> , 2020, 32, 106121.	0.5	25
522	Mutational profiling of POT1 gene and its interaction with TPP1 in cancer- A computational approach. <i>Informatics in Medicine Unlocked</i> , 2020, 20, 100389.	1.9	0
523	In-silico study reveals immunological signaling pathways, their genes, and potential herbal drug targets in ovarian cancer. <i>Informatics in Medicine Unlocked</i> , 2020, 20, 100422.	1.9	15
524	Positive Selection and Gene Expression Analyses from Salivary Glands Reveal Discrete Adaptations within the Ecologically Diverse Bat Family Phyllostomidae. <i>Genome Biology and Evolution</i> , 2020, 12, 1419-1428.	1.1	7
525	Discovering lethal alleles across the turkey genome using a transmission ratio distortion approach. <i>Animal Genetics</i> , 2020, 51, 876-889.	0.6	12
526	Noise Exposures Causing Hearing Loss Generate Proteotoxic Stress and Activate the Proteostasis Network. <i>Cell Reports</i> , 2020, 33, 108431.	2.9	33
527	Rumen epithelial transcriptome and microbiome profiles of rumen epithelium and contents of beef cattle with and without liver abscesses. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	10

#	ARTICLE	IF	CITATIONS
528	Effect of ladostigil treatment of aging rats on gene expression in four brain areas associated with regulation of memory. <i>Neuropharmacology</i> , 2020, 177, 108229.	2.0	8
529	Quantitative Proteomic Changes after Organophosphorous Nerve Agent Exposure in the Rat Hippocampus. <i>ACS Chemical Neuroscience</i> , 2020, 11, 2638-2648.	1.7	5
530	Serum Protein Profiling Reveals a Landscape of Inflammation and Immune Signaling in Early-stage COVID-19 Infection. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1749-1759.	2.5	45
531	BAHCC1 binds H3K27me3 via a conserved BAH module to mediate gene silencing and oncogenesis. <i>Nature Genetics</i> , 2020, 52, 1384-1396.	9.4	57
532	Emerging Biomarkers for Prediction and Early Diagnosis of Necrotizing Enterocolitis in the Era of Metabolomics and Proteomics. <i>Frontiers in Pediatrics</i> , 2020, 8, 602255.	0.9	38
533	Changes in Honey Bee Head Proteome in Response to Dietary 24-Methylenecholesterol. <i>Insects</i> , 2020, 11, 743.	1.0	1
534	Genomically Aided Diagnosis of Severe Developmental Disorders. <i>Annual Review of Genomics and Human Genetics</i> , 2020, 21, 327-349.	2.5	3
535	Classification and functional analyses of putative virulence factors of <i>Mycobacterium tuberculosis</i> : A combined sequence and structure based study. <i>Computational Biology and Chemistry</i> , 2020, 87, 107270.	1.1	0
536	Proteomic data of seminal plasma and spermatozoa of four purebred dogs. <i>Data in Brief</i> , 2020, 30, 105498.	0.5	7
537	Remethylation of <i>Dnmt3a</i> hematopoietic cells is associated with partial correction of gene dysregulation and reduced myeloid skewing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3123-3134.	3.3	27
538	MIPPIE: the mouse integrated protein-protein interaction reference. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	14
539	The mitochondrial protein PGAM5 suppresses energy consumption in brown adipocytes by repressing expression of uncoupling protein 1. <i>Journal of Biological Chemistry</i> , 2020, 295, 5588-5601.	1.6	9
540	Multi-omic analysis of the effects of low frequency ventilation during cardiopulmonary bypass surgery. <i>International Journal of Cardiology</i> , 2020, 309, 40-47.	0.8	1
541	CRISPR-based gene knockout screens reveal deubiquitinases involved in HIV-1 latency in two Jurkat cell models. <i>Scientific Reports</i> , 2020, 10, 5350.	1.6	30
542	Hepatic transcriptome of the freeze-tolerant <i>Copeia</i> 's gray treefrog, <i>Dryophytes chrysoscelis</i> : responses to cold acclimation and freezing. <i>BMC Genomics</i> , 2020, 21, 226.	1.2	17
543	Identification of Blood Circular RNAs as Potential Biomarkers for Acute Ischemic Stroke. <i>Frontiers in Neuroscience</i> , 2020, 14, 81.	1.4	34
544	Investigation of spectroscopic and proteomic alterations underlying prostate carcinogenesis. <i>Journal of Proteomics</i> , 2020, 226, 103888.	1.2	7
545	Gibberellin recovers seed germination in rice with impaired brassinosteroid signalling. <i>Plant Science</i> , 2020, 293, 110435.	1.7	41

#	ARTICLE	IF	CITATIONS
546	Using SNP Weights Derived From Gene Expression Modules to Improve GWAS Power for Feed Efficiency in Pigs. <i>Frontiers in Genetics</i> , 2019, 10, 1339.	1.1	11
547	Rigorous characterization of urinary extracellular vesicles (uEVs) in the low centrifugation pellet - a neglected source for uEVs. <i>Scientific Reports</i> , 2020, 10, 3701.	1.6	45
548	Salmonella enterica Serovar Typhi exposure elicits deliberate physiological alterations and triggers the involvement of ubiquitin mediated proteolysis pathway in <i>Caenorhabditis elegans</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 149, 215-233.	3.6	8
549	Gene Expression in Patient-Derived Neural Progenitors Implicates WNT5A Signaling in the Etiology of Schizophrenia. <i>Biological Psychiatry</i> , 2020, 88, 236-247.	0.7	28
550	The regulatory function of dIno80 correlates with its DNA binding activity. <i>Gene</i> , 2020, 732, 144368.	1.0	1
551	Cytoprotective Effect of Ascorbic Acid and Rutin against Oxidative Changes in the Proteome of Skin Fibroblasts Cultured in a Three-Dimensional System. <i>Nutrients</i> , 2020, 12, 1074.	1.7	30
552	Milk lactoperoxidase decreases ID1 and ID3 expression in human oral squamous cell carcinoma cell lines. <i>Scientific Reports</i> , 2020, 10, 5836.	1.6	4
553	A Phenotypic Characterization of Two Isolates of a Multidrug-Resistant Outbreak Strain of <i>Mycobacterium tuberculosis</i> with Opposite Epidemiological Fitness. <i>BioMed Research International</i> , 2020, 2020, 1-9.	0.9	2
554	Transcriptional Profiling of the Adult Hair Follicle Mesenchyme Reveals R-spondin as a Novel Regulator of Dermal Progenitor Function. <i>IScience</i> , 2020, 23, 101019.	1.9	31
555	Colony-level pesticide exposure affects honey bee ( <i>Apis mellifera</i> L.) royal jelly production and nutritional composition. <i>Chemosphere</i> , 2021, 263, 128183.	4.2	37
556	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. <i>Nucleic Acids Research</i> , 2021, 49, D1452-D1463.	6.5	83
557	FunRich enables enrichment analysis of OMICs datasets. <i>Journal of Molecular Biology</i> , 2021, 433, 166747.	2.0	144
558	Deferoxamine mesylate improves splicing and GAA activity of the common c.-32-13T>G allele in late-onset PD patient fibroblasts. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 20, 227-236.	1.8	5
559	Identification and Downstream Analyses of Domains Amplified in Plant Genomes: The Case of StAR-Related Lipid Transfer (START) Domains in Rice. <i>Methods in Molecular Biology</i> , 2021, 2238, 325-338.	0.4	1
561	Bayesian parameter estimation for automatic annotation of gene functions using observational data and phylogenetic trees. <i>PLoS Computational Biology</i> , 2021, 17, e1007948.	1.5	0
562	Proteomics Approach of Rapamycin Anti-Tumoral Effect on Primary and Metastatic Canine Mammary Tumor Cells In Vitro. <i>Molecules</i> , 2021, 26, 1213.	1.7	2
563	Latent trait modeling of tau neuropathology in progressive supranuclear palsy. <i>Acta Neuropathologica</i> , 2021, 141, 667-680.	3.9	5
564	The regulatory enzymes and protein substrates for the lysine $\epsilon^2$ -hydroxybutyrylation pathway. <i>Science Advances</i> , 2021, 7, .	4.7	87



#	ARTICLE	IF	CITATIONS
565	SMURF2-mediated ubiquitin signaling plays an essential role in the regulation of PARP1 PARylating activity, molecular interactions, and functions in mammalian cells. <i>FASEB Journal</i> , 2021, 35, e21436.	0.2	4
566	Extracellular vesicle microRNA in early versus late pregnancy with birth outcomes in the MADRES study. <i>Epigenetics</i> , 2022, 17, 269-285.	1.3	14
567	Editor's introduction to this issue (Genomics and Informatics, 2021, 19, e1).	0.4	2
569	The Transposable Element Environment of Human Genes Differs According to Their Duplication Status and Essentiality. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	1
570	Knock out of specific maternal vitellogenins in zebrafish ( <i>Danio rerio</i> ) evokes vital changes in egg proteomic profiles that resemble the phenotype of poor quality eggs. <i>BMC Genomics</i> , 2021, 22, 308.	1.2	14
572	In-Silico Study of Immune System Associated Genes in Case of Type-2 Diabetes With Insulin Action and Resistance, and/or Obesity. <i>Frontiers in Endocrinology</i> , 2021, 12, 641888.	1.5	17
575	MetaGSCA: A tool for meta-analysis of gene set differential coexpression. <i>PLoS Computational Biology</i> , 2021, 17, e1008976.	1.5	2
576	Chromosomal instability by mutations in the novel minor spliceosome component <i>CENATAC</i> . <i>EMBO Journal</i> , 2021, 40, e106536.	3.5	26
577	Proteomic analysis of human frontal and temporal cortex using iTRAQ-based 2D LC-MS/MS. <i>Chinese Neurosurgical Journal</i> , 2021, 7, 27.	0.3	2
578	<i>ABCA1</i> , <i>TCF7</i> , <i>NFATC1</i> , <i>PRKCZ</i> , and <i>PDGFA</i> DNA methylation as potential epigenetic-sensitive targets in acute coronary syndrome via network analysis. <i>Epigenetics</i> , 2022, 17, 547-563.	1.3	9
579	In silico analysis and prediction of transcription factors of the proteins interacting with astrocyte elevated gene-1. <i>Computational Biology and Chemistry</i> , 2021, 92, 107478.	1.1	3
580	Levetiracetam Treatment Normalizes Levels of Presynaptic Endocytosis Machinery and Restores Nonamyloidogenic APP Processing in <i>App</i> Knock-in Mice. <i>Journal of Proteome Research</i> , 2021, 20, 3580-3589.	1.8	9
581	A protein interactions map of multiple organ systems associated with COVID-19 disease. <i>Genomics and Informatics</i> , 2021, 19, e14.	0.4	2
582	RNA editing affects cis-regulatory elements and predicts adverse cancer survival. <i>Cancer Medicine</i> , 2021, 10, 6114-6127.	1.3	5
583	Bothrops Jararaca Snake Venom Modulates Key Cancer-Related Proteins in Breast Tumor Cell Lines. <i>Toxins</i> , 2021, 13, 519.	1.5	5
584	Proteome remodeling in the <i>Mycobacterium tuberculosis</i> PknG knockout: Molecular evidence for the role of this kinase in cell envelope biogenesis and hypoxia response. <i>Journal of Proteomics</i> , 2021, 244, 104276.	1.2	6
585	Employing bioinformatics analysis to identify hub genes and microRNAs involved in colorectal cancer. <i>Medical Oncology</i> , 2021, 38, 114.	1.2	11
586	A chromosome-level genome assembly of the striped catfish ( <i>Pangasianodon hypophthalmus</i> ). <i>Genomics</i> , 2021, 113, 3349-3356.	1.3	18

#	ARTICLE	IF	CITATIONS
587	Gonadotropin-releasing hormone receptor pathway affects the function of human EBV-transformed B lymphocytes in an age-independent way. <i>Experimental Gerontology</i> , 2021, 152, 111471.	1.2	1
590	Understanding the role of potential pathways and its components including hypoxia and immune system in case of oral cancer. <i>Scientific Reports</i> , 2021, 11, 19576.	1.6	16
591	Metformin inhibits polyphosphate-induced hyper-permeability and inflammation. <i>International Immunopharmacology</i> , 2021, 99, 107937.	1.7	5
592	Liquid Chromatography and Tandem Mass Spectrometry in Label-Free of Zebrafish ( <i>Danio rerio</i> ) Eggs. <i>Methods in Molecular Biology</i> , 2021, 2218, 277-290.	0.4	1
593	Striatal RGS7 Regulates Depression-Related Behaviors and Stress-Induced Reinstatement of Cocaine Conditioned Place Preference. <i>ENeuro</i> , 2021, 8, ENEURO.0365-20.2020.	0.9	7
594	Bioinformatics Methods to Deduce Biological Interpretation from Proteomics Data. <i>Methods in Molecular Biology</i> , 2017, 1549, 147-161.	0.4	2
595	Functional Interaction Network Construction and Analysis for Disease Discovery. <i>Methods in Molecular Biology</i> , 2017, 1558, 235-253.	0.4	96
596	Generation and Interpretation of Context-Specific Human Protein-Protein Interaction Networks with HIPPIE. <i>Methods in Molecular Biology</i> , 2020, 2074, 135-144.	0.4	4
597	The <i>C. difficile</i> toxin B membrane translocation machinery is an evolutionarily conserved protein delivery apparatus. <i>Nature Communications</i> , 2020, 11, 432.	5.8	20
598	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
599	LegumelP V3: from models to crops—an integrative gene discovery platform for translational genomics in legumes. <i>Nucleic Acids Research</i> , 2021, 49, D1472-D1479.	6.5	25
614	Prognostic value and co-expression patterns of metabolic pathways in cancers. <i>BMC Genomics</i> , 2020, 21, 860.	1.2	5
615	Dynamic transcriptome changes during adipose tissue energy expenditure reveal critical roles for long noncoding RNA regulators. <i>PLoS Biology</i> , 2017, 15, e2002176.	2.6	81
616	TFAP2 paralogs regulate melanocyte differentiation in parallel with MITF. <i>PLoS Genetics</i> , 2017, 13, e1006636.	1.5	78
617	Identification of RNA Binding Proteins Associated with Dengue Virus RNA in Infected Cells Reveals Temporally Distinct Host Factor Requirements. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004921.	1.3	56
618	Comparison of monocyte gene expression among patients with neurocysticercosis-associated epilepsy, Idiopathic Epilepsy and idiopathic headaches in India. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005664.	1.3	9
619	Machine Learning of Protein Interactions in Fungal Secretory Pathways. <i>PLoS ONE</i> , 2016, 11, e0159302.	1.1	7
620	The Influenza Virus Protein PB1-F2 Increases Viral Pathogenesis through Neutrophil Recruitment and NK Cells Inhibition. <i>PLoS ONE</i> , 2016, 11, e0165361.	1.1	33

#	ARTICLE	IF	CITATIONS
621	Combination treatment with 6-mercaptopurine and allopurinol in HepG2 and HEK293 cells – Effects on gene expression levels and thiopurine metabolism. PLoS ONE, 2017, 12, e0173825.	1.1	6
622	Enhancement of Arabidopsis growth characteristics using genome interrogation with artificial transcription factors. PLoS ONE, 2017, 12, e0174236.	1.1	7
623	Characterization of basal and lipopolysaccharide-induced microRNA expression in equine peripheral blood mononuclear cells using Next-Generation Sequencing. PLoS ONE, 2017, 12, e0177664.	1.1	7
624	Gene signature associated with benign neurofibroma transformation to malignant peripheral nerve sheath tumors. PLoS ONE, 2017, 12, e0178316.	1.1	3
625	PpTFDB: A pigeonpea transcription factor database for exploring functional genomics in legumes. PLoS ONE, 2017, 12, e0179736.	1.1	13
626	Genomic and transcriptomic comparison of allergen and silver nanoparticle-induced mast cell degranulation reveals novel non-immunoglobulin E mediated mechanisms. PLoS ONE, 2018, 13, e0193499.	1.1	12
627	Honey can repairing damage of liver tissue due to protein energy malnutrition through induction of endogenous stem cells. Veterinary World, 2017, 10, 711-715.	0.7	12
628	TU-Tagging: A Method for Identifying Layer-Enriched Neuronal Genes in Developing Mouse Visual Cortex. ENeuro, 2017, 4, ENEURO.0181-17.2017.	0.9	13
629	DEVELOPMENT OF METHODS FOR AUTOMATIC EXTRACTION OF KNOWLEDGE FROM TEXTS OF SCIENTIFIC PUBLICATIONS FOR THE CREATION OF A KNOWLEDGE BASE SOLANUM TUBEROSUM. Sel'skokhozyaistvennaya Biologiya, 2017, 52, 63-74.	0.1	4
630	Gene Ontology: A Resource for Analysis and Interpretation of Alzheimer's Disease Data. , 0, , 23-36.		9
631	Construction and evaluation of yeast expression networks by database-guided predictions. Microbial Cell, 2016, 3, 236-247.	1.4	7
632	<i>In silico</i> predicted structural and functional insights of all missense mutations on 2B domain of <i>K1/K10</i> causing genodermatoses. Oncotarget, 2016, 7, 52766-52780.	0.8	5
633	Comparative proteomics of a model MCF10A-KRasG12V cell line reveals a distinct molecular signature of the KRasG12V cell surface. Oncotarget, 2016, 7, 86948-86971.	0.8	23
634	Characterization of urinary extracellular vesicle proteins in muscle-invasive bladder cancer. Oncotarget, 2017, 8, 91199-91208.	0.8	51
635	Host cell transcriptome modification upon exogenous HPV16 L2 protein expression. Oncotarget, 2017, 8, 90730-90747.	0.8	2
636	Genetic identification and molecular modeling characterization reveal a novel <i>PROM1</i> mutation in Stargardt4-like macular dystrophy. Oncotarget, 2018, 9, 122-141.	0.8	32
637	A Bioinformatics Pipeline for Whole Exome Sequencing: Overview of the Processing and Steps from Raw Data to Downstream Analysis. Bio-protocol, 2018, 8, .	0.2	6
638	Targeted Gene Sequencing of Gallbladder Carcinoma Identifies High-impact Somatic and Rare Germline Mutations. Cancer Genomics and Proteomics, 2017, 14, 495-506.	1.0	11

#	ARTICLE	IF	CITATIONS
639	<i>Fasciola hepatica</i> isolates induce different immune responses in unmaturation bovine macrophages. <i>Journal of Veterinary Research (Poland)</i> , 2019, 63, 63-70.	0.3	5
640	Characterization of exosomes from body fluids of dairy cows. <i>Journal of Animal Science</i> , 2017, 95, 3893.	0.2	28
641	Similarities and Differences in Extracellular Vesicle Profiles between Ischaemic Stroke and Myocardial Infarction. <i>Biomedicines</i> , 2021, 9, 8.	1.4	16
642	The IFN Response in Bats Displays Distinctive IFN-Stimulated Gene Expression Kinetics with Atypical RNASEL Induction. <i>Journal of Immunology</i> , 2018, 200, 209-217.	0.4	73
643	Proteomic profile of follicular fluid from patients with polycystic ovary syndrome (PCOS) submitted to in vitro fertilization (IVF) compared to oocyte donors. <i>Jornal Brasileiro De Reproducao Assistida</i> , 2019, 23, 367-391.	0.3	9
644	In silico Meta-Analysis of Circulatory microRNAs in Prostate Cancer. <i>Journal of Analytical Oncology</i> , 2017, 6, 107-116.	0.1	1
645	Direct screening for chromatin status on DNA barcodes in yeast delineates the regulome of H3K79 methylation by Dot1. <i>ELife</i> , 2016, 5, .	2.8	22
646	Atrophia controls developmental signaling pathways via interactions with Trithorax-like. <i>ELife</i> , 2017, 6, .	2.8	15
647	Insights into electrosensory organ development, physiology and evolution from a lateral line-enriched transcriptome. <i>ELife</i> , 2017, 6, .	2.8	38
648	Robust manipulation of the behavior of <i>Drosophila melanogaster</i> by a fungal pathogen in the laboratory. <i>ELife</i> , 2018, 7, .	2.8	58
649	Genome-wide quantification of the effects of DNA methylation on human gene regulation. <i>ELife</i> , 2018, 7, .	2.8	96
650	Changes in mRNA abundance drive shuttling of RNA binding proteins, linking cytoplasmic RNA degradation to transcription. <i>ELife</i> , 2018, 7, .	2.8	85
651	Genetic and environmental perturbations lead to regulatory decoherence. <i>ELife</i> , 2019, 8, .	2.8	34
652	Dynamics and genetic diversification of <i>Escherichia coli</i> during experimental adaptation to an anaerobic environment. <i>PeerJ</i> , 2017, 5, e3244.	0.9	14
653	Integrated Proteotranscriptomics of Human Myometrium in Labor Landscape Reveals the Increased Molecular Associated With Inflammation Under Hypoxia Stress. <i>Frontiers in Immunology</i> , 2021, 12, 722816.	2.2	14
654	Population genomic, olfactory, dietary, and gut microbiota analyses demonstrate the unique evolutionary trajectory of feral pigs. <i>Molecular Ecology</i> , 2022, 31, 220-237.	2.0	16
655	A GO catalogue of human DNA-binding transcription factors. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194765.	0.9	15
656	Computational algorithmic and molecular dynamics study of functional and structural impacts of non-synonymous single nucleotide polymorphisms in human DHFR gene. <i>Computational Biology and Chemistry</i> , 2021, 95, 107587.	1.1	2

#	ARTICLE	IF	CITATIONS
681	Identification of Candidate Genes Responsible for Age-Related Macular Degeneration Using Microarray Data. , 2019, , 969-1001.		0
682	Purification and Proteomic Analysis of Alphavirus Particles from Sindbis Virus Grown in Mammalian and Insect Cells. Bio-protocol, 2019, 9, e3239.	0.2	1
684	A Systems-Based Map of Human Brain Cell-Type Enriched Genes and Malignancy-Associated Endothelial Changes. SSRN Electronic Journal, 0, , .	0.4	0
692	Proteome Bioinformatics Methods for Studying Histidine Phosphorylation. Methods in Molecular Biology, 2020, 2077, 237-250.	0.4	0
693	Transcriptome analysis revealed that delaying first colostrum feeding postponed ileum immune system development of neonatal calves. Genomics, 2021, 113, 4116-4125.	1.3	1
694	Gene Expression Profiling of Early Acute Febrile Stage of Dengue Infection and Its Comparative Analysis With Streptococcus pneumoniae Infection. Frontiers in Cellular and Infection Microbiology, 2021, 11, 707905.	1.8	11
696	Discovering Biomarkers in Parkinsonâ€™s Disease Using Module Correspondence and Pathway Information. Advances in Intelligent Systems and Computing, 2021, , 249-261.	0.5	1
697	Microarray expression profiling identifies genes, including cytokines, and biofunctions, as diapedesis, associated with a brain metastasis from a papillary thyroid carcinoma. American Journal of Cancer Research, 2016, 6, 2140-2161.	1.4	10
698	MK2a inhibitor CMPD1 abrogates chikungunya virus infection by modulating actin remodeling pathway. PLoS Pathogens, 2021, 17, e1009667.	2.1	7
699	Bidirectional Introgression between <i>Mus musculus domesticus</i> and <i>Mus spretus</i> . Genome Biology and Evolution, 2022, 14, .	1.1	11
700	In-silico profiling of SLC6A19, for identification of deleterious ns-SNPs to enhance the Hartnup disease diagnosis. Computational Toxicology, 2022, 22, 100215.	1.8	0
701	<i>In silico</i> assessment of DNA damage response gene variants associated with head and neck cancer. Journal of Biomolecular Structure and Dynamics, 2023, 41, 2090-2107.	2.0	1
702	Trafficking-defective mutant PROKR2 cycles between endoplasmic reticulum and Golgi to attenuate endoplasmic reticulum stress. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	2
703	MonaGO: a novel gene ontology enrichment analysis visualisation system. BMC Bioinformatics, 2022, 23, 69.	1.2	12
705	The Emerging Role of E3 Ubiquitin Ligase SMURF2 in the Regulation of Transcriptional Co-Repressor KAP1 in Untransformed and Cancer Cells and Tissues. Cancers, 2022, 14, 1607.	1.7	2
706	The E3 ubiquitin ligase SMURF2 stabilizes RNA editase ADAR1p110 and promotes its adenosine-to-inosine (A-to-I) editing function. Cellular and Molecular Life Sciences, 2022, 79, 237.	2.4	2
737	Multi-staged gene expression profiling reveals potential genes and the critical pathways in kidney cancer. Scientific Reports, 2022, 12, 7240.	1.6	10
740	A human adipose tissue cell-type transcriptome atlas. Cell Reports, 2022, 40, 111046.	2.9	30

#	ARTICLE	IF	CITATIONS
742	Comprehensive Multiomics Analysis Reveals Potential Diagnostic and Prognostic Biomarkers in Adrenal Cortical Carcinoma. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-33.	0.7	0
743	Transformer Neural Networks for Protein Family and Interaction Prediction Tasks. <i>Journal of Computational Biology</i> , 2023, 30, 95-111.	0.8	3
744	Synthesis of Silver Nano Particles Using Myricetin and the In-Vitro Assessment of Anti-Colorectal Cancer Activity: In-Silico Integration. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11024.	1.8	11
745	Gene expression of axenically-isolated clinical <i>Entamoeba histolytica</i> strains and its impact on disease severity of amebiasis. <i>PLoS Pathogens</i> , 2022, 18, e1010880.	2.1	5
746	Spatiotemporal dynamics of the tomato fruit transcriptome under prolonged water stress. <i>Plant Physiology</i> , 2022, 190, 2557-2578.	2.3	6
748	Propagation, detection and correction of errors using the sequence database network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	6
749	Glutamyl-prolyl-tRNA synthetase 1 coordinates early endosomal anti-inflammatory AKT signaling. <i>Nature Communications</i> , 2022, 13, .	5.8	1
751	Proteomic characterization of spinal cord synaptoneuroosomes from Tg-SOD1/G93A mice supports a role for MNK1 and local translation in the early stages of amyotrophic lateral sclerosis. <i>Molecular and Cellular Neurosciences</i> , 2022, 123, 103792.	1.0	1
752	Ai>ç curated collection of human vaccination response signatures. <i>Scientific Data</i> , 2022, 9, .	2.4	3
753	Elaborating the Functional Roles of a Leucine-Rich Repeat Protein from &lt;i>Arabidopsis thaliana&lt;/i>. <i>American Journal of Plant Sciences</i> , 2022, 13, 1381-1401.	0.3	0
754	Salmonella Typhimurium induces genome-wide expression and phosphorylation changes that modulate immune response, intracellular survival and vesicle transport in infected neutrophils. <i>Developmental and Comparative Immunology</i> , 2023, 140, 104597.	1.0	4
755	Potential target identification for osteosarcoma treatment: Gene expression re-analysis and drug repurposing. <i>Gene</i> , 2023, 856, 147106.	1.0	0
756	Genomic profiling and network-level understanding uncover the potential genes and the pathways in hepatocellular carcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
757	An Approach for Systems-Level Understanding of Prostate Cancer from High-Throughput Data Integration to Pathway Modeling and Simulation. <i>Cells</i> , 2022, 11, 4121.	1.8	7
758	Transcriptome analysis of the binucleate ciliate <i>Tetrahymena thermophila</i> with asynchronous nuclear cell cycles. <i>Molecular Biology of the Cell</i> , 2023, 34, .	0.9	3
759	Role of ZNF143 and Its Association with Gene Expression Patterns, Noncoding Mutations, and the Immune System in Human Breast Cancer. <i>Life</i> , 2023, 13, 27.	1.1	1
760	Interrogation of an ovine serum peptide spectral library to annotate ambiguous clinicopathological biomarkers using data-independent acquisition. <i>F1000Research</i> , 0, 11, 1433.	0.8	0
761	Transcriptome profiling reveals the underlying mechanism of grape post-harvest pathogen <i>Penicillium olsonii</i> against the metabolites of <i>Bacillus velezensis</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2

#	ARTICLE	IF	CITATIONS
762	Molecular Pathways of Diabetic Kidney Disease Inferred from Proteomics. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 0, Volume 16, 117-128.	1.1	1
765	Genome-wide association study reveals novel genetic loci involved in anaerobic germination tolerance in <i>Indica</i> rice. <i>Molecular Breeding</i> , 2023, 43, .	1.0	1
766	Genome-Wide Prediction of Disease Resistance Gene Analogs in Flax. <i>Compendium of Plant Genomes</i> , 2023, , 217-233.	0.3	0
767	Dysregulation of metalloproteins in ischemic heart disease patients with systolic dysfunction. <i>International Journal of Biological Macromolecules</i> , 2023, 232, 123435.	3.6	2
768	A complex genomic architecture underlies reproductive isolation in a North American oriole hybrid zone. <i>Communications Biology</i> , 2023, 6, .	2.0	0
769	ProteInfer, deep neural networks for protein functional inference. <i>ELife</i> , 0, 12, .	2.8	31
770	Predictive analytics with multiomics data. , 2023, , 171-183.		0