PANTHER in 2013: modeling the evolution of gene funct the context of phylogenetic trees

Nucleic Acids Research

41, D377-D386

DOI: 10.1093/nar/gks1118

#	ARTICLE	IF	CITATIONS
1	RNAseq versus genome-predicted transcriptomes: a large population of novel transcripts identified in an Illumina-454 Hydra transcriptome. BMC Genomics, 2013, 14, 204.	1.2	61
2	Large-scale gene function analysis with the PANTHER classification system. Nature Protocols, 2013, 8, 1551-1566.	5.5	2,276
3	Proteomic techniques for characterisation of mesenchymal stem cell secretome. Biochimie, 2013, 95, 2196-2211.	1.3	231
4	The evolution of lineage-specific clusters of single nucleotide substitutions in the human genome. Molecular Phylogenetics and Evolution, 2013, 69, 276-285.	1.2	3
5	Tethering preferences of domain families co-occurring in multi-domain proteins. Molecular BioSystems, 2013, 9, 1708.	2.9	1
6	On Identifying and Analyzing Significant Nodes in Protein-Protein Interaction Networks. , 2013, , .		1
7	Exploring the role of post-translational modifications on proteinâ€“protein interactions with survivin. Archives of Biochemistry and Biophysics, 2013, 538, 64-70.	1.4	25
8	Web Apollo: a web-based genomic annotation editing platform. Genome Biology, 2013, 14, R93.	13.9	329
9	Role of genomic architecture in the expression dynamics of long noncoding RNAs during differentiation of human neuroblastoma cells. BMC Systems Biology, 2013, 7, S11.	3.0	24
10	Conversion of KEGG metabolic pathways to SBGN maps including automatic layout. BMC Bioinformatics, 2013, 14, 250.	1.2	13
11	A systems biology approach using metabolomic data reveals genes and pathways interacting to modulate divergent growth in cattle. BMC Genomics, 2013, 14, 798.	1.2	76
12	Gene variants associated with antisocial behaviour: a latent variable approach. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2013, 54, 1074-1085.	3.1	16
13	Crosstalk between B16 melanoma cells and B-1 lymphocytes induces global changes in tumor cell gene expression. Immunobiology, 2013, 218, 1293-1303.	0.8	11
14	Differential in Gel Electrophoresis (DIGE) Comparative Proteomic Analysis of Macrophages Cell Cultures in Response to Perthamide C Treatment. Marine Drugs, 2013, 11, 1288-1299.	2.2	7
15	Oxidative Bioactivation of Abacavir in Subcellular Fractions of Human Antigen Presenting Cells. Chemical Research in Toxicology, 2013, 26, 1064-1072.	1.7	12
16	Pathway Databases: Making Chemical and Biological Sense of the Genomic Data Flood. Chemistry and Biology, 2013, 20, 629-635.	6.2	20
17	HMPAS: Human Membrane Protein Analysis System. Proteome Science, 2013, 11, S7.	0.7	10
18	SILAC-based phosphoproteomics reveals an inhibitory role of KSR1 in p53 transcriptional activity via modulation of DBC1. British Journal of Cancer, 2013, 109, 2675-2684.	2.9	16

#	ARTICLE	IF	CITATIONS
19	In-depth bioinformatic analysis of lung cancer-associated microRNA targets. Oncology Reports, 2013, 30, 2945-2956.	1.2	4
20	Epigenome-wide profiling identifies significant differences in DNA methylation between matched-pairs of T- and B-lymphocytes from healthy individuals. Epigenetics, 2013, 8, 1188-1197.	1.3	42
21	Genome-wide identification of genes regulated in<i>trans</i>by transposable element small interfering RNAs. RNA Biology, 2013, 10, 1379-1395.	1.5	91
22	TATN-1 Mutations Reveal a Novel Role for Tyrosine as a Metabolic Signal That Influences Developmental Decisions and Longevity in Caenorhabditis elegans. PLoS Genetics, 2013, 9, e1004020.	1.5	41
23	Linking Transcriptional Changes over Time in Stimulated Dendritic Cells to Identify Gene Networks Activated during the Innate Immune Response. PLoS Computational Biology, 2013, 9, e1003323.	1.5	24
24	Systemically Circulating Viral and Tumor-Derived MicroRNAs in KSHV-Associated Malignancies. PLoS Pathogens, 2013, 9, e1003484.	2.1	140
25	Integrated virus-host methylome analysis in head and neck squamous cell carcinoma. Epigenetics, 2013, 8, 953-961.	1.3	31
26	Phosphoproteomicsâ€based network medicine. FEBS Journal, 2013, 280, 5696-5704.	2.2	16
27	Comparing the Chemical Structure and Protein Content of ChEMBL, DrugBank, Human Metabolome Database and the Therapeutic Target Database. Molecular Informatics, 2013, 32, 881-897.	1.4	28
28	Distinctive patterns of DNA methylation associated with Parkinson disease. Epigenetics, 2013, 8, 1030-1038.	1.3	275
29	Nuclear targeting of dystroglycan promotes the expression of androgen regulated transcription factors in prostate cancer. Scientific Reports, 2013, 3, 2792.	1.6	30
30	Complementation Test ofRpe65Knockout and Tvrm148. , 2013, 54, 5111.		9
31	Deep sequencing identifies circulating mouse miRNAs that are functionally implicated in manifestations of aging and responsive to calorie restriction. Aging, 2013, 5, 130-141.	1.4	67
32	Celiac Anti-Type 2 Transglutaminase Antibodies Induce Phosphoproteome Modification in Intestinal Epithelial Caco-2 Cells. PLoS ONE, 2013, 8, e84403.	1.1	13
33	Application of Fluorescence Two-Dimensional Difference In-Gel Electrophoresis as a Proteomic Biomarker Discovery Tool in Muscular Dystrophy Research. Biology, 2013, 2, 1438-1464.	1.3	37
34	Construction of a Public CHO Cell Line Transcript Database Using Versatile Bioinformatics Analysis Pipelines. PLoS ONE, 2014, 9, e85568.	1.1	57
35	FRA2 Is a STAT5 Target Gene Regulated by IL-2 in Human CD4 T Cells. PLoS ONE, 2014, 9, e90370.	1.1	12
36	Comparative 2D-DIGE Proteomic Analysis of Bovine Mammary Epithelial Cells during Lactation Reveals Protein Signatures for Lactation Persistency and Milk Yield. PLoS ONE, 2014, 9, e102515.	1.1	49

#	ARTICLE	IF	CITATIONS
37	Prioritisation and Network Analysis of Crohn's Disease Susceptibility Genes. PLoS ONE, 2014, 9, e108624.	1.1	4
38	Serum Amyloid A and Clusterin as Potential Predictive Biomarkers for Severe Hand, Foot and Mouth Disease by 2D-DIGE Proteomics Analysis. PLoS ONE, 2014, 9, e108816.	1.1	8
39	Genome-Wide Microarray Expression and Genomic Alterations by Array-CGH Analysis in Neuroblastoma Stem-Like Cells. PLoS ONE, 2014, 9, e113105.	1.1	5
40	An RNA Interference Screen for Genes Required to Shape the Anteroposterior Compartment Boundary in Drosophila Identifies the Eph Receptor. PLoS ONE, 2014, 9, e114340.	1.1	22
41	The Role of 8-Oxoguanine DNA Glycosylase-1 in Inflammation. International Journal of Molecular Sciences, 2014, 15, 16975-16997.	1.8	96
42	Defining the nociceptor transcriptome. Frontiers in Molecular Neuroscience, 2014, 7, 87.	1.4	131
43	POEAS: Automated Plant Phenomic Analysis Using Plant Ontology. Bioinformatics and Biology Insights, 2014, 8, BBI.S19057.	1.0	6
44	Databases, Standards, and Modeling Platforms for Systems Biology. , 2014, , 169-182.		0
45	Mycobacterium Tuberculosis Proteome Microarray for Global Studies of Protein Function and Immunogenicity. Cell Reports, 2014, 9, 2317-2329.	2.9	77
46	Genome sequencing and analysis of Mangalica, a fatty local pig of Hungary. BMC Genomics, 2014, 15, 761.	1.2	40
47	Profiling gene promoter occupancy of Sox2 in two phenotypically distinct breast cancer cell subsets using chromatin immunoprecipitation and genome-wide promoter microarrays. Breast Cancer Research, 2014, 16, 470.	2.2	13
48	MOPED 2.5â€"An Integrated Multi-Omics Resource: Multi-Omics Profiling Expression Database Now Includes Transcriptomics Data. OMICS A Journal of Integrative Biology, 2014, 18, 335-343.	1.0	42
49	Mouse genetics and proteomic analyses demonstrate a critical role for complement in a model of DHRD/ML, an inherited macular degeneration. Human Molecular Genetics, 2014, 23, 52-68.	1.4	47
50	Proteomic identification of early changes in the renal cytoskeleton in obstructive uropathy. American Journal of Physiology - Renal Physiology, 2014, 306, F1429-F1441.	1.3	7
51	Transforming Growth Factor-Beta (TGF-<i>Î²</i>) Signaling in Paravertebral Muscles in Juvenile and Adolescent Idiopathic Scoliosis. BioMed Research International, 2014, 2014, 1-14.	0.9	19
52	Big data and other challenges in the quest for orthologs. Bioinformatics, 2014, 30, 2993-2998.	1.8	109
53	Depletion of C3orf1/TIMMDC1 Inhibits Migration and Proliferation in 95D Lung Carcinoma Cells. International Journal of Molecular Sciences, 2014, 15, 20555-20571.	1.8	8
54	Intricate effects of primary motor neuronopathy on contractile proteins and metabolic muscle enzymes as revealed by label-free mass spectrometry. Bioscience Reports, 2014, 34, .	1.1	12

#	ARTICLE	IF	CITATIONS
55	In silico identification of genetic variants in glucocerebrosidase (GBA) gene involved in Gaucher's disease using multiple software tools. Frontiers in Genetics, 2014, 5, 148.	1.1	18
56	SUMOylation of the polycomb group protein L3MBTL2 facilitates repression of its target genes. Nucleic Acids Research, 2014, 42, 3044-3058.	6.5	22
57	HYPERSENSITIVE TO HIGH LIGHT1 Interacts with LOW QUANTUM YIELD OF PHOTOSYSTEM II1 and Functions in Protection of Photosystem II from Photodamage in <i>Arabidopsis</i>. Plant Cell, 2014, 26, 1213-1229.	3.1	87
58	AlgaePath: comprehensive analysis of metabolic pathways using transcript abundance data from next-generation sequencing in green algae. BMC Genomics, 2014, 15, 196.	1.2	36
59	Most parsimonious reconciliation in the presence of gene duplication, loss, and deep coalescence using labeled coalescent trees. Genome Research, 2014, 24, 475-486.	2.4	69
60	An Unbiased Proteomic Screen Reveals Caspase Cleavage Is Positively and Negatively Regulated by Substrate Phosphorylation. Molecular and Cellular Proteomics, 2014, 13, 1184-1197.	2.5	39
61	Data in support of peptidomic analysis of spermatozoa during epididymal maturation. Data in Brief, 2014, 1, 79-84.	0.5	2
62	Pathoproteomics of testicular tissue deficient in the GARP component VPS54: The wobbler mouse model of globozoospermia. Proteomics, 2014, 14, 839-852.	1.3	19
64	Interatrial differences of basal molecular setâ€up and changes in tachycardiaâ€induced heart failureâ€“a proteomic profiling study. European Journal of Heart Failure, 2014, 16, 835-845.	2.9	9
65	Identification of miRâ€494 direct targets involved in senescence of human diploid fibroblasts. FASEB Journal, 2014, 28, 3720-3733.	0.2	34
66	Regulating life or death: Potential role of microRNA in rescue of the corpus luteum. Molecular and Cellular Endocrinology, 2014, 398, 78-88.	1.6	37
67	Mapping genetic modifiers of survival in a mouse model of Dravet syndrome. Genes, Brain and Behavior, 2014, 13, 163-172.	1.1	145
68	Advances in urinary proteome analysis and applications in systems biology. Bioanalysis, 2014, 6, 2549-2569.	0.6	17
69	Analysis of Global Changes in Gene Expression Induced by Human Polynucleotide Phosphorylase (<i>hPNPase^{oldâ€35}</i>). Journal of Cellular Physiology, 2014, 229, 1952-1962.	2.0	9
70	Proteomic identification of potential prognostic biomarkers in resectable pancreatic ductal adenocarcinoma. Proteomics, 2014, 14, 945-955.	1.3	44
71	PP2A inhibition overcomes acquired resistance to HER2 targeted therapy. Molecular Cancer, 2014, 13, 157.	7.9	38
72	From sequence to enzyme mechanism using multi-label machine learning. BMC Bioinformatics, 2014, 15, 150.	1.2	17
73	Genome-wide Twist1 occupancy in endocardial cushion cells, embryonic limb buds, and peripheral nerve sheath tumor cells. BMC Genomics, 2014, 15, 821.	1.2	12

#	ARTICLE	IF	CITATIONS
74	A Comparison of RNA-Seq and Exon Arrays for Whole Genome Transcription Profiling of the L5 Spinal Nerve Transection Model of Neuropathic Pain in the Rat. Molecular Pain, 2014, 10, 1744-8069-10-7.	1.0	75
75	TreeFam v9: a new website, more species and orthology-on-the-fly. Nucleic Acids Research, 2014, 42, D922-D925.	6.5	125
76	Bioprospecting in the Genomic Age. Advances in Applied Microbiology, 2014, 87, 111-146.	1.3	10
77	Entropy-driven partitioning of the hierarchical protein space. Bioinformatics, 2014, 30, i624-i630.	1.8	2
78	Polytomy refinement for the correction of dubious duplications in gene trees. Bioinformatics, 2014, 30, i519-i526.	1.8	18
79	PortEco: a resource for exploring bacterial biology through high-throughput data and analysis tools. Nucleic Acids Research, 2014, 42, D677-D684.	6.5	25
80	Identification of Small Ubiquitin-like Modifier Substrates with Diverse Functions Using the Xenopus Egg Extract System. Molecular and Cellular Proteomics, 2014, 13, 1659-1675.	2.5	12
81	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. Nucleic Acids Research, 2014, 42, D897-D902.	6.5	264
82	Pharmacogenomics of 17-alpha hydroxyprogesterone caproate for recurrent preterm birth prevention. American Journal of Obstetrics and Gynecology, 2014, 210, 321.e1-321.e21.	0.7	23
83	Biological Overlap of Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder: Evidence From Copy Number Variants. Journal of the American Academy of Child and Adolescent Psychiatry, 2014, 53, 761-770.e26.	0.3	105
84	Computational Approaches and Resources in Single Amino Acid Substitutions Analysis Toward Clinical Research. Advances in Protein Chemistry and Structural Biology, 2014, 94, 365-423.	1.0	22
85	H ₂ O ₂ Production in Species of the Lactobacillus acidophilus Group: a Central Role for a Novel NADH-Dependent Flavin Reductase. Applied and Environmental Microbiology, 2014, 80, 2229-2239.	1.4	130
86	Application of Evolutionary Based in Silico Methods to Predict the Impact of Single Amino Acid Substitutions in Vitelliform Macular Dystrophy. Advances in Protein Chemistry and Structural Biology, 2014, 94, 177-267.	1.0	10
87	Systems-Level Analysis of Innate Immunity. Annual Review of Immunology, 2014, 32, 547-577.	9.5	53
88	What's that gene (or protein)? Online resources for exploring functions of genes, transcripts, and proteins. Molecular Biology of the Cell, 2014, 25, 1187-1201.	0.9	13
89	Ensembl Genomes 2013: scaling up access to genome-wide data. Nucleic Acids Research, 2014, 42, D546-D552.	6.5	205
90	An Overview of the Challenges in Designing, Integrating, and Delivering BARD: A Public Chemical-Biology Resource and Query Portal for Multiple Organizations, Locations, and Disciplines. Journal of Biomolecular Screening, 2014, 19, 614-627.	2.6	22
91	Convergent evolution in European and Rroma populations reveals pressure exerted by plague on Toll-like receptors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2668-2673.	3.3	88

#	Article	IF	Citations
92	Effect of deltamethrin (pyrethroid insecticide) on two clones of Daphnia magna (Crustacea,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 T	1.9	30
93	Resources for Functional Genomics Studies in <i>Drosophila melanogaster</i>. Genetics, 2014, 197, 1-18.	1.2	61
94	InterProScan 5: genome-scale protein function classification. Bioinformatics, 2014, 30, 1236-1240.	1.8	6,553
95	<i><scp>DECR</scp>1</i> and <i><scp>ME</scp>1</i> genotypes are associated with lipid composition traits in <scp>D</scp>uroc pigs. Journal of Animal Breeding and Genetics, 2014, 131, 46-52.	0.8	16
96	In-depth Characterization of the Cerebrospinal Fluid (CSF) Proteome Displayed Through the CSF Proteome Resource (CSF-PR). Molecular and Cellular Proteomics, 2014, 13, 3152-3163.	2.5	130
97	Identification of DNA methylation changes at<i>cis</i>-regulatory elements during early steps of HSC differentiation using tagmentation-based whole genome bisulfite sequencing. Cell Cycle, 2014, 13, 3476-3487.	1.3	39
98	Comprehensive Analysis of Stop Codon Usage in Bacteria and Its Correlation with Release Factor Abundance. Journal of Biological Chemistry, 2014, 289, 30334-30342.	1.6	66
99	Inflammatory cytokines, interleukin-1 beta and tumor necrosis factor-alpha, upregulated in glioblastoma multiforme, raise the levels of CRYAB in exosomes secreted by U373 glioma cells. Biochemical and Biophysical Research Communications, 2014, 453, 326-331.	1.0	94
100	Chronic PFOS exposure alters the expression of neuronal development-related human homologues in Eisenia fetida. Ecotoxicology and Environmental Safety, 2014, 110, 288-297.	2.9	10
101	High-throughput single nucleotide variant discovery in E14 mouse embryonic stem cells provides a new reference genome assembly. Genomics, 2014, 104, 121-127.	1.3	13
102	<i>GALNS</i> mutations in Indian patients with mucopolysaccharidosis IVA. American Journal of Medical Genetics, Part A, 2014, 164, 2793-2801.	0.7	31
103	Insights into Three Whole-Genome Duplications Gleaned from the<i>Paramecium caudatum</i>Genome Sequence. Genetics, 2014, 197, 1417-1428.	1.2	67
104	Sex differences in microRNA expression during developmentin rat cortex. Neurochemistry International, 2014, 77, 24-32.	1.9	32
105	Identification of candidate odorant degrading gene/enzyme systems in the antennal transcriptome of Drosophila melanogaster. Insect Biochemistry and Molecular Biology, 2014, 53, 30-43.	1.2	124
106	Proteomic analysis underlines the usefulness of both primary adherent and stem-like cell lines for studying proteins involved in human glioblastoma. Journal of Proteomics, 2014, 110, 7-19.	1.2	3
107	Differential retention and divergent resolution of duplicate genes following whole-genome duplication. Genome Research, 2014, 24, 1665-1675.	2.4	111
108	Conserved and host-specific features of influenza virion architecture. Nature Communications, 2014, 5, 4816.	5.8	214
109	Analysis of structural diversity in wolf-like canids reveals post-domestication variants. BMC Genomics, 2014, 15, 465.	1.2	16

#	ARTICLE	IF	CITATIONS
110	Next generation sequencing gives an insight into the characteristics of highly selected breeds versus non-breed horses in the course of domestication. BMC Genomics, 2014, 15, 562.	1.2	24
111	A feasibility study to identify proteins in the residual Pap test fluid of women with normal cytology by mass spectrometry-based proteomics. Clinical Proteomics, 2014, 11, 30.	1.1	16
112	Modular organization and reticulate evolution of the ORF1 of Jockey superfamily transposable elements. Mobile DNA, 2014, 5, 19.	1.3	11
113	The genetic landscape of infantile spasms. Human Molecular Genetics, 2014, 23, 4846-4858.	1.4	156
114	Quantitative Proteomics by SWATH-MS Reveals Altered Expression of Nucleic Acid Binding and Regulatory Proteins in HIV-1-Infected Macrophages. Journal of Proteome Research, 2014, 13, 2109-2119.	1.8	65
115	Efficiency and Safety of O⁶-Methylguanine DNA Methyltransferase (MGMT^{P140K})-Mediated<i>In Vivo</i>Selection in a Humanized Mouse Model. Human Gene Therapy, 2014, 25, 144-155.	1.4	8
116	Characterization of Glycoproteins in Pancreatic Cyst Fluid Using a High-Performance Multiple Lectin Affinity Chromatography Platform. Journal of Proteome Research, 2014, 13, 289-299.	1.8	25
117	SNP2GO: Functional Analysis of Genome-Wide Association Studies. Genetics, 2014, 197, 285-289.	1.2	30
118	Widespread Signals of Convergent Adaptation to High Altitude in Asia and America. American Journal of Human Genetics, 2014, 95, 394-407.	2.6	131
119	Broad-Enrich: functional interpretation of large sets of broad genomic regions. Bioinformatics, 2014, 30, i393-i400.	1.8	21
120	Transcriptome profiling reveals that the SM22Î±-regulated molecular pathways contribute to vascular pathology. Journal of Molecular and Cellular Cardiology, 2014, 72, 263-272.	0.9	23
121	Unpredictable neonatal stress enhances adult anxiety and alters amygdala gene expression related to serotonin and GABA. Neuroscience, 2014, 258, 147-161.	1.1	61
122	Gene expression in teratogenic exposures: A new approach to understanding individual risk. Reproductive Toxicology, 2014, 45, 94-104.	1.3	14
123	In the secretory endometria of women, luminal epithelia exhibit gene and protein expressions that differ from those of glandular epithelia. Fertility and Sterility, 2014, 102, 307-317.e7.	0.5	20
124	An integrated perspective and functional impact of the mitochondrial acetylome. Expert Review of Proteomics, 2014, 11, 383-394.	1.3	14
125	Expression of 19 microRNAs in glioblastoma and comparison with other brain neoplasia of grades Iâ€“III. Molecular Oncology, 2014, 8, 417-430.	2.1	96
126	Common features of microRNA target prediction tools. Frontiers in Genetics, 2014, 5, 23.	1.1	356
127	A meta-approach for improving the prediction and the functional annotation of ortholog groups. BMC Genomics, 2014, 15, S16.	1.2	20

#	ARTICLE	IF	CITATIONS
128	PlantCAZyme: a database for plant carbohydrate-active enzymes. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	1.4	38
129	Optimisation of miRNA-mRNA relationship prediction using biological features. International Journal of Computational Biology and Drug Design, 2014, 7, 45.	0.3	2
130	Proteomic comparison between abdominal and thoracic aortic aneurysms. International Journal of Molecular Medicine, 2014, 33, 1035-1047.	1.8	18
131	Atypical Femoral Fracture in Osteoporosis Pseudoglioma Syndrome Associated with Two Novel Compound Heterozygous Mutations in <i>LRP5</i>. Journal of Bone and Mineral Research, 2015, 30, 615-620.	3.1	25
132	Comparative twoâ€dimensional polyacrylamide gel electrophoresis of the salivary proteome of children with autism spectrum disorder. Journal of Cellular and Molecular Medicine, 2015, 19, 2664-2678.	1.6	39
133	Activity-Dependent Neuroprotective Protein (ADNP): A Case Study for Highly Conserved Chordata-Specific Genes Shaping the Brain and Mutated in Cancer. Journal of Alzheimer's Disease, 2015, 45, 57-73.	1.2	44
134	<scp>HMGB</scp>1 facilitates repair of mitochondrial <scp>DNA</scp> damage and extends the lifespan of mutant ataxinâ€1 knockâ€in mice. EMBO Molecular Medicine, 2015, 7, 78-101.	3.3	66
135	Characterization and quantification of proteins secreted by single human embryos prior to implantation. EMBO Molecular Medicine, 2015, 7, 1465-1479.	3.3	36
136	A Systems Level Analysis of Vasopressin-mediated Signaling Networks in Kidney Distal Convoluted Tubule Cells. Scientific Reports, 2015, 5, 12829.	1.6	21
137	A comparison of the transcriptome of Drosophila melanogaster in response to entomopathogenic fungus, ionizing radiation, starvation and cold shock. BMC Genomics, 2015, 16, S8.	1.2	76
138	DDX3Y gene rescue of a Y chromosome AZFa deletion restores germ cell formation and transcriptional programs. Scientific Reports, 2015, 5, 15041.	1.6	63
139	Why do Sequence Signatures Predict Enzyme Mechanism? Homology versus Chemistry. Evolutionary Bioinformatics, 2015, 11, EBO.S31482.	0.6	4
140	Competition-cooperation relationship networks characterize the competition and cooperation between proteins. Scientific Reports, 2015, 5, 11619.	1.6	3
141	Human metabolic atlas: an online resource for human metabolism. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav068.	1.4	76
142	Reconstructing a SuperGeneTree minimizing reconciliation. BMC Bioinformatics, 2015, 16, S4.	1.2	5
143	Multiple target drug cocktail design for attacking the core network markers of four cancers using ligand-based and structure-based virtual screening methods. BMC Medical Genomics, 2015, 8, S4.	0.7	15
144	ESEA: Discovering the Dysregulated Pathways based on Edge Set Enrichment Analysis. Scientific Reports, 2015, 5, 13044.	1.6	31
145	Proteomic analysis of tylosin-resistant Mycoplasma gallisepticum reveals enzymatic activities associated with resistance. Scientific Reports, 2015, 5, 17077.	1.6	6

#	Article	IF	Citations
146	Positional plasticity in regenerating Amybstoma mexicanum limbs is associated with cell proliferation and pathways of cellular differentiation. BMC Developmental Biology, 2015, 15, 45.	2.1	30
147	Runs of homozygosity reveal signatures of positive selection for reproduction traits in breed and non-breed horses. BMC Genomics, 2015, 16, 764.	1.2	125
148	A human 3â€²UTR clone collection to study post-transcriptional gene regulation. BMC Genomics, 2015, 16, 1036.	1.2	7
149	Gene set analysis: A stepâ€byâ€step guide. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 517-527.	1.1	66
150	Novel CDKN2A mutations in Austrian melanoma patients. Melanoma Research, 2015, 25, 412-420.	0.6	10
151	A weighted and integrated drug-target interactome: drug repurposing for schizophrenia as a use case. BMC Systems Biology, 2015, 9, S2.	3.0	10
152	Blood-based lung cancer biomarkers identified through proteomic discovery in cancer tissues, cell lines and conditioned medium. Clinical Proteomics, 2015, 12, 18.	1.1	35
153	Label-free mass spectrometric analysis reveals complex changes in the brain proteome from the mdx-4cv mouse model of Duchenne muscular dystrophy. Clinical Proteomics, 2015, 12, 27.	1.1	27
154	Genome-wide scan for selection signatures in six cattle breeds in South Africa. Genetics Selection Evolution, 2015, 47, 92.	1.2	96
155	Genomic population structure and prevalence of copy number variations in South African Nguni cattle. BMC Genomics, 2015, 16, 894.	1.2	46
156	Transcriptomes of post-mitotic neurons identify the usage of alternative pathways during adult and embryonic neuronal differentiation. BMC Genomics, 2015, 16, 1100.	1.2	21
157	Development of an efficient RNA interference method by feeding for the microcrustacean Daphnia. BMC Biotechnology, 2015, 15, 91.	1.7	28
158	Characterization of genome-wide H3K27ac profiles reveals a distinct PM2.5-associated histone modification signature. Environmental Health, 2015, 14, 65.	1.7	37
159	Proteomic analysis of HIV-1 Gag interacting partners using proximity-dependent biotinylation. Virology Journal, 2015, 12, 138.	1.4	38
160	Midgut proteome of an argasid tick, Ornithodoros erraticus: a comparison between unfed and engorged females. Parasites and Vectors, 2015, 8, 525.	1.0	30
161	Label-free LC-MS analysis of HER2+ breast cancer cell line response to HER2 inhibitor treatment. DARU, Journal of Pharmaceutical Sciences, 2015, 23, 40.	0.9	21
162	Cellular response to empty and palladiumâ€conjugated aminoâ€polystyrene nanospheres uptake: A proteomic study. Proteomics, 2015, 15, 34-43.	1.3	11
163	Large-scale identification of secretome glycoproteins recognized by<i>Wisteria floribunda</i>agglutinin: A glycoproteomic approach to biomarker discovery. Proteomics, 2015, 15, 2921-2933.	1.3	18

#	Article	IF	Citations
164	Viral infection causes a shift in the self peptide repertoire presented by human MHC class I molecules. Proteomics - Clinical Applications, 2015, 9, 1035-1052.	0.8	16
165	Relationship of intratumoural protein expression patterns to age and <scp>E</scp>psteinâ€•<scp>B</scp>arr virus status in classical <scp>H</scp>odgkin lymphoma. European Journal of Haematology, 2015, 95, 137-149.	1.1	8
166	LymPHOS 2.0: an update of a phosphosite database of primary human T cells. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav115.	1.4	15
167	Labelâ€•free mass spectrometric analysis of the <i>mdxâ€•4cv</i> diaphragm identifies the matricellular protein periostin as a potential factor involved in dystrophinopathyâ€•related fibrosis. Proteomics, 2015, 15, 2318-2331.	1.3	51
168	Global cPILOT analysis of the APP/PSâ€•1 mouse liver proteome. Proteomics - Clinical Applications, 2015, 9, 872-884.	0.8	25
169	Global quantitative proteomic analysis of human glioma cells profiled host protein expression in response to enterovirus type 71 infection. Proteomics, 2015, 15, 3784-3796.	1.3	13
170	Discovery of novel vitamin Dâ€•regulated proteins in INSâ€•1 cells: a proteomic approach. Diabetes/Metabolism Research and Reviews, 2015, 31, 481-491.	1.7	6
171	Intrinsically Disordered Proteins: Controlled Chaos or Random Walk. International Journal of Plant Biology, 2015, 6, 6191.	1.1	1
172	Understanding Xeroderma Pigmentosum Complementation Groups Using Gene Expression Profiling after UV-Light Exposure. International Journal of Molecular Sciences, 2015, 16, 15985-15996.	1.8	16
173	Concurrent Label-Free Mass Spectrometric Analysis of Dystrophin Isoform Dp427 and the Myofibrosis Marker Collagen in Crude Extracts from mdx-4cv Skeletal Muscles. Proteomes, 2015, 3, 298-327.	1.7	29
174	Metabolomics, Standards, and Metabolic Modeling for Synthetic Biology in Plants. Frontiers in Bioengineering and Biotechnology, 2015, 3, 167.	2.0	15
175	Simultaneous Pathoproteomic Evaluation of the Dystrophin-Glycoprotein Complex and Secondary Changes in the mdx-4cv Mouse Model of Duchenne Muscular Dystrophy. Biology, 2015, 4, 397-423.	1.3	37
176	Comparative Label-Free Mass Spectrometric Analysis of Mildly versus Severely Affected mdx Mouse Skeletal Muscles Identifies Annexin, Lamin, and Vimentin as Universal Dystrophic Markers. Molecules, 2015, 20, 11317-11344.	1.7	44
177	AnGeLi: A Tool for the Analysis of Gene Lists from Fission Yeast. Frontiers in Genetics, 2015, 6, 330.	1.1	65
178	A Genome-Wide siRNA Screen in Mammalian Cells for Regulators of S6 Phosphorylation. PLoS ONE, 2015, 10, e0116096.	1.1	10
179	Protein Interactome of Muscle Invasive Bladder Cancer. PLoS ONE, 2015, 10, e0116404.	1.1	12
180	Proteomics-Driven Analysis of Ovine Whey Colostrum. PLoS ONE, 2015, 10, e0117433.	1.1	21
181	Proteomic Signature of the Murine Intervertebral Disc. PLoS ONE, 2015, 10, e0117807.	1.1	23

#	ARTICLE	IF	CITATIONS
182	slc7a6os Gene Plays a Critical Role in Defined Areas of the Developing CNS in Zebrafish. PLoS ONE, 2015, 10, e0119696.	1.1	6
183	The Active Tamoxifen Metabolite Endoxifen (4OHNDtam) Strongly Down-Regulates Cytokeratin 6 (CK6) in MCF-7 Breast Cancer Cells. PLoS ONE, 2015, 10, e0122339.	1.1	3
184	Fine Mapping of a GWAS-Derived Obesity Candidate Region on Chromosome 16p11.2. PLoS ONE, 2015, 10, e0125660.	1.1	12
185	Stress Responses of Small Heat Shock Protein Genes in Lepidoptera Point to Limited Conservation of Function across Phylogeny. PLoS ONE, 2015, 10, e0132700.	1.1	19
186	Epstein-Barr Virus MicroRNA Expression Increases Aggressiveness of Solid Malignancies. PLoS ONE, 2015, 10, e0136058.	1.1	29
187	Assessing the Metabolic Diversity of Streptococcus from a Protein Domain Point of View. PLoS ONE, 2015, 10, e0137908.	1.1	8
188	Normal and Cystic Fibrosis Human Bronchial Epithelial Cells Infected with Pseudomonas aeruginosa Exhibit Distinct Gene Activation Patterns. PLoS ONE, 2015, 10, e0140979.	1.1	22
189	Genome-Wide Association Study of Staphylococcus aureus Carriage in a Community-Based Sample of Mexican-Americans in Starr County, Texas. PLoS ONE, 2015, 10, e0142130.	1.1	17
190	Conserved Molecular Underpinnings and Characterization of a Role for Caveolin-1 in the Tumor Microenvironment of Mature T-Cell Lymphomas. PLoS ONE, 2015, 10, e0142682.	1.1	14
191	Cyclophilin C Participates in the US2-Mediated Degradation of Major Histocompatibility Complex Class I Molecules. PLoS ONE, 2015, 10, e0145458.	1.1	9
192	Analysis of BRCA gene missense mutations. Journal of Biomedical Engineering and Informatics, 2015, 2, 91.	0.2	0
193	Systematic Analysis and Prediction of<i>In Situ</i>Cross Talk of O-GlcNAcylation and Phosphorylation. BioMed Research International, 2015, 2015, 1-12.	0.9	9
194	Monitoring of Serial Presurgical and Postsurgical Changes in the Serum Proteome in a Series of Patients with Calcific Aortic Stenosis. Disease Markers, 2015, 2015, 1-11.	0.6	8
195	Hypoxia Strongly Affects Mitochondrial Ribosomal Proteins and Translocases, as Shown by Quantitative Proteomics of HeLa Cells. International Journal of Proteomics, 2015, 2015, 1-9.	2.0	22
196	Optimal bayesian feature filtering. , 2015, , .		8
197	Molecular basis of cleft palates in mice. World Journal of Biological Chemistry, 2015, 6, 121.	1.7	36
198	Araport: the Arabidopsis Information Portal. Nucleic Acids Research, 2015, 43, D1003-D1009.	6.5	193
199	Transcriptomic landscape of lncRNAs in inflammatory bowel disease. Genome Medicine, 2015, 7, 39.	3.6	171

#	ARTICLE	IF	CITATIONS
200	Roles of Progesterone Receptor A and B Isoforms During Human Endometrial Decidualization. Molecular Endocrinology, 2015, 29, 882-895.	3.7	79
201	A Combined Shotgun and Targeted Mass Spectrometry Strategy for Breast Cancer Biomarker Discovery. Journal of Proteome Research, 2015, 14, 2807-2818.	1.8	33
202	The molecular correlates of organ loss: the case of insect Malpighian tubules. Biology Letters, 2015, 11, 20150154.	1.0	11
203	Correlated gene expression supports synchronous activity in brain networks. Science, 2015, 348, 1241-1244.	6.0	532
204	Developmental Transcriptome for a Facultatively Eusocial Bee, Megalopta genalis. G3: Genes, Genomes, Genetics, 2015, 5, 2127-2135.	0.8	18
205	Long-term neural and physiological phenotyping of a single human. Nature Communications, 2015, 6, 8885.	5.8	353
206	The language of the protein universe. Current Opinion in Genetics and Development, 2015, 35, 50-56.	1.5	27
207	Transcriptomes of lineage-specific <i>Drosophila</i> neuroblasts profiled via genetic targeting and robotic sorting. Development (Cambridge), 2015, 143, 411-21.	1.2	49
208	Proteomic analysis and functional characterization of mouse brain mitochondria during aging reveal alterations in energy metabolism. Proteomics, 2015, 15, 1574-1586.	1.3	38
209	Mass spectrometry and bioinformatics analysis data. Data in Brief, 2015, 2, 21-25.	0.5	3
210	Quantitative Proteomics Reveals an Altered Cystic Fibrosis<i>In Vitro</i>Bronchial Epithelial Secretome. American Journal of Respiratory Cell and Molecular Biology, 2015, 53, 22-32.	1.4	49
211	Expanded microbial genome coverage and improved protein family annotation in the COG database. Nucleic Acids Research, 2015, 43, D261-D269.	6.5	1,345
212	Liver Preservation With Machine Perfusion and a Newly Developed Cell-Free Oxygen Carrier Solution Under Subnormothermic Conditions. American Journal of Transplantation, 2015, 15, 381-394.	2.6	111
213	Prediction of the pathogenicity of antithrombin sequence variations by in silico methods. Thrombosis Research, 2015, 135, 404-409.	0.8	16
214	Gene expression profile in cardiovascular disease and preeclampsia: AÂmeta-analysis of the transcriptome based on raw data from human studies deposited in Gene Expression Omnibus. Placenta, 2015, 36, 170-178.	0.7	35
215	Bioinformatic analysis of a PLP-dependent enzyme superfamily suitable for biocatalytic applications. Biotechnology Advances, 2015, 33, 566-604.	6.0	193
216	Effect of Occupational Exposures on Lung Cancer Susceptibility: A Study of Geneâ€“Environment Interaction Analysis. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 570-579.	1.1	14
217	Differential regulation of cytotoxicity pathway discriminating between HIV, HCV mono- and co-infection identified by transcriptome profiling of PBMCs. Virology Journal, 2015, 12, 4.	1.4	4

#	ARTICLE	IF	CITATIONS
218	Effects of sublethal doses of silver nanoparticles on <i>Bacillus subtilis</i> planktonic and sessile cells. Journal of Applied Microbiology, 2015, 118, 1103-1115.	1.4	46
219	EHFPI: a database and analysis resource of essential host factors for pathogenic infection. Nucleic Acids Research, 2015, 43, D946-D955.	6.5	13
220	Gestational Diabetes Alters Offspring DNA Methylation Profiles in Human and Rat: Identification of Key Pathways Involved in Endocrine System Disorders, Insulin Signaling, Diabetes Signaling, and ILK Signaling. Endocrinology, 2015, 156, 2222-2238.	1.4	63
221	Beyond protein expression, MOPED goes multi-omics. Nucleic Acids Research, 2015, 43, D1145-D1151.	6.5	17
222	Whole-genome sequencing reveals oncogenic mutations in mycosis fungoides. Blood, 2015, 126, 508-519.	0.6	193
223	Beyond the usual suspects: a multidimensional genetic exploration of infant attachment disorganization and security. Attachment and Human Development, 2015, 17, 288-301.	1.2	16
224	The Lineage-Specific Transcription Factor PU.1 Prevents Polycomb-Mediated Heterochromatin Formation at Macrophage-Specific Genes. Molecular and Cellular Biology, 2015, 35, 2610-2625.	1.1	8
225	Dynamic Proteomics. Methods in Enzymology, 2015, 561, 219-276.	0.4	57
226	Acute myocardial infarction activates distinct inflammation and proliferation pathways in circulating monocytes, prior to recruitment, and identified through conserved transcriptional responses in mice and humans. European Heart Journal, 2015, 36, 1923-1934.	1.0	88
227	The history of the CATH structural classification of protein domains. Biochimie, 2015, 119, 209-217.	1.3	34
228	Granulocyte-Macrophage Colony Stimulating Factor Exerts Protective and Immunomodulatory Effects in Cortical Trauma. Journal of Neuroimmunology, 2015, 278, 162-173.	1.1	30
229	A rule-based expert system for inferring functional annotation. Applied Soft Computing Journal, 2015, 35, 373-385.	4.1	5
230	Molecular mechanisms of the non-coenzyme action of thiamin in brain: biochemical, structural and pathway analysis. Scientific Reports, 2015, 5, 12583.	1.6	96
231	An integrated genomic analysis of papillary renal cell carcinoma type 1 uncovers the role of focal adhesion and extracellular matrix pathways. Molecular Oncology, 2015, 9, 1667-1677.	2.1	21
232	Contribution of proteomics to the management of vascular disorders. Translational Proteomics, 2015, 7, 3-14.	1.2	3
233	Agriproteomics of Bread Wheat: Comparative Proteomics and Network Analyses of Grain Size Variation. OMICS A Journal of Integrative Biology, 2015, 19, 372-382.	1.0	1
234	Identification of functional candidates amongst hypothetical proteins of <i>Mycobacterium leprae</i> Br4923, a causative agent of leprosy. Genome, 2015, 58, 25-42.	0.9	16
235	Genome-Wide Identification and Evolution of HECT Genes in Soybean. International Journal of Molecular Sciences, 2015, 16, 8517-8535.	1.8	15

#	ARTICLE	IF	CITATIONS
236	Genenames.org: the HGNC resources in 2015. Nucleic Acids Research, 2015, 43, D1079-D1085.	6.5	463
237	Whole transcriptome analysis reveals changes in expression of immune-related genes during and after bleaching in a reef-building coral. Royal Society Open Science, 2015, 2, 140214.	1.1	189
238	Characterization of host response to Cryptococcus neoformans through quantitative proteomic analysis of cryptococcal meningitis co-infected with HIV. Molecular BioSystems, 2015, 11, 2529-2540.	2.9	10
239	Using quantitative PCR with retrotransposon-based insertion polymorphisms as markers in sugarcane. Journal of Experimental Botany, 2015, 66, 4239-4250.	2.4	10
240	The BioPlex Network: A Systematic Exploration of the Human Interactome. Cell, 2015, 162, 425-440.	13.5	1,241
241	Comparative Study of Three Methods of Sample Preparation for Proteomics Research. Chinese Journal of Analytical Chemistry, 2015, 43, 808-813.	0.9	4
242	Autoantibody profile of patients infected with knowlesi malaria. Clinica Chimica Acta, 2015, 448, 33-38.	0.5	8
243	Recent Positive Selection Has Acted on Genes Encoding Proteins with More Interactions within the Whole Human Interactome. Genome Biology and Evolution, 2015, 7, 1141-1154.	1.1	59
244	Determination of the protein expression profiles of breast cancer cell lines by quantitative proteomics using iTRAQ labelling and tandem mass spectrometry. Journal of Proteomics, 2015, 124, 50-78.	1.2	32
245	Subcellular quantitative proteomic analysis reveals host proteins involved in human cytomegalovirus infection. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 967-978.	1.1	11
246	Identifying the Biological Basis of GWAS Hits for Endometriosis1. Biology of Reproduction, 2015, 92, 87.	1.2	55
247	Maintenance and Loss of Duplicated Genes by Dosage Subfunctionalization. Molecular Biology and Evolution, 2015, 32, 2141-2148.	3.5	160
248	A Major Human Oral Lysophosphatidic Acid Species, LPA 18:1, Regulates Novel Genes in Human Gingival Fibroblasts. Journal of Periodontology, 2015, 86, 713-725.	1.7	8
249	Biochemical functional predictions for protein structures of unknown or uncertain function. Computational and Structural Biotechnology Journal, 2015, 13, 182-191.	1.9	77
250	Inorganic Arsenic-induced cellular transformation is coupled with genome wide changes in chromatin structure, transcriptome and splicing patterns. BMC Genomics, 2015, 16, 212.	1.2	43
251	Plasmodium vivax inhibits erythroid cell growth through altered phosphorylation of the cytoskeletal protein ezrin. Malaria Journal, 2015, 14, 138.	0.8	10
252	The OMA orthology database in 2015: function predictions, better plant support, synteny view and other improvements. Nucleic Acids Research, 2015, 43, D240-D249.	6.5	201
253	Temporal lobe proteins implicated in synaptic failure exhibit differential expression and deamidation in vascular dementia. Neurochemistry International, 2015, 80, 87-98.	1.9	26

#	ARTICLE	IF	CITATIONS
254	Comparative transcriptome profiling approach to glean virulence and immunomodulation-related genes of Fasciola hepatica. BMC Genomics, 2015, 16, 366.	1.2	15
255	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	9.4	663
256	Comparison of human cell signaling pathway databasesâ€"evolution, drawbacks and challenges. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	1.4	86
257	Biocompatibility assessment of haemodialysis membrane materials by proteomic investigations. Molecular BioSystems, 2015, 11, 1633-1643.	2.9	35
258	Brg1 promotes both tumor-suppressive and oncogenic activities at distinct stages of pancreatic cancer formation. Genes and Development, 2015, 29, 658-671.	2.7	129
259	Global Analysis of Protein Folding Thermodynamics for Disease State Characterization. Journal of Proteome Research, 2015, 14, 2287-2297.	1.8	28
260	Onco-proteogenomics identifies urinary S100A9 and GRN as potential combinatorial biomarkers for early diagnosis of hepatocellular carcinoma. BBA Clinical, 2015, 3, 205-213.	4.1	33
261	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. Human Molecular Genetics, 2015, 24, 1185-1199.	1.4	71
262	Sustained Î²â€catenin activity in dermal fibroblasts promotes fibrosis by upâ€regulating expression of extracellular matrix proteinâ€coding genes. Journal of Pathology, 2015, 235, 686-697.	2.1	89
263	The Promise of Multi-Omics and Clinical Data Integration to Identify and Target Personalized Healthcare Approaches in Autism Spectrum Disorders. OMICS A Journal of Integrative Biology, 2015, 19, 197-208.	1.0	84
264	ElemeNT: a computational tool for detecting core promoter elements. Transcription, 2015, 6, 41-50.	1.7	66
265	Serum proteomic profiling of major depressive disorder. Translational Psychiatry, 2015, 5, e599-e599.	2.4	100
266	The Lingula genome provides insights into brachiopod evolution and the origin of phosphate biomineralization. Nature Communications, 2015, 6, 8301.	5.8	159
267	Functional classification of CATH superfamilies: a domain-based approach for protein function annotation. Bioinformatics, 2015, 31, 3460-3467.	1.8	93
268	Quantitative Differences in the Urinary Proteome of Siblings Discordant for Type 1 Diabetes Include Lysosomal Enzymes. Journal of Proteome Research, 2015, 14, 3123-3135.	1.8	26
269	Harnessing Connectivity in a Large-Scale Small-Molecule Sensitivity Dataset. Cancer Discovery, 2015, 5, 1210-1223.	7.7	575
270	Protein profiling of mefloquine resistant Plasmodium falciparum using mass spectrometry-based proteomics. International Journal of Mass Spectrometry, 2015, 391, 82-92.	0.7	12
271	Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. GigaScience, 2015, 4, 38.	3.3	84

#	Article	IF	Citations
272	The octopus genome and the evolution of cephalopod neural and morphological novelties. Nature, 2015, 524, 220-224.	13.7	506
273	14-3-3Î¶ coordinates adipogenesis of visceral fat. Nature Communications, 2015, 6, 7671.	5.8	62
274	Radiation dose-rate effects on gene expression for human biodosimetry. BMC Medical Genomics, 2015, 8, 22.	0.7	92
275	Metabolic Pathway Databases: A Word of Caution. Methods in Pharmacology and Toxicology, 2015, , 27-63.	0.1	1
276	Metabolic changes in type 2 diabetes are reflected in peripheral blood cells, revealing aberrant cytotoxicity, a viral signature, and hypoxia inducible factor activity. BMC Medical Genomics, 2015, 8, 20.	0.7	20
277	A glutamatergic network mediates lithium response in bipolar disorder as defined by epigenome pathway analysis. Pharmacogenomics, 2015, 16, 1547-1563.	0.6	34
278	Genome-Wide Analysis of<i>PHOSPHOLIPID</i>:<i>DIACYLGLYCEROL ACYLTRANSFERASE</i>(<i>PDAT</i>) Genes in Plants Reveals the Eudicot-Wide<i>PDAT</i>Gene Expansion and Altered Selective Pressures Acting on the Core Eudicot<i>PDAT</i>Paralogs Â. Plant Physiology, 2015, 167, 887-904.	2.3	39
279	The Phenome-Wide Distribution of Genetic Variance. American Naturalist, 2015, 186, 15-30.	1.0	26
280	Phosphoproteomic Analysis of Aurora Kinase Inhibition in Monopolar Cytokinesis. Journal of Proteome Research, 2015, 14, 4087-4098.	1.8	14
281	Identification of Caveolar Resident Proteins in Ventricular Myocytes Using a Quantitative Proteomic Approach: Dynamic Changes in Caveolar Composition Following Adrenoceptor Activation. Molecular and Cellular Proteomics, 2015, 14, 596-608.	2.5	25
282	YPED: An Integrated Bioinformatics Suite and Database for Mass Spectrometry-based Proteomics Research. Genomics, Proteomics and Bioinformatics, 2015, 13, 25-35.	3.0	15
283	Comparative Genomics Suggests Primary Homothallism of <i>Pneumocystis</i> Species. MBio, 2015, 6, .	1.8	38
284	Endothelial inflammatory transcriptional responses to an altered plasma exposome following inhalation of diesel emissions. Inhalation Toxicology, 2015, 27, 272-280.	0.8	21
285	SILAC-based quantitative proteomics identified lysosome as a fast response target to PDT agent Gd-N induced oxidative stress in human ovarian cancer IGROV1 cells. Molecular BioSystems, 2015, 11, 3059-3067.	2.9	6
286	Insights into the proline hydroxylase (PHD) family, molecular evolution and its impact on human health. Biochimie, 2015, 116, 114-124.	1.3	17
287	Mating induces the expression of immune- and pH-regulatory genes in the utero-vaginal junction containing mucosal sperm-storage tubuli of hens. Reproduction, 2015, 150, 473-483.	1.1	27
288	In Vivo Effects of Mesenchymal Stromal Cells in Two Patients With Severe Acute Respiratory Distress Syndrome. Stem Cells Translational Medicine, 2015, 4, 1199-1213.	1.6	131
289	Increased hepatocellular protein carbonylation in human end-stage alcoholic cirrhosis. Free Radical Biology and Medicine, 2015, 89, 1144-1153.	1.3	14

#	ARTICLE	IF	CITATIONS
290	Data set of the protein expression profiles of Luminal A, Claudin-low and overexpressing HER2 + breast cancer cell lines by iTRAQ labelling and tandem mass spectrometry. Data in Brief, 2015, 4, 292-301.	0.5	2
291	Diversity in protein domain superfamilies. Current Opinion in Genetics and Development, 2015, 35, 40-49.	1.5	38
292	Transcriptome analysis of GVHD reveals aurora kinase A as a targetable pathway for disease prevention. Science Translational Medicine, 2015, 7, 315ra191.	5.8	64
293	Characteristic molecular and proteomic signatures of drugâ€induced liver injury in a rat model. Journal of Applied Toxicology, 2015, 35, 152-164.	1.4	14
294	Pooled assembly of marine metagenomic datasets: enriching annotation through chimerism. Bioinformatics, 2015, 31, 311-317.	1.8	26
295	Gene Ontology Consortium: going forward. Nucleic Acids Research, 2015, 43, D1049-D1056.	6.5	2,743
296	Investigation of serum proteome alterations in human endometriosis. Journal of Proteomics, 2015, 114, 182-196.	1.2	36
297	Schistosome infections induce significant changes in the host biliary proteome. Journal of Proteomics, 2015, 114, 71-82.	1.2	6
298	Bioinformatics approaches for the functional interpretation of protein lists: From ontology term enrichment to network analysis. Proteomics, 2015, 15, 981-996.	1.3	27
299	Behavioral and Proteomic Analysis of Stress Response in Zebrafish (<i>Danio rerio</i>). Journal of Proteome Research, 2015, 14, 943-952.	1.8	14
300	Brief Report: Distinct Dysregulation of the Small Leucineâ€Rich Repeat Protein Family in Osteoarthritic Acetabular Labrum Compared to Articular Cartilage. Arthritis and Rheumatology, 2015, 67, 435-441.	2.9	20
301	Novel genomic signals of recent selection in an Ethiopian population. European Journal of Human Genetics, 2015, 23, 1085-1092.	1.4	25
302	Detecting time periods of differential gene expression using Gaussian processes: an application to endothelial cells exposed to radiotherapy dose fraction. Bioinformatics, 2015, 31, 728-735.	1.8	28
303	Quantitative proteomic analysis of global effect of LLL12 on U87 cell's proteome: An insight into the molecular mechanism of LLL12. Journal of Proteomics, 2015, 113, 127-142.	1.2	20
304	How to learn about gene function: text-mining or ontologies?. Methods, 2015, 74, 3-15.	1.9	24
305	MicroRNA miR145 Regulates TGFBR2 Expression and Matrix Synthesis in Vascular Smooth Muscle Cells. Circulation Research, 2015, 116, 23-34.	2.0	72
306	Prediction of Ebolavirus Genomes Encoded MicroRNA-Like Small RNAs Using Bioinformatics Approaches. , 0, , .		1
307	Inorganic Arsenicâ€"Related Changes in the Stromal Tumor Microenvironment in a Prostate Cancer Cellâ€"Conditioned Media Model. Environmental Health Perspectives, 2016, 124, 1009-1015.	2.8	14

#	ARTICLE	IF	CITATIONS
308	Proteomic Upregulation of Fatty Acid Synthase and Fatty Acid Binding Protein 5 and Identification of Cancer- and Race-Specific Pathway Associations in Human Prostate Cancer Tissues. Journal of Cancer, 2016, 7, 1452-1464.	1.2	38
309	Unraveling Molecular Differences of Gastric Cancer by Label-Free Quantitative Proteomics Analysis. International Journal of Molecular Sciences, 2016, 17, 69.	1.8	31
310	Glucose or Altered Ceramide Biosynthesis Mediate Oxygen Deprivation Sensitivity Through Novel Pathways Revealed by Transcriptome Analysis in<i>Caenorhabditis elegans</i>. G3: Genes, Genomes, Genetics, 2016, 6, 3149-3160.	0.8	15
311	Decay of sexual trait genes in an asexual parasitoid wasp. Genome Biology and Evolution, 2016, 8, evw273.	1.1	33
312	Vitamin D Induces Global Gene Transcription in Human Corneal Epithelial Cells: Implications for Corneal Inflammation. , 2016, 57, 2689.		10
313	Identification of the First<i>De Novo UBIAD1</i>Gene Mutation Associated with Schnyder Corneal Dystrophy. Journal of Ophthalmology, 2016, 2016, 1-9.	0.6	9
314	In Silico Designing and Analysis of Inhibitors against Target Protein Identified through Host-Pathogen Protein Interactions in Malaria. International Journal of Medicinal Chemistry, 2016, 2016, 1-13.	2.2	6
315	Lamina Associated Polypeptide 1 (LAP1) Interactome and Its Functional Features. Membranes, 2016, 6, 8.	1.4	19
316	Transcriptome profiling of the rumen epithelium of beef cattle differing in residual feed intake. BMC Genomics, 2016, 17, 592.	1.2	93
317	PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. Frontiers in Microbiology, 2016, 7, 118.	1.5	153
318	Scale Invariant Disordered Nanotopography Promotes Hippocampal Neuron Development and Maturation with Involvement of Mechanotransductive Pathways. Frontiers in Cellular Neuroscience, 2016, 10, 267.	1.8	64
319	Characterization of AQPs in Mouse, Rat, and Human Colon and Their Selective Regulation by Bile Acids. Frontiers in Nutrition, 2016, 3, 46.	1.6	38
320	Computational Identification of the Paralogs and Orthologs of Human Cytochrome P450 Superfamily and the Implication in Drug Discovery. International Journal of Molecular Sciences, 2016, 17, 1020.	1.8	23
321	Comparing Simplification Strategies for the Skeletal Muscle Proteome. Proteomes, 2016, 4, 10.	1.7	2
322	Genome-wide gene expression and RNA half-life measurements allow predictions of regulation and metabolic behavior in Methanosarcina acetivorans. BMC Genomics, 2016, 17, 924.	1.2	22
323	IGDD: a database of intronless genes in dicots. BMC Bioinformatics, 2016, 17, 289.	1.2	23
324	Clinical significance of mitofusin-2 and its signaling pathways in hepatocellular carcinoma. World Journal of Surgical Oncology, 2016, 14, 179.	0.8	20
325	WORMHOLE: Novel Least Diverged Ortholog Prediction through Machine Learning. PLoS Computational Biology, 2016, 12, e1005182.	1.5	21

#	Article	IF	Citations
326	Advanced Running Performance by Genetic Predisposition in Male Dummerstorf Marathon Mice (DUhTP) Reveals Higher Sterol Regulatory Element-Binding Protein (SREBP) Related mRNA Expression in the Liver and Higher Serum Levels of Progesterone. PLoS ONE, 2016, 11, e0146748.	1.1	6
327	In-Silico Computing of the Most Deleterious nsSNPs in HBA1 Gene. PLoS ONE, 2016, 11, e0147702.	1.1	38
328	Transcriptional Analysis of T Cells Resident in Human Skin. PLoS ONE, 2016, 11, e0148351.	1.1	29
329	Major Transcriptome Changes Accompany the Growth of Pseudomonas aeruginosa in Blood from Patients with Severe Thermal Injuries. PLoS ONE, 2016, 11, e0149229.	1.1	31
330	A Systems Biology Approach to the Coordination of Defensive and Offensive Molecular Mechanisms in the Innate and Adaptive Hostâ€"Pathogen Interaction Networks. PLoS ONE, 2016, 11, e0149303.	1.1	10
331	The Genomic Scrapheap Challenge; Extracting Relevant Data from Unmapped Whole Genome Sequencing Reads, Including Strain Specific Genomic Segments, in Rats. PLoS ONE, 2016, 11, e0160036.	1.1	5
332	B Cell Receptor Activation Predominantly Regulates AKT-mTORC1/2 Substrates Functionally Related to RNA Processing. PLoS ONE, 2016, 11, e0160255.	1.1	33
333	Transcriptomic Changes Associated with Pregnancy in a Marsupial, the Gray Short-Tailed Opossum Monodelphis domestica. PLoS ONE, 2016, 11, e0161608.	1.1	20
334	Transcriptomic Analysis of Soil-Grown Arabidopsis thaliana Roots and Shoots in Response to a Drought Stress. Frontiers in Plant Science, 2016, 7, 180.	1.7	94
335	A continuum of mRNP complexes in embryonic microRNA-mediated silencing. Nucleic Acids Research, 2017, 45, gkw872.	6.5	20
336	Somatic gene mutation analysis of triple negative breast cancers. Breast, 2016, 29, 202-207.	0.9	23
337	Adaptive divergence despite strong genetic drift: genomic analysis of the evolutionary mechanisms causing genetic differentiation in the island fox (Urocyon littoralis). Molecular Ecology, 2016, 25, 2176-2194.	2.0	114
338	Protein turnover analysis in <i>Salmonella</i> Typhimurium during infection by dynamic SILAC, Topograph, and quantitative proteomics. Journal of Basic Microbiology, 2016, 56, 801-811.	1.8	8
339	Gene expression analysis during acute hepatitis C virus infection associates dendritic cell activation with viral clearance. Journal of Medical Virology, 2016, 88, 843-851.	2.5	3
340	Determining synthesis rates of individual proteins in zebrafish (<i>Danio rerio</i>) with low levels of a stable isotope labelled amino acid. Proteomics, 2016, 16, 1398-1406.	1.3	2
341	Sequence Determinants of Intracellular Phase Separation by Complex Coacervation of a Disordered Protein. Molecular Cell, 2016, 63, 72-85.	4.5	622
342	Pathway analysis in attention deficit hyperactivity disorder: An ensemble approach. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 815-826.	1.1	38
343	Ensembl comparative genomics resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav096.	1.4	344

#	ARTICLE	IF	CITATIONS
344	Neuronal cell lines as model dorsal root ganglion neurons. Molecular Pain, 2016, 12, 174480691664611.	1.0	81
345	MINERVAâ€"a platform for visualization and curation of molecular interaction networks. Npj Systems Biology and Applications, 2016, 2, 16020.	1.4	68
346	Dysregulated immune system networks in war veterans with PTSD is an outcome of altered miRNA expression and DNA methylation. Scientific Reports, 2016, 6, 31209.	1.6	74
347	A novel mutant allele of SSI2 confers a better balance between disease resistance and plant growth inhibition on Arabidopsis thaliana. BMC Plant Biology, 2016, 16, 208.	1.6	21
348	Altered microRNA expression and pre-mRNA splicing events reveal new mechanisms associated with early stage Mycobacterium avium subspecies paratuberculosis infection. Scientific Reports, 2016, 6, 24964.	1.6	47
349	Nuclear myosin I regulates cell membrane tension. Scientific Reports, 2016, 6, 30864.	1.6	26
350	Age-related neurogenesis decline in the subventricular zone is associated with specific cell cycle regulation changes in activated neural stem cells. Scientific Reports, 2016, 6, 21505.	1.6	77
351	Extensive local adaptation within the chemosensory system following Drosophila melanogasterâ€™s global expansion. Nature Communications, 2016, 7, ncomms11855.	5.8	48
352	Combination of the histone deacetylase inhibitor depsipeptide and 5-fluorouracil upregulates major histocompatibility complex class II and p21 genes and activates caspase-3/7 in human colon cancer HCT-116 cells. Oncology Reports, 2016, 36, 1875-1885.	1.2	32
353	Cardiovascular proteomics in the era of big data: experimental and computational advances. Clinical Proteomics, 2016, 13, 23.	1.1	9
354	Bioinformatics Tools for Proteomics Data Interpretation. Advances in Experimental Medicine and Biology, 2016, 919, 281-341.	0.8	20
355	Altered DNA methylation associated with an abnormal liver phenotype in a cattle model with a high incidence of perinatal pathologies. Scientific Reports, 2016, 6, 38869.	1.6	17
356	Global quantitative proteomics reveal up-regulation of endoplasmic reticulum stress response proteins upon depletion of eIF5A in HeLa cells. Scientific Reports, 2016, 6, 25795.	1.6	43
357	Kat3 coactivators in somatic stem cells and cancer stem cells: biological roles, evolution, and pharmacologic manipulation. Cell Biology and Toxicology, 2016, 32, 61-81.	2.4	42
358	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	9.0	198
359	Proteomics of cellâ€"cell interactions in health and disease. Proteomics, 2016, 16, 328-344.	1.3	12
360	Altered neural signaling and immune pathways in peripheral blood mononuclear cells of schizophrenia patients with cognitive impairment: A transcriptome analysis. Brain, Behavior, and Immunity, 2016, 53, 194-206.	2.0	30
361	Global proteome profiling of dental cementum under experimentally-induced apposition. Journal of Proteomics, 2016, 141, 12-23.	1.2	20

#	Article	IF	Citations
362	Dysregulated signaling hubs of liver lipid metabolism reveal hepatocellular carcinoma pathogenesis. Nucleic Acids Research, 2016, 44, 5529-5539.	6.5	35
363	In silico transcriptional regulation and functional analysis of dengue shock syndrome associated SNPs in PLCE1 and MICB genes. Functional and Integrative Genomics, 2016, 16, 335-345.	1.4	5
364	A proteomic signature of ovarian cancer tumor fluid identified by highthroughput and verified by targeted proteomics. Journal of Proteomics, 2016, 145, 226-236.	1.2	33
365	PANTHER-PSEP: predicting disease-causing genetic variants using position-specific evolutionary preservation. Bioinformatics, 2016, 32, 2230-2232.	1.8	228
366	Data set for transcriptional response to depletion of the Shoc2 scaffolding protein. Data in Brief, 2016, 7, 770-778.	0.5	4
367	Computational prediction of virusâ€“human proteinâ€“protein interactions using embedding kernelized heterogeneous data. Molecular BioSystems, 2016, 12, 1976-1986.	2.9	17
368	Improvement of Mitochondria Extract from<i>Saccharomyces cerevisiae</i>Characterization in Shotgun Proteomics Using Sheathless Capillary Electrophoresis Coupled to Tandem Mass Spectrometry. Journal of Chromatographic Science, 2016, 54, 653-663.	0.7	16
369	Overexpression of Sly41 suppresses COPII vesicleâ€“tethering deficiencies by elevating intracellular calcium levels. Molecular Biology of the Cell, 2016, 27, 1635-1649.	0.9	4
370	Bioactive peptides in plant-derived foodstuffs. Journal of Proteomics, 2016, 147, 140-155.	1.2	142
371	Protein biomarkers of susceptibility and resilience to stress in a rat model of depression. Molecular and Cellular Neurosciences, 2016, 74, 87-95.	1.0	41
372	Asialoglycoprotein receptor 1 is a specific cell-surface marker for isolating hepatocytes derived from human pluripotent stem cells. Development (Cambridge), 2016, 143, 1475-1481.	1.2	47
373	A high-quality carrot genome assembly provides new insights into carotenoid accumulation and asterid genome evolution. Nature Genetics, 2016, 48, 657-666.	9.4	432
374	Dopamine pathway is highly diverged in primate species that differ markedly in social behavior. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6178-6181.	3.3	33
375	Homology-Based Annotation of Large Protein Datasets. Methods in Molecular Biology, 2016, 1415, 153-176.	0.4	0
376	Gene expression analysis of disabled and re-induced isoprene emission by the tropical tree<i>Ficus septica</i>before and after cold ambient temperature exposure. Tree Physiology, 2016, 36, 873-882.	1.4	11
377	Comparative interactomics analysis of different ALS-associated proteins identifies converging molecular pathways. Acta Neuropathologica, 2016, 132, 175-196.	3.9	113
378	Ataxin-1 regulates the cerebellar bioenergetics proteome through the GSK3Î²-mTOR pathway which is altered in Spinocerebellar ataxia type 1 (SCA1). Human Molecular Genetics, 2016, 25, 4021-4040.	1.4	43
379	Behavioral Genetic Toolkits. Current Topics in Developmental Biology, 2016, 119, 157-204.	1.0	46

#	Article	IF	Citations
380	A method for whole protein isolation from human cranial bone. Analytical Biochemistry, 2016, 515, 33-39.	1.1	14
381	Molecular Diversity of Midbrain Development in Mouse, Human, and Stem Cells. Cell, 2016, 167, 566-580.e19.	13.5	687
382	InÂvitro secretomics study of pterygium-derived fibroblasts by iTRAQ-based quantitative proteomics strategy. Experimental Eye Research, 2016, 153, 14-22.	1.2	7
383	Chromatin structureâ€"based prediction of recurrent noncoding mutations in cancer. Nature Genetics, 2016, 48, 1321-1326.	9.4	29
384	Towards Consensus Gene Ages. Genome Biology and Evolution, 2016, 8, 1812-1823.	1.1	63
385	Comparative Proteomic Analysis of Extracellular Vesicles Isolated by Acoustic Trapping or Differential Centrifugation. Analytical Chemistry, 2016, 88, 8577-8586.	3.2	36
386	Normal human mitral valve proteome: A preliminary investigation by gelâ€based and gelâ€free proteomic approaches. Electrophoresis, 2016, 37, 2633-2643.	1.3	3
387	Approach for Identifying Human Leukocyte Antigen (HLA)-DR Bound Peptides from Scarce Clinical Samples. Molecular and Cellular Proteomics, 2016, 15, 3017-3029.	2.5	46
388	Prp40 and early events in splice site definition. Wiley Interdisciplinary Reviews RNA, 2016, 7, 17-32.	3.2	27
389	Characterization of the direct targets of <scp>FOXO</scp> transcription factors throughout evolution. Aging Cell, 2016, 15, 673-685.	3.0	177
390	New insights on the mitochondrial proteome plasticity in Parkinson's disease. Proteomics - Clinical Applications, 2016, 10, 416-429.	0.8	11
391	Genomeâ€wide analysis reveals conserved transcriptional responses downstream of resting potential change in <i>Xenopus</i> embryos, axolotl regeneration, and human mesenchymal cell differentiation. Regeneration (Oxford, England), 2016, 3, 3-25.	6.3	53
392	Visceral motor neuron diversity delineates a cellular basis for nipple- and pilo-erection muscle control. Nature Neuroscience, 2016, 19, 1331-1340.	7.1	91
393	Impact of outdated gene annotations on pathway enrichment analysis. Nature Methods, 2016, 13, 705-706.	9.0	113
394	A Genomic Resource for the Development, Improvement, and Exploitation of Sorghum for Bioenergy. Genetics, 2016, 204, 21-33.	1.2	115
395	DNA methylation patterns associated with oxidative stress in an ageing population. BMC Medical Genomics, 2016, 9, 72.	0.7	37
396	Quantitative Proteomics Reveals the Mechanism of Oxygen Treatment on Lenses of Alzheimerâ€™s Disease Model Mice. Journal of Alzheimer's Disease, 2016, 54, 275-286.	1.2	14
397	Cells release subpopulations of exosomes with distinct molecular and biological properties. Scientific Reports, 2016, 6, 22519.	1.6	728

#	ARTICLE	IF	CITATIONS
398	A Comprehensive Characterization of the Function of LincRNAs in Transcriptional Regulation Through Long-Range Chromatin Interactions. Scientific Reports, 2016, 6, 36572.	1.6	19
399	Serum proteomic profiles of depressive subtypes. Translational Psychiatry, 2016, 6, e851-e851.	2.4	56
400	A proteomic analysis of chondrogenic, osteogenic and tenogenic constructs from ageing mesenchymal stem cells. Stem Cell Research and Therapy, 2016, 7, 133.	2.4	24
401	Tissue enrichment analysis for C. elegans genomics. BMC Bioinformatics, 2016, 17, 366.	1.2	155
402	What Signatures Dominantly Associate with Gene Age?. Genome Biology and Evolution, 2016, 8, 3083-3089.	1.1	39
403	Candidate adaptive genes associated with lineage divergence: identifying <scp>SNP</scp>s via nextâ€generation targeted resequencing in mule deer (<i>Odocoileus hemionus</i>). Molecular Ecology Resources, 2016, 16, 1165-1172.	2.2	14
404	Developmental alcohol exposure leads to a persistent change on astrocyte secretome. Journal of Neurochemistry, 2016, 137, 730-743.	2.1	22
405	Origin and Functional Prediction of Pollen Allergens in Plants. Plant Physiology, 2016, 172, 341-357.	2.3	33
406	Effect of Heme Oxygenase-1 Deficiency on Glomerular Proteomics. American Journal of Nephrology, 2016, 43, 441-450.	1.4	5
407	Transcriptomic Profiling Maps Anatomically Patterned Subpopulations among Single Embryonic Cardiac Cells. Developmental Cell, 2016, 39, 491-507.	3.1	218
408	Identification of mutations, gene expression changes and fusion transcripts by whole transcriptome RNAseq in docetaxel resistant prostate cancer cells. SpringerPlus, 2016, 5, 1861.	1.2	15
409	REST is a hypoxia-responsive transcriptional repressor. Scientific Reports, 2016, 6, 31355.	1.6	60
410	Variant detection and runs of homozygosity in next generation sequencing data elucidate the genetic background of Lundehund syndrome. BMC Genomics, 2016, 17, 535.	1.2	12
411	Head Transcriptomes of Two Closely Related Species of Fruit Flies of the<i>Anastrepha fraterculus</i>Group Reveals Divergent Genes in Species with Extensive Gene Flow. G3: Genes, Genomes, Genetics, 2016, 6, 3283-3295.	0.8	18
412	HMGB4 is expressed by neuronal cells and affects the expression of genes involved in neural differentiation. Scientific Reports, 2016, 6, 32960.	1.6	14
413	Specification of jaw identity by the Hand2 transcription factor. Scientific Reports, 2016, 6, 28405.	1.6	21
414	MiR-125a-3p timely inhibits oligodendroglial maturation and is pathologically up-regulated in human multiple sclerosis. Scientific Reports, 2016, 6, 34503.	1.6	55
416	Transcriptional profile of SH-SY5Y human neuroblastoma cells transfected by Toxoplasma rhoptry protein 16. Molecular Medicine Reports, 2016, 14, 4099-4108.	1.1	5

#	Article	IF	Citations
417	Hypoxia causes transgenerational impairments in reproduction of fish. Nature Communications, 2016, 7, 12114.	5.8	134
418	BcCluster: A Bladder Cancer Database at the Molecular Level. Bladder Cancer, 2016, 2, 65-76.	0.2	4
419	Accumulation of isolevuglandin-modified protein in normal and fibrotic lung. Scientific Reports, 2016, 6, 24919.	1.6	21
420	A Bayesian algorithm for detecting differentially expressed proteins and its application in breast cancer research. Scientific Reports, 2016, 6, 30159.	1.6	4
421	Heritability and Genome-Wide Association Analyses of Sleep Duration in Children: The EAGLE Consortium. Sleep, 2016, 39, 1859-1869.	0.6	34
422	Saliva-Induced Clotting Captures Streptococci: Novel Roles for Coagulation and Fibrinolysis in Host Defense and Immune Evasion. Infection and Immunity, 2016, 84, 2813-2823.	1.0	12
423	Comprehensive coverage of cardiovascular disease data in the disease portals at the Rat Genome Database. Physiological Genomics, 2016, 48, 589-600.	1.0	3
424	Identification and preliminary characterization of chemosensory perception-associated proteins in the melon fly Bactrocera cucurbitae using RNA-seq. Scientific Reports, 2016, 6, 19112.	1.6	29
425	SorghumFDB: sorghum functional genomics database with multidimensional network analysis. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw099.	1.4	47
426	The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw100.	1.4	1,085
427	GO annotation in InterPro: why stability does not indicate accuracy in a sea of changing annotations. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw027.	1.4	19
428	Characterization of patients at high risk of melanoma in Austria. British Journal of Dermatology, 2016, 174, 1308-1317.	1.4	10
429	The walnut (<i>Juglans regia</i>) genome sequence reveals diversity in genes coding for the biosynthesis of nonâ€structural polyphenols. Plant Journal, 2016, 87, 507-532.	2.8	233
430	Myeloid translocation genes differentially regulate colorectal cancer programs. Oncogene, 2016, 35, 6341-6349.	2.6	11
431	Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. Nucleic Acids Research, 2016, 44, W90-W97.	6.5	7,240
432	Characterization of frataxin gene network in Friedreich's ataxia fibroblasts using the RNA-Seq technique. Mitochondrion, 2016, 30, 59-66.	1.6	9
433	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. Nature Methods, 2016, 13, 651-656.	9.0	147
434	Proteomic Analysis of Mouse Oocytes Identifies PRMT7 as a Reprogramming Factor that Replaces SOX2 in the Induction of Pluripotent Stem Cells. Journal of Proteome Research, 2016, 15, 2407-2421.	1.8	42

#	Article	IF	Citations
435	A sunflower WRKY transcription factor stimulates the mobilization of seed-stored reserves during germination and post-germination growth. Plant Cell Reports, 2016, 35, 1875-1890.	2.8	27
436	Accelerating Adverse Outcome Pathway Development Using Publicly Available Data Sources. Current Environmental Health Reports, 2016, 3, 53-63.	3.2	64
437	Increased expression of AT-1/SLC33A1 causes an autistic-like phenotype in mice by affecting dendritic branching and spine formation. Journal of Experimental Medicine, 2016, 213, 1267-1284.	4.2	27
438	Screening of whole genome sequences identified high-impact variants for stallion fertility. BMC Genomics, 2016, 17, 288.	1.2	21
439	The link between orthology relations and gene trees: a correction perspective. Algorithms for Molecular Biology, 2016, 11, 4.	0.3	26
440	Old genes experience stronger translational selection than young genes. Gene, 2016, 590, 29-34.	1.0	11
441	RNA-Seq of Huntingtonâ€™s disease patient myeloid cells reveals innate transcriptional dysregulation associated with proinflammatory pathway activation. Human Molecular Genetics, 2016, 25, ddw142.	1.4	47
442	Mouse genome database 2016. Nucleic Acids Research, 2016, 44, D840-D847.	6.5	80
443	systemsDock: a web server for network pharmacology-based prediction and analysis. Nucleic Acids Research, 2016, 44, W507-W513.	6.5	135
444	ncRNA orthologies in the vertebrate lineage. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav127.	1.4	19
445	Chemoproteomic Approach to Explore the Target Profile of GPCR ligands: Application to 5â€HT_{1A} and 5â€HT₆ Receptors. Chemistry - A European Journal, 2016, 22, 1313-1321.	1.7	15
446	IQSEC2 and X-linked syndromal intellectual disability. Psychiatric Genetics, 2016, 26, 101-108.	0.6	15
447	Mutation analysis of Swedish haemophilia B families â€“ high frequency of unique mutations. Haemophilia, 2016, 22, 440-445.	1.0	17
448	The Proteome of Filter-Grown Caco-2 Cells With a Focus on Proteins Involved in Drug Disposition. Journal of Pharmaceutical Sciences, 2016, 105, 817-827.	1.6	58
449	Proteomic analysis for the identification of serum diagnostic markers for joint hypermobility syndrome. International Journal of Molecular Medicine, 2016, 37, 461-467.	1.8	11
450	Quantitative phosphoproteomics reveals genistein as a modulator of cell cycle and DNA damage response pathways in triple-negative breast cancer cells. International Journal of Oncology, 2016, 48, 1016-1028.	1.4	41
451	Piwi maintains germline stem cells and oogenesis in Drosophila through negative regulation of Polycomb group proteins. Nature Genetics, 2016, 48, 283-291.	9.4	46
452	Equine Arteritis Virus Uses Equine CXCL16 as an Entry Receptor. Journal of Virology, 2016, 90, 3366-3384.	1.5	19

#	Article	IF	Citations
453	Integrated Genomic and Network-Based Analyses of Complex Diseases and Human Disease Network. Journal of Genetics and Genomics, 2016, 43, 349-367.	1.7	21
454	Integrative genetic analysis of mouse and human AML identifies cooperating disease alleles. Journal of Experimental Medicine, 2016, 213, 25-34.	4.2	25
455	ALCOdb: Gene Coexpression Database for Microalgae. Plant and Cell Physiology, 2016, 57, e3-e3.	1.5	35
456	Quantitative tissue proteomic investigation of invasive ductal carcinoma of breast with luminal B HER2 positive and HER2 enriched subtypes towards potential diagnostic and therapeutic biomarkers. Journal of Proteomics, 2016, 132, 112-130.	1.2	25
457	Transcription factor ATF4 directs basal and stress-induced gene expression in the unfolded protein response and cholesterol metabolism in the liver. Molecular Biology of the Cell, 2016, 27, 1536-1551.	0.9	156
458	Identification of proteins that are differentially expressed in brains with Alzheimer's disease using iTRAQ labeling and tandem mass spectrometry. Journal of Proteomics, 2016, 139, 103-121.	1.2	48
459	Proteomic analysis of dystrophin deficiency and associated changes in the aged mdx-4cv heart model of dystrophinopathy-related cardiomyopathy. Journal of Proteomics, 2016, 145, 24-36.	1.2	46
460	M-sec regulates polarized secretion of inflammatory endothelial chemokines and facilitates CCL2-mediated lymphocyte transendothelial migration. Journal of Leukocyte Biology, 2016, 99, 1045-1055.	1.5	14
461	Transcription-associated processes cause DNA double-strand breaks and translocations in neural stem/progenitor cells. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2258-2263.	3.3	88
462	An epigenome-wide association meta-analysis of prenatal maternal stress in neonates: A model approach for replication. Epigenetics, 2016, 11, 140-149.	1.3	80
463	Citrullination-acetylation interplay guides E2F-1 activity during the inflammatory response. Science Advances, 2016, 2, e1501257.	4.7	64
464	Sperm proteomics: potential impact on male infertility treatment. Expert Review of Proteomics, 2016, 13, 285-296.	1.3	29
465	A potential endophenotype for Alzheimer's disease: cerebrospinal fluid clusterin. Neurobiology of Aging, 2016, 37, 208.e1-208.e9.	1.5	44
466	Arabidopsis CML38, a Calcium Sensor That Localizes to Ribonucleoprotein Complexes under Hypoxia Stress. Plant Physiology, 2016, 170, 1046-1059.	2.3	87
467	Identification of differentially methylated regions in new genes associated with knee osteoarthritis. Gene, 2016, 576, 312-318.	1.0	28
468	Ontology-Based Prediction and Prioritization of Gene Functional Annotations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 248-260.	1.9	18
469	Shoc2-tranduced ERK1/2 motility signals â€" Novel insights from functional genomics. Cellular Signalling, 2016, 28, 448-459.	1.7	13
470	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. Biotechnology Advances, 2016, 34, 663-686.	6.0	30

#	Article	IF	Citations
471	Exosomes as therapeutics: The implications of molecular composition and exosomal heterogeneity. Journal of Controlled Release, 2016, 228, 179-190.	4.8	279
472	PANTHER version 10: expanded protein families and functions, and analysis tools. Nucleic Acids Research, 2016, 44, D336-D342.	6.5	790
473	Extracellular Vesicles Originate from the Conceptus and Uterus During Early Pregnancy in Sheep1. Biology of Reproduction, 2016, 94, 56.	1.2	136
474	Cross-organism learning method to discover new gene functionalities. Computer Methods and Programs in Biomedicine, 2016, 126, 20-34.	2.6	17
475	The transcriptome of nitrofen-induced pulmonary hypoplasia in the rat model of congenital diaphragmatic hernia. Pediatric Research, 2016, 79, 766-775.	1.1	20
476	Ensembl 2016. Nucleic Acids Research, 2016, 44, D710-D716.	6.5	1,372
477	The Arabidopsis NRG2 Protein Mediates Nitrate Signaling and Interacts with and Regulates Key Nitrate Regulators. Plant Cell, 2016, 28, 485-504.	3.1	154
478	Large-scale inference of protein tissue origin in gram-positive sepsis plasma using quantitative targeted proteomics. Nature Communications, 2016, 7, 10261.	5.8	88
479	GTA: a game theoretic approach to identifying cancer subnetwork markers. Molecular BioSystems, 2016, 12, 818-825.	2.9	11
480	Nano-MoO₃-mediated synthesis of bioactive thiazolidin-4-ones acting as anti-bacterial agents and their mode-of-action analysis using in silico target prediction, docking and similarity searching. New Journal of Chemistry, 2016, 40, 2189-2199.	1.4	4
481	Exome arrays capture polygenic rare variant contributions to schizophrenia. Human Molecular Genetics, 2016, 25, 1001-1007.	1.4	54
482	Profiling of differential gene expression in the hypothalamus of broiler-type Taiwan country chickens in response to acute heat stress. Theriogenology, 2016, 85, 483-494.e8.	0.9	38
483	Fuzzy Correlated Association Mining: Selecting altered associations among the genes, and some possible marker genes mediating certain cancers. Applied Soft Computing Journal, 2016, 38, 587-605.	4.1	13
484	Human microRNAs profiling in response to influenza A viruses (subtypes pH1N1, H3N2, and H5N1). Experimental Biology and Medicine, 2016, 241, 409-420.	1.1	50
485	Differential expression profile of membrane proteins in L-02 cells exposed to trichloroethylene. Toxicology and Industrial Health, 2016, 32, 1774-1783.	0.6	1
486	NKX6.1 functions as a metastatic suppressor through epigenetic regulation of the epithelialâ€“mesenchymal transition. Oncogene, 2016, 35, 2266-2278.	2.6	26
487	Effect of Prolonged Simulated Microgravity on Metabolic Proteins in Rat Hippocampus: Steps toward Safe Space Travel. Journal of Proteome Research, 2016, 15, 29-37.	1.8	34
488	The application of multi-omics and systems biology to identify therapeutic targets in chronic kidney disease. Nephrology Dialysis Transplantation, 2016, 31, 2003-2011.	0.4	101

#	Article	IF	Citations
489	Protein function annotation using protein domain family resources. Methods, 2016, 93, 24-34.	1.9	32
490	Anti-amyloid compounds protect from silica nanoparticle-induced neurotoxicity in the nematode<i>C. elegans</i>. Nanotoxicology, 2016, 10, 426-435.	1.6	44
491	Microarray analyses to quantify advantages of 2D and 3D hydrogel culture systems in maintaining the native valvular interstitial cell phenotype. Biomaterials, 2016, 74, 31-41.	5.7	104
492	BVES regulates c-Myc stability via PP2A and suppresses colitis-induced tumourigenesis. Gut, 2017, 66, 852-862.	6.1	43
493	Genome-wide identification of Wnt/Î²-catenin transcriptional targets during Xenopus gastrulation. Developmental Biology, 2017, 426, 165-175.	0.9	42
494	Proteomic analysis of ovarian cancer cells during epithelial-mesenchymal transition (EMT) induced by epidermal growth factor (EGF) reveals mechanisms of cell cycle control. Journal of Proteomics, 2017, 151, 2-11.	1.2	40
495	Quantitative proteomic analysis of HIVâ€•1 Tatâ€•induced dysregulation in SHâ€•SY5Y neuroblastoma cells. Proteomics, 2017, 17, 1600236.	1.3	8
496	Transcriptomic analysis of human norovirus NS1-2 protein highlights a multifunctional role in murine monocytes. BMC Genomics, 2017, 18, 39.	1.2	32
497	TOP2A , HELLS , ATAD2 , and TET3 Are Novel Prognostic Markers in Renal Cell Carcinoma. Urology, 2017, 102, 265.e1-265.e7.	0.5	42
498	Extracellular MicroRNA Signature of Human Helper T Cell Subsets in Health and Autoimmunity. Journal of Biological Chemistry, 2017, 292, 2903-2915.	1.6	63
499	A novel embryo culture media supplement that improves pregnancy rates in mice. Reproduction, 2017, 153, 327-340.	1.1	7
500	In silico analysis of the deleterious nsSNPs (missense) in the homeobox domain of human <i>HOXB13</i> gene responsible for hereditary prostate cancer. Chemical Biology and Drug Design, 2017, 90, 188-199.	1.5	9
501	Genomic characterization of the evolutionary potential of the sea urchin <i>Strongylocentrotus droebachiensis</i> facing ocean acidification. Genome Biology and Evolution, 2016, 8, evw272.	1.1	11
502	Early differences in islets from prediabetic NOD mice: combined microarray and proteomic analysis. Diabetologia, 2017, 60, 475-489.	2.9	31
503	Caste-biased gene expression in a facultatively eusocial bee suggests a role for genetic accommodation in the evolution of eusociality. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20162228.	1.2	41
504	<i>IRAV</i> (<i>FLJ11286</i>), an Interferon-Stimulated Gene with Antiviral Activity against Dengue Virus, Interacts with MOV10. Journal of Virology, 2017, 91, .	1.5	54
505	Expression profiling and bioinformatic analyses suggest new target genes and pathways for human hair follicle related microRNAs. BMC Dermatology, 2017, 17, 3.	2.1	35
506	Blood Proteomic Profiling in Inherited (ATTRm) and Acquired (ATTRwt) Forms of Transthyretin-Associated Cardiac Amyloidosis. Journal of Proteome Research, 2017, 16, 1659-1668.	1.8	56

#	Article	IF	Citations
507	Annotating Mutational Effects on Proteins and Protein Interactions: Designing Novel and Revisiting Existing Protocols. Methods in Molecular Biology, 2017, 1550, 235-260.	0.4	18
508	Proteomic analysis of chondromodulin-I-induced differentiation of mesenchymal stem cells into chondrocytes. Journal of Proteomics, 2017, 159, 1-18.	1.2	3
509	IL-7Î´5 protein is expressed in human tissues and induces expression of the oxidized low density lipoprotein receptor 1 (OLR1) in CD14+ monocytes. International Journal of Infectious Diseases, 2017, 59, 29-36.	1.5	2
511	Toward Understanding the Cold, Hot, and Neutral Nature of Chinese Medicines Using in Silico Mode-of-Action Analysis. Journal of Chemical Information and Modeling, 2017, 57, 468-483.	2.5	59
512	Genomic characterisation of EÎ¼-Myc mouse lymphomas identifies Bcor as a Myc co-operative tumour-suppressor gene. Nature Communications, 2017, 8, 14581.	5.8	33
513	Triploid Atlantic salmon shows similar performance, fatty acid composition and proteome response to diploids during early freshwater rearing. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 22, 67-77.	0.4	13
514	Proteomic Profiling Analysis Reveals a Link between Experimental Autoimmune Uveitis and Complement Activation in Rats. Scandinavian Journal of Immunology, 2017, 85, 331-342.	1.3	9
515	Semi-synthetic sapogenin exerts neuroprotective effects by skewing the brain ischemia reperfusion transcriptome towards inflammatory resolution. Brain, Behavior, and Immunity, 2017, 64, 103-115.	2.0	2
516	Longitudinal peripheral blood transcriptional analysis of a patient with severe Ebola virus disease. Science Translational Medicine, 2017, 9, .	5.8	23
517	Noumeavirus replication relies on a transient remote control of the host nucleus. Nature Communications, 2017, 8, 15087.	5.8	91
518	Association between mutation status and left ventricular reverse remodelling in dilated cardiomyopathy. Heart, 2017, 103, 1704-1710.	1.2	64
519	Proteomic profiling of mdx-4cv serum reveals highly elevated levels of the inflammation-induced plasma marker haptoglobin in muscular dystrophy. International Journal of Molecular Medicine, 2017, 39, 1357-1370.	1.8	34
520	CBP/Catenin antagonists: Targeting LSCsâ€™ Achilles heel. Experimental Hematology, 2017, 52, 1-11.	0.2	13
521	Methodological Guidelines to Study Extracellular Vesicles. Circulation Research, 2017, 120, 1632-1648.	2.0	728
522	Multipronged quantitative proteomics reveals serum proteome alterations in breast cancer intrinsic subtypes. Journal of Proteomics, 2017, 163, 1-13.	1.2	18
523	Carbon dioxide-dependent regulation of NF-Îº B family members RelB and p100 gives molecular insight into CO2-dependent immune regulation. Journal of Biological Chemistry, 2017, 292, 11561-11571.	1.6	25
524	3â€² UTR G-quadruplexes regulate miRNA binding. Rna, 2017, 23, 1172-1179.	1.6	97
525	Proteome-Wide Protein Expression Profiling Across Five Pancreatic Cell Lines. Pancreas, 2017, 46, 690-698.	0.5	18

#	Article	IF	Citations
526	Differential gene expression in narrowâ€•and broadâ€headed European glass eels (<i>Anguilla) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74 chemotaxis. Molecular Ecology, 2017, 26, 3943-3953.	2.0	10
527	Quantitative proteomic analysis of EZH2 inhibition in acute myeloid leukemia reveals the targets and pathways that precede the induction of cell death. Proteomics - Clinical Applications, 2017, 11, 1700013.	0.8	5
528	Evolutionary History of Chemosensory-Related Gene Families across the Arthropoda. Molecular Biology and Evolution, 2017, 34, 1838-1862.	3.5	157
529	The Classification of Protein Domains. Methods in Molecular Biology, 2017, 1525, 137-164.	0.4	14
530	Information Visualization for Biological Data. Methods in Molecular Biology, 2017, 1526, 403-415.	0.4	2
531	Changes in the fine root proteome of Fagus sylvatica L. trees associated with P-deficiency and amelioration of P-deficiency. Journal of Proteomics, 2017, 169, 33-40.	1.2	10
532	Ageing and hypoxia cause protein aggregation in mitochondria. Cell Death and Differentiation, 2017, 24, 1730-1738.	5.0	40
533	MIDAS: Mining differentially activated subpaths of KEGG pathways from multi-class RNA-seq data. Methods, 2017, 124, 13-24.	1.9	15
534	Pathview Web: user friendly pathway visualization and data integration. Nucleic Acids Research, 2017, 45, W501-W508.	6.5	326
535	Comparative analysis of MBD-seq and MeDIP-seq and estimation of gene expression changes in a rodent model of schizophrenia. Genomics, 2017, 109, 204-213.	1.3	21
536	Proteomic analysis of bronchoalveolar lavage fluid (BALF) from lung cancer patients using label-free mass spectrometry. BBA Clinical, 2017, 7, 97-104.	4.1	25
537	Computational predictors fail to identify amino acid substitution effects at rheostat positions. Scientific Reports, 2017, 7, 41329.	1.6	47
538	Plant cholesterol biosynthetic pathway overlaps with phytosterol metabolism. Nature Plants, 2017, 3, 16205.	4.7	201
539	HMGB1 downâ€regulation mediates terameprocol vascular antiâ€proliferative effect in experimental pulmonary hypertension. Journal of Cellular Physiology, 2017, 232, 3128-3138.	2.0	5
540	Global Analysis of Protein Expression of Inner Ear Hair Cells. Journal of Neuroscience, 2017, 37, 1320-1339.	1.7	55
541	Evaluating Functional Annotations of Enzymes Using the Gene Ontology. Methods in Molecular Biology, 2017, 1446, 111-132.	0.4	14
542	Mobile-phone radiation-induced perturbation of gene-expression profiling, redox equilibrium and sporadic-apoptosis control in the ovary of<i>Drosophila melanogaster</i>. Fly, 2017, 11, 75-95.	0.9	11
543	Signatures of Selection and Interspecies Introgression in the Genome of Chinese Domestic Pigs. Genome Biology and Evolution, 2017, 9, 2592-2603.	1.1	43

#	ARTICLE	IF	CITATIONS
544	Alterations in mRNA 3â€² UTR Isoform Abundance Accompany Gene Expression Changes in Human Huntingtonâ€™s Disease Brains. Cell Reports, 2017, 20, 3057-3070.	2.9	40
545	Conserved expression of ultra-conserved noncoding RNA in mammalian nervous system. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 1159-1168.	0.9	14
546	Modelling the evolution of transcription factor binding preferences in complex eukaryotes. Scientific Reports, 2017, 7, 7596.	1.6	22
547	InÂVivo Expression of miR-32 Induces Proliferation in Prostate Epithelium. American Journal of Pathology, 2017, 187, 2546-2557.	1.9	16
548	A Systems Biology Approach to Understanding Alcoholic Liver Disease Molecular Mechanism: The Development of Static and Dynamic Models. Bulletin of Mathematical Biology, 2017, 79, 2450-2473.	0.9	5
549	The <i>Arabidopsis CPSF30â€Ł</i> gene plays an essential role in nitrate signaling and regulates the nitrate transceptor gene <i><scp>NRT</scp>1.1</i>. New Phytologist, 2017, 216, 1205-1222.	3.5	59
550	Serum Proteomic Variability Associated with Clinical Phenotype in Familial Transthyretin Amyloidosis (ATTRm). Journal of Proteome Research, 2017, 16, 4104-4112.	1.8	5
551	Global Analysis of Membrane-associated Protein Oligomerization Using Protein Correlation Profiling. Molecular and Cellular Proteomics, 2017, 16, 1972-1989.	2.5	32
552	NFATc1 controls the cytotoxicity of CD8+ T cells. Nature Communications, 2017, 8, 511.	5.8	150
553	Molecular modeling and structure-based drug discovery approach reveals protein kinases as off-targets for novel anticancer drug RH1. Medical Oncology, 2017, 34, 176.	1.2	7
554	Candidate genes for male and female reproductive traits in Canchim beef cattle. Journal of Animal Science and Biotechnology, 2017, 8, 67.	2.1	32
555	Genome reconstruction in Cynara cardunculus taxa gains access to chromosome-scale DNA variation. Scientific Reports, 2017, 7, 5617.	1.6	30
556	Mutation intolerant genes and targets of FMRP are enriched for nonsynonymous alleles in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 724-731.	1.1	19
557	Evolutionary dynamics of the kinetochore network in eukaryotes as revealed by comparative genomics. EMBO Reports, 2017, 18, 1559-1571.	2.0	206
558	MicroRNA-200b regulates distal airway development by maintaining epithelial integrity. Scientific Reports, 2017, 7, 6382.	1.6	34
559	Proteomic profiling of the dystrophin complex and membrane fraction from dystrophic mdx muscle reveals decreases in the cytolinker desmoglein and increases in the extracellular matrix stabilizers biglycan and fibronectin. Journal of Muscle Research and Cell Motility, 2017, 38, 251-268.	0.9	34
560	DNA hypermethylation induced by Epstein-Barr virus in the development of Epstein-Barr virus-associated gastric carcinoma. Archives of Pharmacal Research, 2017, 40, 894-905.	2.7	17
561	Progranulin deficiency causes impairment of autophagy and TDP-43 accumulation. Journal of Experimental Medicine, 2017, 214, 2611-2628.	4.2	101

#	ARTICLE	IF	CITATIONS
562	Genomic assessment in Lactobacillus plantarum links the butyrogenic pathway with glutamine metabolism. Scientific Reports, 2017, 7, 15975.	1.6	25
563	Recent advances and clinical insights into the use of proteomics in the study of atherosclerosis. Expert Review of Proteomics, 2017, 14, 701-713.	1.3	6
564	Best Practices in Manual Annotation with the Gene Ontology. Methods in Molecular Biology, 2017, 1446, 41-54.	0.4	21
565	Medium term water deficit elicits distinct transcriptome responses in Eucalyptus species of contrasting environmental origin. BMC Genomics, 2017, 18, 284.	1.2	16
566	Whole genome sequencing identifies missense mutation in MTBP in Shar-Pei affected with Autoinflammatory Disease (SPAID). BMC Genomics, 2017, 18, 348.	1.2	9
567	Proteomic analysis of mucopolysaccharidosis I mouse brain with two-dimensional polyacrylamide gel electrophoresis. Molecular Genetics and Metabolism, 2017, 120, 101-110.	0.5	12
568	Connectome Disconnectivity and Cortical Gene Expression in Patients With Schizophrenia. Biological Psychiatry, 2017, 81, 495-502.	0.7	163
569	Proteomic level changes associated with S3I201 treated U87 glioma cells. Journal of Proteomics, 2017, 150, 341-350.	1.2	6
570	Development of a RNA-Seq Based Prognostic Signature in Lung Adenocarcinoma. Journal of the National Cancer Institute, 2017, 109, djw200.	3.0	150
571	MeSH term-based semantic analysis of microRNA regulation on glucocorticoid resistance in pediatric acute lymphoblastic leukemia. , 2017, , .		1
572	The Human Blood-Nerve Barrier Transcriptome. Scientific Reports, 2017, 7, 17477.	1.6	33
573	Proteomic characterization of paired non-malignant and malignant African-American prostate epithelial cell lines distinguishes them by structural proteins. BMC Cancer, 2017, 17, 480.	1.1	6
574	Gene annotations prediction using singular value decomposition and independent component analysis. , 2017, , .		0
575	Phosphoproteomic analysis of the antitumor effects of ginsenoside Rg3 in human breast cancer cells. Oncology Letters, 2017, 15, 2889-2898.	0.8	10
576	De novo genome assembly and annotation of Australia's largest freshwater fish, the Murray cod (Maccullochella peelii), from Illumina and Nanopore sequencing read. GigaScience, 2017, 6, 1-6.	3.3	57
577	Response of Turkey Muscle Satellite Cells to Thermal Challenge. II. Transcriptome Effects in Differentiating Cells. Frontiers in Physiology, 2017, 8, 948.	1.3	15
578	Transcriptomic Response of Purple Willow (Salix purpurea) to Arsenic Stress. Frontiers in Plant Science, 2017, 8, 1115.	1.7	32
579	Big Regeneration Mechanisms via Systems Biology and Big Database Mining Methods. , 2017, , 373-430.		0

#	ARTICLE	IF	CITATIONS
580	Impaired response of the bronchial epithelium to inflammation characterizes severe equine asthma. BMC Genomics, 2017, 18, 708.	1.2	32
581	In vivo Host-Pathogen Interaction as Revealed by Global Proteomic Profiling of Zebrafish Larvae. Frontiers in Cellular and Infection Microbiology, 2017, 7, 334.	1.8	48
582	Isogenic Cellular Systems Model the Impact of Genetic Risk Variants in the Pathogenesis of Type 1 Diabetes. Frontiers in Endocrinology, 2017, 8, 276.	1.5	17
583	A Comprehensive Gene Expression Meta-analysis Identifies Novel Immune Signatures in Rheumatoid Arthritis Patients. Frontiers in Immunology, 2017, 8, 74.	2.2	35
584	InlL from Listeria monocytogenes Is Involved in Biofilm Formation and Adhesion to Mucin. Frontiers in Microbiology, 2017, 8, 660.	1.5	59
585	Time-Dependent, HIV-Tat-Induced Perturbation of Human Neurons In Vitro: Towards a Model for the Molecular Pathology of HIV-Associated Neurocognitive Disorders. Frontiers in Molecular Neuroscience, 2017, 10, 163.	1.4	6
586	Involvement of Chromatin Remodeling Genes and the Rho GTPases RhoB and CDC42 in Ovarian Clear Cell Carcinoma. Frontiers in Oncology, 2017, 7, 109.	1.3	20
587	Tubulin Beta-3 Chain as a New Candidate Protein Biomarker of Human Skin Aging: A Preliminary Study. Oxidative Medicine and Cellular Longevity, 2017, 2017, 1-21.	1.9	16
588	Genomic regions associated with host response to porcine reproductive and respiratory syndrome vaccination and co-infection in nursery pigs. BMC Genomics, 2017, 18, 865.	1.2	18
589	Impact of genetic variation on three dimensional structure and function of proteins. PLoS ONE, 2017, 12, e0171355.	1.1	55
590	A sorghum (Sorghum bicolor) mutant with altered carbon isotope ratio. PLoS ONE, 2017, 12, e0179567.	1.1	5
591	CytoGTA: A cytoscape plugin for identifying discriminative subnetwork markers using a game theoretic approach. PLoS ONE, 2017, 12, e0185016.	1.1	5
592	Investigation of mutations in the HBB gene using the 1,000 genomes database. PLoS ONE, 2017, 12, e0174637.	1.1	29
593	Highly accessible AU-rich regions in 3â€™ untranslated regions are hotspots for binding of regulatory factors. PLoS Computational Biology, 2017, 13, e1005460.	1.5	47
594	A proteomic insight into the midgut proteome of Ornithodoros moubata females reveals novel information on blood digestion in argasid ticks. Parasites and Vectors, 2017, 10, 366.	1.0	33
595	Whole transcriptome RNA-Seq analysis reveals extensive cell type-specific compartmentalization in Volvox carteri. BMC Biology, 2017, 15, 111.	1.7	19
596	Differential gene expression in disease: a comparison between high-throughput studies and the literature. BMC Medical Genomics, 2017, 10, 59.	0.7	66
597	Genome-wide scan for runs of homozygosity identifies potential candidate genes associated with local adaptation in Valle del Belice sheep. Genetics Selection Evolution, 2017, 49, 84.	1.2	146

#	ARTICLE	IF	CITATIONS
598	Orthonome â€" a new pipeline for predicting high quality orthologue gene sets applicable to complete and draft genomes. BMC Genomics, 2017, 18, 673.	1.2	11
599	Genomewide association of piglet responses to infection with one of two porcine reproductive and respiratory syndrome virus isolates1. Journal of Animal Science, 2017, 95, 16-38.	0.2	26
600	042 Genome-wide association of myoglobin concentrations in pork loins. Journal of Animal Science, 2017, 95, 20-20.	0.2	2
601	An investigation of methyl tert-butyl ether-induced cytotoxicity and protein profile in Chinese hamster ovary cells. Molecular Medicine Reports, 2017, 16, 8595-8604.	1.1	6
602	Quantitative proteomics analysis of the role of tetraspanin-8 in the drug resistance of gastric cancer. International Journal of Oncology, 2018, 52, 473-484.	1.4	7
603	Proteomic profiling of early degenerative retina of RCS rats. International Journal of Ophthalmology, 2017, 10, 878-889.	0.5	6
604	Big Drug Design Mechanisms via Systems Biology and Big Database Mining. , 2017, , 737-845.		1
605	Exploring autophagy with Gene Ontology. Autophagy, 2018, 14, 419-436.	4.3	64
606	Pathway and Network Analysis of Differentially Expressed Genes in Transcriptomes. Methods in Molecular Biology, 2018, 1751, 35-55.	0.4	4
607	Systematic Protein Prioritization for Targeted Proteomics Studies through Literature Mining. Journal of Proteome Research, 2018, 17, 1383-1396.	1.8	16
608	RSRC1 mutation affects intellect and behaviour through aberrant splicing and transcription, downregulating IGFBP3. Brain, 2018, 141, 961-970.	3.7	20
609	The Substrates of Nonsense-Mediated mRNA Decay in<i>Caenorhabditis elegans</i>. G3: Genes, Genomes, Genetics, 2018, 8, 195-205.	0.8	18
610	Zinc oxide nanoparticles induce murine photoreceptor cell death via mitochondria-related signaling pathway. Artificial Cells, Nanomedicine and Biotechnology, 2018, 46, 1102-1113.	1.9	27
611	Changes in transcriptomic profile of trout larvae obtained with frozen sperm. Aquaculture, 2018, 492, 306-320.	1.7	10
612	RNA-Seq-mediated transcriptomic analysis of heat stress response in a polar Chlorella sp. (Trebouxiophyceae, Chlorophyta). Journal of Applied Phycology, 2018, 30, 3103-3119.	1.5	16
613	<i>Bombyx mori</i> epidermal growth factor receptor is required for nucleopolyhedrovirus replication. Insect Molecular Biology, 2018, 27, 464-477.	1.0	9
614	IreA Controls Endoplasmic Reticulum Stress-Induced Autophagy and Survival through Homeostasis Recovery. Molecular and Cellular Biology, 2018, 38, .	1.1	14
615	Genomic analysis of synchronous intracranial meningiomas with different histological grades. Journal of Neuro-Oncology, 2018, 138, 41-48.	1.4	2

#	ARTICLE	IF	CITATIONS
616	The vesicle trafficking regulator PN_SCD1 is demethylated and overexpressed in florets of apomictic Paspalum notatum genotypes. Scientific Reports, 2018, 8, 3030.	1.6	16
617	Quantitative genetic methods depending on the nature of the phenotypic trait. Annals of the New York Academy of Sciences, 2018, 1422, 29-47.	1.8	56
618	Development of a Photo-Cross-Linkable Diaminoquinazoline Inhibitor for Target Identification in <i>Plasmodium falciparum</i>. ACS Infectious Diseases, 2018, 4, 523-530.	1.8	20
619	A quantitative and temporal map of proteostasis during heat shock in<i>Saccharomyces cerevisiae</i>. Molecular Omics, 2018, 14, 37-52.	1.4	17
620	The Wnt/Î²â€catenin pathway determines the predisposition and efficiency of liverâ€toâ€pancreas reprogramming. Hepatology, 2018, 68, 1589-1603.	3.6	18
621	The genome sequence of the soft-rot fungus <i>Penicillium purpurogenum</i> reveals a high gene dosage for lignocellulolytic enzymes. Mycology, 2018, 9, 59-69.	2.0	12
622	Amniotic fluid stem cell exosomes: Therapeutic perspective. BioFactors, 2018, 44, 158-167.	2.6	42
623	Personalized Proteomics in Proliferative Vitreoretinopathy Implicate Hematopoietic Cell Recruitment and mTOR as a Therapeutic Target. American Journal of Ophthalmology, 2018, 186, 152-163.	1.7	34
624	Wnt Signaling in Stem Cells and Cancer Stem Cells: A Tale of Two Coactivators. Progress in Molecular Biology and Translational Science, 2018, 153, 209-244.	0.9	40
625	Network-based technologies for early drug discovery. Drug Discovery Today, 2018, 23, 626-635.	3.2	72
626	Systems Biology Modeling to Study Pathogenâ€“Host Interactions. Methods in Molecular Biology, 2018, 1734, 97-112.	0.4	13
627	Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism. Nature Genetics, 2018, 50, 6-11.	9.4	327
628	Human DNA Repair Genes Possess Potential G-Quadruplex Sequences in Their Promoters and 5â€²-Untranslated Regions. Biochemistry, 2018, 57, 991-1002.	1.2	55
629	The MEROPS database of proteolytic enzymes, their substrates and inhibitors in 2017 and a comparison with peptidases in the PANTHER database. Nucleic Acids Research, 2018, 46, D624-D632.	6.5	1,234
630	MicroRNA-7 mediates cross-talk between metabolic signaling pathways in the liver. Scientific Reports, 2018, 8, 361.	1.6	24
631	A Proteomic-Based Approach to Study the Mechanism of Cytotoxicity Induced by Interleukin-1Î± and Cycloheximide. Chromatographia, 2018, 81, 47-56.	0.7	2
632	Unraveling the human protein atlas of metastatic melanoma in the course of ultraviolet radiation-derived photo-therapy. Journal of Proteomics, 2018, 188, 119-138.	1.2	4
633	Liver proteome response of pre-harvest Atlantic salmon following exposure to elevated temperature. BMC Genomics, 2018, 19, 133.	1.2	43

#	Article	IF	Citations
634	Analysis of human ES cell differentiation establishes that the dominant isoforms of the lncRNAs RMST and FIRRE are circular. BMC Genomics, 2018, 19, 276.	1.2	43
635	Constraints on signaling network logic reveal functional subgraphs on Multiple Myeloma OMIC data. BMC Systems Biology, 2018, 12, 32.	3.0	3
636	Functional and structural characterization of osteocytic MLO-Y4 cell proteins encoded by genes differentially expressed in response to mechanical signals in vitro. Scientific Reports, 2018, 8, 6716.	1.6	11
637	Genome-wide identification of runs of homozygosity islands and associated genes in local dairy cattle breeds. Animal, 2018, 12, 2480-2488.	1.3	65
638	Germline Variants in the POT1-Gene in High-Risk Melanoma Patients in Austria. G3: Genes, Genomes, Genetics, 2018, 8, 1475-1480.	0.8	12
639	Deregulated microRNA and mRNA expression profiles in the peripheral blood of patients with Marfan syndrome. Journal of Translational Medicine, 2018, 16, 60.	1.8	23
640	Clinical genetic strategies for early onset neurodegenerative diseases. Molecular and Cellular Toxicology, 2018, 14, 123-142.	0.8	20
641	Monitoring Transcriptomic Changes in Soil-Grown Roots and Shoots of Arabidopsis thaliana Subjected to a Progressive Drought Stress. Methods in Molecular Biology, 2018, 1761, 223-230.	0.4	3
642	Genome, transcriptome and proteome: the rise of omics data and their integration in biomedical sciences. Briefings in Bioinformatics, 2018, 19, 286-302.	3.2	498
643	Transcriptome sequencing of an Antarctic microalga, Chlorella sp. (Trebouxiophyceae, Chlorophyta) subjected to short-term ultraviolet radiation stress. Journal of Applied Phycology, 2018, 30, 87-99.	1.5	27
644	Pharmacogenomics of 17â€alpha hydroxyprogesterone caproate for recurrent preterm birth: a caseâ€“control study. BJOG: an International Journal of Obstetrics and Gynaecology, 2018, 125, 343-350.	1.1	10
645	Novel clinical and molecular findings in Spanish patients with naevoid basal cell carcinoma syndrome. British Journal of Dermatology, 2018, 178, 198-206.	1.4	5
646	Challenges in defining the role of intron retention in normal biology and disease. Seminars in Cell and Developmental Biology, 2018, 75, 40-49.	2.3	51
647	Nitrogen â€“ essential macronutrient and signal controlling flowering time. Physiologia Plantarum, 2018, 162, 251-260.	2.6	36
648	Comparative transcriptomics of cyprinid minnows and carp in a common wild setting: a resource for ecological genomics in freshwater communities. DNA Research, 2018, 25, 11-23.	1.5	2
649	Identification of Slug and SOX7 as transcriptional repressors binding to the hepatitis B virus core promoter. Journal of Hepatology, 2018, 68, 42-52.	1.8	9
650	Systematic-analysis of mRNA expression profiles in skeletal muscle of patients with type II diabetes: The glucocorticoid was central in pathogenesis. Journal of Cellular Physiology, 2018, 233, 4068-4076.	2.0	8
651	Analysis of neuronal phosphoproteome reveals PINK1 regulation of BAD function and cell death. Cell Death and Differentiation, 2018, 25, 904-917.	5.0	28

#	ARTICLE	IF	CITATIONS
652	A microRNA feedback loop regulates global microRNA abundance during aging. Rna, 2018, 24, 159-172.	1.6	37
653	Synthetic microbial consortia enable rapid assembly of pure translation machinery. Nature Chemical Biology, 2018, 14, 29-35.	3.9	56
654	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. Molecular Psychiatry, 2018, 23, 1169-1180.	4.1	32
655	Rapid microevolution during recent range expansion to harsh environments. BMC Evolutionary Biology, 2018, 18, 187.	3.2	29
656	Comprehensive and critical evaluation of individualized pathway activity measurement tools on pan-cancer data. Briefings in Bioinformatics, 2018, , .	3.2	14
657	Genome-wide methylation study of whole blood cellsï¿½DNA in men with congenital hypopituitarism disease. International Journal of Molecular Medicine, 2019, 43, 155-166.	1.8	3
658	Heterotrimeric Gâ€Proteinâ€Dependent Proteome and Phosphoproteome in Unstimulated Arabidopsis Roots. Proteomics, 2018, 18, e1800323.	1.3	26
659	Functional annotation of differentially expressed fetal cardiac microRNA targets: implication for microRNA-based cardiovascular therapeutics. 3 Biotech, 2018, 8, 494.	1.1	9
660	Dawn regulates guard cell proteins in Arabidopsis thaliana that function in ATP production from fatty acid beta-oxidation. Plant Molecular Biology, 2018, 98, 525-543.	2.0	10
661	A Transcriptome Study of Progeroid Neurocutaneous Syndrome Reveals POSTN As a New Element in Proline Metabolic Disorder. , 2018, 9, 1043.		3
662	Secretory High-Mobility Group Box 1 Protein Affects Regulatory T Cell Differentiation in Neuroblastoma Microenvironment<i>In Vitro</i>. Journal of Oncology, 2018, 2018, 1-12.	0.6	14
663	Melatonin regulation of transcription in the reversal of morphine tolerance: Microarray analysis of differential gene expression. International Journal of Molecular Medicine, 2019, 43, 791-806.	1.8	10
664	Genes known to escape X chromosome inactivation predict coâ€morbid chronic musculoskeletal pain and posttraumatic stress symptom development in women following trauma exposure. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 415-427.	1.1	13
665	Membrane proteome characterization of periodontal ligament cell sets from deciduous and permanent teeth. Journal of Periodontology, 2019, 90, 775-787.	1.7	5
666	Promotion of Myoblast Differentiation by Fkbp5 via Cdk4 Isomerization. Cell Reports, 2018, 25, 2537-2551.e8.	2.9	26
667	Repetitive somatic embryogenesis induced cytological and proteomic changes in embryogenic lines of Pseudotsuga menziesii [Mirb.]. BMC Plant Biology, 2018, 18, 164.	1.6	33
668	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	9.4	169
669	HomodimerizationÂregulates an endothelial specific signature of the SOX18 transcription factor. Nucleic Acids Research, 2018, 46, 11381-11395.	6.5	21

#	ARTICLE	IF	CITATIONS
670	Identification of Kinases and Interactors of p53 Using Kinase-Catalyzed Cross-Linking and Immunoprecipitation. Journal of the American Chemical Society, 2018, 140, 16299-16310.	6.6	12
671	Nuclear Factor I Represses the Notch Effector HEY1 in Glioblastoma. Neoplasia, 2018, 20, 1023-1037.	2.3	24
672	A High-Resolution Proteomic Landscaping of Primary Human Dental Stem Cells: Identification of SHED- and PDLSC-Specific Biomarkers. International Journal of Molecular Sciences, 2018, 19, 158.	1.8	16
673	Whole-transcriptomic Profile of SK-MEL-3 Melanoma Cells Treated with the Histone Deacetylase Inhibitor: Trichostatin A. Cancer Genomics and Proteomics, 2018, 15, 349-364.	1.0	22
674	Comprehensive innate immune profiling of chikungunya virus infection in pediatric cases. Molecular Systems Biology, 2018, 14, e7862.	3.2	66
675	Comparative proteomic analysis of normal and gliotic PVR retina and contribution of MÃ¼ller glia to this profile. Experimental Eye Research, 2018, 177, 197-207.	1.2	17
676	Genomeâ€“wide binding of transcription factor ZEB1 in tripleâ€negative breast cancer cells. Journal of Cellular Physiology, 2018, 233, 7113-7127.	2.0	32
677	Analysis of the impact of corticosteroids adjuvant treatment during experimental invasive meningococcal infection in mice. Steroids, 2018, 136, 32-39.	0.8	2
678	Proteomic changes during adult stage in pre-optic, hypothalamus, hippocampus and pituitary regions of female rat brain following neonatal exposure to estradiol-17Î². General and Comparative Endocrinology, 2018, 266, 126-134.	0.8	3
679	Analysis Methods for Shotgun Metagenomics. Computational Biology, 2018, , 71-112.	0.1	1
680	Theoretical and Applied Aspects of Systems Biology. Computational Biology, 2018, , .	0.1	3
681	A reassessment of DNA-immunoprecipitation-based genomic profiling. Nature Methods, 2018, 15, 499-504.	9.0	92
682	Role of differentially expressed genes and long nonâ€coding RNAs in papillary thyroid carcinoma diagnosis, progression, and prognosis. Journal of Cellular Biochemistry, 2018, 119, 8249-8259.	1.2	35
683	Nudgeâ€nudge, <scp>WNK</scp>â€<scp>WNK</scp> (kinases), say no more?. New Phytologist, 2018, 220, 35-48.	3.5	32
684	CRISPR screens identify genomic ribonucleotides as a source of PARP-trapping lesions. Nature, 2018, 559, 285-289.	13.7	297
685	Drug Targeting and Biomarkers in Head and Neck Cancers: Insights from Systems Biology Analyses. OMICS A Journal of Integrative Biology, 2018, 22, 422-436.	1.0	49
686	A Meta-Analysis Characterizing Stem-Like Gene Expression in the Suprachiasmatic Nucleus and Its Circadian Clock. BioMed Research International, 2018, 2018, 1-11.	0.9	9
687	Nuclear receptor/Wnt beta-catenin interactions are regulated via differential CBP/p300 coactivator usage. PLoS ONE, 2018, 13, e0200714.	1.1	16

#	ARTICLE	IF	CITATIONS
688	The human CIB1â€"EVER1â€"EVER2 complex governs keratinocyte-intrinsic immunity to Î²-papillomaviruses. Journal of Experimental Medicine, 2018, 215, 2289-2310.	4.2	92
689	Plasminogen activator inhibitor-1 and tenascin-C secreted by equine mesenchymal stromal cells stimulate dermal fibroblast migration in vitro and contribute to wound healing in vivo. Cytotherapy, 2018, 20, 1061-1076.	0.3	27
690	A semantics-oriented computational approach to investigate microRNA regulation on glucocorticoid resistance in pediatric acute lymphoblastic leukemia. BMC Medical Informatics and Decision Making, 2018, 18, 57.	1.5	12
691	Implication of OPRM1 A118G Polymorphism in Opioids Addicts in Pakistan: In vitro and In silico Analysis. Journal of Molecular Neuroscience, 2018, 65, 472-479.	1.1	18
692	Development and validation of an updated computational model of Streptomyces coelicolor primary and secondary metabolism. BMC Genomics, 2018, 19, 519.	1.2	20
693	Phosphatidylserine-Liposomes Promote Tolerogenic Features on Dendritic Cells in Human Type 1 Diabetes by Apoptotic Mimicry. Frontiers in Immunology, 2018, 9, 253.	2.2	58
694	Oxytosis/Ferroptosisâ€"(Re-) Emerging Roles for Oxidative Stress-Dependent Non-apoptotic Cell Death in Diseases of the Central Nervous System. Frontiers in Neuroscience, 2018, 12, 214.	1.4	197
695	Data driven point packing for fast clustering. , 2018, , .		3
696	Heterogeneity and interplay of the extracellular vesicle small RNA transcriptome and proteome. Scientific Reports, 2018, 8, 10813.	1.6	118
697	Transcription factor induced conversion of human fibroblasts towards the hair cell lineage. PLoS ONE, 2018, 13, e0200210.	1.1	26
698	GATA3 as a master regulator and therapeutic target in ovarian highâ€grade serous carcinoma stem cells. International Journal of Cancer, 2018, 143, 3106-3119.	2.3	31
699	Potential biomarkers and therapeutic targets in cervical cancer: Insights from the meta-analysis of transcriptomics data within network biomedicine perspective. PLoS ONE, 2018, 13, e0200717.	1.1	89
700	Effect of the sequence data deluge on the performance of methods for detecting protein functional residues. BMC Bioinformatics, 2018, 19, 67.	1.2	4
701	Genomewide binding of transcription factor Snail1 in tripleâ€negative breast cancer cells. Molecular Oncology, 2018, 12, 1153-1174.	2.1	22
702	Proteome analysis of the potential serum biomarkers for chronic benzene poisoning. Environmental Toxicology and Pharmacology, 2018, 60, 157-164.	2.0	4
703	OrthoList 2: A New Comparative Genomic Analysis of Human and <i>Caenorhabditis elegans</i> Genes. Genetics, 2018, 210, 445-461.	1.2	233
704	Genomic analysis reveals recurrent deletion of JAKâ€STAT signaling inhibitors <i>HNRNPK</i> and <i>SOCS1</i> in mycosis fungoides. Genes Chromosomes and Cancer, 2018, 57, 653-664.	1.5	56
705	Neurog3-dependent pancreas dysgenesis causes ectopic pancreas in Hes1 mutants. Development (Cambridge), 2018, 145, .	1.2	15

#	Article	IF	Citations
706	Identification of genomic regions harboring diversity between Holstein and two local endangered breeds, Modenese and Maremmana. Livestock Science, 2018, 216, 75-83.	0.6	3
707	Solid phase chemistry to covalently and reversibly capture thiolated RNA. Nucleic Acids Research, 2018, 46, 6996-7005.	6.5	21
708	Establishing the role of PLVAP in protein-losing enteropathy: a homozygous missense variant leads to an attenuated phenotype. Journal of Medical Genetics, 2018, 55, 779-784.	1.5	14
709	Proteomic analysis of corneal endothelial cell-descemet membrane tissues reveals influence of insulin dependence and disease severity in type 2 diabetes mellitus. PLoS ONE, 2018, 13, e0192287.	1.1	19
710	HMMER Cut-off Threshold Tool (HMMERCTTER): Supervised classification of superfamily protein sequences with a reliable cut-off threshold. PLoS ONE, 2018, 13, e0193757.	1.1	16
711	Kinase Substrate Profiling Using a Proteome-wide Serine-Oriented Human Peptide Library. Biochemistry, 2018, 57, 4717-4725.	1.2	16
712	A novel SRC-2-dependent regulation of epithelial-mesenchymal transition in breast cancer cells. Journal of Steroid Biochemistry and Molecular Biology, 2019, 185, 57-70.	1.2	5
713	Biological Database Searching. , 2019, , 29-38.		0
714	Biological and Medical Ontologies: GO and GOA. , 2019, , 823-831.		1
715	Systems-Based Interactome Analysis for Hematopoiesis Effect of Angelicae sinensis Radix: Regulated Network of Cell Proliferation towards Hemopoiesis. Chinese Journal of Integrative Medicine, 2019, 25, 939-947.	0.7	4
716	lncRNA in worms â€" Time to meet the neighbors. Current Opinion in Systems Biology, 2019, 13, 10-15.	1.3	1
717	Type II Epithelial-Mesenchymal Transition Upregulates Protein N-Glycosylation To Maintain Proteostasis and Extracellular Matrix Production. Journal of Proteome Research, 2019, 18, 3447-3460.	1.8	21
718	Synaptotagmin 17 controls neurite outgrowth and synaptic physiology via distinct cellular pathways. Nature Communications, 2019, 10, 3532.	5.8	26
719	Total Polysaccharides of Lily Bulb Ameliorate Menopause-Like Behavior in Ovariectomized Mice: Multiple Mechanisms Distinct from Estrogen Therapy. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-27.	1.9	8
720	The impact of SOCS1 mutations in diffuse large Bâ€cell lymphoma. British Journal of Haematology, 2019, 187, 627-637.	1.2	15
721	Targeting of lipid metabolism with a metabolic inhibitor cocktail eradicates peritoneal metastases in ovarian cancer cells. Communications Biology, 2019, 2, 281.	2.0	67
722	Transcriptomic characterisation of the optimised rat model of Walker 256 breast cancer cellâ€induced bone pain. Clinical and Experimental Pharmacology and Physiology, 2019, 46, 1201-1215.	0.9	2
723	Mutational analysis of BRCA1 and BRCA2 genes in women with familial breast cancer from different regions of Colombia. Hereditary Cancer in Clinical Practice, 2019, 17, 20.	0.6	6

#	ARTICLE	IF	CITATIONS
724	Quantitative proteomics of milk whey reveals breed and season specific variation in protein abundance in Holstein Friesian cow and Murrah buffalo. Research in Veterinary Science, 2019, 125, 244-252.	0.9	14
725	Estimating dispensable content in the human interactome. Nature Communications, 2019, 10, 3205.	5.8	9
726	Gene expression profile of human T cells following a single stimulation of peripheral blood mononuclear cells with anti-CD3 antibodies. BMC Genomics, 2019, 20, 593.	1.2	12
727	TAF1, associated with intellectual disability in humans, is essential for embryogenesis and regulates neurodevelopmental processes in zebrafish. Scientific Reports, 2019, 9, 10730.	1.6	28
728	Differential gene expression and gene ontologies associated with increasing water-stress in leaf and root transcriptomes of perennial ryegrass (Lolium perenne). PLoS ONE, 2019, 14, e0220518.	1.1	4
729	Global gene expression reveals an increase of HMGB1 and APEX1 proteins and their involvement in oxidative stress, apoptosis and inflammation pathways among betaâ€thalassaemia intermedia and major phenotypes. British Journal of Haematology, 2019, 186, 608-619.	1.2	7
730	Glial Î±â€synuclein promotes neurodegeneration characterized by a distinct transcriptional program in vivo. Glia, 2019, 67, 1933-1957.	2.5	27
731	Proteomic analysis in cells treated with pristine carbon nano-onions and its subcellular localization. Advances in Natural Sciences: Nanoscience and Nanotechnology, 2019, 10, 035011.	0.7	4
732	A Hormone That Lost Its Receptor: Anti-MÃ¼llerian Hormone (AMH) in Zebrafish Gonad Development and Sex Determination. Genetics, 2019, 213, 529-553.	1.2	45
733	Bone Marrow Mesenchymal Stem Cells' Secretome Exerts Neuroprotective Effects in a Parkinson's Disease Rat Model. Frontiers in Bioengineering and Biotechnology, 2019, 7, 294.	2.0	70
734	Co-Localization of DNA i-Motif-Forming Sequences and 5-Hydroxymethyl-cytosines in Human Embryonic Stem Cells. Molecules, 2019, 24, 3619.	1.7	3
735	Discovery of Functional SNPs via Genome-Wide Exploration of Malaysian Pigmented Rice Varieties. International Journal of Genomics, 2019, 2019, 1-12.	0.8	4
736	Considerations and Implications in the Purification of Extracellular Vesicles â€“ A Cautionary Tale. Frontiers in Neuroscience, 2019, 13, 1067.	1.4	39
737	Silenced ZNF154 Is Associated with Longer Survival in Resectable Pancreatic Cancer. International Journal of Molecular Sciences, 2019, 20, 5437.	1.8	7
738	Quantitative Proteomics Reveals Remodeling of Protein Repertoire Across Life Phases of <i>Daphnia pulex</i>. Proteomics, 2019, 19, e1900155.	1.3	2
739	Effects of Iron Oxide Nanoparticles (Î³-Fe2O3) on Liver, Lung and Brain Proteomes following Sub-Acute Intranasal Exposure: A New Toxicological Assessment in Rat Model Using iTRAQ-Based Quantitative Proteomics. International Journal of Molecular Sciences, 2019, 20, 5186.	1.8	12
740	Comparative co-expression network analysis extracts the <i>SlHSP70</i> gene affecting to shoot elongation of tomato. Plant Biotechnology, 2019, 36, 143-153.	0.5	8
741	Gene Cascade Finder: A tool for identification of gene cascades and its application in Caenorhabditis elegans. PLoS ONE, 2019, 14, e0215187.	1.1	5

#	ARTICLE	IF	CITATIONS
742	Comparative Assessment of Seven Docking Programs on a Nonredundant Metalloprotein Subset of the PDBbind Refined. Journal of Chemical Information and Modeling, 2019, 59, 3846-3859.	2.5	35
743	Quantitative Proteome Profiling of Coxiella burnetii Reveals Major Metabolic and Stress Differences Under Axenic and Cell Culture Cultivation. Frontiers in Microbiology, 2019, 10, 2022.	1.5	10
744	Revisiting the Î²-Lactams for Tuberculosis Therapy with a Compound-Compound Synthetic Lethality Approach. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	4
745	Co-culture With Human Breast Adipocytes Differentially Regulates Protein Abundance in Breast Cancer Cells. Cancer Genomics and Proteomics, 2019, 16, 319-332.	1.0	11
746	Wnt signaling regulates trans-differentiation of stem cell like type 2 alveolar epithelial cells to type 1 epithelial cells. Respiratory Research, 2019, 20, 204.	1.4	39
747	Differential expression of novel MicroRNAs from developing fetal heart of Gallus gallus domesticus implies a role in cardiac development. Molecular and Cellular Biochemistry, 2019, 462, 157-165.	1.4	1
748	Identification and Classification of Differentially Expressed Genes and Network Meta-Analysis Reveals Potential Molecular Signatures Associated With Tuberculosis. Frontiers in Genetics, 2019, 10, 932.	1.1	26
749	Genetic Risk of Arrhythmic Phenotypes in Patients With Dilated Cardiomyopathy. Journal of the American College of Cardiology, 2019, 74, 1480-1490.	1.2	167
750	MARK4 protein can explore the active-like conformations in its non-phosphorylated state. Scientific Reports, 2019, 9, 12967.	1.6	4
751	A human endogenous retrovirus encoded protease potentially cleaves numerous cellular proteins. Mobile DNA, 2019, 10, 36.	1.3	9
752	Pathway enrichment analysis and visualization of omics data using g:Profiler, GSEA, Cytoscape and EnrichmentMap. Nature Protocols, 2019, 14, 482-517.	5.5	1,172
753	A large scale proteome analysis of the gefitinib primary resistance overcome by KDAC inhibition in KRAS mutated adenocarcinoma cells overexpressing amphiregulin. Journal of Proteomics, 2019, 195, 114-124.	1.2	10
754	Cytological, Biochemical and Molecular Events of the Embryogenic State in Douglas-fir (Pseudotsuga) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.7	18
755	Comparative Analysis of Developmental Transcriptome Maps of Arabidopsis thaliana and Solanum lycopersicum. Genes, 2019, 10, 50.	1.0	18
756	Proteomic insight into the pathogenesis of CAPN5-vitreoretinopathy. Scientific Reports, 2019, 9, 7608.	1.6	9
757	Proteomics Analysis of Urine to Examine Physical Effects of Warm Nano Mist Sauna Bathing. Healthcare (Switzerland), 2019, 7, 71.	1.0	0
758	Aberrant NFATc1 signaling counteracts TGFÎ²-mediated growth arrest and apoptosis induction in pancreatic cancer progression. Cell Death and Disease, 2019, 10, 446.	2.7	12
759	Spatial proteomics reveal that the protein phosphatase PTP1B interacts with and may modify tyrosine phosphorylation of the rhomboid protease RHBDL4. Journal of Biological Chemistry, 2019, 294, 11486-11497.	1.6	12

#	Article	IF	Citations
760	Hippocampal sub-regional differences in the microRNA response to forebrain ischemia. Molecular and Cellular Neurosciences, 2019, 98, 164-178.	1.0	7
761	Investigating the toxic effects induced by iron oxide nanoparticles on neuroblastoma cell line: an integrative study combining cytotoxic, genotoxic and proteomic tools. Nanotoxicology, 2019, 13, 1021-1040.	1.6	16
762	Identification of Crucial Candidate Genes and Pathways in Glioblastoma Multiform by Bioinformatics Analysis. Biomolecules, 2019, 9, 201.	1.8	33
763	Yap1b, a divergent Yap/Taz family member, cooperates with yap1 in survival and morphogenesis via common transcriptional targets. Development (Cambridge), 2019, 146, .	1.2	10
764	Environmental temperature variation affects brain protein expression and cognitive abilities in adult zebrafish (Danio rerio): A proteomic and behavioural study. Journal of Proteomics, 2019, 204, 103396.	1.2	47
765	A single-cell transcriptional roadmap for cardiopharyngeal fate diversification. Nature Cell Biology, 2019, 21, 674-686.	4.6	78
766	Toxicoproteomic Analysis of Poly(ADP-Ribose)-Associated Proteins Induced by Oxidative Stress in Human Proximal Tubule Cells. Toxicological Sciences, 2019, 171, 117-131.	1.4	0
767	BAL Cell Gene Expression in Severe Asthma Reveals Mechanisms of Severe Disease and Influences of Medications. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 837-856.	2.5	37
768	Diabetesâ€mediated promotion of colon mucosa carcinogenesis is associated with mitochondrial dysfunction. Molecular Oncology, 2019, 13, 1887-1897.	2.1	9
769	Altered Gene Response to Aflatoxin B1 in the Spleens of Susceptible and Resistant Turkeys. Toxins, 2019, 11, 242.	1.5	5
770	A Chinese family with familial hemiplegic migraine type 2 due to a novel missense mutation in <i>ATP1A2</i>. Cephalalgia, 2019, 39, 1382-1395.	1.8	7
771	Differential Effects of Influenza Virus NA, HA Head, and HA Stalk Antibodies on Peripheral Blood Leukocyte Gene Expression during Human Infection. MBio, 2019, 10, .	1.8	8
772	In-depth serum proteomics reveals biomarkers of psoriasis severity and response to traditional Chinese medicine. Theranostics, 2019, 9, 2475-2488.	4.6	76
773	Identification of LIFR, PIK3R1, and MMP12 as Novel Prognostic Signatures in Gallbladder Cancer Using Network-Based Module Analysis. Frontiers in Oncology, 2019, 9, 325.	1.3	15
774	Placental DNA methylation levels at CYP2E1 and IRS2 are associated with child outcome in a prospective autism study. Human Molecular Genetics, 2019, 28, 2659-2674.	1.4	57
775	A novel <i><scp>CDKN</scp>2A</i> variant (p16^{L117P}) in a patient with familial and multiple primary melanomas. Pigment Cell and Melanoma Research, 2019, 32, 734-738.	1.5	7
776	Porcine Epidemic Diarrhea Virus (PEDV) ORF3 Interactome Reveals Inhibition of Virus Replication by Cellular VPS36 Protein. Viruses, 2019, 11, 382.	1.5	15
777	Pristimerin inhibits glioma progression by targeting AGO2 and PTPN1 expression via miR-542-5p. Bioscience Reports, 2019, 39, .	1.1	19

#	Article	IF	Citations
778	Genome-wide identification of alternative splicing events that regulate protein transport across the secretory pathway. Journal of Cell Science, 2019, 132, .	1.2	4
779	Altered keratinocyte differentiation is an early driver of keratin mutation-based palmoplantar keratoderma. Human Molecular Genetics, 2019, 28, 2255-2270.	1.4	25
780	Glycolytic flux in <i>Saccharomyces cerevisiae</i> is dependent on RNA polymerase III and its negative regulator Maf1. Biochemical Journal, 2019, 476, 1053-1082.	1.7	9
781	Brain Imagingâ€Guided Analysis Reveals DNA Methylation Profiles Correlated with Insular Surface Area and Alcohol Use Disorder. Alcoholism: Clinical and Experimental Research, 2019, 43, 628-639.	1.4	3
782	Differential Transcriptome Responses to Aflatoxin B1 in the Cecal Tonsil of Susceptible and Resistant Turkeys. Toxins, 2019, 11, 55.	1.5	10
783	In search of the altering salivary proteome in metastatic breast and ovarian cancers. FASEB BioAdvances, 2019, 1, 191-207.	1.3	11
784	Integrative Omic Profiling Reveals Unique Hypoxia Induced Signatures in Gastric Cancer Associated Myofibroblasts. Cancers, 2019, 11, 263.	1.7	2
785	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	9.4	154
786	Bone extracts immunomodulate and enhance the regenerative performance of dicalcium phosphates bioceramics. Acta Biomaterialia, 2019, 89, 343-358.	4.1	35
787	Multimodal Analysis of SCN1A Missense Variants Improves Interpretation of Clinically Relevant Variants in Dravet Syndrome. Frontiers in Neurology, 2019, 10, 289.	1.1	9
788	Acoel genome reveals the regulatory landscape of whole-body regeneration. Science, 2019, 363, .	6.0	125
789	Cytotoxic effects of parathion, paraoxon, and their methylated derivatives on a mouse neuroblastoma cell line NB41A3. Fundamental Toxicological Sciences, 2019, 6, 45-56.	0.2	4
790	Actomyosin contraction during cellularization is regulated in part by Src64 control of Actin 5C protein levels. Genesis, 2019, 57, e23297.	0.8	4
791	Prioritization of cancer therapeutic targets using CRISPRâ€“Cas9 screens. Nature, 2019, 568, 511-516.	13.7	886
792	Genotype-phenotype relations of the von Hippel-Lindau tumor suppressor inferred from a large-scale analysis of disease mutations and interactors. PLoS Computational Biology, 2019, 15, e1006478.	1.5	24
793	Mining Featured Biomarkers Linked with Epithelial Ovarian Cancer Based on Bioinformatics. Diagnostics, 2019, 9, 39.	1.3	3
794	Proteomics-Derived Biomarker Panel Improves Diagnostic Precision to Classify Endometrioid and High-grade Serous Ovarian Carcinoma. Clinical Cancer Research, 2019, 25, 4309-4319.	3.2	33
795	<i>Hoxa13</i> regulates expression of common <i>Hox</i> target genes involved in cartilage development to coordinate the expansion of the autopodal anlage. Development Growth and Differentiation, 2019, 61, 228-251.	0.6	13

#	Article	IF	Citations
796	Proteomic alterations of HDL in youth with type 1 diabetes and their associations with glycemic control: a caseâ€“control study. Cardiovascular Diabetology, 2019, 18, 43.	2.7	46
797	Comparative Analysis of Brain and Fat Body Gene Splicing Patterns in the Honey Bee, <i>Apis mellifera</i>. G3: Genes, Genomes, Genetics, 2019, 9, 1055-1063.	0.8	5
798	GeM-Pro: a tool for genome functional mining and microbial profiling. Applied Microbiology and Biotechnology, 2019, 103, 3123-3134.	1.7	13
799	Proteomic Quantification of Human Bloodâ€“Brain Barrier SLC and ABC Transporters in Healthy Individuals and Dementia Patients. Molecular Pharmaceutics, 2019, 16, 1220-1233.	2.3	85
800	A Review on Protein Structure Classification. Lecture Notes in Computational Vision and Biomechanics, 2019, , 89-95.	0.5	0
801	Molecular analysis of APOB, SAR1B, ANGPTL3, and MTTP in patients with primary hypocholesterolemia in a clinical laboratory setting: Evidence supporting polygenicity in mutation-negative patients. Atherosclerosis, 2019, 283, 52-60.	0.4	15
802	SELER: a database of super-enhancer-associated lncRNA- directed transcriptional regulation in human cancers. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	17
803	Invasive invertebrates associated with highly duplicated gene content. Molecular Ecology, 2019, 28, 1652-1663.	2.0	14
804	Serum protein profiles suggest a possible link between qi deficiency constitution and Pi-qi-deficiency syndrome of chronic superficial gastritis. Journal of Traditional Chinese Medical Sciences, 2019, 6, 308-314.	0.1	0
805	Proteomics analysis identified serum biomarkers for occupational benzene exposure and chronic benzene poisoning. Medicine (United States), 2019, 98, e16117.	0.4	3
806	Gene expression profiles of dicyemid life-cycle stages may explain how dispersing larvae locate new hosts. Zoological Letters, 2019, 5, 32.	0.7	0
807	HSF1Base: A Comprehensive Database of HSF1 (Heat Shock Factor 1) Target Genes. International Journal of Molecular Sciences, 2019, 20, 5815.	1.8	56
808	Evolutionarily novel genes are expressed in transgenic fish tumors and their orthologs are involved in development of progressive traits in humans. Infectious Agents and Cancer, 2019, 14, 46.	1.2	8
809	Molecular profiling of single neurons of known identity in two ganglia from the crab <i>Cancer borealis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26980-26990.	3.3	26
810	Proteogenomics of Colorectal Cancer Liver Metastases: Complementing Precision Oncology with Phenotypic Data. Cancers, 2019, 11, 1907.	1.7	12
811	Evidence of multifaceted functions of codon usage in translation within the model beetle Tribolium castaneum. DNA Research, 2019, 26, 473-484.	1.5	3
812	An Optimized Method for the Proteomic Analysis of Low Volumes of Cell Culture Media and the Secretome: The Application and the Demonstration of Altered Protein Expression in iPSC-Derived Neuronal Cell Lines from Parkinsonâ€™s Disease Patients. Journal of Proteome Research, 2019, 18, 1198-1207.	1.8	2
813	A Gene Expression Screen in<i>Drosophila melanogaster</i>Identifies Novel JAK/STAT and EGFR Targets During Oogenesis. G3: Genes, Genomes, Genetics, 2019, 9, 47-60.	0.8	27

#	Article	IF	Citations
814	Induction of apoptosis in ovarian cancer cells by miR-493-3p directly targeting AKT2, STK38L, HMGA2, ETS1 and E2F5. Cellular and Molecular Life Sciences, 2019, 76, 539-559.	2.4	28
815	Osteoblasts Regulate Angiogenesis in Response to Mechanical Unloading. Calcified Tissue International, 2019, 104, 344-354.	1.5	12
816	PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. Nucleic Acids Research, 2019, 47, D419-D426.	6.5	2,455
817	Identifying residues that determine palmitoylation using association rule mining. Bioinformatics, 2019, 35, 2887-2890.	1.8	3
818	Ancestral Genomes: a resource for reconstructed ancestral genes and genomes across the tree of life. Nucleic Acids Research, 2019, 47, D271-D279.	6.5	17
819	DeepIsoFun: a deep domain adaptation approach to predict isoform functions. Bioinformatics, 2019, 35, 2535-2544.	1.8	20
820	Genome-wide association study for longevity in the Holstein cattle population. Animal, 2019, 13, 1350-1357.	1.3	12
821	Control principles for complex biological networks. Briefings in Bioinformatics, 2019, 20, 2253-2266.	3.2	46
822	Prediction of proteinâ€“protein interactions between fungus (Magnaporthe grisea) and rice (Oryza) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.2	21
823	A genome-wide association study of tramadol metabolism from post-mortem samples. Pharmacogenomics Journal, 2020, 20, 94-103.	0.9	3
824	Alliance of Genome Resources Portal: unified model organism research platform. Nucleic Acids Research, 2020, 48, D650-D658.	6.5	145
825	Identification of molecular signatures and pathways to identify novel therapeutic targets in Alzheimer's disease: Insights from a systems biomedicine perspective. Genomics, 2020, 112, 1290-1299.	1.3	89
826	AKR2A participates in the regulation of cotton fibre development by modulating biosynthesis of veryâ€longâ€chain fatty acids. Plant Biotechnology Journal, 2020, 18, 526-539.	4.1	20
827	The Class II KNOX genes <i>KNAT3</i> and <i>KNAT7</i> work cooperatively to influence deposition of secondary cell walls that provide mechanical support to Arabidopsis stems. Plant Journal, 2020, 101, 293-309.	2.8	63
828	Endometrial expression of various genes (ISGs, PPARs, RXRs and MUC1) on day 16 post-ovulation in repeat breeder cows, with or without subclinical endometritis. Theriogenology, 2020, 142, 251-259.	0.9	9
829	Curating the gnomAD database: Report of novel variants in the globinâ€coding genes and bioinformatics analysis. Human Mutation, 2020, 41, 81-102.	1.1	8
830	Proteomic profiling of salmon skin mucus for the comparison of sampling methods. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2020, 1138, 121965.	1.2	14
831	InÂVivo RNAi-Mediated eIF3m Knockdown Affects Ribosome Biogenesis and Transcription but Has Limited Impact on mRNA-Specific Translation. Molecular Therapy - Nucleic Acids, 2020, 19, 252-266.	2.3	14

#	Article	IF	Citations
832	Analysis of Differentially Expressed Genes in Coronary Artery Disease by Integrated Microarray Analysis. Biomolecules, 2020, 10, 35.	1.8	12
833	Tumor Microenvironment-Associated Immune-Related Genes for the Prognosis of Malignant Pleural Mesothelioma. Frontiers in Oncology, 2020, 10, 544789.	1.3	11
834	The methylome is altered for plants in a high CO₂ world: Insights into the response of a wild plant population to multigenerational exposure to elevated atmospheric [CO₂]. Global Change Biology, 2020, 26, 6474-6492.	4.2	13
835	Influence of the go-based semantic similarity measures in multi-objective gene clustering algorithm performance. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050038.	0.3	1
836	Clinical Translational Potential in Skin Wound Regeneration for Adipose-Derived, Blood-Derived, and Cellulose Materials: Cells, Exosomes, and Hydrogels. Biomolecules, 2020, 10, 1373.	1.8	26
837	Reference transcriptomes and comparative analyses of six species in the threatened rosewood genus Dalbergia. Scientific Reports, 2020, 10, 17749.	1.6	20
838	Divergent genes in gerbils: prevalence, relation to GC-biased substitution, and phenotypic relevance. BMC Evolutionary Biology, 2020, 20, 134.	3.2	6
839	The <i>FAM171A2</i> gene is a key regulator of progranulin expression and modifies the risk of multiple neurodegenerative diseases. Science Advances, 2020, 6, .	4.7	9
840	Integrative Analysis of Cell Crosstalk within Follicular Lymphoma Cell Niche: Towards a Definition of the FL Supportive Synapse. Cancers, 2020, 12, 2865.	1.7	14
841	Translating Biomarkers of Cholangiocarcinoma for Theranosis: A Systematic Review. Cancers, 2020, 12, 2817.	1.7	4
842	A gene expression signature of TREM2hi macrophages and Î³Î´ T cells predicts immunotherapy response. Nature Communications, 2020, 11, 5084.	5.8	90
843	Transcriptome analysis of turkey (Meleagris gallopavo) reproductive tract revealed key pathways regulating spermatogenesis and post-testicular sperm maturation. Poultry Science, 2020, 99, 6094-6118.	1.5	16
844	IFNT, ISGs, PPARs, RXRs and MUC1 in day 16 embryo and endometrium of repeat-breeder cows, with or without subclinical endometritis. Theriogenology, 2020, 158, 39-49.	0.9	7
845	The Rac2 GTPase contributes to cathepsin H-mediated protection against cytokine-induced apoptosis in insulin-secreting cells. Molecular and Cellular Endocrinology, 2020, 518, 110993.	1.6	9
846	The longevity-associated variant of BPIFB4 improves a CXCR4-mediated striatumâ€"microglia crosstalk preventing disease progression in a mouse model of Huntingtonâ€™s disease. Cell Death and Disease, 2020, 11, 546.	2.7	15
847	BRG1 Loss Predisposes Lung Cancers to Replicative Stress and ATR Dependency. Cancer Research, 2020, 80, 3841-3854.	0.4	32
848	Araport Lives: An Updated Framework for Arabidopsis Bioinformatics. Plant Cell, 2020, 32, 2683-2686.	3.1	28
849	Whole genome resequencing of four Italian sweet pepper landraces provides insights on sequence variation in genes of agronomic value. Scientific Reports, 2020, 10, 9189.	1.6	18

#	ARTICLE	IF	CITATIONS
850	Inflammatory Response of Ischemic Tolerance in Circulating Plasma: Preconditioning-Induced by Transient Ischemic Attack (TIA) Phenomena in Acute Ischemia Patients (AIS). Frontiers in Neurology, 2020, 11, 552470.	1.1	7
851	Protein Corona Gold Nanoparticles Fingerprinting Reveals a Profile of Blood Coagulation Proteins in the Serum of HER2-Overexpressing Breast Cancer Patients. International Journal of Molecular Sciences, 2020, 21, 8449.	1.8	15
852	Gene expression changes occurring at bolting time are associated with leaf senescence in Arabidopsis. Plant Direct, 2020, 4, e00279.	0.8	15
853	Neurotoxic microglia promote TDP-43 proteinopathy in progranulin deficiency. Nature, 2020, 588, 459-465.	13.7	98
854	Noise Exposures Causing Hearing Loss Generate Proteotoxic Stress and Activate the Proteostasis Network. Cell Reports, 2020, 33, 108431.	2.9	33
855	Top-Down Proteomics of Endogenous Membrane Proteins Enabled by Cloud Point Enrichment and Multidimensional Liquid Chromatographyâ€"Mass Spectrometry. Analytical Chemistry, 2020, 92, 15726-15735.	3.2	24
856	ASH2L drives proliferation and sensitivity to bleomycin and other genotoxins in Hodgkinâ€™s lymphoma and testicular cancer cells. Cell Death and Disease, 2020, 11, 1019.	2.7	10
857	Reconstruction of Dementia Gene Network Using Online Bioinformatics Tools. , 2020, , .		0
858	Insertion variants missing in the human reference genome are widespread among human populations. BMC Biology, 2020, 18, 167.	1.7	7
859	Endocrine disrupting chemicals and COVID-19 relationships: A computational systems biology approach. Environment International, 2021, 157, 106232.	4.8	25
860	Genome-Wide Differential DNA Methylation and miRNA Expression Profiling Reveals Epigenetic Regulatory Mechanisms Underlying Nitrogen-Limitation-Triggered Adaptation and Use Efficiency Enhancement in Allotetraploid Rapeseed. International Journal of Molecular Sciences, 2020, 21, 8453.	1.8	10
861	Reference Genome for the Highly Transformable <i>Setaria viridis</i> ME034V. G3: Genes, Genomes, Genetics, 2020, 10, 3467-3478.	0.8	36
862	Bioinformatics resources, databases, and tools for human mtDNA. , 2020, , 277-304.		0
863	Recurrent sequence evolution after independent gene duplication. BMC Evolutionary Biology, 2020, 20, 98.	3.2	8
864	â€œMind the Gapâ€: Hi-C Technology Boosts Contiguity of the Globe Artichoke Genome in Low-Recombination Regions. G3: Genes, Genomes, Genetics, 2020, 10, 3557-3564.	0.8	12
865	Benchmarking gene ontology function predictions using negative annotations. Bioinformatics, 2020, 36, i210-i218.	1.8	12
866	Regeneration in sponge <i>Sycon ciliatum</i> partly mimics postlarval development. Development (Cambridge), 2020, 147, .	1.2	22
867	Cp1/cathepsin L is required for autolysosomal clearance in <i>Drosophila</i>. Autophagy, 2021, 17, 2734-2749.	4.3	9

#	Article	IF	Citations
868	Seminal plasma AnnexinA2 protein is a relevant biomarker for stallions which require removal of seminal plasma for sperm survival upon refrigerationâ€. Biology of Reproduction, 2020, 103, 1275-1288.	1.2	14
869	Analysis of circulating-microRNA expression in lactating Holstein cows under summer heat stress. PLoS ONE, 2020, 15, e0231125.	1.1	14
870	A high-quality chromosome-level genome assembly reveals genetics for important traits in eggplant. Horticulture Research, 2020, 7, 153.	2.9	85
871	Consistency of the Tools That Predict the Impact of Single Nucleotide Variants (SNVs) on Gene Functionality: The BRCA1 Gene. Biomolecules, 2020, 10, 475.	1.8	0
872	Regional sequence expansion or collapse in heterozygous genome assemblies. PLoS Computational Biology, 2020, 16, e1008104.	1.5	31
873	Population Genomics of Organelle Genomes in Crop Plants. Population Genomics, 2020, , 1.	0.2	1
874	G protein-coupled estrogen receptor 1 (GPER-1) and agonist G-1 inhibit growth of ovarian cancer cells by activation of anti-tumoral transcriptome responses: impact of GPER-1 mRNA on survival. Journal of Cancer Research and Clinical Oncology, 2020, 146, 3175-3188.	1.2	13
875	The Coevolution of Cellularity and Metabolism Following the Origin of Life. Journal of Molecular Evolution, 2020, 88, 598-617.	0.8	16
876	Revisiting the clinical impact of variants in EFHC1 in patients with different phenotypes of genetic generalized epilepsy. Epilepsy and Behavior, 2020, 112, 107469.	0.9	5
877	Stepwise cell fate decision pathways during osteoclastogenesis at single-cell resolution. Nature Metabolism, 2020, 2, 1382-1390.	5.1	60
878	multiGSEA: a GSEA-based pathway enrichment analysis for multi-omics data. BMC Bioinformatics, 2020, 21, 561.	1.2	70
879	Autism-associated miR-873 regulates ARID1B, SHANK3 and NRXN2 involved in neurodevelopment. Translational Psychiatry, 2020, 10, 418.	2.4	15
880	Multimerization of Zika Virus-NS5 Causes Ciliopathy and Forces Premature Neurogenesis. Cell Stem Cell, 2020, 27, 920-936.e8.	5.2	18
881	Emerging of composition variations of SARS-CoV-2 spike protein and human ACE2 contribute to the level of infection: in silico approaches. Journal of Biomolecular Structure and Dynamics, 2020, , 1-12.	2.0	5
882	Epigenetic Analysis through MSAP-NGS Coupled Technology: The Case Study of White Poplar Monoclonal Populations/Stands. International Journal of Molecular Sciences, 2020, 21, 7393.	1.8	3
883	Comprehensive Immunoprofiling of Pediatric Zika Reveals Key Role for Monocytes in the Acute Phase and No Effect of Prior Dengue Virus Infection. Cell Reports, 2020, 31, 107569.	2.9	43
884	Detection of runs of homozygosity in conserved and commercial pig breeds in Poland. Journal of Animal Breeding and Genetics, 2020, 137, 571-580.	0.8	19
885	Comprehensive analyses of 723 transcriptomes enhance genetic and biological interpretations for complex traits in cattle. Genome Research, 2020, 30, 790-801.	2.4	97

#	Article	IF	Citations
886	A Genetic Investigation of Island Jersey Cattle, the Foundation of the Jersey Breed: Comparing Population Structure and Selection to Guernsey, Holstein, and United States Jersey Cattle. Frontiers in Genetics, 2020, 11, 366.	1.1	18
887	RAS internal tandem duplication disrupts GTPase-activating protein (GAP) binding to activate oncogenic signaling. Journal of Biological Chemistry, 2020, 295, 9335-9348.	1.6	8
888	The effect of Nannochloropsis oceanica feed inclusion on rabbit muscle proteome. Journal of Proteomics, 2020, 222, 103783.	1.2	11
889	miR-196B-5P and miR-200B-3P Are Differentially Expressed in Medulloblastomas of Adults and Children. Diagnostics, 2020, 10, 265.	1.3	6
890	Complex Analysis of Retroposed Genesâ€™ Contribution to Human Genome, Proteome and Transcriptome. Genes, 2020, 11, 542.	1.0	8
891	Quantitative alterations in bovine milk proteome from healthy, subclinical and clinical mastitis during S. aureus infection. Journal of Proteomics, 2020, 223, 103815.	1.2	19
892	The effects of improving low dietary protein utilization on the proteome of lamb tissues. Journal of Proteomics, 2020, 223, 103798.	1.2	7
893	A myelin basic protein fragment induces sexually dimorphic transcriptome signatures of neuropathic pain in mice. Journal of Biological Chemistry, 2020, 295, 10807-10821.	1.6	15
894	Antigenic membrane proteins of virulent variant of Entamoeba histolytica HM-1:IMSS. Pathogens and Global Health, 2020, 114, 333-342.	1.0	1
895	Single-Cell Transcriptomics Analysis Identifies Nuclear Protein 1 as a Regulator of Docetaxel Resistance in Prostate Cancer Cells. Molecular Cancer Research, 2020, 18, 1290-1301.	1.5	25
896	Blood Serum Stimulates p38-Mediated Proliferation and Changes in Global Gene Expression of Adult Human Cardiac Stem Cells. Cells, 2020, 9, 1472.	1.8	13
897	CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities. Nature, 2020, 580, 136-141.	13.7	203
898	Genetic compensation in a stable slc25a46 mutant zebrafish: A case for using F0 CRISPR mutagenesis to study phenotypes caused by inherited disease. PLoS ONE, 2020, 15, e0230566.	1.1	39
899	Molecular natural history of breast cancer: Leveraging transcriptomics to predict breast cancer progression and aggressiveness. Cancer Medicine, 2020, 9, 3551-3562.	1.3	8
900	Proteomic mapping of Drosophila transgenic elav.L-GAL4/+ brain as a tool to illuminate neuropathology mechanisms. Scientific Reports, 2020, 10, 5430.	1.6	3
901	Functionally Enigmatic Genes in Cancer: Using TCGA Data to Map the Limitations of Annotations. Scientific Reports, 2020, 10, 4106.	1.6	14
902	TP53-Deficient Angiosarcoma Expression Profiling in Rat Model. Cancers, 2020, 12, 1525.	1.7	3
903	HTRA1-Related Cerebral Small Vessel Disease: A Review of the Literature. Frontiers in Neurology, 2020, 11, 545.	1.1	52

#	ARTICLE	IF	CITATIONS
904	Transcriptional analyses of acute per os exposure and co-exposure of 4-vinylcyclohexene and methylmercury-contaminated diet in adults of Drosophila melanogaster. Environmental Pollution, 2020, 263, 114632.	3.7	3
905	Human Virus Transcriptional Regulators. Cell, 2020, 182, 24-37.	13.5	52
906	Identification and classification of differentially expressed genes reveal potential molecular signature associated with SARS-CoV-2 infection in lung adenocarcinomal cells. Informatics in Medicine Unlocked, 2020, 20, 100384.	1.9	15
907	Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. Nucleic Acids Research, 2020, 48, 2312-2331.	6.5	30
908	Aberrant Development Corrected in Adult-Onset Huntington's Disease iPSC-Derived Neuronal Cultures via WNT Signaling Modulation. Stem Cell Reports, 2020, 14, 406-419.	2.3	45
909	Lineage tracing on transcriptional landscapes links state to fate during differentiation. Science, 2020, 367, .	6.0	426
910	Palmoplantar Keratoderma with Leukokeratosis Anogenitalis Caused by KDSR Mutations. Journal of Investigative Dermatology, 2020, 140, 1662-1665.e1.	0.3	6
911	Enhancerâ€“gene maps in the human and zebrafish genomes using evolutionary linkage conservation. Nucleic Acids Research, 2020, 48, 2357-2371.	6.5	32
912	3â€™Pool-seq: an optimized cost-efficient and scalable method of whole-transcriptome gene expression profiling. BMC Genomics, 2020, 21, 64.	1.2	12
913	Influence of Metabolic Status and Diet on Early Pregnant Equine Histotroph Proteome: Preliminary Findings. Journal of Equine Veterinary Science, 2020, 88, 102938.	0.4	5
914	Integrative pathway enrichment analysis of multivariate omics data. Nature Communications, 2020, 11, 735.	5.8	125
915	Comprehensive Molecular Characterization Identifies Distinct Genomic and Immune Hallmarks of Renal Medullary Carcinoma. Cancer Cell, 2020, 37, 720-734.e13.	7.7	74
916	Proteomic profiling of stallion spermatozoa suggests changes in sperm metabolism and compromised redox regulation after cryopreservation. Journal of Proteomics, 2020, 221, 103765.	1.2	26
917	Genetic Screen for Cell Fitness in High or Low Oxygen Highlights Mitochondrial and Lipid Metabolism. Cell, 2020, 181, 716-727.e11.	13.5	126
918	Differentiation Drives Widespread Rewiring of the Neural Stem Cell Chaperone Network. Molecular Cell, 2020, 78, 329-345.e9.	4.5	66
919	Genetic Differentiation of the Two Types of Polish Cold-blooded Horses Included in the National Conservation Program. Animals, 2020, 10, 542.	1.0	4
920	Proximity proteomics identifies novel function of Rab14 in trafficking of Ebola virus matrix protein VP40. Biochemical and Biophysical Research Communications, 2020, 527, 387-392.	1.0	12
921	Development of a Bioinformatics Framework for Identification and Validation of Genomic Biomarkers and Key Immunopathology Processes and Controllers in Infectious and Non-infectious Severe Inflammatory Response Syndrome. Frontiers in Immunology, 2020, 11, 380.	2.2	17

#	ARTICLE	IF	CITATIONS
922	Predicted Cellular and Molecular Actions of Lithium in the Treatment of Bipolar Disorder: An In Silico Study. CNS Drugs, 2020, 34, 521-533.	2.7	1
923	Dysfunction of Hair Follicle Mesenchymal Progenitors Contributes to Age-Associated Hair Loss. Developmental Cell, 2020, 53, 185-198.e7.	3.1	56
924	The Autism-Related Protein SETD5 Controls Neural Cell Proliferation through Epigenetic Regulation of rDNA Expression. IScience, 2020, 23, 101030.	1.9	18
925	Transcriptomics at Maize Embryo/Endosperm Interfaces Identifies a Transcriptionally Distinct Endosperm Subdomain Adjacent to the Embryo Scutellum. Plant Cell, 2020, 32, 833-852.	3.1	60
926	Diversity in AÎ² deposit morphology and secondary proteome insolubility across models of Alzheimer-typeÂamyloidosis. Acta Neuropathologica Communications, 2020, 8, 43.	2.4	16
927	Tet3 ablation in adult brain neurons increases anxiety-like behavior and regulates cognitive function in mice. Molecular Psychiatry, 2021, 26, 1445-1457.	4.1	37
928	The influence of X chromosome variants on trait neuroticism. Molecular Psychiatry, 2021, 26, 483-491.	4.1	17
929	Protein residues determining interaction specificity inÂparalogous families. Bioinformatics, 2021, 37, 1076-1082.	1.8	4
930	Genomeâ€wide assessment of diversity and differentiation between original and modern Brown cattle populations. Animal Genetics, 2021, 52, 21-31.	0.6	20
931	Network analysis of transcriptomics data for the prediction and prioritization of membrane-associated biomarkers for idiopathic pulmonary fibrosis (IPF) by bioinformatics approach. Advances in Protein Chemistry and Structural Biology, 2021, 123, 241-273.	1.0	29
932	Comparative proteomic analysis of dental cementum from deciduous and permanent teeth. Journal of Periodontal Research, 2021, 56, 173-185.	1.4	9
933	Genome-wide analysis reveals the patterns of genetic diversity and population structure of 8 Italian local chicken breeds. Poultry Science, 2021, 100, 441-451.	1.5	18
934	Whole exome sequencing reveals pathogenic variants in MYO3A, MYO15A and COL9A3 and differential frequencies in ancestral alleles in hearing impairment genes among individuals from Cameroon. Human Molecular Genetics, 2021, 29, 3729-3743.	1.4	9
935	Identification of regenerative processes in neonatal spinal cord injury in the opossum (<scp><i>Monodelphis domestica</i></scp>): A transcriptomic study. Journal of Comparative Neurology, 2021, 529, 969-986.	0.9	9
938	Dynamic Module Detection in Temporal Attributed Networks of Cancers. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2219-2230.	1.9	31
939	Differential proteomic analysis of children infected with respiratory syncytial virus. Brazilian Journal of Medical and Biological Research, 2021, 54, e9850.	0.7	10
940	Dysregulated H3K27 Acetylation Is Implicated in Fatty Liver Hemorrhagic Syndrome in Chickens. Frontiers in Genetics, 2020, 11, 574167.	1.1	9
941	Analysis of Human Faecal Host Proteins: Responsiveness to 10-Week Dietary Intervention Modifying Dietary Protein Intake in Elderly Males. Frontiers in Nutrition, 2020, 7, 595905.	1.6	3

#	ARTICLE	IF	CITATIONS
942	MiR-144-3p is associated with pathological inflammation in patients infected with Mycobacteroides abscessus. Experimental and Molecular Medicine, 2021, 53, 136-149.	3.2	16
945	Loss of the fragile X syndrome protein FMRP results in misregulation of nonsense-mediated mRNA decay. Nature Cell Biology, 2021, 23, 40-48.	4.6	23
947	Genomic imbalance determines positive and negative modulation of gene expression in diploid maize. Plant Cell, 2021, 33, 917-939.	3.1	22
948	In silico data mining of human body fluids to unravel the immunomes in breast cancer. Journal of Proteins and Proteomics, 2021, 12, 45-62.	1.0	1
950	Structure-based analyses of Salmonella RcsB variants unravel new features of the Rcs regulon. Nucleic Acids Research, 2021, 49, 2357-2374.	6.5	10
951	Transcriptional response of <i>Candida albicans</i> to <i>Pseudomonas aeruginosa</i> in a polymicrobial biofilm. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	8
952	Gene function finding through cross-organism ensemble learning. BioData Mining, 2021, 14, 14.	2.2	4
953	Circular RNAâ€"MicroRNAâ€"MRNA interaction predictions in SARS-CoV-2 infection. Journal of Integrative Bioinformatics, 2021, 18, 45-50.	1.0	17
954	A De Novo Transcriptome Assembly of<i>Ceratopteris richardii</i>Provides Insights into the Evolutionary Dynamics of Complex Gene Families in Land Plants. Genome Biology and Evolution, 2021, 13, .	1.1	34
955	Peripheral blood transcriptome profiling enables monitoring disease progression in dystrophic mice and patients. EMBO Molecular Medicine, 2021, 13, e13328.	3.3	16
956	Heterogeneous Hunter-Gatherer and Steppe-Related Ancestries in Late Neolithic and Bell Beaker Genomes from Present-Day France. Current Biology, 2021, 31, 1072-1083.e10.	1.8	20
958	Genetics of mouse behavioral and peripheral neural responses to sucrose. Mammalian Genome, 2021, 32, 51-69.	1.0	2
959	A functional screen identifies transcriptional networks that regulate HIV-1 and HIV-2. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	13
960	Exploring a Region on Chromosome 8p23.1 Displaying Positive Selection Signals in Brazilian Admixed Populations: Additional Insights Into Predisposition to Obesity and Related Disorders. Frontiers in Genetics, 2021, 12, 636542.	1.1	4
961	Genomic consequences of humanâ€mediated translocations in margin populations of an endangered amphibian. Evolutionary Applications, 2021, 14, 1623-1634.	1.5	2
962	Exploration of binary proteinâ€"protein interactions between tick-borne flaviviruses and Ixodes ricinus. Parasites and Vectors, 2021, 14, 144.	1.0	11
963	Yeast grown in continuous culture systems can detect mutagens with improved sensitivity relative to the Ames test. PLoS ONE, 2021, 16, e0235303.	1.1	3
964	Genetic controls of Tas1r3-independent sucrose consumption in mice. Mammalian Genome, 2021, 32, 70-93.	1.0	2

#	Article	IF	Citations
965	Density Peak clustering of protein sequences associated to a Pfam clan reveals clear similarities and interesting differences with respect to manual family annotation. BMC Bioinformatics, 2021, 22, 121.	1.2	1
966	Pathway analysis for genome-wide genetic variation data: Analytic principles, latest developments, and new opportunities. Journal of Genetics and Genomics, 2021, 48, 173-183.	1.7	6
967	Identification of the potential function of circRNA in hypertrophic cardiomyopathy based on mutual RNA-RNA and RNA-RBP relationships shown by microarray data. Journal of Electronic Science and Technology, 2021, 19, 100097.	2.0	0
968	RNA-seq and GSEA identifies suppression of ligand-gated chloride efflux channels as the major gene pathway contributing to form deprivation myopia. Scientific Reports, 2021, 11, 5280.	1.6	14
969	Genomeâ€wide ancestry and introgression in a Zambian baboon hybrid zone. Molecular Ecology, 2021, 30, 1907-1920.	2.0	9
970	A Comparison of Differential Gene Expression in Response to the Onset of Water Stress Between Three Hybrid Brachiaria Genotypes. Frontiers in Plant Science, 2021, 12, 637956.	1.7	9
971	Genetic variability in COVID-19-related genes in the Brazilian population. Human Genome Variation, 2021, 8, 15.	0.4	29
972	From Proteomic Mapping to Invasion-Metastasis-Cascade Systemic Biomarkering and Targeted Drugging of Mutant BRAF-Dependent Human Cutaneous Melanomagenesis. Cancers, 2021, 13, 2024.	1.7	5
973	mRNA Expressions of Candidate Genes in Gestational Day 16 Conceptus and Corresponding Endometrium in Repeat Breeder Dairy Cows with Suboptimal Uterine Environment Following Transfer of Different Quality Day 7 Embryos. Animals, 2021, 11, 1092.	1.0	5
974	The molecular signatures of compatible and incompatible pollination in Arabidopsis. BMC Genomics, 2021, 22, 268.	1.2	9
975	Integrated microRNA and mRNA Expression Profiling Identifies Novel Targets and Networks Associated with Ebsteinâ€™s Anomaly. Cells, 2021, 10, 1066.	1.8	5
976	Analysis of astaxanthin molecular targets based on network pharmacological strategies. Journal of Food Biochemistry, 2021, 45, e13717.	1.2	5
977	NASA GeneLab RNA-seq consensus pipeline: Standardized processing of short-read RNA-seq data. IScience, 2021, 24, 102361.	1.9	20
978	Targeting the nucleotide salvage factor DNPH1 sensitizes <i>BRCA</i> -deficient cells to PARP inhibitors. Science, 2021, 372, 156-165.	6.0	68
979	Altered Transcription Factor Expression Responses to Exercise in Insulin Resistance. Frontiers in Physiology, 2021, 12, 649461.	1.3	4
982	Exome sequencing of early-onset patients supports genetic heterogeneity in colorectal cancer. Scientific Reports, 2021, 11, 11135.	1.6	5
983	Selective androgen receptor modulators activate the canonical prostate cancer androgen receptor program and repress cancer growth. Journal of Clinical Investigation, 2021, 131, .	3.9	23
984	Co-expression Network Revealed Roles of RNA m6A Methylation in Human Î²-Cell of Type 2 Diabetes Mellitus. Frontiers in Cell and Developmental Biology, 2021, 9, 651142.	1.8	7

#	Article	IF	Citations
985	LncRNA Mrhl orchestrates differentiation programs in mouse embryonic stem cells through chromatin mediated regulation. Stem Cell Research, 2021, 53, 102250.	0.3	8
986	Overcoming false-positive gene-category enrichment in the analysis of spatially resolved transcriptomic brain atlas data. Nature Communications, 2021, 12, 2669.	5.8	74
988	BBX19 fine-tunes the circadian rhythm by interacting with PSEUDO-RESPONSE REGULATOR proteins to facilitate their repressive effect on morning-phased clock genes. Plant Cell, 2021, 33, 2602-2617.	3.1	38
989	Profilin2 regulates actin rod assembly in neuronal cells. Scientific Reports, 2021, 11, 10287.	1.6	7
990	Comparative transcriptomics between Drosophila mojavensis and D. arizonae reveals transgressive gene expression and underexpression of spermatogenesis-related genes in hybrid testes. Scientific Reports, 2021, 11, 9844.	1.6	12
991	Multiomics reveal pivotal roles of sodium translocation and compartmentation in regulating salinity resistance in allotetraploid rapeseed. Journal of Experimental Botany, 2021, 72, 5687-5708.	2.4	7
992	Effect of Endosulfan Organochlorine-based Insecticide on Human Mental Health at the Molecular Level using Panther. Analytical Chemistry Letters, 2021, 11, 303-314.	0.4	1
993	Per1/Per2â€"Igf2 axisâ€"mediated circadian regulation of myogenic differentiation. Journal of Cell Biology, 2021, 220, .	2.3	18
995	GATA6 defines endoderm fate by controlling chromatin accessibility during differentiation of human-induced pluripotent stem cells. Cell Reports, 2021, 35, 109145.	2.9	32
996	Predicting the Evolution of Synteniesâ€"An Algorithmic Review. Algorithms, 2021, 14, 152.	1.2	3
1000	Sex-Specific Age-Related Changes in Methylation of Certain Genes. Sovremennye Tehnologii V Medicine, 2021, 13, 26.	0.4	2
1001	Oncolytic H-1 parvovirus binds to sialic acid on laminins for cell attachment and entry. Nature Communications, 2021, 12, 3834.	5.8	15
1003	DysPIA: A Novel Dysregulated Pathway Identification Analysis Method. Frontiers in Genetics, 2021, 12, 647653.	1.1	2
1004	Single Nucleotide Polymorphism Discovery and Genetic Differentiation Analysis of Geese Bred in Poland, Using Genotyping-by-Sequencing (GBS). Genes, 2021, 12, 1074.	1.0	8
1005	Bioinformatics Pathway Analysis Pipeline for NGS Transcriptome Profile Data on Nasopharyngeal Carcinoma. IOP Conference Series: Earth and Environmental Science, 2021, 794, 012115.	0.2	1
1006	The TORâ€dependent phosphoproteome and regulation of cellular protein synthesis. EMBO Journal, 2021, 40, e107911.	3.5	7
1007	Cross-species Exon Capture and Whole Exome Sequencing: Application, Utility and Challenges for Genomic Resource Development in Non-model Species. Marine Biotechnology, 2021, 23, 560-575.	1.1	3
1008	A Yeast BiFC-seq Method for Genome-wide Interactome Mapping. Genomics, Proteomics and Bioinformatics, 2022, 20, 795-807.	3.0	0

#	ARTICLE	IF	CITATIONS
1010	TaxaIInomy: an extension of NCBI Taxonomy that produces a hierarchically complete taxonomic tree. BMC Bioinformatics, 2021, 22, 388.	1.2	8
1011	Influence of dietary Spirulina inclusion and lysozyme supplementation on the longissimus lumborum muscle proteome of newly weaned piglets. Journal of Proteomics, 2021, 244, 104274.	1.2	8
1012	A novel view on an old drug, 5-fluorouracil: an unexpected RNA modifier with intriguing impact on cancer cell fate. NAR Cancer, 2021, 3, zcab032.	1.6	22
1014	Proteomics as a tool to disclose the cellular and molecular mechanisms of selected anticancer gold compounds. Coordination Chemistry Reviews, 2021, 438, 213905.	9.5	23
1015	Molecular Characterization and Elucidation of Pathways to Identify Novel Therapeutic Targets in Pulmonary Arterial Hypertension. Frontiers in Physiology, 2021, 12, 694702.	1.3	12
1016	T cell composition and polygenic multiple sclerosis risk: a populationâ€based study in children. European Journal of Neurology, 2021, 28, 3731-3741.	1.7	3
1017	Omics Multi-Layers Networks Provide Novel Mechanistic and Functional Insights Into Fat Storage and Lipid Metabolism in Poultry. Frontiers in Genetics, 2021, 12, 646297.	1.1	9
1018	The Identification of Zinc-Finger Protein 433 as a Possible Prognostic Biomarker for Clear-Cell Renal Cell Carcinoma. Biomolecules, 2021, 11, 1193.	1.8	7
1019	Curating the gnomAD database: Report of novel variants in the thyrogobulin gene using in silico bioinformatics algorithms. Molecular and Cellular Endocrinology, 2021, 534, 111359.	1.6	7
1020	Diverse heterochromatin-associated proteins repress distinct classes of genes and repetitive elements. Nature Cell Biology, 2021, 23, 905-914.	4.6	35
1021	Epistasis for head morphology in <i>Drosophila melanogaster</i>. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	2
1023	MOSGA 2: Comparative genomics and validation tools. Computational and Structural Biotechnology Journal, 2021, 19, 5504-5509.	1.9	4
1024	Muscle-secreted neurturin couples myofiber oxidative metabolism and slow motor neuron identity. Cell Metabolism, 2021, 33, 2215-2230.e8.	7.2	22
1025	Impact of stunning before slaughter on expression of skeletal muscles proteome in sheep. Animal Biotechnology, 2023, 34, 495-502.	0.7	3
1026	APOBEC3C, a nucleolar protein induced by genotoxins, is excluded from DNA damage sites. FEBS Journal, 2022, 289, 808-831.	2.2	5
1027	EnrichVisBox: A Versatile and Powerful Web Toolbox for Visualizing Complex Functional Enrichment Results of Omics Data. Journal of Computational Biology, 2021, 28, 922-930.	0.8	4
1028	Viral Strain-Specific Activation of Pathogen-Associated Molecular Pattern-Triggered Immunity Enhances Symptom Severity in Broad Bean Wilt Virus 2 Infection. Frontiers in Plant Science, 2021, 12, 746543.	1.7	3
1029	Gene expression profiling on effect of aspirin on osteogenic differentiation of periodontal ligament stem cells. BDJ Open, 2021, 7, 35.	0.8	2

#	ARTICLE	IF	CITATIONS
1030	Gestational Diabetes Mellitus-Induced Changes in Proteomes and Glycated/Glycosylated Proteomes of Human Colostrum. Journal of Agricultural and Food Chemistry, 2021, 69, 10749-10759.	2.4	13
1031	De novo Assembly, Annotation, and Analysis of Transcriptome Data of the Ladakh Ground Skink Provide Genetic Information on High-Altitude Adaptation. Genes, 2021, 12, 1423.	1.0	0
1033	Transcriptional Profiling of Tumorspheres Reveals TRPM4 as a Novel Stemness Regulator in Breast Cancer. Biomedicines, 2021, 9, 1368.	1.4	9
1035	RNase E-HupB Dynamic Interaction Fosters Mycobacterial Cell Homeostasis and Fitness. SSRN Electronic Journal, 0, , .	0.4	0
1036	Role of Multiomics Data to Understand Hostâ€"Pathogen Interactions in COVID-19 Pathogenesis. Journal of Proteome Research, 2021, 20, 1107-1132.	1.8	24
1037	Comprehensive analysis of epigenetic signatures of human transcription control. Molecular Omics, 2021, 17, 692-705.	1.4	1
1038	Gene regulatory networks for compatible versus incompatible grafts identify a role for SlWOX4 during junction formation. Plant Cell, 2022, 34, 535-556.	3.1	24
1039	Computational Methods for Intron Retention Identification and Quantification. , 2021, , 63-74.		0
1040	Nuclear Phosphatidylinositol 3,4,5-Trisphosphate Interactome Uncovers an Enrichment in Nucleolar Proteins. Molecular and Cellular Proteomics, 2021, 20, 100102.	2.5	6
1041	Role of an ancient light-harvesting protein of PSI in light absorption and photoprotection. Nature Communications, 2021, 12, 679.	5.8	28
1042	Traceless Cleavage of Proteinâ€"Biotin Conjugates under Biologically Compatible Conditions. ChemBioChem, 2017, 18, 1688-1691.	1.3	7
1043	Transcriptomics Using Axolotls. Methods in Molecular Biology, 2015, 1290, 309-319.	0.4	2
1044	Bioinformatics Tools and Resources for Cancer Immunotherapy Study. Methods in Molecular Biology, 2020, 2055, 649-678.	0.4	7
1045	Comparative Genomics Approaches to Identifying Functionally Related Genes. Lecture Notes in Computer Science, 2014, , 1-24.	1.0	2
1046	Orthology Relation and Gene Tree Correction: Complexity Results. Lecture Notes in Computer Science, 2015, , 66-79.	1.0	9
1047	Synapse Proteomes and Disease. , 2016, , 85-99.		1
1048	Systematic Genome-wide Screening and Prediction of microRNAs in EBOV During the 2014 Ebolavirus Outbreak. Scientific Reports, 2015, 5, 9912.	1.6	44
1049	Chapter 14. Bioinformatics of Genomics in the Assessment of Cancer. Issues in Toxicology, 2016, , 442-483.	0.2	1

#	Article	IF	Citations
1050	Investigation of a common gene expression signature in gastrointestinal cancers using systems biology approaches. Molecular BioSystems, 2017, 13, 2277-2288.	2.9	4
1051	Large-scale inference of gene function through phylogenetic annotation of Gene Ontology terms: case study of the apoptosis and autophagy cellular processes. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw155.	1.4	12
1052	Transcriptome profiling of alphaherpesvirus-infected cells treated with the HIV-integrase inhibitor raltegravir reveals profound and specific alterations in host transcription. Journal of General Virology, 2018, 99, 1115-1128.	1.3	1
1088	Splicing modulation sensitizes chronic lymphocytic leukemia cells to venetoclax by remodeling mitochondrial apoptotic dependencies. JCI Insight, 2018, 3, .	2.3	39
1090	Usp22 controls multiple signaling pathways that are essential for vasculature formation in the mouse placenta. Development (Cambridge), 2019, 146, .	1.2	30
1091	KEGGViewer, a BioJS component to visualize KEGGÂPathways. F1000Research, 2014, 3, 43.	0.8	11
1092	Visualisation of BioPAX Networks using BioLayout Express3D. F1000Research, 2014, 3, 246.	0.8	16
1093	FIH Regulates Cellular Metabolism through Hydroxylation of the Deubiquitinase OTUB1. PLoS Biology, 2016, 14, e1002347.	2.6	78
1094	Improvement in Protein Domain Identification Is Reached by Breaking Consensus, with the Agreement of Many Profiles and Domain Co-occurrence. PLoS Computational Biology, 2016, 12, e1005038.	1.5	38
1095	Comprehensive Transcriptome Meta-analysis to Characterize Host Immune Responses in Helminth Infections. PLoS Neglected Tropical Diseases, 2016, 10, e0004624.	1.3	30
1096	Interaction of CSFV E2 Protein with Swine Host Factors as Detected by Yeast Two-Hybrid System. PLoS ONE, 2014, 9, e85324.	1.1	26
1097	Myc and Max Genome-Wide Binding Sites Analysis Links the Myc Regulatory Network with the Polycomb and the Core Pluripotency Networks in Mouse Embryonic Stem Cells. PLoS ONE, 2014, 9, e88933.	1.1	30
1098	Genome-Wide Transcriptional Profiling of Skin and Dorsal Root Ganglia after Ultraviolet-B-Induced Inflammation. PLoS ONE, 2014, 9, e93338.	1.1	46
1099	Absence of Metalloprotease GP63 Alters the Protein Content of Leishmania Exosomes. PLoS ONE, 2014, 9, e95007.	1.1	98
1100	Gene Expression Profiling Identifies Microphthalmia-Associated Transcription Factor (MITF) and Dickkopf-1 (DKK1) as Regulators of Microenvironment-Driven Alterations in Melanoma Phenotype. PLoS ONE, 2014, 9, e95157.	1.1	26
1101	On the Crucial Cerebellar Wound Healing-Related Pathways and Their Cross-Talks after Traumatic Brain Injury in Danio rerio. PLoS ONE, 2014, 9, e97902.	1.1	20
1102	Neuroproteome Changes after Ischemia/Reperfusion Injury and Tissue Plasminogen Activator Administration in Rats: A Quantitative iTRAQ Proteomics Study. PLoS ONE, 2014, 9, e98706.	1.1	13
1103	Epigenetic Alterations in the Brain Associated with HIV-1 Infection and Methamphetamine Dependence. PLoS ONE, 2014, 9, e102555.	1.1	40

#	Article	IF	Citations
1104	Wnt Pathway Activation Increases Hypoxia Tolerance during Development. PLoS ONE, 2014, 9, e103292.	1.1	8
1105	Expression Profiling of Mitochondrial Voltage-Dependent Anion Channel-1 Associated Genes Predicts Recurrence-Free Survival in Human Carcinomas. PLoS ONE, 2014, 9, e110094.	1.1	28
1106	Expression of Tumor Necrosis Factor-Alpha-Mediated Genes Predicts Recurrence-Free Survival in Lung Cancer. PLoS ONE, 2014, 9, e115945.	1.1	14
1107	A Genome-Wide Scan Reveals Important Roles of DNA Methylation in Human Longevity by Regulating Age-Related Disease Genes. PLoS ONE, 2015, 10, e0120388.	1.1	42
1108	MMP7 Is Required to Mediate Cell Invasion and Tumor Formation upon Plakophilin3 Loss. PLoS ONE, 2015, 10, e0123979.	1.1	41
1109	Telomerase Activity and Telomere Length in Daphnia. PLoS ONE, 2015, 10, e0127196.	1.1	30
1110	Resistance to Inhibitors of Cholinesterase 3 (Ric-3) Expression Promotes Selective Protein Associations with the Human Î±7-Nicotinic Acetylcholine Receptor Interactome. PLoS ONE, 2015, 10, e0134409.	1.1	9
1111	Differentially Expressed Genes and Signature Pathways of Human Prostate Cancer. PLoS ONE, 2015, 10, e0145322.	1.1	36
1112	Correlative Analysis of miRNA Expression and Oncotype Dx Recurrence Score in Estrogen Receptor Positive Breast Carcinomas. PLoS ONE, 2015, 10, e0145346.	1.1	16
1113	Meta-Analyses of Microarray Datasets Identifies ANO1 and FADD as Prognostic Markers of Head and Neck Cancer. PLoS ONE, 2016, 11, e0147409.	1.1	50
1114	Nanonets Collect Cancer Secretome from Pericellular Space. PLoS ONE, 2016, 11, e0154126.	1.1	11
1115	Identifying Aspects of the Post-Transcriptional Program Governing the Proteome of the Green Alga Micromonas pusilla. PLoS ONE, 2016, 11, e0155839.	1.1	7
1116	Proteomic Study of Entamoeba histolytica Trophozoites, Cysts, and Cyst-Like Structures. PLoS ONE, 2016, 11, e0156018.	1.1	26
1117	Whole Exome Sequencing and Segregation Analysis Confirms That a Mutation in COL17A1 Is the Cause of Epithelial Recurrent Erosion Dystrophy in a Large Dominant Pedigree Previously Mapped to Chromosome 10q23-q24. PLoS ONE, 2016, 11, e0157418.	1.1	10
1118	Efficient Gene Tree Correction Guided by Genome Evolution. PLoS ONE, 2016, 11, e0159559.	1.1	42
1119	Decoding the Regulatory Landscape of Ageing in Musculoskeletal Engineered Tissues Using Genome-Wide DNA Methylation and RNASeq. PLoS ONE, 2016, 11, e0160517.	1.1	26
1120	Glutamate Receptor Interacting Protein 1 Mediates Platelet Adhesion and Thrombus Formation. PLoS ONE, 2016, 11, e0160638.	1.1	4
1121	Preliminary Validation of a High Docosahexaenoic Acid (DHA) and -Linolenic Acid (ALA) Dietary Oil Blend: Tissue Fatty Acid Composition and Liver Proteome Response in Atlantic Salmon (Salmo salar) Smolts. PLoS ONE, 2016, 11, e0161513.	1.1	8

#	ARTICLE	IF	CITATIONS
1122	Drosophila Genotype Influences Commensal Bacterial Levels. PLoS ONE, 2017, 12, e0170332.	1.1	42
1123	Deep-proteome mapping of WM-266-4 human metastatic melanoma cells: From oncogenic addiction to druggable targets. PLoS ONE, 2017, 12, e0171512.	1.1	21
1124	Proteome analysis of bronchoalveolar lavage from calves infected with bovine respiratory syncytial virusâ€"Insights in pathogenesis and perspectives for new treatments. PLoS ONE, 2017, 12, e0186594.	1.1	24
1125	Global Gene Expression Profiling in Omental Adipose Tissue of Morbidly Obese Diabetic African Americans. Journal of Endocrinology and Metabolism, 2015, 5, 199-210.	0.1	21
1126	Noninvasive Brain Stimulation Enhances Memory Acquisition and Is Associated with Synaptoneurosome Modification in the Rat Hippocampus. ENeuro, 2019, 6, ENEURO.0311-19.2019.	0.9	7
1127	<scp>LGR</scp> 5 controls extracellular matrix production by stem cells in the developing intestine. EMBO Reports, 2020, 21, e49224.	2.0	21
1128	Alternative splicing coupled mRNA decay shapes the temperatureâ€dependent transcriptome. EMBO Reports, 2020, 21, e51369.	2.0	28
1129	A central role for TOR signalling in a yeast model for juvenile CLN3 disease. Microbial Cell, 2015, 2, 466-480.	1.4	13
1130	Replicative and radiation-induced aging: a comparison of gene expression profiles. Aging, 2019, 11, 2378-2387.	1.4	13
1131	Identification of an immune-related risk signature for predicting prognosis in clear cell renal cell carcinoma. Aging, 2020, 12, 2302-2332.	1.4	48
1132	SPARC overexpression alters microRNA expression profiles involved in tumor progression. Genes and Cancer, 2017, 8, 453-471.	0.6	8
1133	Impact of DLK1-DIO3 imprinted cluster hypomethylation in smoker patients with lung cancer. Oncotarget, 2018, 9, 4395-4410.	0.8	37
1134	Dynamics of PBMC gene expression in hepatitis C virus genotype 1-infected patients during combined peginterferon/ribavirin therapy. Oncotarget, 2016, 7, 61325-61335.	0.8	7
1135	Tristetraprolin disables prostate cancer maintenance by impairing proliferation and metabolic function. Oncotarget, 2016, 7, 83462-83475.	0.8	10
1136	Disabled cell density sensing leads to dysregulated cholesterol synthesis in glioblastoma. Oncotarget, 2017, 8, 14860-14875.	0.8	30
1137	Genome-wide shRNA screen revealed integrated mitogenic signaling between dopamine receptor D2 (DRD2) and epidermal growth factor receptor (EGFR) in glioblastoma. Oncotarget, 2014, 5, 882-893.	0.8	127
1138	Time-course gene profiling and networks in demethylated retinoblastoma cell line. Oncotarget, 2015, 6, 23688-23707.	0.8	6
1139	A Comparative Analysis and Review of lysyl Residues Affected by Posttranslational Modifications. Current Genomics, 2015, 16, 128-138.	0.7	12

#	ARTICLE	IF	CITATIONS
1140	Analysis of K-Ras Interactions by Biotin Ligase Tagging. Cancer Genomics and Proteomics, 2017, 14, 225-239.	1.0	11
1142	Analysis of Differential Expression of microRNAs and Their Target Genes in Prostate Cancer: A Bioinformatics Study on Microarray Gene Expression Data. International Journal of Molecular and Cellular Medicine, 2019, 8, 103-114.	1.1	4
1143	Age-related changes in mesenchymal stem cells identified using a multi-omics approach. , 2016, 31, 136-159.		53
1144	BacillOndex: an integrated data resource for systems and synthetic biology. Journal of Integrative Bioinformatics, 2013, 10, 224.	1.0	4
1145	Genome-Wide Survey of Selection Signatures in Pakistani Cattle Breeds. Pakistan Veterinary Journal, 2018, 38, 214-218.	0.5	6
1146	Computational Verification of Large Logical Modelsâ€"Application to the Prediction of T Cell Response to Checkpoint Inhibitors. Frontiers in Physiology, 2020, 11, 558606.	1.3	18
1147	Serumâ€free culture alters the quantity and protein composition of neuroblastomaâ€derived extracellular vesicles. Journal of Extracellular Vesicles, 2015, 4, 26883.	5.5	131
1148	Lack of <i>Rbl</i>1/p107 Effects on Cell Proliferation and Maturation in the Inner Ear. Journal of Behavioral and Brain Science, 2013, 03, 534-555.	0.2	3
1149	Expression Profiles of the Individual Genes Corresponding to the Genes Generated by Cytotoxicity Experiments with Bortezomib in Multiple Myeloma. Turkish Journal of Haematology, 2016, 33, 286-292.	0.2	2
1150	A Primer for Disease Gene Prioritization Using Next-Generation Sequencing Data. Genomics and Informatics, 2013, 11, 191.	0.4	11
1151	Sequence Analysis of Hypothetical Proteins from<i>Helicobacter pylori</i>26695 to Identify Potential Virulence Factors. Genomics and Informatics, 2016, 14, 125.	0.4	28
1152	Dissecting the pre-placodal transcriptome to reveal presumptive direct targets of Six1 and Eya1 in cranial placodes. ELife, 2016, 5, .	2.8	45
1153	Cell culture-based profiling across mammals reveals DNA repair and metabolism as determinants of species longevity. ELife, 2016, 5, .	2.8	69
1154	Temporal dynamics of the developing lung transcriptome in three common inbred strains of laboratory mice reveals multiple stages of postnatal alveolar development. PeerJ, 2016, 4, e2318.	0.9	47
1155	Evolutionary analysis of vision genes identifies potential drivers of visual differences between giraffe and okapi. PeerJ, 2017, 5, e3145.	0.9	9
1156	Comparative functional analysis of proteins containing low-complexity predicted amyloid regions. PeerJ, 2018, 6, e5823.	0.9	7
1157	Speeding up all-against-all protein comparisons while maintaining sensitivity by considering subsequence-level homology. PeerJ, 2014, 2, e607.	0.9	7
1158	Partial defoliation of<i>Brachypodium distachyon</i>plants grown in petri dishes under low light increases P and other nutrient levels concomitantly with transcriptional changes in the roots. PeerJ, 2019, 7, e7102.	0.9	2

#	ARTICLE	IF	CITATIONS
1159	Amyloid domains in the cell nucleus controlled by nucleoskeletal protein lamin B1 reveal a new pathway of mercury neurotoxicity. PeerJ, 2015, 3, e754.	0.9	15
1160	The sugarcane mitochondrial genome: assembly, phylogenetics and transcriptomics. PeerJ, 2019, 7, e7558.	0.9	15
1161	Computational analysis of the LRRK2 interactome. PeerJ, 2015, 3, e778.	0.9	48
1162	Detection and characterization of microRNA expression profiling and its target genes in response to canine parvovirus in Crandell Reese Feline Kidney cells. PeerJ, 2020, 8, e8522.	0.9	8
1163	Computational analysis of microRNA-mediated interactions in SARS-CoV-2 infection. PeerJ, 2020, 8, e9369.	0.9	164
1165	Transcription Factor Action Orchestrates the Complex Expression Pattern of CRABS CLAW in Arabidopsis. Genes, 2021, 12, 1663.	1.0	5
1166	Toward Integrated Multi-Omics Intervention: Rice Trait Improvement and Stress Management. Frontiers in Plant Science, 2021, 12, 741419.	1.7	14
1167	Taking the road less traveled â€“ the therapeutic potential of CBP/Î²-catenin antagonists. Expert Opinion on Therapeutic Targets, 2021, 25, 701-719.	1.5	6
1168	Inhibition of USP28 overcomes Cisplatin-resistance of squamous tumors by suppression of the Fanconi anemia pathway. Cell Death and Differentiation, 2022, 29, 568-584.	5.0	16
1169	Human Genome. Computational Biology, 2013, , 249-262.	0.1	0
1170	Quantitative Proteomics Analysis of Differentially Expressed Proteins Involved in Renal Clear Cell Carcinoma by Shotgun Approach Coupled with Stable Isotope Dimethyl Labeling. Journal of Proteomics and Bioinformatics, 2014, s7, .	0.4	1
1171	Shotgun Proteomics Analysis of Differentially Expressed Urinary Proteins Involved in the Hepatocellular Carcinoma. Journal of Proteomics and Bioinformatics, 2014, 07, .	0.4	0
1172	BioJS InterMineTable Component: A BioJS componentÂfor displaying data from InterMine compatible webserviceÂendpoints. F1000Research, 0, 3, 46.	0.8	1
1173	treeWidget: a BioJS component to visualise phylogenetic trees. F1000Research, 0, 3, 49.	0.8	1
1175	Proteomic analysis of thyroid tissue in Graves' disease and toxic multinodular goiter. Endocrine Abstracts, 0, , .	0.0	0
1176	Identification of Biologically Significant Elements Using Correlation Networks in High Performance Computing Environments. Lecture Notes in Computer Science, 2015, , 607-619.	1.0	0
1177	Modifying the Classical F Test for Microarray Experiments. Journal of Biostatistics and Biometric Applications, 2016, 1, .	0.3	0
1181	Integration of Transcriptomic and Proteomic Data for Disease Insights. Neuromethods, 2017, , 325-356.	0.2	0

#	ARTICLE	IF	CITATIONS
1196	Enhanced Kat3A/Catenin transcription: a common mechanism of therapeutic resistance. , 2019, 2, 917-932.		0
1220	Studying RNAâ€"Protein Interaction Using. Methods in Molecular Biology, 2021, 2170, 213-218.	0.4	0
1221	Extracellular vesicles in patients in the acute phase of psychosis and after clinical improvement: an explorative study. PeerJ, 2020, 8, e9714.	0.9	6
1224	Capillary Electrophoresis Assessment of Plasma Protein Changes in an African Penguin (<i>Spheniscus) Tj ETQq1 1 0.784314 rgBT /Ove	1.6	5
1225	Identifying Potential Biomarkers in Colorectal Cancer and Developing Non-invasive Diagnostic Models Using Bioinformatics Approaches. Avicenna Journal of Medical Biochemistry, 2020, 8, 99-111.	0.5	0
1229	A phylogenetic analysis between humans and D. melanogaster: A repertoire of solute carriers in humans and flies. Gene, 2022, 809, 146033.	1.0	2
1230	A Survey on Applications of Artificial Intelligence in Fighting Against COVID-19. ACM Computing Surveys, 2022, 54, 1-32.	16.1	55
1234	Genomic Insights Into the Archaea Inhabiting an Australian Radioactive Legacy Site. Frontiers in Microbiology, 2021, 12, 732575.	1.5	5
1235	Metabolic Imbalance Effect on Retinal MÃ¼ller Glial Cells Reprogramming Capacity: Involvement of Histone Deacetylase SIRT6. Frontiers in Genetics, 2021, 12, 769723.	1.1	9
1236	Proteomic characterization of GSK3Î² knockout shows altered cell adhesion and metabolic pathway utilisation in colorectal cancer cells. PLoS ONE, 2021, 16, e0246707.	1.1	0
1238	iTRAQâ€'based proteomic analysis reveals potential regulatory networks in dust miteâ€'related asthma treated with subcutaneous allergen immunotherapy. Molecular Medicine Reports, 2020, 22, 3607-3620.	1.1	2
1242	Acarbose has sex-dependent and -independent effects on age-related physical function, cardiac health, and lipid biology. JCI Insight, 2020, 5, .	2.3	16
1243	Fine mapping of variants associated with endometriosis in the WNT4 region on chromosome 1p36. International Journal of Molecular Epidemiology and Genetics, 2013, 4, 193-206.	0.4	16
1244	Computational methods and opportunities for phosphorylation network medicine. Translational Cancer Research, 2014, 3, 266-278.	0.4	8
1245	Transcriptome analysis of aging mouse meibomian glands. Molecular Vision, 2016, 22, 518-27.	1.1	14
1246	Mutation near the binding interfaces at Î±-hemoglobin stabilizing protein is highly pathogenic. American Journal of Translational Research (discontinued), 2016, 8, 4224-4232.	0.0	12
1247	Morpho-Physiological and Proteomic Response of Bt-Cotton and Non-Bt Cotton to Drought Stress. Frontiers in Plant Science, 2021, 12, 663576.	1.7	0
1248	Prediction of Key Proteins Via Topological Analysis of Protein-Protein Interaction Network. Galen, 2018, 7, e1129.	0.6	1

#	ARTICLE	IF	CITATIONS
1249	Transcriptomic Changes in the Rumen Epithelium of Cattle after the Induction of Acidosis. Archives of Razi Institute, 2020, 75, 109-121.	0.4	0
1250	HRD1-mediated METTL14 degradation regulates m6A mRNA modification to suppress ER proteotoxic liver disease. Molecular Cell, 2021, 81, 5052-5065.e6.	4.5	24
1252	Data-Dependent Acquisition Ladder for Capillary Electrophoresis Mass Spectrometry-Based Ultrasensitive (Neuro)Proteomics. Analytical Chemistry, 2021, 93, 15964-15972.	3.2	18
1253	Detection of molecular signatures and pathways shared by Alzheimerâ€™s disease and type 2 diabetes. Gene, 2022, 810, 146070.	1.0	11
1254	Gene Regulation Analysis Reveals Perturbations of Autism Spectrum Disorder during Neural System Development. Genes, 2021, 12, 1901.	1.0	4
1256	Differential Kat3 Usage Orchestrates the Integration of Cellular Metabolism with Differentiation. Cancers, 2021, 13, 5884.	1.7	4
1257	Expression and associated epigenetic mechanisms of the Ca2+-signaling genes in breast cancer subtypes and epithelial-to-mesenchymal transition. Journal of Cell Communication and Signaling, 2022, 16, 461-474.	1.8	3
1258	The Transcription Factor FEZF1, a Direct Target of EWSR1-FLI1 in Ewing Sarcoma Cells, Regulates the Expression of Neural-Specific Genes. Cancers, 2021, 13, 5668.	1.7	4
1260	A comprehensive in silico investigation into the nsSNPs of Drd2 gene predicts significant functional consequences in dopamine signaling and pharmacotherapy. Scientific Reports, 2021, 11, 23212.	1.6	7
1261	Multi-Omics Integration and Network Analysis Reveal Potential Hub Genes and Genetic Mechanisms Regulating Bovine Mastitis. Current Issues in Molecular Biology, 2022, 44, 309-328.	1.0	11
1262	Identification of key regulators in parathyroid adenoma using an integrative gene network analysis. Bioinformation, 2020, 16, 910-922.	0.2	3
1263	Comparative proteomic analysis of hybrid maize MR2008 and its parental lines. Journal of Agricultural Science, 2021, 159, 570-579.	0.6	1
1264	Possible Role of Prep1 Homeodomain Transcription Factor in Cardiac Mesenchymal Stromal Cells. Molecular Biology, 2021, 55, 847-853.	0.4	0
1266	Integrated Metabolomics and Proteomics Dynamics of Serum Samples Reveals Dietary Zeolite Clinoptilolite Supplementation Restores Energy Balance in High Yielding Dairy Cows. Metabolites, 2021, 11, 842.	1.3	6
1267	Identification of Prognostic Biomarkers in Papillary Thyroid Cancer and Developing Non-Invasive Diagnostic Models Through Integrated Bioinformatics Analysis. MicroRNA (Shariqah, United Arab) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	6
1268	miRNome Profiling Detects miR-101-3p and miR-142-5p as Putative Blood Biomarkers of Frailty Syndrome. Genes, 2022, 13, 231.	1.0	10
1269	Comparative Proteomics of <i>Coxiella</i> like Endosymbionts (CLEs) in the Symbiotic Organs of Rhipicephalus sanguineus Ticks. Microbiology Spectrum, 2022, 10, e0167321.	1.2	5
1270	Effect of dietary incorporation of Chlorella vulgaris and CAZyme supplementation on the hepatic proteome of finishing pigs. Journal of Proteomics, 2022, 256, 104504.	1.2	5

#	ARTICLE	IF	CITATIONS
1271	Enrichment of Newly Synthesized Proteins following treatment of C2C12 Myotubes with Endotoxin and Interferon-Î³. Inflammation, 2022, , 1.	1.7	1
1272	Skeletal muscle transcriptomics identifies common pathways in nerve crush injury and ageing. Skeletal Muscle, 2022, 12, 3.	1.9	5
1273	Identifying individualized risk subpathways reveals pan-cancer molecular classification based on multi-omics data. Computational and Structural Biotechnology Journal, 2022, 20, 838-849.	1.9	2
1274	Evolution of a New Testis-Specific Functional Promoter Within the Highly Conserved Map2k7 Gene of the Mouse. Frontiers in Genetics, 2021, 12, 812139.	1.1	1
1275	Pseudouridine synthases modify human pre-mRNA co-transcriptionally and affect pre-mRNA processing. Molecular Cell, 2022, 82, 645-659.e9.	4.5	75
1276	Systematic Pharmacology Mechanisms of Starfish in the Treatment of Peptic Ulcer. International Journal of Pharmacology, 2022, 18, 248-261.	0.1	0
1277	The P522R protective variant of PLCG2 promotes the expression of antigen presentation genes by human microglia in an Alzheimer's disease mouse model. Alzheimer's and Dementia, 2022, 18, 1765-1778.	0.4	19
1278	Identification of Molecular Signatures and Candidate Drugs in Vascular Dementia by Bioinformatics Analyses. Frontiers in Molecular Neuroscience, 2022, 15, 751044.	1.4	10
1279	Transcriptome signature changes in the liver of a migratory passerine. Genomics, 2022, 114, 110283.	1.3	8
1280	The short isoform of the host antiviral protein ZAP acts as an inhibitor of SARS-CoV-2 programmed ribosomal frameshifting. Nature Communications, 2021, 12, 7193.	5.8	49
1282	Characterization of the 3'UTR of the BTD gene and identification of regulatory elements and microRNAs. Genetics and Molecular Biology, 2022, 45, e20200432.	0.6	2
1283	Transcriptional Profiling of Early and Late Phases of Bovine Tuberculosis. Infection and Immunity, 2022, 90, IAI0031321.	1.0	4
1284	PUCHI represses early meristem formation in developing lateral roots of <i>Arabidopsis thaliana</i>. Journal of Experimental Botany, 2022, 73, 3496-3510.	2.4	11
1285	Identification of phenotype-specific networks from paired gene expressionâ€“cell shape imaging data. Genome Research, 2022, 32, 750-765.	2.4	5
1287	The evolution of de novo <scp>humanâ€specific microRNA</scp> genes on chromosome 21. American Journal of Biological Anthropology, 2022, 178, 223-243.	0.6	2
1288	Precise tumor immune rewiring via synthetic CRISPRa circuits gated by concurrent gain/loss of transcription factors. Nature Communications, 2022, 13, 1454.	5.8	6
1289	Multivariate genomic and transcriptomic determinants of imaging-derived personalized therapeutic needs in Parkinsonâ€™s disease. Scientific Reports, 2022, 12, 5483.	1.6	3
1290	Comparative Proteomic Analysis of the Diatom Phaeodactylum tricornutum Reveals New Insights Into Intra- and Extra-Cellular Protein Contents of Its Oval, Fusiform, and Triradiate Morphotypes. Frontiers in Plant Science, 2022, 13, 673113.	1.7	4

#	ARTICLE	IF	CITATIONS
1291	Multiple Profile Models Extract Features from Protein Sequence Data and Resolve Functional Diversity of Very Different Protein Families. Molecular Biology and Evolution, 2022, 39, .	3.5	7
1293	Genome-Wide Survey and Development of the First Microsatellite Markers Database (AnCorDB) in Anemone coronaria L.. International Journal of Molecular Sciences, 2022, 23, 3126.	1.8	13
1294	HIV-1 Tat and cocaine coexposure impacts piRNAs to affect astrocyte energy metabolism. Epigenomics, 2022, 14, 261-278.	1.0	2
1295	Human gut bacteria produce Î—17-modulating bileÂacid metabolites. Nature, 2022, 603, 907-912.	13.7	210
1296	The Non-pregnant and Pregnant Human Cervix: a Systematic Proteomic Analysis. Reproductive Sciences, 2022, 29, 1542-1559.	1.1	4
1298	Transcriptome analysis of infected Crandell Rees Feline Kidney (CRFK) cells by canine parvovirus type 2c Laotian isolates. Gene, 2022, 822, 146324.	1.0	2
1299	Proteomic Analysis of Autoimmune Retinopathy Implicates Neuronal Cell Adhesion Molecule as a Potential Biomarker. Ophthalmology Science, 2022, 2, 100131.	1.0	4
1300	VPS32, a member of the ESCRT complex, modulates adherence to host cells in the parasite Trichomonas vaginalis by affecting biogenesis and cargo sorting of released extracellular vesicles. Cellular and Molecular Life Sciences, 2022, 79, 11.	2.4	8
1301	Effects of the Expression of Random Sequence Clones on Growth and Transcriptome Regulation in Escherichia coli. Genes, 2022, 13, 53.	1.0	9
1302	FOXO3 regulates a common genomic program in aging and glioblastoma stem cells. Aging and Cancer, 2021, 2, 137-159.	0.5	3
1303	FertilityOnline: A Straightforward Pipeline for Functional Gene Annotation and Disease Mutation Discovery. Genomics, Proteomics and Bioinformatics, 2022, 20, 455-465.	3.0	3
1304	Characterization of SLC34A2 as a Potential Prognostic Marker of Oncological Diseases. Biomolecules, 2021, 11, 1878.	1.8	4
1305	Proteolytic Profiling of Streptococcal Pyrogenic Exotoxin B (SpeB) by Complementary HPLC-MS Approaches. International Journal of Molecular Sciences, 2022, 23, 412.	1.8	7
1306	From drug repositioning to target repositioning: prediction of therapeutic targets using genetically perturbed transcriptomic signatures. Bioinformatics, 2022, 38, i68-i76.	1.8	3
1307	RNase E and HupB dynamics foster mycobacterial cell homeostasis and fitness. IScience, 2022, 25, 104233.	1.9	2
1308	Whole mitochondrial genome sequencing of Malaysian patients with cardiomyopathy. PeerJ, 2022, 10, e13265.	0.9	1
1359	Morpho-Physiological and Proteomic Response of Bt-Cotton and Non-Bt Cotton to Drought Stress. Frontiers in Plant Science, 2021, 12, 663576.	1.7	10
1361	PTEN mutant non-small cell lung cancer require ATM to suppress pro-apoptotic signalling and evade radiotherapy. Cell and Bioscience, 2022, 12, 50.	2.1	9

#	Article	IF	Citations
1362	The Cellular Senescence Factor Extracellular HMGB1 Directly Inhibits Oligodendrocyte Progenitor Cell Differentiation and Impairs CNS Remyelination. Frontiers in Cellular Neuroscience, 2022, 16, 833186.	1.8	7
1363	Expression Analysis in Atlantic Salmon Liver Reveals miRNAs Associated with Smoltification and Seawater Adaptation. Biology, 2022, 11, 688.	1.3	3
1364	Genome-Wide Association Study and Genomic Selection for Proteinogenic Methionine in Soybean Seeds. Frontiers in Plant Science, 2022, 13, 859109.	1.7	8
1365	PRD-Class Homeobox Genes in Bovine Early Embryos: Function, Evolution, and Overlapping Roles. Molecular Biology and Evolution, 2022, 39, .	3.5	3
1366	Chromatin remodeling is restricted by transient GATA6 binding during iPSC differentiation to definitive endoderm. IScience, 2022, 25, 104300.	1.9	3
1367	Differential proteome and interactome analysis reveal the basis of pleiotropy associated with the histidine methyltransferase Hpm1p. Molecular and Cellular Proteomics, 2022, , 100249.	2.5	1
1369	Radiotherapy-activated NBTXR3 nanoparticles modulate cancer cell immunogenicity and TCR repertoire. Cancer Cell International, 2022, 22, .	1.8	8
1371	Dosage-sensitive miRNAs trigger modulation of gene expression during genomic imbalance in maize. Nature Communications, 2022, 13, .	5.8	1
1372	LncRNA <i>RUS</i> shapes the gene expression program towards neurogenesis. Life Science Alliance, 2022, 5, e202201504.	1.3	5
1374	Cultivar-specific miRNA-mediated RNA silencing in grapes. Planta, 2022, 256, .	1.6	0
1375	Widely Targeted Lipidomics and Transcriptomics Analysis Revealed Changes of Lipid Metabolism in Spleen Dendritic Cells in Shrimp Allergy. Foods, 2022, 11, 1882.	1.9	4
1376	Curating the GnomAD Database: Report of Novel Variants in the Thyroid Peroxidase Gene Using In Silico Bioinformatics Algorithms and a Literature Review. SSRN Electronic Journal, 0, , .	0.4	0
1378	Network Pharmacology and In Vivo Experimental Validation to Uncover the Renoprotective Mechanisms of Fangji Huangqi Decoction on Nephrotic Syndrome. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-17.	0.5	1
1379	Bioinformatics roadmap for therapy selection in cancer genomics. Molecular Oncology, 2022, 16, 3881-3908.	2.1	6
1380	Joint Tissue Protective and Immune-Modulating miRNA Landscape of Mesenchymal Stromal Cell-Derived Extracellular Vesicles under Different Osteoarthritis-Mimicking Conditions. Pharmaceutics, 2022, 14, 1400.	2.0	2
1381	Metabolic modeling-based drug repurposing in Glioblastoma. Scientific Reports, 2022, 12, .	1.6	4
1382	Identifying cell stateâ€"associated alternative splicing events and their coregulation. Genome Research, 2022, 32, 1385-1397.	2.4	3
1383	The evolution of the testis transcriptome in pregnant male pipefishes and seahorses. Evolution; International Journal of Organic Evolution, 2022, 76, 2162-2180.	1.1	0

#	Article	IF	Citations
1384	Epigenetically silenced apoptosis-associated tyrosine kinase (AATK) facilitates a decreased expression of Cyclin D1 and WEE1, phosphorylates TP53 and reduces cell proliferation in a kinase-dependent manner. Cancer Gene Therapy, 2022, 29, 1975-1987.	2.2	6
1385	lncRNAâ€“miRNAâ€“mRNA ceRNA Network Involved in Sheep Prolificacy: An Integrated Approach. Genes, 2022, 13, 1295.	1.0	12
1386	Associations between circulating proteins and risk of breast cancer by intrinsic subtypes: a Mendelian randomisation analysis. British Journal of Cancer, 2022, 127, 1507-1514.	2.9	4
1387	The epigenetic reader PHF21B modulates murine social memory and synaptic plasticityâ€“related genes. JCI Insight, 2022, 7, .	2.3	3
1388	Network Tau spreading is vulnerable to the expression gradients of <i>APOE</i> and glutamatergic-related genes. Science Translational Medicine, 2022, 14, .	5.8	19
1389	Dynamic changes in O-GlcNAcylation regulate osteoclast differentiation and bone loss via nucleoporin 153. Bone Research, 2022, 10, .	5.4	8
1390	Cross-platform validation of a mouse blood gene signature for quantitative reconstruction of radiation dose. Scientific Reports, 2022, 12, .	1.6	4
1391	Curating the gnomAD database: Report of novel variants in the thyroid peroxidase gene using in silico bioinformatics algorithms and a literature review. Molecular and Cellular Endocrinology, 2022, 558, 111748.	1.6	0
1392	Acute changes in free and extracellular vesicle-associated circulating miRNAs and myokine profile in professional sky-runners during the Gran Sasso dâ€™Italia vertical run. Frontiers in Molecular Biosciences, 0, 9, .	1.6	3
1393	Molecular and cellular architecture of the larval sensory organ in the cnidarian <i>Nematostella vectensis</i>. Development (Cambridge), 2022, 149, .	1.2	10
1394	Transcriptome response of proliferating muscle satellite cells to thermal challenge in commercial turkey. Frontiers in Physiology, 0, 13, .	1.3	5
1395	Dichotomous <i>cis</i>-regulatory motifs mediate the maturation of the neuromuscular junction by retrograde BMP signaling. Nucleic Acids Research, 0, , .	6.5	0
1396	A systematic review and Meta-analysis of urinary extracellular vesicles proteome in diabetic nephropathy. Frontiers in Endocrinology, 0, 13, .	1.5	6
1397	Insulin and serine metabolism as sex-specific hallmarks of Alzheimerâ€™s disease in the human hippocampus. Cell Reports, 2022, 40, 111271.	2.9	19
1398	A Systems Toxicological Analysis of Oxybenzone Effects on the Metabolic Physiology of Embryo-Larval Zebrafish (Danio Rerio). SSRN Electronic Journal, 0, , .	0.4	0
1399	RTN2, a new member of circadian clock genes identified by database mining and bioinformatics prediction, is highly expressed in ovarian cancer. Molecular Medicine Reports, 2022, 26, .	1.1	0
1400	Mechanism of action of Orthosiphon stamineus against non-alcoholic fatty liver disease: Insights from systems pharmacology and molecular docking approaches. Saudi Pharmaceutical Journal, 2022, , .	1.2	5
1401	Craniofacial, dental, and molecular features of Pyle disease in a South African child. BDJ Open, 2022, 8, .	0.8	0

#	Article	IF	Citations
1402	Pollutants corrupt resilience pathways of aging in the nematode C. elegans. IScience, 2022, 25, 105027.	1.9	6
1404	Expression Analysis of Moritella viscosa-Challenged Atlantic Salmon Identifies Disease-Responding Genes, MicroRNAs and Their Predicted Target Genes and Pathways. International Journal of Molecular Sciences, 2022, 23, 11200.	1.8	6
1406	cAMP-Protein kinase A and stress-activated MAP kinase signaling mediate transcriptional control of autophagy in fission yeast during glucose limitation or starvation. Autophagy, 2023, 19, 1311-1331.	4.3	4
1407	Multiple sclerosis risk variants influence the peripheral Bâ€cell compartment early in life in the general population. European Journal of Neurology, 0, , .	1.7	2
1408	Ethylene emitted by viral pathogen-infected pepper (Capsicum annuum L.) plants is a volatile chemical cue that attracts aphid vectors. Frontiers in Plant Science, 0, 13, .	1.7	4
1412	Correspondence between gene expression and neurotransmitter receptor and transporter density in the human brain. NeuroImage, 2022, 264, 119671.	2.1	20
1413	Comparative transcriptomics analysis pipeline for the meta-analysis of phylogenetically divergent datasets (CoRMAP). BMC Bioinformatics, 2022, 23, .	1.2	2
1414	Using the <i>Arabidopsis</i> Information Resource (TAIR) to Find Information About <i>Arabidopsis</i> Genes. Current Protocols, 2022, 2, .	1.3	11
1415	Prediction of BRAF V600E variant from cancer gene expression data. Translational Cancer Research, 2022, 11, 4051-4056.	0.4	2
1416	Anisomycin has a potential toxicity of promoting cuproptosis in human ovarian cancer stem cells by attenuating YY1/lipoic acid pathway activation. Journal of Cancer, 2022, 13, 3503-3514.	1.2	11
1418	Whole-exome sequencing of epithelial ovarian carcinomas differing in resistance to platinum therapy. Life Science Alliance, 2022, 5, e202201551.	1.3	3
1419	Transcriptome Response of Differentiating Muscle Satellite Cells to Thermal Challenge in Commercial Turkey. Genes, 2022, 13, 1857.	1.0	3
1420	Analyses of Transcriptomics Cell Signalling for Pre-Screening Applications in the Integrated Approach for Testing and Assessment of Non-Genotoxic Carcinogens. International Journal of Molecular Sciences, 2022, 23, 12718.	1.8	6
1421	Analysis of nested alternate open reading frames and their encoded proteins. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	1
1422	A comprehensive survey of the approaches for pathway analysis using multi-omics data integration. Briefings in Bioinformatics, 2022, 23, .	3.2	13
1423	The interplay between prior selection, mild intermittent exposure, and acute severe exposure in phenotypic and transcriptional response to hypoxia. Ecology and Evolution, 2022, 12, .	0.8	7
1424	A systems toxicological analysis of oxybenzone effects on the metabolic physiology of embryo-larval zebrafish (Danio rerio). Environmental Advances, 2022, 9, 100308.	2.2	3
1425	The Prognostic and Therapeutic Implications of the Chemoresistance Gene BIRC5 in Triple-Negative Breast Cancer. Cancers, 2022, 14, 5180.	1.7	7

#	Article	IF	Citations
1426	Cell derived matrices from bovine corneal endothelial cells as a model to study cellular dysfunction. Experimental Eye Research, 2023, 226, 109303.	1.2	3
1428	Prediction of homologous recombination deficiency from cancer gene expression data. Journal of International Medical Research, 2022, 50, 030006052211336.	0.4	0
1429	Integrative omics indicate FMRP sequesters mRNA from translation and deadenylation in human neuronal cells. Molecular Cell, 2022, 82, 4564-4581.e11.	4.5	6
1430	Changes of gene expression in peripheral blood mononuclear cells of lung cancer patients with or without anorexia. Clinical Nutrition, 2023, 42, 9-17.	2.3	0
1431	Pleiotropic fitness effects of the lncRNA Uhg4 in Drosophila melanogaster. BMC Genomics, 2022, 23, .	1.2	0
1432	Single-cell multiomics reveals the complexity of TGFÎ² signalling to chromatin in iPSC-derived kidney organoids. Communications Biology, 2022, 5, .	2.0	3
1433	Bone Marrow Macrophages Induce Inflammation by Efferocytosis of Apoptotic Prostate Cancer Cells via HIF-1Î± Stabilization. Cells, 2022, 11, 3712.	1.8	3
1434	Genome Editing Reveals Both the Crucial Role of OsCOI2 in Jasmonate Signaling and the Functional Diversity of COI1 Homologs in Rice. Plant and Cell Physiology, 2023, 64, 405-421.	1.5	6
1435	The role of genomic signatures of directional selection and demographic history in the population structure of a marine teleost with high gene flow. Ecology and Evolution, 2022, 12, .	0.8	2
1437	Stage-specific and cell type-specific requirements of ikzf1 during haematopoietic differentiation in zebrafish. Scientific Reports, 2022, 12, .	1.6	5
1438	FUS-ALS hiPSC-derived astrocytes impair human motor units through both gain-of-toxicity and loss-of-support mechanisms. Molecular Neurodegeneration, 2023, 18, .	4.4	17
1439	CASC3 biomolecular condensates restrict Turnip crinkle virus by limiting host factor availability. Journal of Molecular Biology, 2023, , 167956.	2.0	3
1441	Medicinal Chemistry Strategies for the Development of Inhibitors Disrupting Î²-Cateninâ€™s Interactions with Its Nuclear Partners. Journal of Medicinal Chemistry, 2023, 66, 1-31.	2.9	6
1442	CPEB3 low-complexity motif regulates local protein synthesis via proteinâ€“protein interactions in neuronal ribonucleoprotein granules. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	6
1444	The Tumor Coagulome as a Transcriptional Target and a Potential Effector of Glucocorticoids in Human Cancers. Cancers, 2023, 15, 1531.	1.7	0
1445	Genomic and immune landscape Of metastatic pheochromocytoma and paraganglioma. Nature Communications, 2023, 14, .	5.8	8
1446	Computational analysis of structural and functional evaluation of the deleterious missense variants in the human <i>CTLA4</i> gene. Journal of Biomolecular Structure and Dynamics, 2023, 41, 14179-14196.	2.0	0
1449	Complement system dysregulation in synovial fluid from patients with persistent inflammation following anterior cruciate ligament reconstruction surgery. Journal of Cartilage & Joint Preservation, 2023, , 100114.	0.2	0

#	ARTICLE	IF	CITATIONS
1451	In silico Identification of Hypoxic Signature followed by reverse transcription-quantitative PCR Validation in Cancer Cell Lines. Iranian Biomedical Journal, 2023, 27, 23-33.	0.4	1
1452	Metabolic responses in blood-stage malaria parasites associated with increased and decreased sensitivity to PfATP4 inhibitors. Malaria Journal, 2023, 22, .	0.8	1
1453	Use of an Integrated Multi-Omics Approach To Identify Molecular Mechanisms and Critical Factors Involved in the Pathogenesis of <i>Leptospira</i>. Microbiology Spectrum, 2023, 11, .	1.2	3
1454	Convergence or redundancy: alternative views about the evolutionary genomics of character displacement. Evolution; International Journal of Organic Evolution, 0, , .	1.1	0
1455	Genesâ€toâ€Pathways Species Conservation Analysis: Enabling the Exploration of Conservation of Biological Pathways and Processes Across Species. Environmental Toxicology and Chemistry, 2023, 42, 1152-1166.	2.2	4
1456	Transcriptome analyses of the cortex and white matter of focal cortical dysplasia type II: Insights into pathophysiology and tissue characterization. Frontiers in Neurology, 0, 14, .	1.1	4
1457	The P-body protein 4E-T represses translation to regulate the balance between cell genesis and establishment of the postnatal NSC pool. Cell Reports, 2023, 42, 112242.	2.9	1
1459	Longitudinal multi-omic changes in the transcriptome and proteome of peripheral blood cells after a 4ÂGy total body radiation dose to Rhesus macaques. BMC Genomics, 2023, 24, .	1.2	1
1460	Insights into Common Octopus (Octopus vulgaris) Ink Proteome and Bioactive Peptides Using Proteomic Approaches. Marine Drugs, 2023, 21, 206.	2.2	2
1461	Peripheral signature of altered synaptic integrity in young onset cannabis use disorder: A proteomic study of circulating extracellular vesicles. World Journal of Biological Psychiatry, 2023, 24, 603-613.	1.3	0
1464	Metaboverse enables automated discovery and visualization of diverse metabolic regulatory patterns. Nature Cell Biology, 2023, 25, 616-625.	4.6	4
1465	Expansion and collapse of VEGF diversity in major clades of the animal kingdom. Angiogenesis, 0, , .	3.7	1
1466	Genetic and genomic analyses of <i>Drosophila melanogaster</i> models of chromatin modification disorders. Genetics, 2023, 224, .	1.2	2
1530	Bioinformatics in Pathway Identification, Design, Modelling, and Simulation. , 2024, , 181-198.		0