

# PANTHER version 11: expanded annotation data from Gene Ontology pathways, and data analysis tool enhancements

Nucleic Acids Research

45, D183-D189

DOI: [10.1093/nar/gkw1138](https://doi.org/10.1093/nar/gkw1138)

Citation Report

#	ARTICLE	IF	CITATIONS
3	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017, 45, D331-D338.	6.5	1,838
4	Quantitative Proteomic and Phosphoproteomic Analysis of H37Ra and H37Rv Strains of <i>Mycobacterium tuberculosis</i> . <i>Journal of Proteome Research</i> , 2017, 16, 1632-1645.	1.8	55
5	Proteomic Analysis of Chorion-Derived Mesenchymal Stem Cells: Combination of 2D Nano-HPLC in Tandem with ESI Mass Spectrometry. <i>Chromatographia</i> , 2017, 80, 201-207.	0.7	1
6	miRNA engineering of CHO cells facilitates production of difficult-to-express proteins and increases success in cell line development. <i>Biotechnology and Bioengineering</i> , 2017, 114, 1495-1510.	1.7	40
7	Changes of Cerebrospinal Fluid Peptides due to Tauopathy. <i>Journal of Alzheimer's Disease</i> , 2017, 58, 507-520.	1.2	6
8	Exercise alters mouse sperm small noncoding RNAs and induces a transgenerational modification of male offspring conditioned fear and anxiety. <i>Translational Psychiatry</i> , 2017, 7, e1114-e1114.	2.4	134
9	Impact of cytosine methylation on DNA binding specificities of human transcription factors. <i>Science</i> , 2017, 356, .	6.0	912
10	DOT1L safeguards cartilage homeostasis and protects against osteoarthritis. <i>Nature Communications</i> , 2017, 8, 15889.	5.8	112
11	The effect of histone deacetylase inhibitor trichostatin A on porcine mesenchymal stem cell transcriptome. <i>Biochimie</i> , 2017, 139, 56-73.	1.3	8
12	The microprotein Minion controls cell fusion and muscle formation. <i>Nature Communications</i> , 2017, 8, 15664.	5.8	195
13	Role of Ambient Gas Composition on Cold Physical Plasma-Elicited Cell Signaling in Keratinocytes. <i>Biophysical Journal</i> , 2017, 112, 2397-2407.	0.2	40
14	Generation of Single-Cell Transcript Variability by Repression. <i>Current Biology</i> , 2017, 27, 1811-1817.e3.	1.8	43
15	The genome draft of coconut ( <i>Cocos nucifera</i> ). <i>GigaScience</i> , 2017, 6, 1-11.	3.3	96
16	Bivalent complexes of PRC1 with orthologs of BRD4 and MOZ/MORF target developmental genes in <i>Drosophila</i> . <i>Genes and Development</i> , 2017, 31, 1988-2002.	2.7	25
17	Adenovirus E1A TRRAP-targeting domain-mediated enhancement of MYC association with the NuA4 complex activates a panel of MYC target genes enriched for gene expression and ribosome biogenesis. <i>Virology</i> , 2017, 512, 172-179.	1.1	2
18	Growth in spaceflight hardware results in alterations to the transcriptome and proteome. <i>Life Sciences in Space Research</i> , 2017, 15, 88-96.	1.2	28
19	Low-dose rapamycin extends lifespan in a mouse model of mtDNA depletion syndrome. <i>Human Molecular Genetics</i> , 2017, 26, 4588-4605.	1.4	70
20	Meta-analysis of Liver and Heart Transcriptomic Data for Functional Annotation Transfer in Mammalian Orthologs. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 425-432.	1.9	3

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21	Global issues in allergy and immunology: Parasitic infections and allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 1217-1228.	1.5	61
22	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213.	13.7	3,500
23	Quantitative Analysis of Proteome Modulations in Alveolar Epithelial Type II Cells in Response to Pulmonary <i>Aspergillus fumigatus</i> Infection. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2184-2198.	2.5	26
24	Gene expression during delayed hatching in fish-out-of-water. <i>Ecological Genetics and Genomics</i> , 2017, 3-5, 52-59.	0.3	7
25	Differential carbonylation of proteins in end-stage human fatty and nonfatty NASH. <i>Free Radical Biology and Medicine</i> , 2017, 113, 280-290.	1.3	7
26	The Omics Dashboard for interactive exploration of gene-expression data. <i>Nucleic Acids Research</i> , 2017, 45, 12113-12124.	6.5	57
27	New Insight of Common Regulatory Pathways in Human Trabecular Meshwork Cells in Response to Dexamethasone and Prednisolone Using an Integrated Quantitative Proteomics: SWATH and MRM-HR Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017, 16, 3753-3765.	1.8	19
28	Silencing of retrotransposons by SETDB1 inhibits the interferon response in acute myeloid leukemia. <i>Journal of Cell Biology</i> , 2017, 216, 3535-3549.	2.3	144
29	Quantitative Proteomics Reveals the Regulatory Networks of Circular RNA CDR1as in Hepatocellular Carcinoma Cells. <i>Journal of Proteome Research</i> , 2017, 16, 3891-3902.	1.8	77
30	Long read reference genome-free reconstruction of a full-length transcriptome from <i>Astragalus membranaceus</i> reveals transcript variants involved in bioactive compound biosynthesis. <i>Cell Discovery</i> , 2017, 3, 17031.	3.1	95
31	Integrating Prior Information with Bayesian Feature Selection. , 2017, , .		6
32	Proteomics of Parma Dry-Cured Ham: Analysis of Salting Exudates. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 6307-6316.	2.4	27
33	EWS/FLI is a Master Regulator of Metabolic Reprogramming in Ewing Sarcoma. <i>Molecular Cancer Research</i> , 2017, 15, 1517-1530.	1.5	39
34	Activating transcription factor 3 promotes loss of the acinar cell phenotype in response to cerulein-induced pancreatitis in mice. <i>Molecular Biology of the Cell</i> , 2017, 28, 2347-2359.	0.9	21
35	Identification of a gene expression profile associated with the regulation of angiogenesis in endometrial cancer. <i>Molecular Medicine Reports</i> , 2017, 16, 2547-2555.	1.1	13
36	Whole Genome Sequencing of <i>Mycobacterium tuberculosis</i> Isolates From Extrapulmonary Sites. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 413-425.	1.0	22
37	BIME2, a novel gene required for interhomolog meiotic recombination in the protist model organism <i>Tetrahymena</i> . <i>Chromosome Research</i> , 2017, 25, 291-298.	1.0	4
38	Silencing of Repetitive DNA Is Controlled by a Member of an Unusual <i>Caenorhabditis elegans</i> Gene Family. <i>Genetics</i> , 2017, 207, 529-545.	1.2	37

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39	Elucidating the in vivo interactome of HIV-1 RNA by hybridization capture and mass spectrometry. <i>Scientific Reports</i> , 2017, 7, 16965.	1.6	36
40	YY1 Is a Structural Regulator of Enhancer-Promoter Loops. <i>Cell</i> , 2017, 171, 1573-1588.e28.	13.5	749
41	Using the <i>Arabidopsis</i> Information Resource (TAIR) to Find Information About <i>Arabidopsis</i> Genes. <i>Current Protocols in Bioinformatics</i> , 2017, 60, 1.11.1-1.11.45.	25.8	44
42	Whole Exome Sequencing reveals new candidate genes in host genomic susceptibility to Respiratory Syncytial Virus Disease. <i>Scientific Reports</i> , 2017, 7, 15888.	1.6	29
43	FMRFamide-like peptides expand the behavioral repertoire of a densely connected nervous system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10726-E10735.	3.3	64
44	Sumoylation Contributes to Timekeeping and Temperature Compensation of the Plant Circadian Clock. <i>Journal of Biological Rhythms</i> , 2017, 32, 560-569.	1.4	23
45	Development of multivariable models to predict change in Body Mass Index within a clinical trial population of psychotic individuals. <i>Scientific Reports</i> , 2017, 7, 14738.	1.6	16
46	Evidence for rRNA 2 <sup>â€²</sup> -O-methylation plasticity: Control of intrinsic translational capabilities of human ribosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12934-12939.	3.3	197
47	JMJD8 is a novel endoplasmic reticulum protein with a JmjC domain. <i>Scientific Reports</i> , 2017, 7, 15407.	1.6	13
48	Comprehensive analysis of gene expression patterns in Friedreich's ataxia fibroblasts by RNA sequencing reveals altered levels of protein synthesis factors and solute carriers. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 1353-1369.	1.2	38
49	Intrinsic MYH7 expression regulation contributes to tissue level allelic imbalance in hypertrophic cardiomyopathy. <i>Journal of Muscle Research and Cell Motility</i> , 2017, 38, 291-302.	0.9	22
50	Structure-mediated modulation of mRNA abundance by A-to-I editing. <i>Nature Communications</i> , 2017, 8, 1255.	5.8	65
51	Genome-wide mapping and characterization of microsatellites in the swamp eel genome. <i>Scientific Reports</i> , 2017, 7, 3157.	1.6	23
52	Elucidating Protein-DNA Interactions in Human Aliphoid Chromatin via Hybridization Capture and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017, 16, 3433-3442.	1.8	12
53	Genome-wide identification and characterization of phased small interfering RNA genes in response to <i>Botrytis cinerea</i> infection in <i>Solanum lycopersicum</i> . <i>Scientific Reports</i> , 2017, 7, 3019.	1.6	13
54	The role of human host genetics in tuberculosis resistance. <i>Expert Review of Respiratory Medicine</i> , 2017, 11, 721-737.	1.0	16
55	Clinical responses to ERK inhibition in BRAF V600E-mutant colorectal cancer predicted using a computational model. <i>Npj Systems Biology and Applications</i> , 2017, 3, 14.	1.4	45
56	Characterizing the reproductive transcriptomic correlates of acute dehydration in males in the desert-adapted rodent, <i>Peromyscus eremicus</i> . <i>BMC Genomics</i> , 2017, 18, 473.	1.2	10

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57	Cross-Species Genome-Wide Identification of Evolutionary Conserved MicroProteins. <i>Genome Biology and Evolution</i> , 2017, 9, 777-789.	1.1	23
58	Transcriptome analyses reveal SR45 to be a neutral splicing regulator and a suppressor of innate immunity in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2017, 18, 772.	1.2	64
59	Optimal Bayesian feature filtering for single-nucleotide polymorphism data. , 2017, , .		2
60	A Conserved Carbon Starvation Response Underlies Bud Dormancy in Woody and Herbaceous Species. <i>Frontiers in Plant Science</i> , 2017, 8, 788.	1.7	88
61	Unravelling Protein-Protein Interaction Networks Linked to Aliphatic and Indole Glucosinolate Biosynthetic Pathways in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 2028.	1.7	21
62	Systematic Selection of Reference Genes for the Normalization of Circulating RNA Transcripts in Pregnant Women Based on RNA-Seq Data. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1709.	1.8	26
63	Alignment of Mitotic Chromosomes in Human Cells Involves SR-Like Splicing Factors Btf and TRAP150. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1956.	1.8	4
64	Differential Expression Profile of lncRNAs from Primary Human Hepatocytes Following DEET and Fipronil Exposure. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2104.	1.8	14
65	The Stearoyl-CoA Desaturase-1 (Desat1) in <i>Drosophila</i> cooperated with Myc to Induce Autophagy and Growth, a Potential New Link to Tumor Survival. <i>Genes</i> , 2017, 8, 131.	1.0	9
66	Low-Dose Alkylphenol Exposure Promotes Mammary Epithelium Alterations and Transgenerational Developmental Defects, But Does Not Enhance Tumorigenic Behavior of Breast Cancer Cells. <i>Frontiers in Endocrinology</i> , 2017, 8, 272.	1.5	9
67	Analysis of Purified Pancreatic Islet Beta and Alpha Cell Transcriptomes Reveals 11 $\beta$ -Hydroxysteroid Dehydrogenase (Hsd11b1) as a Novel Disallowed Gene. <i>Frontiers in Genetics</i> , 2017, 08, 41.	1.1	60
68	Family History of Early Infant Death Correlates with Earlier Age at Diagnosis But Not Shorter Time to Diagnosis for Severe Combined Immunodeficiency. <i>Frontiers in Immunology</i> , 2017, 8, 808.	2.2	34
69	â€œHotspotsâ€™ of Antigen Presentation Revealed by Human Leukocyte Antigen Ligandomics for Neoantigen Prioritization. <i>Frontiers in Immunology</i> , 2017, 8, 1367.	2.2	133
70	The Networks of Genes Encoding Palmitoylated Proteins in Axonal and Synaptic Compartments Are Affected in PPT1 Overexpressing Neuronal-Like Cells. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 266.	1.4	17
71	Intrinsically disordered linkers determine the interplay between phase separation and gelation in multivalent proteins. <i>ELife</i> , 2017, 6, .	2.8	514
72	Tsc2 disruption in mesenchymal progenitors results in tumors with vascular anomalies overexpressing Lgals3. <i>ELife</i> , 2017, 6, .	2.8	13
73	Relating protein functional diversity to cell type number identifies genes that determine dynamic aspects of chromatin organisation as potential contributors to organismal complexity. <i>PLoS ONE</i> , 2017, 12, e0185409.	1.1	4
74	Serial-omics characterization of equine urine. <i>PLoS ONE</i> , 2017, 12, e0186258.	1.1	4

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75	Functional annotation of Alzheimer's disease associated loci revealed by GWASs. PLoS ONE, 2017, 12, e0179677.	1.1	30
76	An autonomous metabolic role for Spen. PLoS Genetics, 2017, 13, e1006859.	1.5	19
77	Vulvar squamous cell carcinoma aggressiveness is associated with differential expression of collagen and STAT1. Clinical Proteomics, 2017, 14, 40.	1.1	2
78	Pan-genome and phylogeny of <i>Bacillus cereus sensu lato</i> . BMC Evolutionary Biology, 2017, 17, 176.	3.2	92
79	RNA sequencing identifies novel non-coding RNA and exon-specific effects associated with cigarette smoking. BMC Medical Genomics, 2017, 10, 58.	0.7	48
80	Protein recoding by ADAR1-mediated RNA editing is not essential for normal development and homeostasis. Genome Biology, 2017, 18, 166.	3.8	64
81	A putative causal relationship between genetically determined female body shape and posttraumatic stress disorder. Genome Medicine, 2017, 9, 99.	3.6	31
82	The Gene Ontology of eukaryotic cilia and flagella. Cilia, 2017, 6, 10.	1.8	6
83	Multiclass Bayesian feature selection. , 2017, , .		2
84	The pennycress ( <i>Thlaspi arvense</i> L.) nectary: structural and transcriptomic characterization. BMC Plant Biology, 2017, 17, 201.	1.6	23
85	The Carboxy Terminus of YCF1 Contains a Motif Conserved throughout >500 Myr of Streptophyte Evolution. Genome Biology and Evolution, 2017, 9, 473-479.	1.1	14
86	A time-series analysis of altered histone H3 acetylation and gene expression during the course of MMAIII-induced malignant transformation of urinary bladder cells. Carcinogenesis, 2017, 38, 378-390.	1.3	6
87	Computational Analysis of Regulatory Network in Psoriasis by Top-Down Approach: An Initiation towards Identifying a Novel Biomarker to Diagnose and Treat Psoriasis in Future. Medical Reports & Case Studies, 2017, 02, .	0.0	0
88	Transcriptomic analysis of boron hyperaccumulation mechanisms in <i>Puccinellia distans</i> . Chemosphere, 2018, 199, 390-401.	4.2	17
89	Label-Free Quantitative Phosphoproteomics Reveals Regulation of Vasodilator-Stimulated Phosphoprotein upon Stathmin-1 Silencing in a Pair of Isogenic Colorectal Cancer Cell Lines. Proteomics, 2018, 18, e1700242.	1.3	10
90	Morphological and transcriptomic analyses reveal three discrete primary stages of postembryonic development in the common fire salamander, <i>Salamandra salamandra</i> . Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2018, 330, 96-108.	0.6	10
91	Comparative Protein Interaction Network Analysis Identifies Shared and Distinct Functions for the Human ROCO Proteins. Proteomics, 2018, 18, e1700444.	1.3	34
92	Advances in <i>Fasciola hepatica</i> research using omics™ technologies. International Journal for Parasitology, 2018, 48, 321-331.	1.3	39

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93	Proteomic profiling of extracellular vesicles released from vascular smooth muscle cells during initiation of phosphate-induced mineralization. <i>Connective Tissue Research</i> , 2018, 59, 55-61.	1.1	22
94	Single-molecule, full-length transcript sequencing provides insight into the extreme metabolism of the ruby-throated hummingbird <i>Archilochus colubris</i> . <i>GigaScience</i> , 2018, 7, 1-12.	3.3	67
95	Comparative <i>i</i> TRAQ analysis of protein abundance in the human sinoatrial node and working cardiomyocytes. <i>Journal of Anatomy</i> , 2018, 232, 956-964.	0.9	4
96	Scalable, cGMP-compatible purification of extracellular vesicles carrying bioactive human heterodimeric IL-15/lactadherin complexes. <i>Journal of Extracellular Vesicles</i> , 2018, 7, 1442088.	5.5	106
97	Epigenetic modifiers promote mitochondrial biogenesis and oxidative metabolism leading to enhanced differentiation of neuroprogenitor cells. <i>Cell Death and Disease</i> , 2018, 9, 360.	2.7	29
98	Proteomic profiling of HIV-infected T-cells by SWATH mass spectrometry. <i>Virology</i> , 2018, 516, 246-257.	1.1	6
99	dbSWEET: An Integrated Resource for SWEET Superfamily to Understand, Analyze and Predict the Function of Sugar Transporters in Prokaryotes and Eukaryotes. <i>Journal of Molecular Biology</i> , 2018, 430, 2203-2211.	2.0	7
100	Donor-dependent variation of human umbilical cord blood mesenchymal stem cells in response to hypoxic preconditioning and amelioration of limb ischemia. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-15.	3.2	56
101	Analysis of 182 cerebral palsy transcriptomes points to dysregulation of trophic signalling pathways and overlap with autism. <i>Translational Psychiatry</i> , 2018, 8, 88.	2.4	22
102	Endocrine disruptor exposure during development increases incidence of uterine fibroids by altering DNA repair in myometrial stem cells. <i>Biology of Reproduction</i> , 2018, 99, 735-748.	1.2	25
103	Transcriptome of the bivalve <i>Limecola balthica</i> L. from Western Pacific: A new resource for studies of European populations. <i>Marine Genomics</i> , 2018, 40, 58-63.	0.4	4
104	Detection of genetic variants between different Polish Landrace and Puławska pigs by means of RNA-seq analysis. <i>Animal Genetics</i> , 2018, 49, 215-225.	0.6	13
105	Interferon-Stimulated Genes Are Involved in Cross-resistance to Radiotherapy in Tamoxifen-Resistant Breast Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 3397-3408.	3.2	68
106	<i>INPP4B</i> overexpression and <i>KIT</i> downregulation in human achalasia. <i>Neurogastroenterology and Motility</i> , 2018, 30, e13346.	1.6	6
107	Different Neuronal Activity Patterns Induce Different Gene Expression Programs. <i>Neuron</i> , 2018, 98, 530-546.e11.	3.8	262
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111	Cold Shock as a Screen for Genes Involved in Cold Acclimatization in <i>Neurospora crassa</i> . G3: Genes, Genomes, Genetics, 2018, 8, 1439-1454.	0.8	3
112	Repurposing tofacitinib as an anti-myeloma therapeutic to reverse growth-promoting effects of the bone marrow microenvironment. Haematologica, 2018, 103, 1218-1228.	1.7	30
113	Liver regeneration during the associating liver partition and portal vein ligation for staged hepatectomy procedure in <i>Sus scrofa</i> is positively modulated by stem cells. Oncology Letters, 2018, 15, 6309-6321.	0.8	2
114	Baseline mRNA expression differs widely between common laboratory strains of zebrafish. Scientific Reports, 2018, 8, 4780.	1.6	18
115	Alterations in Serum MicroRNA Profile During Hemodialysis - Potential Biological Implications. Cellular Physiology and Biochemistry, 2018, 46, 793-801.	1.1	2
116	A novel genotoxin-specific qPCR array based on the metabolically competent human HepaRG <sub>h</sub> cell line as a rapid and reliable tool for improved in vitro hazard assessment. Archives of Toxicology, 2018, 92, 1593-1608.	1.9	17
117	Liquid biopsy by <i>NGS</i> : differential presence of exons ( <i>DPE</i> ) in cell-free <i>DNA</i> reveals different patterns in metastatic and nonmetastatic colorectal cancer. Cancer Medicine, 2018, 7, 1706-1716.	1.3	16
118	One signal stimulates different transcriptional activation mechanisms. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2018, 1861, 178-189.	0.9	16
119	Polylysine is a Proteostasis Network-Engaging Structural Determinant. Journal of Proteome Research, 2018, 17, 1967-1977.	1.8	11
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121	DNA Repair Network Analysis Reveals Shieldin as a Key Regulator of NHEJ and PARP Inhibitor Sensitivity. Cell, 2018, 173, 972-988.e23.	13.5	349
122	Silencing Arabidopsis <i>CARBOXYL</i> <i>TERMINAL DOMAIN PHOSPHATASE</i> <i>LIKE</i> 4 induces cytokinin <sup>oversensitive</sup> <i>de novo</i> shoot organogenesis. Plant Journal, 2018, 94, 799-812.	2.8	6
123	Analysis of Human Nuclear Protein Complexes by Quantitative Mass Spectrometry Profiling. Proteomics, 2018, 18, e1700427.	1.3	26
124	Transcriptomic Biomarkers for Huntington's Disease: Are Gene Expression Signatures in Whole Blood Reliable Biomarkers?. OMICS A Journal of Integrative Biology, 2018, 22, 283-294.	1.0	9
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126	Common basis for orofacial clefting and cortical interneuronopathy. Translational Psychiatry, 2018, 8, 8.	2.4	14
127	Identifying the molecular targets of <i>Salvia miltiorrhiza</i> (SM) in ox-LDL induced macrophage-derived foam cells based on the integration of metabolomics and network pharmacology. RSC Advances, 2018, 8, 3760-3767.	1.7	5
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129	Molecular characterization of colorectal adenomas with and without malignancy reveals distinguishing genome, transcriptome and methylome alterations. <i>Scientific Reports</i> , 2018, 8, 3161.	1.6	35
130	Whole-Transcriptome Analysis of Mouse Models with MPTP-Induced Early Stages of Parkinson's Disease Reveals Stage-Specific Response of Transcriptome and a Possible Role of Myelin-Linked Genes in Neurodegeneration. <i>Molecular Neurobiology</i> , 2018, 55, 7229-7241.	1.9	14
131	MGAT1 and Complex N-Glycans Regulate ERK Signaling During Spermatogenesis. <i>Scientific Reports</i> , 2018, 8, 2022.	1.6	16
132	Genetics of type 1 diabetes. <i>Current Opinion in Genetics and Development</i> , 2018, 50, 7-16.	1.5	58
133	Defining the molecular signatures of human right heart failure. <i>Life Sciences</i> , 2018, 196, 118-126.	2.0	23
134	Genomewide Transcriptional Responses of Iron-Starved <i>Chlamydia trachomatis</i> Reveal Prioritization of Metabolic Precursor Synthesis over Protein Translation. <i>MSystems</i> , 2018, 3, .	1.7	38
135	BIM and NOXA are mitochondrial effectors of TAF61-driven apoptosis. <i>Cell Death and Disease</i> , 2018, 9, 70.	2.7	9
136	The Planteome database: an integrated resource for reference ontologies, plant genomics and phenomics. <i>Nucleic Acids Research</i> , 2018, 46, D1168-D1180.	6.5	133
137	Development of a Photo-Cross-Linkable Diaminoquinazoline Inhibitor for Target Identification in <i>Plasmodium falciparum</i> . <i>ACS Infectious Diseases</i> , 2018, 4, 523-530.	1.8	20
138	Highly Efficient Exosome Isolation and Protein Analysis by an Integrated Nanomaterial-Based Platform. <i>Analytical Chemistry</i> , 2018, 90, 2787-2795.	3.2	65
139	Synthetic MicroProteins: Versatile Tools for Posttranslational Regulation of Target Proteins. <i>Plant Physiology</i> , 2018, 176, 3136-3145.	2.3	22
140	Eomes-positive CD4 <sup>+</sup> T <sub>H</sub> cells are increased in PTPN22 (1858T) risk allele carriers. <i>European Journal of Immunology</i> , 2018, 48, 655-669.	1.6	33
141	A new miRNA regulator, miR-672, reduces cardiac hypertrophy by inhibiting JUN expression. <i>Gene</i> , 2018, 648, 21-30.	1.0	12
142	Proteomics in biomanufacturing control: Protein dynamics of CHO-K1 cells and conditioned media during apoptosis and necrosis. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1509-1520.	1.7	15
143	Regulation of insulin resistance and type II diabetes by hepatitis C virus infection: A driver function of circulating miRNAs. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 2071-2085.	1.6	17
144	Statistical analysis of human microarray data shows that dietary intervention with n-3 fatty acids, flavonoids and resveratrol enriches for immune response and disease pathways. <i>British Journal of Nutrition</i> , 2018, 119, 239-249.	1.2	9
145	Glutaredoxin-1 Silencing Induces Cell Senescence via p53/p21/p16 Signaling Axis. <i>Journal of Proteome Research</i> , 2018, 17, 1091-1100.	1.8	54
146	Global Quantitative Proteomics reveal Deregulation of Cytoskeletal and Apoptotic Signalling Proteins in Oral Tongue Squamous Cell Carcinoma. <i>Scientific Reports</i> , 2018, 8, 1567.	1.6	18

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147	Genome-Wide DNA Methylation Profiling Identifies Differential Methylation in Uninvolved Psoriatic Epidermis. <i>Journal of Investigative Dermatology</i> , 2018, 138, 1088-1093.	0.3	39
148	Adenosine-to-Inosine Editing of MicroRNA-487b Alters Target Gene Selection After Ischemia and Promotes Neovascularization. <i>Circulation Research</i> , 2018, 122, 444-456.	2.0	53
149	Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism. <i>Nature Genetics</i> , 2018, 50, 6-11.	9.4	327
150	Proteomic diversity of high-density lipoprotein explains its association with clinical outcome in patients with heart failure. <i>European Journal of Heart Failure</i> , 2018, 20, 260-267.	2.9	30
151	Mesenchymal stem cell-derived extracellular vesicles attenuate pulmonary vascular permeability and lung injury induced by hemorrhagic shock and trauma. <i>Journal of Trauma and Acute Care Surgery</i> , 2018, 84, 245-256.	1.1	76
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1074	Predicted Drosophila Interactome Resource and web tool for functional interpretation of differentially expressed genes. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	8
1075	Novel Insights into the Protective Properties of ACTH(4-7)PGP (Semax) Peptide at the Transcriptome Level Following Cerebral Ischaemiaâ€™Reperfusion in Rats. <i>Genes</i> , 2020, 11, 681.	1.0	17
1076	A Conserved Amino Acid in the C Terminus of Human Papillomavirus E7 Mediates Binding to PTPN14 and Repression of Epithelial Differentiation. <i>Journal of Virology</i> , 2020, 94, .	1.5	24
1077	Transcriptome analysis of testis reveals the effects of developmental exposure to bisphenol a or 17Î±-ethinylestradiol in medaka ( <i>Oryzias latipes</i> ). <i>Aquatic Toxicology</i> , 2020, 225, 105553.	1.9	11
1078	Maternal dietary resistant starch does not improve pigletâ€™s gut and liver metabolism when challenged with a high fat diet. <i>BMC Genomics</i> , 2020, 21, 439.	1.2	2
1079	Transcriptome Analyses of <i>Candida albicans</i> Biofilms, Exposed to Arachidonic Acid and Fluconazole, Indicates Potential Drug Targets. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3099-3108.	0.8	11
1080	Identification of Novel Molecular Markers of Human Th17 Cells. <i>Cells</i> , 2020, 9, 1611.	1.8	27
1081	Data on miRNome changes in human cells exposed to nano- or ionic- forms of Cadmium. <i>Data in Brief</i> , 2020, 30, 105636.	0.5	3
1082	<i>Drosophila</i> models of pathogenic copy-number variant genes show global and non-neuronal defects during development. <i>PLoS Genetics</i> , 2020, 16, e1008792.	1.5	9
1083	Understanding the early cold response mechanism in IR64 indica rice variety through comparative transcriptome analysis. <i>BMC Genomics</i> , 2020, 21, 425.	1.2	21
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1085	PRC2-mediated H3K27me3 modulates shoot iron homeostasis in <i>Arabidopsis thaliana</i> . <i>Plant Signaling and Behavior</i> , 2020, 15, 1784549.	1.2	10
1086	<i>Bacillus subtilis</i> inhibits <i>Aspergillus carbonarius</i> by producing iturin A, which disturbs the transport, energy metabolism, and osmotic pressure of fungal cells as revealed by transcriptomics analysis. <i>International Journal of Food Microbiology</i> , 2020, 330, 108783.	2.1	54
1087	Proteomic identification of aerobic glycolysis as a potential metabolic target for methylglyoxal in adipocytes. <i>Nutrition Research</i> , 2020, 80, 66-77.	1.3	3
1088	MicroRNA-19a-PTEN Axis Is Involved in the Developmental Decline of Axon Regenerative Capacity in Retinal Ganglion Cells. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 21, 251-263.	2.3	20
1089	Proteomic Analysis of <i>Saccharomyces cerevisiae</i> Response to Oxidative Stress Mediated by Cocoa Polyphenols Extract. <i>Molecules</i> , 2020, 25, 452.	1.7	5
1090	MicroRNA-205-5p Promotes Unstable Atherosclerotic Plaque Formation In Vivo. <i>Cardiovascular Drugs and Therapy</i> , 2020, 34, 25-39.	1.3	14

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1092	Altered Hippocampal Epigenetic Regulation Underlying Reduced Cognitive Development in Response to Early Life Environmental Insults. <i>Genes</i> , 2020, 11, 162.	1.0	8
1093	RNA-Seq analysis reveals pluripotency-associated genes and their interaction networks in human embryonic stem cells. <i>Computational Biology and Chemistry</i> , 2020, 85, 107239.	1.1	17
1094	De novo transcriptome assembly and sex-biased gene expression in the gonads of Amur catfish ( <i>Silurus</i> ) Tj ETQq1 1.0.784314.rgBT / Ove	1.3	17
1095	Exploring Integrative Analysis Using the BioMedical Evidence Graph. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 147-159.	1.0	4
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1097	Developmental and molecular characterization of novel staminodes in <i>Aquilegia</i> . <i>Annals of Botany</i> , 2020, 126, 231-243.	1.4	9
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1101	Recent advances in functional research in <i>Giardia intestinalis</i> . <i>Advances in Parasitology</i> , 2020, 107, 97-137.	1.4	22
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1104	Investigating cone photoreceptor development using patient-derived NRL null retinal organoids. <i>Communications Biology</i> , 2020, 3, 82.	2.0	62
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1108	Proteomic Analysis of Mucopolysaccharidosis IIIB Mouse Brain. <i>Biomolecules</i> , 2020, 10, 355.	1.8	30

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1110	Causes and consequences of mitochondrial proteome size variation in animals. <i>Mitochondrion</i> , 2020, 52, 100-107.	1.6	2
1111	Computational Identification of the Proteins Associated With Quorum Sensing and Biofilm Formation in <i>Mycobacterium tuberculosis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3011.	1.5	19
1112	Genetic disruption of <i>slc4a10</i> alters the capacity for cellular metabolism and vectorial ion transport in the choroid plexus epithelium. <i>Fluids and Barriers of the CNS</i> , 2020, 17, 2.	2.4	9
1113	NCBP2 modulates neurodevelopmental defects of the 3q29 deletion in <i>Drosophila</i> and <i>Xenopus laevis</i> models. <i>PLoS Genetics</i> , 2020, 16, e1008590.	1.5	30
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1116	Transcriptome profiling and pathway analysis in squamous cell carcinoma of buccal mucosa. <i>Experimental and Molecular Pathology</i> , 2020, 113, 104378.	0.9	9
1117	Silencing Trisomy 21 with XIST in Neural Stem Cells Promotes Neuronal Differentiation. <i>Developmental Cell</i> , 2020, 52, 294-308.e3.	3.1	41
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1128	<i>APOE</i> genotype regulates pathology and disease progression in synucleinopathy. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	102
1129	Ovarian Transcriptomic Analyses in the Urban Human Health Pest, the Western Black Widow Spider. <i>Genes</i> , 2020, 11, 87.	1.0	1
1130	NAPAbench 2: A network synthesis algorithm for generating realistic protein-protein interaction (PPI) network families. <i>PLoS ONE</i> , 2020, 15, e0227598.	1.1	5
1131	Prostate cancer cell-intrinsic interferon signaling regulates dormancy and metastatic outgrowth in bone. <i>EMBO Reports</i> , 2020, 21, e50162.	2.0	58
1132	Inflammatory priming enhances mesenchymal stromal cell secretome potential as a clinical product for regenerative medicine approaches through secreted factors and EV-miRNAs: the example of joint disease. <i>Stem Cell Research and Therapy</i> , 2020, 11, 165.	2.4	76
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1134	Transcriptomic analysis of adhesive capsulitis of the shoulder. <i>Journal of Orthopaedic Research</i> , 2020, 38, 2280-2289.	1.2	14
1135	A Similar Genetic Architecture Underlies the Convergent Evolution of the Selfing Syndrome in <i>Capsella</i> . <i>Plant Cell</i> , 2020, 32, 935-949.	3.1	19
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1142	Stress-mediated convergence of splicing landscapes in male and female rock doves. <i>BMC Genomics</i> , 2020, 21, 251.	1.2	5
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1148	Redox-Regulated Adaptation of <i>Streptococcus oligofermentans</i> to Hydrogen Peroxide Stress. <i>MSystems</i> , 2020, 5, .	1.7	7
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1152	Genetic Networks Underlying Natural Variation in Basal and Induced Activity Levels in <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1247-1260.	0.8	12
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1156	Novel FMRP interaction networks linked to cellular stress. <i>FEBS Journal</i> , 2021, 288, 837-860.	2.2	31
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1164	Intercellular Mitochondria Transfer to Macrophages Regulates White Adipose Tissue Homeostasis and Is Impaired in Obesity. <i>Cell Metabolism</i> , 2021, 33, 270-282.e8.	7.2	160
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1166	Transcriptional regulator-induced phenotype screen reveals drug potentiators in <i>Mycobacterium tuberculosis</i> . <i>Nature Microbiology</i> , 2021, 6, 44-50.	5.9	15
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1188	HIR V2: a human interactome resource for the biological interpretation of differentially expressed genes via gene set linkage analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, , 2021, .	1.4	3
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1644	Predicted mouse interactome and network-based interpretation of differentially expressed genes. <i>PLoS ONE</i> , 2022, 17, e0264174.	1.1	0
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1936	Constraint-Based, Score-Based and Hybrid Algorithms to Construct Bayesian Gene Networks in the Bovine Transcriptome. <i>Animals</i> , 2022, 12, 1305.	1.0	0
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1940	Molecular response of <i>Sargassum vulgare</i> to acidification at volcanic $\text{CO}_2$ vents: Insights from proteomic and metabolite analyses. <i>Molecular Ecology</i> , 2022, 31, 3844-3858.	2.0	4
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1952	Transcriptome Studies of Salmonid Fishes of the Genus <i>Oncorhynchus</i> . <i>Russian Journal of Genetics</i> , 2022, 58, 757-772.	0.2	0
1953	Analyzing BMP2, FGFR, and TGF Beta Expressions in High-Grade Osteosarcoma Untreated and Treated Autografts Using Proteomic Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7409.	1.8	1
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1959	Potential molecular mechanism in self-renewal is associated with miRNA dysregulation in sacral chordoma – A next-generation RNA sequencing study. <i>Heliyon</i> , 2022, 8, e10227.	1.4	0
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1962	Exploration of the Crucial Genes and Molecular Mechanisms Mediating Atherosclerosis and Abnormal Endothelial Shear Stress. <i>Disease Markers</i> , 2022, 2022, 1-22.	0.6	1
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1964	Impact of dietary walnuts, a nutraceutical option, on circulating markers of metabolic dysregulation in a rodent cachectic tumor model. <i>Biomedicine and Pharmacotherapy</i> , 2022, 155, 113728.	2.5	1
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1980	Serum proteomic analysis reveals the differential dose effects of crocodile oil from <i>Crocodylus siamensis</i> on energy metabolism in rats. <i>Open Veterinary Journal</i> , 2022, 12, 697.	0.3	3
1981	Predicted landscape of <scp>RETINOBLASTOMAâ€RELATED LxCxE</scp> â€mediated interactions across the Chloroplastida. <i>Plant Journal</i> , 0, , .	2.8	1
1983	De novo genome assembly and annotation of <i>Holothuria scabra</i> (Jaeger, 1833) from nanopore sequencing reads. <i>Genes and Genomics</i> , 2022, 44, 1487-1498.	0.5	3
1985	An Integrated Bioinformatics Approach to Identify Network-Derived Hub Genes in Starving Zebrafish. <i>Animals</i> , 2022, 12, 2724.	1.0	1
1986	Hyaline Cartilage Microtissues Engineered from Adult Dedifferentiated Chondrocytes: Safety and Role of WNT Signaling. <i>Stem Cells Translational Medicine</i> , 0, , .	1.6	4
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2000	A mass spectrometry-based approach for the identification of KpnÎ²1 binding partners in cancer cells. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
2001	Structural variation and eQTL analysis in two experimental populations of chickens divergently selected for feather-pecking behavior. <i>Neurogenetics</i> , 0, , .	0.7	1
2002	Comprehensive analysis of pre-mRNA alternative splicing regulated by m6A methylation in pig oxidative and glycolytic skeletal muscles. <i>BMC Genomics</i> , 2022, 23, .	1.2	3

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2006	Fatty acids derived from the probiotic <i>Lactocaseibacillus rhamnosus</i> HA-114 suppress age-dependent neurodegeneration. <i>Communications Biology</i> , 2022, 5, .	2.0	12
2007	Genome-Wide Association Analysis Reveals Novel Loci Related with Visual Score Traits in Nellore Cattle Raised in Pasture-Based Systems. <i>Animals</i> , 2022, 12, 3526.	1.0	3
2008	Pleiotropic fitness effects of a <i>Drosophila</i> odorant-binding protein. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	0
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2011	Breast cancer prevention by short-term inhibition of TGF $\beta$ 2 signaling. <i>Nature Communications</i> , 2022, 13, .	5.8	4
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2019	Transcriptomic profiling identified altered expression of genes associated with testicular functions in adult F1 rats exposed to carbimazole during fetal period. <i>Journal of Proteomics</i> , 2023, 274, 104811.	1.2	2
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