

The Gene Ontology Resource: 20 years and still GOing s

Nucleic Acids Research

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A dominant-negative effect drives selection of TP53 missense mutations in myeloid malignancies. <i>Science</i> , 2019, 365, 599-604.	6.0	265
2	Long Non-Coding RNA Expression Levels Modulate Cell-Type-Specific Splicing Patterns by Altering Their Interaction Landscape with RNA-Binding Proteins. <i>Genes</i> , 2019, 10, 593.	1.0	16
3	Evidence of association of the DISC1 interactome gene set with schizophrenia from GWAS. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2019, 95, 109729.	2.5	16
4	MEK inhibition remodels the active chromatin landscape and induces SOX10 genomic recruitment in BRAF(V600E) mutant melanoma cells. <i>Epigenetics and Chromatin</i> , 2019, 12, 50.	1.8	12
5	PropaNet: Time-Varying Condition-Specific Transcriptional Network Construction by Network Propagation. <i>Frontiers in Plant Science</i> , 2019, 10, 698.	1.7	6
6	EpiFIT: functional interpretation of transcription factors based on combination of sequence and epigenetic information. <i>Quantitative Biology</i> , 2019, 7, 233-243.	0.3	4
7	Mammalian Annotation Database for improved annotation and functional classification of Omics datasets from less well-annotated organisms. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	13
8	Biological Random Walks: Integrating heterogeneous data in disease gene prioritization. , 2019, , .		6
9	Omics Driven Understanding of the Intestines of Parasitic Nematodes. <i>Frontiers in Genetics</i> , 2019, 10, 652.	1.1	13
10	RNA polymerase II (RNAP II)-associated factors are recruited to tRNA loci, revealing that RNAP II and RNAP III-mediated transcriptions overlap in yeast. <i>Journal of Biological Chemistry</i> , 2019, 294, 12349-12358.	1.6	2
11	Identification of key pathways and genes in different types of chronic kidney disease based on WGCNA. <i>Molecular Medicine Reports</i> , 2019, 20, 2245-2257.	1.1	12
12	Dysregulation of DNA methylation patterns may identify patients with breast cancer resistant to endocrine therapy: A predictive classifier based on differentially methylated regions. <i>Oncology Letters</i> , 2019, 18, 1287-1303.	0.8	11
13	Ligand Binding Site Structure Shapes Folding, Assembly and Degradation of Homomeric Protein Complexes. <i>Journal of Molecular Biology</i> , 2019, 431, 3871-3888.	2.0	5
14	Using MARRVEL v1.2 for Bioinformatics Analysis of Human Genes and Variant Pathogenicity. <i>Current Protocols in Bioinformatics</i> , 2019, 67, e85.	25.8	14
15	Identification and characterization of sexual dimorphism-linked gene expression profile in hepatocellular carcinoma. <i>Oncology Reports</i> , 2019, 42, 937-952.	1.2	10
16	A Cyclin A-Myb-Muv-Aurora B network regulates the choice between mitotic cycles and polyploid endoreplication cycles. <i>PLoS Genetics</i> , 2019, 15, e1008253.	1.5	30
17	Cloudy with a Chance of Insights: Context Dependent Gene Regulation and Implications for Evolutionary Studies. <i>Genes</i> , 2019, 10, 492.	1.0	21
18	Comprehensive in vivo identification of the c-Myc mRNA protein interactome using HyPR-MS. <i>Rna</i> , 2019, 25, 1337-1352.	1.6	15

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19	Prediction of disease-associated mutations in the transmembrane regions of proteins with known 3D structure. <i>PLoS ONE</i> , 2019, 14, e0219452.	1.1	19
20	Making the Most of Trait-Based Approaches for Microbial Ecology. <i>Trends in Microbiology</i> , 2019, 27, 814-823.	3.5	49
21	Estimating dispensable content in the human interactome. <i>Nature Communications</i> , 2019, 10, 3205.	5.8	9
22	Genome-wide identification of binding sites and gene targets of Alx1, a pivotal regulator of echinoderm skeletogenesis. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	23
23	Integrated identification of key genes and pathways in Alzheimer's disease via comprehensive bioinformatical analyses. <i>Hereditas</i> , 2019, 156, 25.	0.5	32
24	Genetically diverse <i>Pseudomonas aeruginosa</i> populations display similar transcriptomic profiles in a cystic fibrosis explanted lung. <i>Nature Communications</i> , 2019, 10, 3397.	5.8	68
25	Differential gene expression and gene ontologies associated with increasing water-stress in leaf and root transcriptomes of perennial ryegrass (<i>Lolium perenne</i>). <i>PLoS ONE</i> , 2019, 14, e0220518.	1.1	4
26	Identification of diagnostic long non-coding RNA biomarkers in patients with hepatocellular carcinoma. <i>Molecular Medicine Reports</i> , 2019, 20, 1121-1130.	1.1	29
27	Screening key genes and signaling pathways in colorectal cancer by integrated bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2019, 20, 1259-1269.	1.1	28
28	Analysis of potential functional significance of microRNA-3613-3p in human umbilical vein endothelial cells affected by heat stress. <i>Molecular Medicine Reports</i> , 2019, 20, 1846-1856.	1.1	1
29	Isatin inhibits the invasion of human neuroblastoma SH-SY5Y cells, based on microarray analysis. <i>Molecular Medicine Reports</i> , 2019, 20, 1700-1706.	1.1	4
30	Multi-tissue network analysis for drug prioritization in knee osteoarthritis. <i>Scientific Reports</i> , 2019, 9, 15176.	1.6	13
31	GENAVI: a shiny web application for gene expression normalization, analysis and visualization. <i>BMC Genomics</i> , 2019, 20, 745.	1.2	40
32	DNAproDB: an expanded database and web-based tool for structural analysis of DNA-protein complexes. <i>Nucleic Acids Research</i> , 2019, 48, D277-D287.	6.5	41
33	Binding to medium and long chain fatty acyls is a common property of HEAT and ARM repeat modules. <i>Scientific Reports</i> , 2019, 9, 14226.	1.6	3
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35	Biological Network Approaches and Applications in Rare Disease Studies. <i>Genes</i> , 2019, 10, 797.	1.0	30
36	CAGEfightR: analysis of 5'-end data using R/Bioconductor. <i>BMC Bioinformatics</i> , 2019, 20, 487.	1.2	59

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37	Myo-REG: A Portal for Signaling Interactions in Muscle Regeneration. <i>Frontiers in Physiology</i> , 2019, 10, 1216.	1.3	8
38	Loss of methionine sulfoxide reductases increases resistance to oxidative stress. <i>Free Radical Biology and Medicine</i> , 2019, 145, 374-384.	1.3	14
39	SilkDB 3.0: visualizing and exploring multiple levels of data for silkworm. <i>Nucleic Acids Research</i> , 2020, 48, D749-D755.	6.5	59
40	LnCeVar: a comprehensive database of genomic variations that disturb ceRNA network regulation. <i>Nucleic Acids Research</i> , 2020, 48, D111-D117.	6.5	59
41	Bovine Genome Database: new annotation tools for a new reference genome. <i>Nucleic Acids Research</i> , 2019, 48, D676-D681.	6.5	18
42	Spectrum Recovery for Clutter Removal in Penetrating Radar Imaging. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , 2019, 57, 6650-6665.	2.7	6
43	A network-based analysis for mining the risk pathways in glioblastoma. <i>Oncology Letters</i> , 2019, 18, 2712-2717.	0.8	0
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47	The Year of the Rat: The Rat Genome Database at 20: a multi-species knowledgebase and analysis platform. <i>Nucleic Acids Research</i> , 2020, 48, D731-D742.	6.5	92
48	Mapping the perturbome network of cellular perturbations. <i>Nature Communications</i> , 2019, 10, 5140.	5.8	40
49	Expression of Protein-Coding Gene Orthologs in Zebrafish and Mouse Inner Ear Non-sensory Supporting Cells. <i>Frontiers in Neuroscience</i> , 2019, 13, 1117.	1.4	12
50	P38-Mediated Cellular Senescence in Conjunctivochalasis Fibroblasts. , 2019, 60, 4643.		10
51	Phosphoproteomics of Acute Cell Stressors Targeting Exercise Signaling Networks Reveal Drug Interactions Regulating Protein Secretion. <i>Cell Reports</i> , 2019, 29, 1524-1538.e6.	2.9	30
52	A Genome-Wide Screen for Wortmannin-Resistant Mutants in <i>Schizosaccharomyces pombe</i> : The Phosphorylation-Impaired Mutants Are Resistant to Signaling Defect. <i>DNA and Cell Biology</i> , 2019, 38, 1427-1436.	0.9	0
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54	Intraocular VEGF deprivation induces degeneration and fibrogenic response in retina. <i>FASEB Journal</i> , 2019, 33, 13920-13934.	0.2	5

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56	Phellem Cell-Wall Components Are Discriminants of Cork Quality in <i>Quercus suber</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 944.	1.7	10
57	Size-dependent elasticity of gold nanoparticle measured by atomic force microscope based nanoindentation. <i>Applied Physics Letters</i> , 2019, 115, .	1.5	11
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60	Identification of microRNA-181 as a promising biomarker for predicting the poor survival in colorectal cancer. <i>Cancer Medicine</i> , 2019, 8, 5995-6009.	1.3	15
61	Navigating MARRVEL, a Web-Based Tool that Integrates Human Genomics and Model Organism Genetics Information. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	20
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64	Identification of modules and functional analysis in CRC subtypes by integrated bioinformatics analysis. <i>PLoS ONE</i> , 2019, 14, e0221772.	1.1	6
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66	A human endogenous retrovirus encoded protease potentially cleaves numerous cellular proteins. <i>Mobile DNA</i> , 2019, 10, 36.	1.3	9
67	Druggable Transcriptional Networks in the Human Neurogenic Epigenome. <i>Pharmacological Reviews</i> , 2019, 71, 520-538.	7.1	11
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69	Signatures of cell death and proliferation in perturbation transcriptomics data from confounding factor to effective prediction. <i>Nucleic Acids Research</i> , 2019, 47, 10010-10026.	6.5	50
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71	The application of omics-based human liver platforms for investigating the mechanism of drug-induced hepatotoxicity in vitro. <i>Archives of Toxicology</i> , 2019, 93, 3067-3098.	1.9	21
72	Diesel exhaust particles dysregulate multiple immunological pathways in murine macrophages: Lessons from microarray and scRNA-seq technologies. <i>Archives of Biochemistry and Biophysics</i> , 2019, 678, 108116.	1.4	10

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73	Gene Ontology Causal Activity Modeling (GO-CAM) moves beyond GO annotations to structured descriptions of biological functions and systems. <i>Nature Genetics</i> , 2019, 51, 1429-1433.	9.4	76
74	Ten quick tips for biocuration. <i>PLoS Computational Biology</i> , 2019, 15, e1006906.	1.5	21
75	Protein interactions and consensus clustering analysis uncover insights into herpesvirus virion structure and function relationships. <i>PLoS Biology</i> , 2019, 17, e3000316.	2.6	18
76	Muscle strain injury exudate favors acute tissue healing and prolonged connective tissue formation in humans. <i>FASEB Journal</i> , 2019, 33, 10369-10382.	0.2	8
77	Identification of differentially expressed genes in small and non-small cell lung cancer based on meta-analysis of mRNA. <i>Heliyon</i> , 2019, 5, e01707.	1.4	20
78	First-generation predictors of biological protein phase separation. <i>Current Opinion in Structural Biology</i> , 2019, 58, 88-96.	2.6	119
79	Culturing C2C12 myotubes on micromolded gelatin hydrogels accelerates myotube maturation. <i>Skeletal Muscle</i> , 2019, 9, 17.	1.9	80
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81	SynGO: An Evidence-Based, Expert-Curated Knowledge Base for the Synapse. <i>Neuron</i> , 2019, 103, 217-234.e4.	3.8	518
82	NetR and AttR, Two New Bioinformatic Tools to Integrate Diverse Datasets into Cytoscape Network and Attribute Files. <i>Genes</i> , 2019, 10, 423.	1.0	1
83	Bioinformatics analysis of the regulatory lncRNA-miRNA-mRNA network and drug prediction in patients with hypertrophic cardiomyopathy. <i>Molecular Medicine Reports</i> , 2019, 20, 549-558.	1.1	24
84	Development of a Zebrafish S1500+ Sentinel Gene Set for High-Throughput Transcriptomics. <i>Zebrafish</i> , 2019, 16, 331-347.	0.5	5
85	Comparative transcriptome analysis of trout skin pigment cells. <i>BMC Genomics</i> , 2019, 20, 359.	1.2	25
86	INGA 2.0: improving protein function prediction for the dark proteome. <i>Nucleic Acids Research</i> , 2019, 47, W373-W378.	6.5	24
87	A panel of serum exosomal microRNAs as predictive markers for chemoresistance in advanced colorectal cancer. <i>Cancer Chemotherapy and Pharmacology</i> , 2019, 84, 315-325.	1.1	97
88	Sustained DDB-2 and TRX transcriptional response of quercetin-treated lymphocytes exposed to Co-60 radiation. <i>Gene Reports</i> , 2019, 16, 100416.	0.4	0
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90	Promiscuous Targeting of Cellular Proteins by Vpr Drives Systems-Level Proteomic Remodeling in HIV-1 Infection. <i>Cell Reports</i> , 2019, 27, 1579-1596.e7.	2.9	75

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91	Med15: Glutamine-Rich Mediator Subunit with Potential for Plasticity. Trends in Biochemical Sciences, 2019, 44, 737-751.	3.7	15
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103	Differential expression profile analysis of cisplatin-regulated miRNAs in a human gastric cancer cell line. Molecular Medicine Reports, 2019, 20, 1966-1976.	1.1	6
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105	The Alliance of Genome Resources: Building a Modern Data Ecosystem for Model Organism Databases. Genetics, 2019, 213, 1189-1196.	1.2	41
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110	Mutational Forks: Inferring Deregulated Flow of Signal Transduction Based on Patient-Specific Mutations. , 2019, , .		1
111	Visualizing multifunctional PPI network with Gene Ontology annotation. , 2019, , .		0
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116	Mechanistic Dissection of RNA-Binding Proteins in Regulated Gene Expression at Chromatin Levels. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2019, 84, 55-66.	2.0	4
117	The Use of Whole Exome Sequencing in a Cohort of Transgender Individuals to Identify Rare Genetic Variants. <i>Scientific Reports</i> , 2019, 9, 20099.	1.6	18
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120	The essentiality landscape of cell cycle related genes in human pluripotent and cancer cells. <i>Cell Division</i> , 2019, 14, 15.	1.1	13
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131	The JAX Synteny Browser for mouse-human comparative genomics. <i>Mammalian Genome</i> , 2019, 30, 353-361.	1.0	18
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143	Mouse Genome Database (MGD) 2019. <i>Nucleic Acids Research</i> , 2019, 47, D801-D806.	6.5	625
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147	KnockTF: a comprehensive human gene expression profile database with knockdown/knockout of transcription factors. <i>Nucleic Acids Research</i> , 2020, 48, D93-D100.	6.5	72
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150	Randomized trial of weight loss in primary breast cancer: Impact on body composition, circulating biomarkers and tumor characteristics. <i>International Journal of Cancer</i> , 2020, 146, 2784-2796.	2.3	36
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152	Exploring lithium's transcriptional mechanisms of action in bipolar disorder: a multi-step study. <i>Neuropsychopharmacology</i> , 2020, 45, 947-955.	2.8	24
153	High content phenotypic screening identifies serotonin receptor modulators with selective activity upon breast cancer cell cycle and cytokine signaling pathways. <i>Bioorganic and Medicinal Chemistry</i> , 2020, 28, 115209.	1.4	26
154	Screening and Identification of Key Biomarkers in Pancreatic Cancer: Evidence from Bioinformatic Analysis. <i>Journal of Computational Biology</i> , 2020, 27, 1079-1091.	0.8	2
155	Dysregulated immunological and metabolic functions discovered by a polygenic integrative analysis for PCOS. <i>Reproductive BioMedicine Online</i> , 2020, 40, 160-167.	1.1	11
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1973	Using mRNA deep sequencing to analyze differentially expressed genes during Panax notoginseng saponin treatment of ischemic stroke. <i>Molecular Medicine Reports</i> , 2020, 22, 4743-4753.	1.1	0
1974	Integrated microarray analysis of key genes and a miRNA-mRNA regulatory network of early-onset preeclampsia. <i>Molecular Medicine Reports</i> , 2020, 22, 4772-4782.	1.1	0

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1975	Gene expression profile of lipopolysaccharide-induced apoptosis of nucleus pulposus cells reversed by syringic acid. <i>Molecular Medicine Reports</i> , 2020, 22, 5012-5022.	1.1	0
1976	Integrated Bioinformatics Analysis of Hub Genes and Pathways Associated with a Compression Model of Spinal Cord Injury in Rats. <i>Medical Science Monitor</i> , 2020, 26, e927107.	0.5	3
1977	Mesenchymal stem cells negatively regulate CD4 ⁺ T cell activation in patients with primary Sjögren syndrome through the miRNA-125b and miRNA-155 TCR pathway. <i>Molecular Medicine Reports</i> , 2021, 23, .	1.1	1
1978	Identification of Dysregulated Genes for Late-Onset Alzheimer's Disease Using Gene Expression Data in Brain. , 2020, 10, .		0
1979	IL-17 signaling pathway plays a key role in laryngeal squamous cell carcinoma with ethnic specificity. <i>American Journal of Cancer Research</i> , 2021, 11, 2684-2695.	1.4	1
1980	Comparison of critical biomarkers in 2 erectile dysfunction models based on GEO and NOS-cGMP-PDE5 pathway. <i>Medicine (United States)</i> , 2021, 100, e27508.	0.4	0
1981	Foundations for a Realism-Based Ontology of Protein Aggregates. <i>CEUR Workshop Proceedings</i> , 2020, 2807, K1-K10.	2.3	0
1982	ABC Transporters are Hub Genes in Response of Resistant E. Coli ST131 to Ciprofloxacin. <i>Archives of Pharmacy Practice</i> , 2021, 12, 82-88.	0.2	1
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1984	Comparison of critical biomarkers in 2 erectile dysfunction models based on GEO and NOS-cGMP-PDE5 pathway. <i>Medicine (United States)</i> , 2021, 100, e27508.	0.4	2
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1986	Single-cell analysis identifies dynamic gene expression networks that govern B cell development and transformation. <i>Nature Communications</i> , 2021, 12, 6843.	5.8	36
1987	The differentiation state of the Schwann cell progenitor drives phenotypic variation between two contagious cancers. <i>PLoS Pathogens</i> , 2021, 17, e1010033.	2.1	3
1988	Knowledge-guided artificial intelligence technologies for decoding complex multiomics interactions in cells. <i>Clinical and Experimental Pediatrics</i> , 2022, 65, 239-249.	0.9	2
1989	In Silico Characterization and Expression Profiles of Heat Shock Transcription Factors (HSFs) in Maize (<i>Zea mays</i> L.). <i>Agronomy</i> , 2021, 11, 2335.	1.3	13
1990	Landscape genomics of the streamside salamander: Implications for species management in the face of environmental change. <i>Evolutionary Applications</i> , 2022, 15, 220-236.	1.5	4
1991	Altered cell and RNA isoform diversity in aging Down syndrome brains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	38
1992	Follicular T cells are clonally and transcriptionally distinct in B cell-driven mouse autoimmune disease. <i>Nature Communications</i> , 2021, 12, 6687.	5.8	12

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1993	Identification of Potential circRNA-microRNA-mRNA Regulatory Network in Skeletal Muscle. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 762185.	1.6	15
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1996	Titanium with nanotopography attenuates the osteoclast-induced disruption of osteoblast differentiation by regulating histone methylation. <i>Materials Science and Engineering C</i> , 2022, 134, 112548.	3.8	10
1997	Hsa-mir-3163 and CCNB1 may be potential biomarkers and therapeutic targets for androgen receptor positive triple-negative breast cancer. <i>PLoS ONE</i> , 2021, 16, e0254283.	1.1	9
1999	The disease-associated proteins <i>Drosophila</i> Nab2 and Ataxin-2 interact with shared RNAs and coregulate neuronal morphology. <i>Genetics</i> , 2022, 220, .	1.2	4
2000	Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. <i>New Phytologist</i> , 2022, 233, 1317-1330.	3.5	23
2001	Genetic Evidence for Congenital Vascular Disorders in Patients with VACTERL Association. <i>European Journal of Pediatric Surgery</i> , 2022, 32, 061-066.	0.7	0
2003	A Standardized Brain Molecular Atlas: A Resource for Systems Modeling and Simulation. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 604559.	1.4	3
2004	Microarray profiling predicts early neurological and immune phenotypic traits in advance of CNS disease during disease progression in <i>Trypanosoma b. brucei</i> infected CD1 mouse brains. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009892.	1.3	3
2005	Inferred expression regulator activities suggest genes mediating cardiometabolic genetic signals. <i>PLoS Computational Biology</i> , 2021, 17, e1009563.	1.5	3
2006	Toll-Like Receptor (TLR) Signaling Enables Cyclic GMP-AMP Synthase (cGAS) Sensing of HIV-1 Infection in Macrophages. <i>MBio</i> , 2021, 12, e0281721.	1.8	13
2007	APOBEC Mutagenesis Inhibits Breast Cancer Growth through Induction of T cell-Mediated Antitumor Immune Responses. <i>Cancer Immunology Research</i> , 2022, 10, 70-86.	1.6	20
2008	The Alimant to Bodily Condition knowledgebase (ABCKb): a database connecting plants and human health. <i>BMC Research Notes</i> , 2021, 14, 433.	0.6	1
2010	Grundlagen und Anwendungen von KI. <i>Wissenschaftsethik Und Technikfolgenbeurteilung</i> , 2022, , 13-42.	0.8	1
2011	Quantitative dissection of multilocus pathogenic variation in an Egyptian infant with severe neurodevelopmental disorder resulting from multiple molecular diagnoses. <i>American Journal of Medical Genetics, Part A</i> , 2022, 188, 735-750.	0.7	14
2012	Binge Ethanol Exposure in Mice Represses Expression of Genes Involved in Osteoblast Function and Induces Expression of Genes Involved in Osteoclast Differentiation Independently of Endogenous Catalase. <i>Toxicological Sciences</i> , 2022, 185, 232-245.	1.4	2
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2015	Identification of Galectin-3 as Potential Biomarkers for Renal Fibrosis by RNA-Sequencing and Clinicopathologic Findings of Kidney Biopsy. <i>Frontiers in Medicine</i> , 2021, 8, 748225.	1.2	14
2016	Extensive mitochondrial proteome disturbance occurs during the early stages of acute myocardial ischemia. <i>Experimental and Therapeutic Medicine</i> , 2021, 23, 85.	0.8	5
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2019	A Novel Autophagy-Related Long Non-Coding RNA Signature to Predict Prognosis and Therapeutic Response in Esophageal Squamous Cell Carcinoma. <i>International Journal of General Medicine</i> , 2021, Volume 14, 8325-8339.	0.8	13
2020	Comprehensive Analysis Uncovers Prognostic and Immunogenic Characteristics of Cellular Senescence for Lung Adenocarcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 780461.	1.8	28
2021	Splice-Variant Knock-Out of TGF β 2 Receptors Perturbates the Proteome of Ovarian Carcinoma Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12647.	1.8	1
2022	Delayed DNA replication in haploid human embryonic stem cells. <i>Genome Research</i> , 2021, 31, 2155-2169.	2.4	5
2023	MicroRNA Analysis of Human Stroke Brain Tissue Resected during Decompressive Craniectomy/Stroke-Ectomy Surgery. <i>Genes</i> , 2021, 12, 1860.	1.0	9
2024	Whole-transcriptome analysis of aluminum-exposed rat hippocampus and identification of ceRNA networks to investigate neurotoxicity of Al. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 26, 1401-1417.	2.3	12
2025	Identification of discriminative gene-level and protein-level features associated with pathogenic gain-of-function and loss-of-function variants. <i>American Journal of Human Genetics</i> , 2021, 108, 2301-2318.	2.6	21
2026	Identification of copy number variation-driven molecular subtypes informative for prognosis and treatment in pancreatic adenocarcinoma of a Chinese cohort. <i>EBioMedicine</i> , 2021, 74, 103716.	2.7	14
2027	Transcriptomic Profiling and Microsatellite Identification in Cobia (<i>Rachycentron canadum</i>), Using High-Throughput RNA Sequencing. <i>Marine Biotechnology</i> , 2022, 24, 255-262.	1.1	6
2028	Genome-Wide RNAi Screening Identifies Novel Pathways/Genes Involved in Oxidative Stress and Repurposable Drugs to Preserve Cystic Fibrosis Airway Epithelial Cell Integrity. <i>Antioxidants</i> , 2021, 10, 1936.	2.2	3
2029	Multiscale interactome analysis coupled with off-target drug predictions reveals drug repurposing candidates for human coronavirus disease. <i>Scientific Reports</i> , 2021, 11, 23315.	1.6	10
2030	Transcriptomic dataset for <i>Sardina pilchardus</i> : Assembly, annotation, and expression of nine tissues. <i>Data in Brief</i> , 2021, 39, 107583.	0.5	1
2031	Integrated genome and tissue engineering enables screening of cancer vulnerabilities in physiologically relevant perfusable ex vivo cultures. <i>Biomaterials</i> , 2022, 280, 121276.	5.7	5
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2035	The Power of Universal Contextualized Protein Embeddings in Cross-species Protein Function Prediction. <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432110626.	0.6	4
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2037	Post-transcriptional regulation of frog innate immunity: discovery of frog microRNAs associated with antiviral responses and ranavirus infection using a <i>Xenopus laevis</i> skin epithelial-like cell line. <i>Facets</i> , 2021, 6, 2058-2083.	1.1	3
2038	Anc2vec: embedding gene ontology terms by preserving ancestors relationships. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	9
2039	Structure-function relationships of the disease-linked A218T oxytocin receptor variant. <i>Molecular Psychiatry</i> , 2022, 27, 907-917.	4.1	17
2040	Ebola virus delta peptide is an enterotoxin. <i>Cell Reports</i> , 2022, 38, 110172.	2.9	3
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2042	Systems Approaches to Unravel Molecular Function: High-content siRNA Screen Identifies TMEM16A Traffic Regulators as Potential Drug Targets for Cystic Fibrosis. <i>Journal of Molecular Biology</i> , 2022, 434, 167436.	2.0	3
2043	RNAseq reveals extensive metabolic disruptions in the sensitive SF-295 cell line treated with schweinfurthins. <i>Scientific Reports</i> , 2022, 12, 359.	1.6	1
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2046	Integrated Bioinformatics Analysis of Hub Genes and Pathways Associated with a Compression Model of Spinal Cord Injury in Rats. <i>Medical Science Monitor</i> , 2020, 26, e927107.	0.5	6
2047	Using mRNA deep sequencing to analyze differentially expressed genes during <i>Panax notoginseng</i> saponin treatment of ischemic stroke. <i>Molecular Medicine Reports</i> , 2020, 22, 4743-4753.	1.1	1
2048	Integrated microarray analysis of key genes and a miRNA-mRNA regulatory network of early-onset preeclampsia. <i>Molecular Medicine Reports</i> , 2020, 22, 4772-4782.	1.1	4
2049	Short hairpin RNA attenuates liver fibrosis by regulating the PPAR α and NF κ B pathways in HBV-induced liver fibrosis in mice. <i>International Journal of Oncology</i> , 2020, 57, 1116-1128.	1.4	4
2050	[Corrigendum] Cellular expression profiles of Epstein-Barr virus-transformed B-lymphoblastoid cell lines. <i>Biomedical Reports</i> , 2020, 14, 1-1.	0.9	0
2051	Gene expression profile of lipopolysaccharide-induced apoptosis of nucleus pulposus cells reversed by syringic acid. <i>Molecular Medicine Reports</i> , 2020, 22, 5012-5022.	1.1	0

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2053	Multi-species Protein Association Prediction Using Residual Graph Convolutional Network. , 2020, , .		0
2054	Visualizing and Annotating Protein Sequences using A Deep Neural Network. , 2020, , .		3
2055	Mesenchymal stem cells negatively regulate CD4 ⁺ T cell activation in patients with primary Sjögren syndrome through the miRNA-125b and miRNA-155 TCR pathway. <i>Molecular Medicine Reports</i> , 2020, 23, 1-1.	1.1	8
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2057	Identifying the temporal electrophysiological and molecular changes that contribute to TSC-associated epileptogenesis. <i>JCI Insight</i> , 2021, 6, .	2.3	7
2058	8-Hydroxydaidzein Downregulates JAK/STAT, MMP, Oxidative Phosphorylation, and PI3K/AKT Pathways in K562 Cells. <i>Biomedicines</i> , 2021, 9, 1907.	1.4	11
2059	A novel gene functional similarity calculation model by utilizing the specificity of terms and relationships in gene ontology. <i>BMC Bioinformatics</i> , 2022, 23, 47.	1.2	0
2060	Bioactive peptides from broccoli stems strongly enhance regenerative keratinocytes by stimulating controlled proliferation. <i>Pharmaceutical Biology</i> , 2022, 60, 235-246.	1.3	6
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2062	AgroLD: A Knowledge Graph Database for Plant Functional Genomics. <i>Methods in Molecular Biology</i> , 2022, 2443, 527-540.	0.4	2
2064	High-speed fluorescence image-enabled cell sorting. <i>Science</i> , 2022, 375, 315-320.	6.0	121
2065	Haploidy in somatic cells is induced by mature oocytes in mice. <i>Communications Biology</i> , 2022, 5, 95.	2.0	7
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2069	Utilizing network pharmacology and experimental validation to explore the potential molecular mechanisms of BanXia-YiYiRen in treating insomnia. <i>Bioengineered</i> , 2022, 13, 3148-3170.	1.4	7
2070	Integrative analysis of immune-related multi-omics profiles identifies distinct prognosis and tumor microenvironment patterns in osteosarcoma. <i>Molecular Oncology</i> , 2022, 16, 2174-2194.	2.1	14
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2072	Prediction of lncRNA-disease association based on a Laplace normalized random walk with restart algorithm on heterogeneous networks. <i>BMC Bioinformatics</i> , 2022, 23, 5.	1.2	16

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2074	PlantGF: an analysis and annotation platform for plant gene families. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	3
2075	MOET: a web-based gene set enrichment tool at the Rat Genome Database for multiontology and multispecies analyses. <i>Genetics</i> , 2022, 220, .	1.2	7
2076	Getting Started with the IDG KMC Datasets and Tools. <i>Current Protocols</i> , 2022, 2, e355.	1.3	6
2077	Considerations for constructing a protein sequence database for metaproteomics. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 937-952.	1.9	22
2078	An in silico analysis identifies drugs potentially modulating the cytokine storm triggered by SARS-CoV-2 infection. <i>Scientific Reports</i> , 2022, 12, 1626.	1.6	4
2079	The Mechanism Study of Common Flavonoids on Antiglioma Based on Network Pharmacology and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-15.	0.5	3
2080	Endothelial Cell RNA-Seq Data: Differential Expression and Functional Enrichment Analyses to Study Phenotypic Switching. <i>Methods in Molecular Biology</i> , 2022, 2441, 369-426.	0.4	1
2081	Making sense of the linear genome, gene function and TADs. <i>Epigenetics and Chromatin</i> , 2022, 15, 4.	1.8	15
2082	ICEO, a biological ontology for representing and analyzing bacterial integrative and conjugative elements. <i>Scientific Data</i> , 2022, 9, 11.	2.4	5
2084	HESML: a real-time semantic measures library for the biomedical domain with a reproducible survey. <i>BMC Bioinformatics</i> , 2022, 23, 23.	1.2	3
2085	Age-dependent pathogenic characteristics of SARS-CoV-2 infection in ferrets. <i>Nature Communications</i> , 2022, 13, 21.	5.8	31
2086	Assigning protein function from domain-function associations using DomFun. <i>BMC Bioinformatics</i> , 2022, 23, 43.	1.2	8
2087	Biallelic Variants in PYROXD2 Cause a Severe Infantile Metabolic Disorder Affecting Mitochondrial Function. <i>International Journal of Molecular Sciences</i> , 2022, 23, 986.	1.8	5
2089	Transcriptomic Profile of Canine DH82 Macrophages Infected by <i>Leishmania infantum</i> Promastigotes with Different Virulence Behavior. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1466.	1.8	4
2090	Identification of potential biomarkers in hepatocellular carcinoma: A network-based approach. <i>Informatics in Medicine Unlocked</i> , 2022, 28, 100864.	1.9	4
2092	Druggable genetic targets in endometrial cancer. <i>Cancer Treatment and Research Communications</i> , 2022, 30, 100502.	0.7	3
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2095	Systems Biology and Bioinformatics approach to Identify blood based signatures molecules and drug targets of patient with COVID-19. <i>Informatics in Medicine Unlocked</i> , 2022, 28, 100840.	1.9	22
2096	Inferring early-life host and microbiome functions by mass spectrometry-based metaproteomics and metabolomics. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 274-286.	1.9	5
2097	Scripting Analyses of Genomes in Ensembl Plants. <i>Methods in Molecular Biology</i> , 2022, 2443, 27-55.	0.4	6
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2099	Tissue-specific multi-omics analysis of atrial fibrillation. <i>Nature Communications</i> , 2022, 13, 441.	5.8	17
2101	Proteomic screen reveals diverse protein transport between connected neurons in the visual system. <i>Cell Reports</i> , 2022, 38, 110287.	2.9	10
2102	Tumor microenvironment-related multigene prognostic prediction model for breast cancer. <i>Aging</i> , 2022, 14, 845-868.	1.4	2
2103	The DOMINO web-server for active module identification analysis. <i>Bioinformatics</i> , 2022, 38, 2364-2366.	1.8	2
2104	GAAP: A GUI-based Genome Assembly and Annotation Package. <i>Current Genomics</i> , 2022, 23, 77-82.	0.7	3
2105	A novel variant in SMC9 causes intellectual disability, confirming a role for nonsense-mediated decay components in neurocognitive development. <i>European Journal of Human Genetics</i> , 2022, 30, 619-627.	1.4	6
2106	Sperm acquire epididymis-derived proteins through epididymosomes. <i>Human Reproduction</i> , 2022, 37, 651-668.	0.4	34
2107	Deep learning program to predict protein functions based on sequence information. <i>MethodsX</i> , 2022, 9, 101622.	0.7	4
2108	The initial expression alterations occurring to transcription factors during the formation of breast cancer: Evidence from bioinformatics. <i>Cancer Medicine</i> , 2022, 11, 1371-1395.	1.3	6
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2111	Neuropeptidergic regulation of compulsive ethanol seeking in <i>C. elegans</i> . <i>Scientific Reports</i> , 2022, 12, 1804.	1.6	3
2112	Student biocuration projects as a learning environment. <i>F1000Research</i> , 0, 10, 1023.	0.8	0

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2116	Differential Expression of RAD51AP1 in Ovarian Cancer: Effects of siRNA In Vitro. <i>Journal of Personalized Medicine</i> , 2022, 12, 201.	1.1	1
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2120	Multimodal reasoning based on knowledge graph embedding for specific diseases. <i>Bioinformatics</i> , 2022, 38, 2235-2245.	1.8	15
2121	Genomic basis for skin phenotype and cold adaptation in the extinct Steller's sea cow. <i>Science Advances</i> , 2022, 8, eabl6496.	4.7	9
2123	In silico prediction of HIV-1-host molecular interactions and their directionality. <i>PLoS Computational Biology</i> , 2022, 18, e1009720.	1.5	0
2124	SuperDendrix algorithm integrates genetic dependencies and genomic alterations across pathways and cancer types. <i>Cell Genomics</i> , 2022, 2, 100099.	3.0	2
2125	blitzGSEA: efficient computation of gene set enrichment analysis through gamma distribution approximation. <i>Bioinformatics</i> , 2022, 38, 2356-2357.	1.8	9
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2128	Gene-Interaction-Sensitive enrichment analysis in congenital heart disease. <i>BioData Mining</i> , 2022, 15, 4.	2.2	2
2129	MHC-II Signature Correlates With Anti-Tumor Immunity and Predicts anti-PD-L1 Response of Bladder Cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 757137.	1.8	13
2130	Role of mitochondrial genetic interactions in determining adaptation to high altitude human population. <i>Scientific Reports</i> , 2022, 12, 2046.	1.6	4
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2136	Machine learning prediction and tau-based screening identifies potential Alzheimer's disease genes relevant to immunity. <i>Communications Biology</i> , 2022, 5, 125.	2.0	18
2137	Identification of recurrent genetic patterns from targeted sequencing panels with advanced data science: a case-study on sporadic and genetic neurodegenerative diseases. <i>BMC Medical Genomics</i> , 2022, 15, 26.	0.7	4
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