

KEGG: new perspectives on genomes, pathways, disease

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Citation Report

#	ARTICLE	IF	CITATIONS
3	Comparative pan genome analysis of oral <i>Prevotella</i> species implicated in periodontitis. <i>Functional and Integrative Genomics</i> , 2017, 17, 513-536.	1.4	49
4	The core regulatory network in human cells. <i>Biochemical and Biophysical Research Communications</i> , 2017, 484, 348-353.	1.0	4
5	Bioresources inner-recycling between bioflocculation of <i>Microcystis aeruginosa</i> and its reutilization as a substrate for bioflocculant production. <i>Scientific Reports</i> , 2017, 7, 43784.	1.6	16
6	From sequencing data to gene functions: co-functional network approaches. <i>Animal Cells and Systems</i> , 2017, 21, 77-83.	0.8	27
7	Global gene expression profiling of healthy human brain and its application in studying neurological disorders. <i>Scientific Reports</i> , 2017, 7, 897.	1.6	52
8	minepath.org: a free interactive pathway analysis web server. <i>Nucleic Acids Research</i> , 2017, 45, W116-W121.	6.5	8
9	High-Throughput Sequencing and Co-Expression Network Analysis of lncRNAs and mRNAs in Early Brain Injury Following Experimental Subarachnoid Haemorrhage. <i>Scientific Reports</i> , 2017, 7, 46577.	1.6	42
10	Defining Genetic Fitness Determinants and Creating Genomic Resources for an Oral Pathogen. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	22
11	PharmMapper 2017 update: a web server for potential drug target identification with a comprehensive target pharmacophore database. <i>Nucleic Acids Research</i> , 2017, 45, W356-W360.	6.5	802
12	Predictive Genomic Analyses Inform the Basis for Vitamin Metabolism and Provisioning in Bacteria-Arthropod Endosymbioses. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1887-1898.	0.8	8
13	Metabolic reprogramming in clear cell renal cell carcinoma. <i>Nature Reviews Nephrology</i> , 2017, 13, 410-419.	4.1	323
14	Serum glycopattern and <i>Maackia amurensis</i> lectin-II binding glycoproteins in autism spectrum disorder. <i>Scientific Reports</i> , 2017, 7, 46041.	1.6	19
15	Tissue Proteome Analysis of Different Grades of Human Gliomas Provides Major Cues for Glioma Pathogenesis. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 275-284.	1.0	23
16	Bioinformatics tools for quantitative and functional metagenome and metatranscriptome data analysis in microbes. <i>Briefings in Bioinformatics</i> , 2018, 19, 1415-1429.	3.2	34
17	The Bologna Annotation Resource (BAR 3.0): improving protein functional annotation. <i>Nucleic Acids Research</i> , 2017, 45, W285-W290.	6.5	18
18	Exercise-induced modification of the skeletal muscle transcriptome in Arabian horses. <i>Physiological Genomics</i> , 2017, 49, 318-326.	1.0	29
19	Sirtuin E is a fungal global transcriptional regulator that determines the transition from the primary growth to the stationary phase. <i>Journal of Biological Chemistry</i> , 2017, 292, 11043-11054.	1.6	20
20	lncRNAs2Pathways: Identifying the pathways influenced by a set of lncRNAs of interest based on a global network propagation method. <i>Scientific Reports</i> , 2017, 7, 46566.	1.6	24

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22	Mobilization and integration of bacterial phenotypic data—Enabling next generation biodiversity analysis through the Bac Dive metadatabase. <i>Journal of Biotechnology</i> , 2017, 261, 187-193.	1.9	8
23	Constraint-based modeling identifies new putative targets to fight colistin-resistant <i>A. baumannii</i> infections. <i>Scientific Reports</i> , 2017, 7, 3706.	1.6	47
24	Establishment of the model system between phytochemicals and gene expression profiles in Macrosclereid cells of <i>Medicago truncatula</i> . <i>Scientific Reports</i> , 2017, 7, 2580.	1.6	14
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29	Large-Scale Prediction of Drug-Target Interaction: a Data-Centric Review. <i>AAPS Journal</i> , 2017, 19, 1264-1275.	2.2	39
30	Biallelic Mutations in CFAP43 and CFAP44 Cause Male Infertility with Multiple Morphological Abnormalities of the Sperm Flagella. <i>American Journal of Human Genetics</i> , 2017, 100, 854-864.	2.6	220
31	Differential carriage of virulence-associated loci in the New Zealand Rangipo outbreak strain of <i>Mycobacterium tuberculosis</i> . <i>Infectious Diseases</i> , 2017, 49, 680-688.	1.4	13
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37	RNA sequence analysis of rat acute experimental pancreatitis with and without fatty liver: a gene expression profiling comparative study. <i>Scientific Reports</i> , 2017, 7, 734.	1.6	13
38	Transcriptome-based investigation of cirrus development and identifying microsatellite markers in rattan (<i>Daemonorops jenkinsiana</i>). <i>Scientific Reports</i> , 2017, 7, 46107.	1.6	16

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1846	Comparisons of Transcriptome Profiles from <i>Bacillus subtilis</i> Cells Grown in Space versus High Aspect Ratio Vessel (HARV) Clinostats Reveal a Low Degree of Concordance. <i>Astrobiology</i> , 2020, 20, 1498-1509.	1.5	5
1847	<i>Coccoloba alnifolia</i> Leaf Extract as a Potential Antioxidant Molecule Using In Vitro and In Vivo Assays. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-12.	1.9	2
1848	Preclinical validation of therapeutic targets predicted by tensor factorization on heterogeneous graphs. <i>Scientific Reports</i> , 2020, 10, 18250.	1.6	30
1849	Development of a novel immune-related genes prognostic signature for osteosarcoma. <i>Scientific Reports</i> , 2020, 10, 18402.	1.6	17
1850	P0049 IDENTIFYING HUB GENES ASSOCIATED WITH CLINICAL CHARACTERISTICS IN IGA NEPHROPATHY BY WGCNA. <i>Nephrology Dialysis Transplantation</i> , 2020, 35, .	0.4	0
1851	Predicting the Clinical Outcome of Lung Adenocarcinoma Using a Novel Gene Pair Signature Related to RNA-Binding Protein. <i>BioMed Research International</i> , 2020, 2020, 1-14.	0.9	3
1852	Methylome and transcriptome profiles in three yak tissues revealed that DNA methylation and the transcription factor ZGPAT co-regulate milk production. <i>BMC Genomics</i> , 2020, 21, 731.	1.2	4
1853	Oral Treatment With Ileal Spores Triggers Immunometabolic Shifts in Chicken Gut. <i>Frontiers in Veterinary Science</i> , 2020, 7, 629.	0.9	7
1854	Integrated genomic and transcriptomic analysis revealed mutation patterns of de-differentiated liposarcoma and leiomyosarcoma. <i>BMC Cancer</i> , 2020, 20, 1035.	1.1	6

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1856	Uncovering the genomic potential of the Amazon River microbiome to degrade rainforest organic matter. <i>Microbiome</i> , 2020, 8, 151.	4.9	18
1857	Upregulation of miRâ€”9 and miRâ€”193b over human Th17 cell differentiation. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1538.	0.6	5
1858	New insight into the molecular basis of chromium exposure of <i>Litopenaeus vannamei</i> by transcriptome analysis. <i>Marine Pollution Bulletin</i> , 2020, 160, 111673.	2.3	13
1859	A novel lung alveolar cell model for exploring volatile biomarkers of particle-induced lung injury. <i>Scientific Reports</i> , 2020, 10, 15700.	1.6	2
1860	Gap between pediatric and adult approvals of molecular targeted drugs. <i>Scientific Reports</i> , 2020, 10, 17145.	1.6	9
1861	Transcriptomic profile of Pea3 family members reveal regulatory codes for axon outgrowth and neuronal connection specificity. <i>Scientific Reports</i> , 2020, 10, 18162.	1.6	6
1862	Metabolic drug targets of the cytosine metabolism pathways in the dromedary camel (<i>Camelus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 52, 3337-3358.	0.5	1
1863	Recognizing novel chemicals/drugs for anatomical therapeutic chemical classes with a heat diffusion algorithm. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165910.	1.8	10
1864	Google matrix analysis of bi-functional SIGNOR network of proteinâ€”protein interactions. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2020, 559, 125019.	1.2	8
1865	The impact of miR-9 in osteosarcoma. <i>Medicine (United States)</i> , 2020, 99, e21902.	0.4	5
1866	Beneficial rhizobacteria <i>Pseudomonas simiae</i> WCS417 induce major transcriptional changes in plant sugar transport. <i>Journal of Experimental Botany</i> , 2020, 71, 7301-7315.	2.4	35
1867	Exploring the Diversity and Metabolic Profiles of Bacterial Communities Associated With Antarctic Sponges (Terra Nova Bay, Ross Sea). <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	14
1868	Genome-wide identification of differentially methylated promoters and enhancers associated with response to anti-PD-1 therapy in non-small cell lung cancer. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1550-1563.	3.2	99
1869	Transcriptomic profiling in Cutaneous Leishmaniasis patients. <i>Expert Review of Proteomics</i> , 2020, 17, 533-541.	1.3	4
1870	Unveiling Sex-Based Differences in the Effects of Alcohol Abuse: A Comprehensive Functional Meta-Analysis of Transcriptomic Studies. <i>Genes</i> , 2020, 11, 1106.	1.0	19
1871	An unanticipated tumor-suppressive role of the SUMO pathway in the intestine unveiled by Ubc9 haploinsufficiency. <i>Oncogene</i> , 2020, 39, 6692-6703.	2.6	10
1872	Identification and Functional Analysis of Long Non-coding RNAs in Autism Spectrum Disorders. <i>Frontiers in Genetics</i> , 2020, 11, 849.	1.1	5

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1873	Identification of hub genes in colon cancer via bioinformatics analysis. <i>Journal of International Medical Research</i> , 2020, 48, 030006052095323.	0.4	6
1874	Skeletal muscle and cardiac transcriptomics of a regionally endothermic fish, the Pacific bluefin tuna, <i>Thunnus orientalis</i> . <i>BMC Genomics</i> , 2020, 21, 642.	1.2	2
1875	Functional genomic landscape of cancer-intrinsic evasion of killing by T cells. <i>Nature</i> , 2020, 586, 120-126.	13.7	249
1876	Next-generation metabolic engineering approaches towards development of plant cell suspension cultures as specialized metabolite producing biofactories. <i>Biotechnology Advances</i> , 2020, 45, 107635.	6.0	43
1877	Microbial high throughput phenomics: The potential of an irreplaceable omics. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2290-2299.	1.9	26
1878	Network pharmacology analysis of the therapeutic mechanisms of the traditional Chinese herbal formula Lian Hua Qing Wen in Corona virus disease 2019 (COVID-19), gives fundamental support to the clinical use of LHQW. <i>Phytomedicine</i> , 2020, 79, 153336.	2.3	64
1879	PAWER: protein array web exploreR. <i>BMC Bioinformatics</i> , 2020, 21, 411.	1.2	4
1880	Identification of hub genes and its correlation with the prognosis of acute myeloid leukemia based on high-throughput data analysis. <i>Precision Radiation Oncology</i> , 2020, 4, 49-56.	0.4	4
1881	A comprehensive CHO SWATH-MS spectral library for robust quantitative profiling of 10,000 proteins. <i>Scientific Data</i> , 2020, 7, 263.	2.4	17
1882	The small compound, TD-198946, protects against intervertebral degeneration by enhancing glycosaminoglycan synthesis in nucleus pulposus cells. <i>Scientific Reports</i> , 2020, 10, 14190.	1.6	6
1883	Ontological approach to the knowledge systematization of a toxic process and toxic course representation framework for early drug risk management. <i>Scientific Reports</i> , 2020, 10, 14581.	1.6	2
1884	Integrative transcriptomics reveals genotypic impact on sugar beet storability. <i>Plant Molecular Biology</i> , 2020, 104, 359-378.	2.0	9
1885	Comprehensive Proteomic Analysis of Lysine Ubiquitination in Seedling Leaves of <i>Nicotiana tabacum</i> . <i>ACS Omega</i> , 2020, 5, 20122-20133.	1.6	7
1886	Elucidation of resistance signaling and identification of powdery mildew resistant mapping loci (ClAPMR2) during watermelon- <i>Podosphaera xanthii</i> interaction using RNA-Seq and whole-genome resequencing approach. <i>Scientific Reports</i> , 2020, 10, 14038.	1.6	10
1887	Study of Osteoarthritis-Related Hub Genes Based on Bioinformatics Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	11
1888	Study on Intervention Mechanism of Yiqi Huayu Jiedu Decoction on ARDS Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-16.	0.5	2
1889	Transcriptomic Analysis of <i>Rhodococcus opacus</i> R7 Grown on <i>o</i> -Xylene by RNA-Seq. <i>Frontiers in Microbiology</i> , 2020, 11, 1808.	1.5	10
1890	GRIA: Graphical Regularization for Integrative Analysis. , 2020, 2020, 604-612.		1

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1892	Systematic analysis of gut microbiota in pregnant women and its correlations with individual heterogeneity. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 32.	2.9	61
1893	<p>Favorable Immune Microenvironment in Patients with EGFR and MAPK Co-Mutations</p>. <i>Lung Cancer: Targets and Therapy</i> , 2020, Volume 11, 59-71.	1.3	0
1894	Construction and analysis of the protein-protein interaction network for the olfactory system of the silkworm <i>Bombyx mori</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 105, e21737.	0.6	9
1895	3,3'-Dichlorobiphenyl Is Metabolized to a Complex Mixture of Oxidative Metabolites, Including Novel Methoxylated Metabolites, by HepG2 Cells. <i>Environmental Science & Technology</i> , 2020, 54, 12345-12357.	4.6	14
1896	<i>Mycobacterium tuberculosis</i> curli pili (MTP) deficiency is associated with alterations in cell wall biogenesis, fatty acid metabolism and amino acid synthesis. <i>Metabolomics</i> , 2020, 16, 97.	1.4	4
1897	An algorithm to quantify intratumor heterogeneity based on alterations of gene expression profiles. <i>Communications Biology</i> , 2020, 3, 505.	2.0	50
1898	3D curvature-instructed endothelial flow response and tissue vascularization. <i>Science Advances</i> , 2020, 6, .	4.7	45
1899	Predicting biomarkers from classifier for liver metastasis of colorectal adenocarcinomas using machine learning models. <i>Cancer Medicine</i> , 2020, 9, 6667-6678.	1.3	13
1900	Biomarkers, Master Regulators and Genomic Fabric Remodeling in a Case of Papillary Thyroid Carcinoma. <i>Genes</i> , 2020, 11, 1030.	1.0	9
1901	Identification of a metabolism-related gene expression prognostic model in endometrial carcinoma patients. <i>BMC Cancer</i> , 2020, 20, 864.	1.1	21
1902	The precursor of PI(3,4,5)P3 alleviates aging by activating daf-18(Pten) and independent of daf-16. <i>Nature Communications</i> , 2020, 11, 4496.	5.8	19
1903	DEAD-Box Helicase 4 (Ddx4)+ Stem Cells Sustain Tumor Progression in Non-Serous Ovarian Cancers. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6096.	1.8	2
1904	Integration of molecular profiles in a longitudinal wellness profiling cohort. <i>Nature Communications</i> , 2020, 11, 4487.	5.8	66
1905	mRNA and miRNA profiling of Zika virus-infected human umbilical cord mesenchymal stem cells identifies miR-142-5p as an antiviral factor. <i>Emerging Microbes and Infections</i> , 2020, 9, 2061-2075.	3.0	27
1906	Transcriptome Analysis of <i>Solanum Tuberosum</i> Genotype RH89-039-16 in Response to Chitosan. <i>Frontiers in Plant Science</i> , 2020, 11, 1193.	1.7	16
1907	Metagenomic and Metatranscriptomic Study of Microbial Metal Resistance in an Acidic Pit Lake. <i>Microorganisms</i> , 2020, 8, 1350.	1.6	15
1908	ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 2115-2125.	2.5	145

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1909	Finding semantic patterns in omics data using concept rule learning with an ontology-based refinement operator. <i>BioData Mining</i> , 2020, 13, 13.	2.2	1
1910	Biodegradation of Amoxicillin, Tetracyclines and Sulfonamides in Wastewater Sludge. <i>Water (Switzerland)</i> , 2020, 12, 2147.	1.2	59
1911	De novo transcriptome analysis of <i>Lantana camara</i> L. revealed candidate genes involved in phenylpropanoid biosynthesis pathway. <i>Scientific Reports</i> , 2020, 10, 13726.	1.6	17
1912	Molecular causes of an evolutionary shift along the parasitism–mutualism continuum in a bacterial symbiont. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21658-21666.	3.3	12
1913	Potential Molecular Mechanism of the <i>NPPB</i> Gene in Postischemic Heart Failure with and without T2DM. <i>BioMed Research International</i> , 2020, 2020, 1-17.	0.9	2
1914	Identification of key pathways and differentially expressed genes in bronchopulmonary dysplasia using bioinformatics analysis. <i>Biotechnology Letters</i> , 2020, 42, 2569-2580.	1.1	7
1915	Large freshwater phages with the potential to augment aerobic methane oxidation. <i>Nature Microbiology</i> , 2020, 5, 1504-1515.	5.9	66
1916	Extracellular Vesicles Derived From Colorectal Cancer Affects CD8 T Cells: An Analysis Based on Body Mass Index. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 564648.	1.8	6
1917	The Association between the Usage of Non-Steroidal Anti-Inflammatory Drugs and Cognitive Status: Analysis of Longitudinal and Cross-Sectional Studies from the Global Alzheimer's Association Interactive Network and Transcriptomic Data. <i>Brain Sciences</i> , 2020, 10, 961.	1.1	10
1918	Gene Function Similarity Method Based on Data Fusion. , 2020, , .		0
1919	The identification of co-expressed gene modules in <i>Streptococcus pneumoniae</i> from colonization to infection to predict novel potential virulence genes. <i>BMC Microbiology</i> , 2020, 20, 376.	1.3	0
1920	Role of IRE1 β in podocyte proteostasis and mitochondrial health. <i>Cell Death Discovery</i> , 2020, 6, 128.	2.0	10
1921	Molecular insights into the mechanisms of susceptibility of <i>Labeo rohita</i> against oomycete <i>Aphanomyces invadans</i> . <i>Scientific Reports</i> , 2020, 10, 19531.	1.6	11
1922	mTORC1 Transcriptional Regulation of Ribosome Subunits, Protein Synthesis, and Molecular Transport in Primary Human Trophoblast Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 583801.	1.8	22
1923	Identification of Key Modules and Hub Genes Involved in Esophageal Squamous Cell Carcinoma Tumorigenesis Using WCGNA. <i>Cancer Control</i> , 2020, 27, 107327482097881.	0.7	15
1924	Tear proteomic profile in three distinct ocular surface diseases: keratoconus, pterygium, and dry eye related to graft-versus-host disease. <i>Clinical Proteomics</i> , 2020, 17, 42.	1.1	17
1925	Comparative genomics of <i>Klebsiella michiganensis</i> BD177 and related members of <i>Klebsiella</i> sp. reveal the symbiotic relationship with <i>Bactrocera dorsalis</i> . <i>BMC Genetics</i> , 2020, 21, 138.	2.7	5
1926	Analysis of Pan-omics Data in Human Interactome Network (APODHIN). <i>Frontiers in Genetics</i> , 2020, 11, 589231.	1.1	7

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1928	Comprehensive Profiling of Gene Expression in the Cerebral Cortex and Striatum of BTBRTF/ArtRbrc Mice Compared to C57BL/6J Mice. <i>Frontiers in Cellular Neuroscience</i> , 2020, 14, 595607.	1.8	8
1929	Identify and Validate the Transcriptomic, Functional Network, and Predictive Validity of FBXL19-AS1 in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 609601.	1.3	4
1930	First identification of dopamine receptors in pikeperch, <i>Sander lucioperca</i> , during the pre-ovulatory period. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 36, 100747.	0.4	0
1931	miR-140-5p in Small Extracellular Vesicles From Human Papilla Cells Stimulates Hair Growth by Promoting Proliferation of Outer Root Sheath and Hair Matrix Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 593638.	1.8	18
1932	Proteomic Changes of Porcine Oocytes After Vitrification and Subsequent in vitro Maturation: A Tandem Mass Tag-Based Quantitative Analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 614577.	1.8	13
1933	Phosphoproteomics to Characterize Host Response During H3N2 Canine Influenza Virus Infection of Dog Lung. <i>Frontiers in Veterinary Science</i> , 2020, 7, 585071.	0.9	1
1934	Transcriptional Landscape of <i>Waddlia chondrophila</i> Aberrant Bodies Induced by Iron Starvation. <i>Microorganisms</i> , 2020, 8, 1848.	1.6	5
1935	Stress Response of <i>Mesosutterella multiformis</i> Mediated by Nitrate Reduction. <i>Microorganisms</i> , 2020, 8, 2003.	1.6	3
1936	Platelet microparticles load a repertoire of miRNAs programmed to drive osteogenic phenotype. <i>Journal of Biomedical Materials Research - Part A</i> , 2021, 109, 1502-1511.	2.1	6
1937	Co-expression of cancer driver genes: IDH-wildtype glioblastoma-derived tumorspheres. <i>Journal of Translational Medicine</i> , 2020, 18, 482.	1.8	4
1938	Lipid metabolic signatures deviate in sepsis survivors compared to non-survivors. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3678-3691.	1.9	15
1939	Genes, pathways and networks responding to drought stress in oil palm roots. <i>Scientific Reports</i> , 2020, 10, 21303.	1.6	21
1940	A blood transcriptome-based analysis of disease progression, immune regulation, and symptoms in coronavirus-infected patients. <i>Cell Death Discovery</i> , 2020, 6, 141.	2.0	28
1941	Hepatic transcriptome and DNA methylation patterns following perinatal and chronic BPS exposure in male mice. <i>BMC Genomics</i> , 2020, 21, 881.	1.2	3
1942	The ATP-Binding Cassette (ABC) Transport Systems in <i>Mycobacterium tuberculosis</i> : Structure, Function, and Possible Targets for Therapeutics. <i>Biology</i> , 2020, 9, 443.	1.3	20
1943	Comparative analysis of metabolic and transcriptomic features of <i>Nothobranchius furzeri</i> . <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200217.	1.5	2
1944	Comparative proteomics of three Chinese potato cultivars to improve understanding of potato molecular response to late blight disease. <i>BMC Genomics</i> , 2020, 21, 880.	1.2	5

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1946	OsteoBLAST: Computational Routine of Global Molecular Analysis Applied to Biomaterials Development. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 565901.	2.0	4
1947	Genome-scale metabolic reconstruction of the non-model yeast <i>Issatchenkia orientalis</i> SD108 and its application to organic acids production. <i>Metabolic Engineering Communications</i> , 2020, 11, e00148.	1.9	20
1948	Comparison of the gut microbiota of short-term and long-term medical workers and non-medical controls: a cross-sectional analysis. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1285-1292.	2.8	6
1949	Broad genic repression domains signify enhanced silencing of oncogenes. <i>Nature Communications</i> , 2020, 11, 5560.	5.8	10
1950	Co-Administration of Propionate or Protocatechuic Acid Does Not Affect DHA-Specific Transcriptional Effects on Lipid Metabolism in Cultured Hepatic Cells. <i>Nutrients</i> , 2020, 12, 2952.	1.7	2
1951	A Comparison of Transcriptional Diversity of Swine Macrophages Infected With TgHB1 Strain of <i>Toxoplasma gondii</i> Isolated in China. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 526876.	1.8	2
1952	Ubiquitinome Profiling Reveals the Landscape of Ubiquitination Regulation in Rice Young Panicles. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 305-320.	3.0	18
1953	KEGG-expressed genes and pathways in triple negative breast cancer. <i>Medicine (United States)</i> , 2020, 99, e19986.	0.4	19
1954	Conjoint analysis of lncRNA and mRNA expression in rotator cuff tendinopathy. <i>Annals of Translational Medicine</i> , 2020, 8, 335-335.	0.7	13
1955	DGDFS: Dependence Guided Discriminative Feature Selection for Predicting Adverse Drug-Drug Interaction. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2020, , 1-1.	4.0	9
1956	Promiscuous Enzymes Cause Biosynthesis of Diverse Siderophores in <i>Shewanella oneidensis</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	10
1957	Genome-Scale Investigation of the Metabolic Determinants Generating Bacterial Fastidious Growth. <i>MSystems</i> , 2020, 5, .	1.7	16
1958	RNA-Seq and secondary metabolite analyses reveal a putative defence-transcriptome in Norway spruce (<i>Picea abies</i>) against needle bladder rust (<i>Chrysomyxa rhododendri</i>) infection. <i>BMC Genomics</i> , 2020, 21, 336.	1.2	13
1959	Design, synthesis and anticancer/antiestrogenic activities of novel indole-benzimidazoles. <i>Bioorganic Chemistry</i> , 2020, 100, 103929.	2.0	28
1960	Subtractive proteomics and systems biology analysis revealed novel drug targets in <i>Mycoplasma genitalium</i> strain G37. <i>Microbial Pathogenesis</i> , 2020, 145, 104231.	1.3	5
1961	Investigation of Early Death-Induced Changes in Rat Brain by Solid Phase Microextraction via Untargeted High Resolution Mass Spectrometry: <i>In Vivo</i> versus Postmortem Comparative Study. <i>ACS Chemical Neuroscience</i> , 2020, 11, 1827-1840.	1.7	19
1962	The F-Box-Like Protein FBL17 Is a Regulator of DNA-Damage Response and Colocalizes with RETINOBLASTOMA RELATED1 at DNA Lesion Sites. <i>Plant Physiology</i> , 2020, 183, 1295-1305.	2.3	22

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1963	Repurposed Analog of GLP-1 Ameliorates Hyperglycemia in Type 1 Diabetic Mice Through Pancreatic Cell Reprogramming. <i>Frontiers in Endocrinology</i> , 2020, 11, 258.	1.5	15
1964	Sorghum Growth Promotion by <i>Paraburkholderia tropica</i> and <i>Herbaspirillum frisingense</i> : Putative Mechanisms Revealed by Genomics and Metagenomics. <i>Microorganisms</i> , 2020, 8, 725.	1.6	34
1965	Quantifying genetic effects on disease mediated by assayed gene expression levels. <i>Nature Genetics</i> , 2020, 52, 626-633.	9.4	191
1966	<p>Identification of Pannexin 2 as a Novel Marker Correlating with Ferroptosis and Malignant Phenotypes of Prostate Cancer Cells</p>. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 4411-4421.	1.0	24
1967	Identified plasma proteins related to vascular structure are associated with coarctation of the aorta in children. <i>Italian Journal of Pediatrics</i> , 2020, 46, 63.	1.0	0
1968	A Drug-Induced Liver Injury Prediction Model using Transcriptional Response Data with Graph Neural Network. , 2020, , .		5
1969	Balancing selection in Pattern Recognition Receptor signalling pathways is associated with gene function and pleiotropy in a wild rodent. <i>Molecular Ecology</i> , 2020, 29, 1990-2003.	2.0	8
1970	Evaluation of plant sources for antiinfective lead compound discovery by correlating phylogenetic, spatial, and bioactivity data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12444-12451.	3.3	19
1971	A Genome-scale CRISPR Screen Identifies the ERBB and mTOR Signaling Networks as Key Determinants of Response to PI3K Inhibition in Pancreatic Cancer. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 1423-1435.	1.9	14
1972	MyoMiner: explore gene co-expression in normal and pathological muscle. <i>BMC Medical Genomics</i> , 2020, 13, 67.	0.7	7
1973	Cellular Environment Remodels the Genomic Fabrics of Functional Pathways in Astrocytes. <i>Genes</i> , 2020, 11, 520.	1.0	10
1974	Whole genome sequence analysis of <i>Cupriavidus campinensis</i> S14E4C, a heavy metal resistant bacterium. <i>Molecular Biology Reports</i> , 2020, 47, 3973-3985.	1.0	16
1975	Draft Genome of the Liver Fluke <i>Fasciola gigantica</i>. <i>ACS Omega</i> , 2020, 5, 11084-11091.	1.6	25
1976	Antigen-stimulated PBMC transcriptional protective signatures for malaria immunization. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	33
1977	The comprehensive upstream transcription and downstream targeting regulation network of miRNAs reveal potential diagnostic roles in gastric cancer. <i>Life Sciences</i> , 2020, 253, 117741.	2.0	6
1978	Metabolic coessentiality mapping identifies C12orf49 as a regulator of SREBP processing and cholesterol metabolism. <i>Nature Metabolism</i> , 2020, 2, 487-498.	5.1	32
1979	A strategy for large-scale comparison of evolutionary- and reaction-based classifications of enzyme function. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	5
1980	HIF1A expression correlates with increased tumor immune and stromal signatures and aggressive phenotypes in human cancers. <i>Cellular Oncology (Dordrecht)</i> , 2020, 43, 877-888.	2.1	25

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1981	The use of -omics tools for assessing biodeterioration of cultural heritage: A review. <i>Journal of Cultural Heritage</i> , 2020, 45, 351-361.	1.5	30
1982	Network-based strategies in metabolomics data analysis and interpretation: from molecular networking to biological interpretation. <i>Expert Review of Proteomics</i> , 2020, 17, 243-255.	1.3	70
1983	Genome Subtraction and Comparison for the Identification of Novel Drug Targets against <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> . <i>Pathogens</i> , 2020, 9, 368.	1.2	12
1984	Mining the role of angiotensin-like protein family in gastric cancer and seeking potential therapeutic targets by integrative bioinformatics analysis. <i>Cancer Medicine</i> , 2020, 9, 4850-4863.	1.3	12
1985	A computational subtractive genome analysis for the characterization of novel drug targets in <i>Klebsiella pneumonia</i> strain PittNDM01. <i>Microbial Pathogenesis</i> , 2020, 146, 104245.	1.3	1
1986	PathWalks: identifying pathway communities using a disease-related map of integrated information. <i>Bioinformatics</i> , 2020, 36, 4070-4079.	1.8	7
1987	De novo transcriptome analysis unravels tissue-specific expression of candidate genes involved in major secondary metabolite biosynthetic pathways of <i>Plumbago zeylanica</i> : implication for pharmacological potential. <i>3 Biotech</i> , 2020, 10, 271.	1.1	4
1988	Metabolomics and the Microbiome: Characterizing Molecular Diversity in Complex Microbial Communities. , 2020, , 502-518.		2
1989	An information and statistical analysis pipeline for microbial metagenomic sequencing data. <i>Handbook of Statistics</i> , 2020, 43, 67-80.	0.4	0
1990	Towards Unraveling Macroecological Patterns in Rhizosphere Microbiomes. <i>Trends in Plant Science</i> , 2020, 25, 1017-1029.	4.3	42
1991	Genomic competition for noise reduction shaped evolutionary landscape of mir-4673. <i>Npj Systems Biology and Applications</i> , 2020, 6, 12.	1.4	4
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2456	In Situ Localization of Plant Lipid Metabolites by Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry Imaging (MALDI-MSI). <i>Methods in Molecular Biology</i> , 2021, 2295, 417-438.	0.4	5
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2458	Metabolic Pathway Prediction using Non-negative Matrix Factorization with Improved Precision. <i>Lecture Notes in Computer Science</i> , 2021, , 33-44.	1.0	2

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2468	The Metano Modeling Toolbox MMTB: An Intuitive, Web-Based Toolbox Introduced by Two Use Cases. <i>Metabolites</i> , 2021, 11, 113.	1.3	2
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2491	Ranking cancer drivers via betweenness-based outlier detection and random walks. <i>BMC Bioinformatics</i> , 2021, 22, 62.	1.2	6
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2498	A neuronal blood marker is associated with mortality in old age. <i>Nature Aging</i> , 2021, 1, 218-225.	5.3	30

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2504	Screening of Candidate Key Genes Associated with Congenital Heart Disease Using Bioinformatics Data Analysis. <i>Journal of Physics: Conference Series</i> , 2021, 1813, 012038.	0.3	0
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2514	A Bayesian hierarchically structured prior for rare variant association testing. <i>Genetic Epidemiology</i> , 2021, 45, 413-424.	0.6	2
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2529	Expression and molecular profiles of the AlkB family in ovarian serous carcinoma. <i>Aging</i> , 2021, 13, 9679-9692.	1.4	21
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2535	Comparison of plasma and cerebrospinal fluid proteomes identifies gene products guiding adult neurogenesis and neural differentiation in birds. <i>Scientific Reports</i> , 2021, 11, 5312.	1.6	1
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2556	<i>Pseudomonas aeruginosa</i> : An Audacious Pathogen with an Adaptable Arsenal of Virulence Factors. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3128.	1.8	230
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2567	Quantitative acetylome analysis reveals histone modifications that may predict prognosis in hepatitis B-related hepatocellular carcinoma. <i>Clinical and Translational Medicine</i> , 2021, 11, e313.	1.7	19
2568	Anti-Inflammatory and Immune Modulatory Effects of Synbio-Glucan in an Atopic Dermatitis Mouse Model. <i>Nutrients</i> , 2021, 13, 1090.	1.7	3
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2573	Fasting alters the gut microbiome reducing blood pressure and body weight in metabolic syndrome patients. <i>Nature Communications</i> , 2021, 12, 1970.	5.8	108
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2580	Genome-Based Drug Target Identification in Human Pathogen <i>Streptococcus gallolyticus</i> . <i>Frontiers in Genetics</i> , 2021, 12, 564056.	1.1	17
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2588	M2 Macrophage Co-Expression Factors Correlate With Immune Phenotype and Predict Prognosis of Bladder Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 609334.	1.3	19
2589	Prognostic Alternative mRNA Splicing in Adrenocortical Carcinoma. <i>Frontiers in Endocrinology</i> , 2021, 12, 538364.	1.5	4
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2597	Identification and Analysis of Potential Key Genes Associated With Hepatocellular Carcinoma Based on Integrated Bioinformatics Methods. <i>Frontiers in Genetics</i> , 2021, 12, 571231.	1.1	25
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2607	Viral genomic, metagenomic and human transcriptomic characterization and prediction of the clinical forms of COVID-19. <i>PLoS Pathogens</i> , 2021, 17, e1009416.	2.1	30
2608	A novel seven-gene panel predicts the sensitivity and prognosis of head and neck squamous cell carcinoma treated with platinum-based radio(chemo)therapy. <i>European Archives of Oto-Rhino-Laryngology</i> , 2021, 278, 3523-3531.	0.8	4

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2610	How to Get Started with Single Cell RNA Sequencing Data Analysis. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 1279-1292.	3.0	19
2612	Ciprofloxacin increased abundance of antibiotic resistance genes and shaped microbial community in epiphytic biofilm on <i>Vallisneria spiralis</i> in mesocosmic wetland. <i>Bioresource Technology</i> , 2021, 323, 124574.	4.8	39
2614	AutoDTI++: deep unsupervised learning for DTI prediction by autoencoders. <i>BMC Bioinformatics</i> , 2021, 22, 204.	1.2	24
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2618	Prediction of host-pathogen protein interactions by extended network model. <i>Turkish Journal of Biology</i> , 2021, 45, 138-148.	2.1	4
2619	Network pharmacology and RNA-sequencing reveal the molecular mechanism of Xuebijing injection on COVID-19-induced cardiac dysfunction. <i>Computers in Biology and Medicine</i> , 2021, 131, 104293.	3.9	14
2620	Identification of pivotal genes associated with the prognosis of gastric carcinoma through integrated analysis. <i>Bioscience Reports</i> , 2021, 41, .	1.1	7
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2623	Differential Epigenetic Marks Are Associated with Apospory Expressivity in Diploid Hybrids of <i>Paspalum rufum</i> . <i>Plants</i> , 2021, 10, 793.	1.6	5
2624	Dynamic Changes in Fecal Microbial Communities of Neonatal Dairy Calves by Aging and Diarrhea. <i>Animals</i> , 2021, 11, 1113.	1.0	36
2625	Prognostic biomarkers and therapeutic targets in oral squamous cell carcinoma: a study based on cross-database analysis. <i>Hereditas</i> , 2021, 158, 15.	0.5	14
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