DAVID-WS: a stateful web service to facilitate gene/pro

**Bioinformatics** 

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Citation Report

#	Article	IF	CITATIONS
1	CellLineNavigator: a workbench for cancer cell line analysis. Nucleic Acids Research, 2012, 41, D942-D948.	6.5	15
2	Transcriptional profiling of adult Drosophila antennae by high-throughput sequencing. Zoological Studies, 2013, 52, .	0.3	25
3	The emerging field of chemo―and pharmacoproteomics. Proteomics - Clinical Applications, 2013, 7, 171-180.	0.8	15
4	Glycolytic enzymes PGK1 and PKM2 as novel transcriptional targets of PPARγ in breast cancer pathophysiology. Journal of Drug Targeting, 2013, 21, 161-174.	2.1	44
5	Glycocapture-Assisted Global Quantitative Proteomics (gagQP) Reveals Multiorgan Responses in Serum Toxicoproteome. Journal of Proteome Research, 2013, 12, 2034-2044.	1.8	17
6	Synergistic interactions between camptothecin and EGFR or RAC1 inhibitors and between imatinib and Notch signaling or RAC1 inhibitors in glioblastoma cell lines. Cancer Chemotherapy and Pharmacology, 2013, 72, 329-340.	1.1	12
7	RDAVIDWebService: a versatile <i>R</i> interface to DAVID. Bioinformatics, 2013, 29, 2810-2811.	1.8	191
8	Long non-coding RNA identification over mouse brain development by integrative modeling of chromatin and genomic features. Nucleic Acids Research, 2013, 41, 10044-10061.	6.5	65
9	Elucidating Novel Serum Biomarkers Associated with Pulmonary Tuberculosis Treatment. PLoS ONE, 2013, 8, e61002.	1.1	95
10	Nuclear Receptor-Mediated Alleviation of Alcoholic Fatty Liver by Polyphenols Contained in Alcoholic Beverages. PLoS ONE, 2014, 9, e87142.	1.1	15
11	Neighbor Preferences of Amino Acids and Context-Dependent Effects of Amino Acid Substitutions in Human, Mouse, and Dog. International Journal of Molecular Sciences, 2014, 15, 15963-15980.	1.8	4
12	Spatial regulation dominates gene function in the ganglia chain. Bioinformatics, 2014, 30, 310-316.	1.8	6
13	The Proteomic Landscape of the Suprachiasmatic Nucleus Clock Reveals Large-Scale Coordination of Key Biological Processes. PLoS Genetics, 2014, 10, e1004695.	1.5	63
14	Microarray comparison of the gene expression profiles in the adult vs. embryonic day 14 rat liver. Biomedical Reports, 2014, 2, 664-670.	0.9	6
15	Using a large-scale knowledge database on reactions and regulations to propose key upstream regulators of various sets of molecules participating in cell metabolism. BMC Systems Biology, 2014, 8, 32.	3.0	5
16	Genomics and Proteomics for Clinical Discovery and Development. Translational Bioinformatics, 2014,	0.0	3
17	Advances in urinary proteome analysis and applications in systems biology. Bioanalysis, 2014, 6, 2549-2569.	0.6	17
18	Genome-Wide Analysis of Functional and Evolutionary Features of <i>Tele</i> -Enhancers. G3: Genes, Genomes, Genetics, 2014, 4, 579-593.	0.8	3

#	Article	IF	CITATIONS
19	Evaluation and validation of a robust single cell RNA-amplification protocol through transcriptional profiling of enriched lung cancer initiating cells. BMC Genomics, 2014, 15, 1129.	1.2	19
20	CopraRNA and IntaRNA: predicting small RNA targets, networks and interaction domains. Nucleic Acids Research, 2014, 42, W119-W123.	6.5	347
21	BioMet Toolbox 2.0: genome-wide analysis of metabolism and omics data. Nucleic Acids Research, 2014, 42, W175-W181.	6.5	40
22	INsPeCT: INtegrative Platform for Cancer Transcriptomics. Cancer Informatics, 2014, 13, CIN.S13630.	0.9	9
23	Coregulation of Genetic Programs by the Transcription Factors NFIB and STAT5. Molecular Endocrinology, 2014, 28, 758-767.	3.7	16
24	ISAAC - InterSpecies Analysing Application using Containers. BMC Bioinformatics, 2014, 15, 18.	1.2	5
25	Functional genomics suggest neurogenesis in the adult human olfactory bulb. Brain Structure and Function, 2014, 219, 1991-2000.	1.2	45
26	Fine Tuning of Proteomic Technologies to Improve Biological Findings: Advancements in 2011–2013. Analytical Chemistry, 2014, 86, 176-195.	3.2	18
27	Annotation of the Zebrafish Genome through an Integrated Transcriptomic and Proteomic Analysis. Molecular and Cellular Proteomics, 2014, 13, 3184-3198.	2.5	52
28	Affinity purification–mass spectrometry and network analysis to understand protein-protein interactions. Nature Protocols, 2014, 9, 2539-2554.	5.5	169
29	Poly (ADP-ribose) polymerase inhibitor efficacy in head and neck cancer. Oral Oncology, 2014, 50, 825-831.	0.8	7
30	CSF1/CSF1R Blockade Reprograms Tumor-Infiltrating Macrophages and Improves Response to T-cell Checkpoint Immunotherapy in Pancreatic Cancer Models. Cancer Research, 2014, 74, 5057-5069.	0.4	1,030
31	Expression-based network biology identifies immune-related functional modules involved in plant defense. BMC Genomics, 2014, 15, 421.	1.2	36
32	A knowledge base for the discovery of function, diagnostic potential and drug effects on cellular and extracellular miRNAs. BMC Genomics, 2014, 15, S4.	1.2	25
33	Bioinformatic analysis of proteomics data. BMC Systems Biology, 2014, 8, S3.	3.0	131
34	Chromosome-centric Human Proteome Project (C-HPP): Chromosome 12. Journal of Proteome Research, 2014, 13, 3160-3165.	1.8	4
35	An integrated perspective and functional impact of the mitochondrial acetylome. Expert Review of Proteomics, 2014, 11, 383-394.	1.3	14
36	Retrotransposons and piRNA: The missing link in central nervous system. Neurochemistry International, 2014, 77, 94-102.	1.9	20

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#	ARTICLE	IF	CITATIONS
37	Microarray data analysis of neuroblastoma: Expression of SOX2 downregulates the expression of MYCN. Molecular Medicine Reports, 2015, 12, 6867-6872.	1.1	1
38	LENS: web-based lens for enrichment and network studies of human proteins. BMC Medical Genomics, 2015, 8, S2.	0.7	27
39	Circadian and feeding rhythms differentially affect rhythmic mRNA transcription and translation in mouse liver. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6579-88.	3.3	199
40	Memory acquisition and retrieval impact different epigenetic processes that regulate gene expression. BMC Genomics, 2015, 16, S5.	1.2	50
41	High-throughput mRNA and miRNA profiling of epithelial-mesenchymal transition in MDCK cells. BMC Genomics, 2015, 16, 944.	1.2	29
42	Identification and profiling of micro <scp>RNA</scp> s associated with white and black plumage pigmentation in the white and black feather bulbs of ducks by <scp>RNA</scp> sequencing. Animal Genetics, 2015, 46, 627-635.	0.6	10
43	Retrovirus-Mediated Expression of E2A-PBX1 Blocks Lymphoid Fate but Permits Retention of Myeloid Potential in Early Hematopoietic Progenitors. PLoS ONE, 2015, 10, e0130495.	1.1	3
44	Transcriptator: An Automated Computational Pipeline to Annotate Assembled Reads and Identify Non Coding RNA. PLoS ONE, 2015, 10, e0140268.	1.1	14
45	Nonsynonymous Single-Nucleotide Variations on Some Posttranslational Modifications of Human Proteins and the Association with Diseases. Computational and Mathematical Methods in Medicine, 2015, 2015, 1-12.	0.7	5
46	Identifying the causative proteins of similar side effect pairs to explore the common molecular basis of these side effects. Molecular BioSystems, 2015, 11, 2060-2067.	2.9	O
47	Longitudinal epigenetic and gene expression profiles analyzed by three-component analysis reveal down-regulation of genes involved in protein translation in human aging. Nucleic Acids Research, 2015, 43, e100-e100.	6.5	35
48	Proteomics and glycoproteomics of pluripotent stemâ€cell surface proteins. Proteomics, 2015, 15, 1152-1163.	1.3	4
49	Acetylome Analysis Reveals the Involvement of Lysine Acetylation in Photosynthesis and Carbon Metabolism in the Model Cyanobacterium <i>Synechocystis</i> sp. PCC 6803. Journal of Proteome Research, 2015, 14, 1275-1286.	1.8	119
50	Proteome mining for drug target identification in Listeria monocytogenes strain EGD-e and structure-based virtual screening of a candidate drug target penicillin binding protein 4. Journal of Microbiological Methods, 2015, 111, 9-18.	0.7	23
51	Identification of Early-Onset Preeclampsia-Related Genes and MicroRNAs by Bioinformatics Approaches. Reproductive Sciences, 2015, 22, 954-963.	1.1	22
52	Sequence and analysis of a whole genome from Kuwaiti population subgroup of Persian ancestry. BMC Genomics, 2015, 16, 92.	1.2	34
53	Dynamic Proteomics. Methods in Enzymology, 2015, 561, 219-276.	0.4	57
54	Regulation of Toll-like Receptor Signaling by the SF3a mRNA Splicing Complex. PLoS Genetics, 2015, 11, e1004932.	1.5	41

#	Article	IF	Citations
55	Cooperative Transcriptional Activation of Antimicrobial Genes by STAT and NF-κB Pathways by Concerted Recruitment of the Mediator Complex. Cell Reports, 2015, 12, 300-312.	2.9	58
56	Acute Targeting of General Transcription Factor IIB Restricts Cardiac Hypertrophy via Selective Inhibition of Gene Transcription. Circulation: Heart Failure, 2015, 8, 138-148.	1.6	22
57	Hepatocellular carcinoma-derived exosomes promote motility of immortalized hepatocyte through transfer of oncogenic proteins and RNAs. Carcinogenesis, 2015, 36, 1008-1018.	1.3	213
58	Integromics network meta-analysis on cardiac aging offers robust multi-layer modular signatures and reveals micronome synergism. BMC Genomics, 2015, 16, 147.	1.2	19
59	Wnt directs the endosomal flux of <scp>LDL</scp> â€derived cholesterol and lipid droplet homeostasis. EMBO Reports, 2015, 16, 741-752.	2.0	43
60	AVIA v2.0: annotation, visualization and impact analysis of genomic variants and genes. Bioinformatics, 2015, 31, 2748-2750.	1.8	15
61	HiTSelect: a comprehensive tool for high-complexity-pooled screen analysis. Nucleic Acids Research, 2015, 43, e16-e16.	6.5	56
62	Simultaneous generation of many RNA-seq libraries in a single reaction. Nature Methods, 2015, 12, 323-325.	9.0	256
64	Genomic alterations in <i>BCL2L1</i> and <i>DLC1</i> contribute to drug sensitivity in gastric cancer. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12492-12497.	3.3	46
65	Heme Oxygenase-1 Induction Prevents Autoimmune Diabetes in Association With Pancreatic Recruitment of M2-Like Macrophages, Mesenchymal Cells, and Fibrocytes. Endocrinology, 2015, 156, 3937-3949.	1.4	19
66	Comparative Tissue Proteomics of Microdissected Specimens Reveals Novel Candidate Biomarkers of Bladder Cancer. Molecular and Cellular Proteomics, 2015, 14, 2466-2478.	2.5	62
67	Discovery of ML358, a Selective Small Molecule Inhibitor of the SKN-1 Pathway Involved in Drug Detoxification and Resistance in Nematodes. ACS Chemical Biology, 2015, 10, 1871-1879.	1.6	9
68	SAMNetWeb: identifying condition-specific networks linking signaling and transcription. Bioinformatics, 2015, 31, 1124-1126.	1.8	14
69	Mass spectrometry based quantitative proteomics and integrative network analysis accentuates modulating roles of annexinâ€1 in mammary tumorigenesis. Proteomics, 2015, 15, 408-418.	1.3	16
70	Leveraging Comparative Genomics to Identify and Functionally Characterize Genes Associated with Sperm Phenotypes in Python bivittatus (Burmese Python). Genetics Research International, 2016, 2016, 1-16.	2.0	0
71	Networks of Host Factors that Interact with NS1 Protein of Influenza A Virus. Frontiers in Microbiology, 2016, 7, 654.	1.5	27
72	First insights into the nature and evolution of antisense transcription in nematodes. BMC Evolutionary Biology, 2016, 16, 165.	3.2	12
73	Global Profiling of the Cellular Alternative RNA Splicing Landscape during Virus-Host Interactions. PLoS ONE, 2016, 11, e0161914.	1.1	58

#	Article	IF	CITATIONS
74	Prediction of Possible Biomarkers and Novel Pathways Conferring Risk to Post-Traumatic Stress Disorder. PLoS ONE, 2016, 11, e0168404.	1.1	12
75	Identification of biological pathways regulated by PGRN and GRN peptide treatments using transcriptome analysis. European Journal of Neuroscience, 2016, 44, 2214-2225.	1.2	13
76	Systematic analysis of the lysine acetylome in Fusarium graminearum. BMC Genomics, 2016, 17, 1019.	1.2	72
77	Systems view of adipogenesis via novel omics-driven and tissue-specific activity scoring of network functional modules. Scientific Reports, 2016, 6, 28851.	1.6	17
78	Microarray data analysis to identify crucial genes regulated by CEBPB in human SNB19 glioma cells. World Journal of Surgical Oncology, 2016, 14, 258.	0.8	19
79	Towards constructing "Super Gene Sets―regulatory networks. , 2016, , .		1
80	A time-resolved molecular map of the macrophage response to VSV infection. Npj Systems Biology and Applications, 2016, 2, 16027.	1.4	42
81	Low-dose oral interferon modulates expression of inflammatory and autoimmune genes in cattle. Veterinary Immunology and Immunopathology, 2016, 172, 64-71.	0.5	7
82	Global profiling of alternative RNA splicing events provides insights into molecular differences between various types of hepatocellular carcinoma. BMC Genomics, 2016, 17, 683.	1.2	47
83	Computational identification of non-synonymous polymorphisms within regions corresponding to protein interaction sites. Computers in Biology and Medicine, 2016, 79, 30-35.	3.9	6
84	Acetylome analysis reveals the involvement of lysine acetylation in diverse biological processes in Phytophthora sojae. Scientific Reports, 2016, 6, 29897.	1.6	59
85	Mice produced by mitotic reprogramming of sperm injected into haploid parthenogenotes. Nature Communications, 2016, 7, 12676.	5.8	23
86	The severity of hereditary porphyria is modulated by the porphyrin exporter and Lan antigen ABCB6. Nature Communications, 2016, 7, 12353.	5.8	37
87	Dynamic changes in global microRNAome and transcriptome reveal complex miRNA-mRNA regulated host response to Japanese Encephalitis Virus in microglial cells. Scientific Reports, 2016, 6, 20263.	1.6	54
88	Complementary Post Transcriptional Regulatory Information is Detected by PUNCH-P and Ribosome Profiling. Scientific Reports, 2016, 6, 21635.	1.6	25
89	Proteome-wide analysis of lysine acetylation in the plant pathogen Botrytis cinerea. Scientific Reports, 2016, 6, 29313.	1.6	77
91	Comprehensive profiling of lysine acetylproteome analysis reveals diverse functions of lysine acetylation in common wheat. Scientific Reports, 2016, 6, 21069.	1.6	87
92	Tetrapod limb and sarcopterygian fin regeneration share a core genetic programme. Nature Communications, 2016, 7, 13364.	5.8	52

#	ARTICLE	IF	CITATIONS
93	A transcription factor hierarchy defines an environmental stress response network. Science, 2016, 354, .	6.0	394
94	Cell types differ in global coordination of splicing and proportion of highly expressed genes. Scientific Reports, 2016, 6, 32249.	1.6	19
95	Blocking senseâ€strand activity improves potency, safety and specificity of antiâ€hepatitis B virus short hairpin <scp>RNA</scp> . EMBO Molecular Medicine, 2016, 8, 1082-1098.	3.3	24
96	Long noncoding RNAs expressed in human hepatic stellate cells form networks with extracellular matrix proteins. Genome Medicine, 2016, 8, 31.	3.6	59
97	Target identification in Fusobacterium nucleatum by subtractive genomics approach and enrichment analysis of host-pathogen protein-protein interactions. BMC Microbiology, 2016, 16, 84.	1.3	49
98	g:Profiler—a web server for functional interpretation of gene lists (2016 update). Nucleic Acids Research, 2016, 44, W83-W89.	6.5	1,179
99	Genomic survey provides insights into the evolutionary changes that occurred during European expansion of the Âinvasive mosquitofish ( <i>Gambusia holbrooki</i> ). Molecular Ecology, 2016, 25, 1089-1105.	2.0	38
100	An essential role for UTX in resolution and activation of bivalent promoters. Nucleic Acids Research, 2016, 44, 3659-3674.	6.5	63
101	RNA-seq reveals the critical role of CspA in regulating Brucella melitensis metabolism and virulence. Science China Life Sciences, 2016, 59, 417-424.	2.3	18
102	Epigenome-Microbiome crosstalk: A potential new paradigm influencing neonatal susceptibility to disease. Epigenetics, 2016, 11, 205-215.	1.3	105
103	High-fat diet reprograms the epigenome of rat spermatozoa and transgenerationally affects metabolism of the offspring. Molecular Metabolism, 2016, 5, 184-197.	3.0	317
104	Identification of potential COPD genes based on multi-omics data at the functional level. Molecular BioSystems, 2016, 12, 191-204.	2.9	8
105	Genome-Scale Identification of Cell-Wall-Related Genes in Switchgrass through Comparative Genomics and Computational Analyses of Transcriptomic Data. Bioenergy Research, 2016, 9, 172-180.	2.2	10
106	Serotonin receptor 2C regulates neurite growth and is necessary for normal retinal processing of visual information. Developmental Neurobiology, 2017, 77, 419-437.	1.5	19
107	Integrated and Quantitative Proteomics of Human Tumors. Methods in Enzymology, 2017, 586, 229-246.	0.4	7
108	Molecular pathways related to the longevity promotion and cognitive improvement of Cistanche tubulosa in Drosophila. Phytomedicine, 2017, 26, 37-44.	2.3	9
109	Microarray Analysis of Hypertension. Methods in Molecular Biology, 2017, 1527, 41-52.	0.4	5
110	Proteomic analysis of chondromodulin-I-induced differentiation of mesenchymal stem cells into chondrocytes. Journal of Proteomics, 2017, 159, 1-18.	1.2	3

#	ARTICLE	IF	CITATIONS
111	Proteome mining for the identification and in-silico characterization of putative drug targets of multi-drug resistant Clostridium difficile strain 630. Journal of Microbiological Methods, 2017, 136, 6-10.	0.7	3
112	Genomic Comparison of Indigenous African and Northern European Chickens Reveals Putative Mechanisms of Stress Tolerance Related to Environmental Selection Pressure. G3: Genes, Genomes, Genetics, 2017, 7, 1525-1537.	0.8	38
113	High prevalence of TP53 mutations is associated with poor survival and an EMT signature in gliosarcoma patients. Experimental and Molecular Medicine, 2017, 49, e317-e317.	3.2	37
114	Systematic analysis of the lysine acetylome reveals diverse functions of lysine acetylation in the oleaginous yeast Yarrowia lipolytica. AMB Express, 2017, 7, 94.	1.4	16
115	Investigation of differentially-expressed microRNAs and genes in cervical cancer using an integrated bioinformatics analysis. Oncology Letters, 2017, 13, 2784-2790.	0.8	16
116	Identification of Sequence Variants within Experimentally Validated Protein Interaction Sites Provides New Insights into Molecular Mechanisms of Disease Development. Molecular Informatics, 2017, 36, 1700017.	1.4	4
117	A Generalized Linear Model for Decomposing <i>Cis</i> regulatory, Parent-of-Origin, and Maternal Effects on Allele-Specific Gene Expression. G3: Genes, Genomes, Genetics, 2017, 7, 2227-2234.	0.8	11
118	Deciphering the Mechanism of Action of Wrightia tinctoria for Psoriasis Based on Systems Pharmacology Approach. Journal of Alternative and Complementary Medicine, 2017, 23, 866-878.	2.1	2
119	Tricyclic Antidepressants Promote Ceramide Accumulation to Regulate Collagen Production in Human Hepatic Stellate Cells. Scientific Reports, 2017, 7, 44867.	1.6	22
120	Synergic Functions of miRNAs Determine Neuronal Fate of Adult Neural Stem Cells. Stem Cell Reports, 2017, 8, 1046-1061.	2.3	49
121	rNAV 2.0: a visualization tool for bacterial sRNA-mediated regulatory networks mining. BMC Bioinformatics, 2017, 18, 188.	1.2	6
123	Malonylome Analysis Reveals the Involvement of Lysine Malonylation in Metabolism and Photosynthesis in Cyanobacteria. Journal of Proteome Research, 2017, 16, 2030-2043.	1.8	28
124	Altered gene expression profiles in the lungs of benzo[a]pyrene-exposed mice in the presence of lipopolysaccharide-induced pulmonary inflammation. Toxicology and Applied Pharmacology, 2017, 336, 8-19.	1.3	19
125	Integrated Analysis of Copy Number Variations and Gene Expression Profiling in Hepatocellular carcinoma. Scientific Reports, 2017, 7, 10570.	1.6	33
126	MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. Nature Immunology, 2017, 18, 1035-1045.	7.0	63
127	A three miRNAs signature predicts survival in cervical cancer using bioinformatics analysis. Scientific Reports, 2017, 7, 5624.	1.6	60
128	Bioinformatics analysis of gene expression profile data to screen key genes involved in pulmonary sarcoidosis. Gene, 2017, 596, 98-104.	1.0	40
129	Interaction profiling of RNA-binding ubiquitin ligases reveals a link between posttranscriptional regulation and the ubiquitin system. Scientific Reports, 2017, 7, 16582.	1.6	17

#	Article	IF	CITATIONS
130	ciaR impacts biofilm formation by regulating an arginine biosynthesis pathway in Streptococcus sanguinis SK36. Scientific Reports, 2017, 7, 17183.	1.6	47
131	Genome variation and conserved regulation identify genomic regions responsible for strain specific phenotypes in rat. BMC Genomics, 2017, 18, 986.	1.2	3
132	Identification and analysis of key genes in osteosarcoma using bioinformatics. Oncology Letters, 2018, 15, 2789-2794.	0.8	29
133	Identification of human exercise-induced physiological function changes based on bioinformatics analysis. Journal of Sports Medicine and Physical Fitness, 2017, 57, 380-387.	0.4	0
134	Transcriptome-wide analysis of alternative RNA splicing events in Epstein-Barr virus-associated gastric carcinomas. PLoS ONE, 2017, 12, e0176880.	1.1	24
135	Screening and validation of differentially expressed extracellular miRNAs in acute pancreatitis. Molecular Medicine Reports, 2017, 16, 6412-6418.	1.1	11
136	MicroRNA profiling of platelets from immune thrombocytopenia and target gene prediction. Molecular Medicine Reports, 2017, 16, 2835-2843.	1.1	20
137	Docking Studies for Multi-Target Drugs. Current Drug Targets, 2017, 18, 592-604.	1.0	39
138	FERMT2 links cortical actin structures, plasma membrane tension and focal adhesion function to stabilize podocyte morphology. Matrix Biology, 2018, 68-69, 263-279.	1.5	27
139	Workflow for a Computational Analysis of an sRNA Candidate in Bacteria. Methods in Molecular Biology, 2018, 1737, 3-30.	0.4	11
140	In silico profiling of systemic effects of drugs to predict unexpected interactions. Scientific Reports, 2018, 8, 1612.	1.6	13
141	VarCards: an integrated genetic and clinical database for coding variants in the human genome. Nucleic Acids Research, 2018, 46, D1039-D1048.	6.5	148
142	Deletion of DGCR8 in VSMCs of adult mice results in loss of vascular reactivity, reduced blood pressure and neointima formation. Scientific Reports, 2018, 8, 1468.	1.6	7
143	Transcriptome Assessment of Erythema Migrans Skin Lesions in Patients With Early Lyme Disease Reveals Predominant Interferon Signaling. Journal of Infectious Diseases, 2018, 217, 158-167.	1.9	34
144	Snf1-RELATED KINASE1-Controlled C/S <sub>1</sub> -bZIP Signaling Activates Alternative Mitochondrial Metabolic Pathways to Ensure Plant Survival in Extended Darkness. Plant Cell, 2018, 30, 495-509.	3.1	142
145	Network-based technologies for early drug discovery. Drug Discovery Today, 2018, 23, 626-635.	3.2	72
146	Integrative omics analysis of p53â€dependent regulation of metabolism. FEBS Letters, 2018, 592, 380-393.	1.3	6
147	Integrated bioinformatics analysis reveals key candidate genes and pathways in breast cancer. Molecular Medicine Reports, 2018, 17, 8091-8100.	1.1	22

#	ARTICLE	IF	CITATIONS
148	Clinical and Genomic Crosstalk between Glucocorticoid Receptor and Estrogen Receptor $\hat{l}_{\pm}$ In Endometrial Cancer. Cell Reports, 2018, 22, 2995-3005.	2.9	52
149	CXXC5 suppresses hepatocellular carcinoma by promoting TGF-β-induced cell cycle arrest and apoptosis. Journal of Molecular Cell Biology, 2018, 10, 48-59.	1.5	33
150	Microarray analysis to identify the similarities and differences of pathogenesis between aortic occlusive disease and abdominal aortic aneurysm. Vascular, 2018, 26, 301-314.	0.4	6
151	Intragraft Molecular Pathways Associated with Tolerance Induction in Renal Transplantation. Journal of the American Society of Nephrology: JASN, 2018, 29, 423-433.	3.0	11
152	Modules of Correlated Genes in a Gene Expression Regulatory Network of CDDP-Resistant Cancer Cells. , 2018, , .		0
153	Identification of hub genes and pathways in glioblastoma by bioinformatics analysis. Oncology Letters, 2019, 17, 1035-1041.	0.8	7
154	Identification of Candidate Genes Responsible for Age-related Macular Degeneration using Microarray Data. International Journal of Service Science, Management, Engineering, and Technology, 2018, 9, 33-60.	0.7	4
155	Selecting Multiple Biomarker Subsets with Similarly Effective Binary Classification Performances. Journal of Visualized Experiments, 2018, , .	0.2	5
156	Integrated whole genome microarray analysis and immunohistochemical assay identifies COL11A1, GJB2 and CTRL as predictive biomarkers for pancreatic cancer. Cancer Cell International, 2018, 18, 174.	1.8	28
157	Comprehensive proteome analyses of lysine acetylation in tea leaves by sensing nitrogen nutrition. BMC Genomics, 2018, 19, 840.	1.2	31
158	A new method for evaluating the impacts of semantic similarity measures on the annotation of gene sets. PLoS ONE, 2018, 13, e0208037.	1.1	3
159	Three differential expression profiles of miRNAs as potential biomarkers for lung adenocarcinoma. Biochemical and Biophysical Research Communications, 2018, 507, 377-382.	1.0	14
160	Robust analysis of novel mRNA–lncRNA cross talk based on ceRNA hypothesis uncovers carcinogenic mechanism and promotes diagnostic accuracy in esophageal cancer. Cancer Management and Research, 2019, Volume 11, 347-358.	0.9	16
161	Potential clinical value and putative biological function of miR‑122‑5p in hepatocellular carcinoma: A comprehensive study using microarray and RNA sequencing data. Oncology Letters, 2018, 16, 6918-6929.	0.8	12
162	Potential four‑miRNA signature associated with Ti¿½stage and prognosis of patients with pancreatic ductal adenocarcinoma identified by co‑expression analysis. Molecular Medicine Reports, 2018, 19, 441-451.	1.1	3
163	SIRT5 deacylates metabolism-related proteins and attenuates hepatic steatosis in ob/ob mice. EBioMedicine, 2018, 36, 347-357.	2.7	44
164	Screening and identification of potential novel biomarker for diagnosis of complicated Plasmodium vivax malaria. Journal of Translational Medicine, 2018, 16, 272.	1.8	23
165	The role of miR-106p-5p in cervical cancer: from expression to molecular mechanism. Cell Death Discovery, 2018, 4, 36.	2.0	19

#	Article	IF	CITATIONS
166	Genetically defined cellular correlates of the baseline brain MRI signal. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E9727-E9736.	3.3	43
167	Genome-wide screening for functional long noncoding RNAs in human cells by Cas9 targeting of splice sites. Nature Biotechnology, 2018, 36, 1203-1210.	9.4	120
168	Is NF2 a Key Player of the Differentially Expressed Gene Between Spinal Cord Ependymoma and Intracranial Ependymoma?. World Neurosurgery, 2018, 118, e906-e917.	0.7	4
169	Interplay between transcription regulators RUNX1 and FUBP1 activates an enhancer of the oncogenec-KITand amplifies cell proliferation. Nucleic Acids Research, 2018, 46, 11214-11228.	6.5	28
170	Genome-Wide Characterization of Selection Signatures and Runs of Homozygosity in Ugandan Goat Breeds. Frontiers in Genetics, 2018, 9, 318.	1.1	126
171	Tolerance to sustained activation of the cAMP/Creb pathway activity in osteoblastic cells is enabled by loss of p53. Cell Death and Disease, 2018, 9, 844.	2.7	12
172	Screening for implicated genes in colorectal cancer using wholeâ€genome gene expression profiling. Molecular Medicine Reports, 2018, 17, 8260-8268.	1.1	8
173	Quantitative SUMO proteomics reveals the modulation of several PML nuclear body associated proteins and an anti-senescence function of UBC9. Scientific Reports, 2018, 8, 7754.	1.6	26
174	TimeXNet Web: identifying cellular response networks from diverse omics time-course data. Bioinformatics, 2018, 34, 3764-3765.	1.8	0
175	Identification of key pathways and genes in the progression of cervical cancer using bioinformatics analysis. Oncology Letters, 2018, 16, 1003-1009.	0.8	20
176	The ATPâ€binding protein FgArb1 is essential for penetration, infectious and normal growth of <i>Fusarium graminearum</i> . New Phytologist, 2018, 219, 1447-1466.	3.5	44
177	A Computational Systems Pharmacology Approach to Investigate Molecular Mechanisms of Herbal Formula Tian-Ma-Gou-Teng-Yin for Treatment of Alzheimer's Disease. Frontiers in Pharmacology, 2018, 9, 668.	1.6	43
178	Cell division cycle 7 kinase is a negative regulator of cell-mediated collagen degradation. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2018, 315, L360-L370.	1.3	3
179	Influence of Glucose Availability and CRP Acetylation on the Genome-Wide Transcriptional Response of Escherichia coli: Assessment by an Optimized Factorial Microarray Analysis. Frontiers in Microbiology, 2018, 9, 941.	1.5	7
180	LncRNA NEAT1 Promotes Deterioration of Hepatocellular Carcinoma Based on In Vitro Experiments, Data Mining, and RT-qPCR Analysis. Cellular Physiology and Biochemistry, 2018, 48, 540-555.	1.1	30
181	Transcriptome analysis of pig intestinal cell monolayers infected with Cryptosporidium parvum asexual stages. Parasites and Vectors, 2018, 11, 176.	1.0	49
182	Streamlined Tandem Mass Tag (SL-TMT) Protocol: An Efficient Strategy for Quantitative (Phospho)proteome Profiling Using Tandem Mass Tag-Synchronous Precursor Selection-MS3. Journal of Proteome Research, 2018, 17, 2226-2236.	1.8	245
183	Harnessing Omics Big Data in Nine Vertebrate Species by Genome-Wide Prioritization of Sequence Variants with the Highest Predicted Deleterious Effect on Protein Function. OMICS A Journal of Integrative Biology, 2018, 22, 410-421.	1.0	7

#	Article	IF	CITATIONS
184	MicroRNA expression in cervical cancer: Novel diagnostic and prognostic biomarkers. Journal of Cellular Biochemistry, 2018, 119, 7080-7090.	1.2	82
185	The effect of Ganoderma lucidum extract on immunological function and identify its anti-tumor immunostimulatory activity based on the biological network. Scientific Reports, 2018, 8, 12680.	1.6	20
186	The CCR4-NOT complex is a tumor suppressor in Drosophila melanogaster eye cancer models. Journal of Hematology and Oncology, 2018, 11, 108.	6.9	15
187	A Swath Label-Free Proteomics insight into the Faahâ^'/â^' Mouse Liver. Scientific Reports, 2018, 8, 12142.	1.6	2
188	Bioinformatic analysis of four miRNAs relevant to metastasis-regulated processes in endometrial carcinoma. Cancer Management and Research, 2018, Volume 10, 2337-2346.	0.9	13
189	A Parametric Targetability Evaluation Approach for Vitiligo Proteome Extracted through Integration of Gene Ontologies and Protein Interaction Topologies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1830-1842.	1.9	8
190	Moving from Empirical to Rational Vaccine Design in the †Omics†Era. Vaccines, 2019, 7, 89.	2.1	19
191	Rinf Regulates Pluripotency Network Genes and Tet Enzymes in Embryonic Stem Cells. Cell Reports, 2019, 28, 1993-2003.e5.	2.9	18
192	Characterizing the heat response of Arabidopsis thaliana from the perspective of codon usage bias and translational regulation. Journal of Plant Physiology, 2019, 240, 153012.	1.6	23
193	DiVenn: An Interactive and Integrated Web-Based Visualization Tool for Comparing Gene Lists. Frontiers in Genetics, 2019, 10, 421.	1.1	85
194	A systems pharmacology approach to investigate the mechanism of Oryeong-san formula for the treatment of hypertension. Journal of Ethnopharmacology, 2019, 244, 112129.	2.0	38
195	Integrative genomic and transcriptomic analysis of genetic markers in Dupuytren's disease. BMC Medical Genomics, 2019, 12, 98.	0.7	11
196	Identification and validation of a prognostic four-genes signature for hepatocellular carcinoma: integrated ceRNA network analysis. Hepatology International, 2019, 13, 618-630.	1.9	44
197	KIAA1429 acts as an oncogenic factor in breast cancer by regulating CDK1 in an N6-methyladenosine-independent manner. Oncogene, 2019, 38, 6123-6141.	2.6	149
198	Identification of genetic variations in Necator americanus through resequencing by whole genome amplification. Journal of International Medical Research, 2019, 47, 4353-4364.	0.4	0
199	LCTL Is a Prognostic Biomarker and Correlates With Stromal and Immune Infiltration in Gliomas. Frontiers in Oncology, 2019, 9, 1083.	1.3	16
200	Analysis of miRNAâ€nRNA regulatory network revealed key genes induced by aflatoxin B1 exposure in primary human hepatocytes. Molecular Genetics & Enomic Medicine, 2019, 7, e971.	0.6	13
201	BioDog, biomarker detection for improving identification power of breast cancer histologic grade in methylomics. Epigenomics, 2019, 11, 1717-1732.	1.0	9

#	Article	IF	CITATIONS
202	Mechanistic insights into autocrine and paracrine roles of endothelial GABA signaling in the embryonic forebrain. Scientific Reports, 2019, 9, 16256.	1.6	9
203	A Long Non-coding RNA Signature to Improve Prognostic Prediction of Pancreatic Ductal Adenocarcinoma. Frontiers in Oncology, 2019, 9, 1160.	1.3	29
204	Candidate genes mediated by estrogenâ€related receptor γ in pancreatic β cells. Journal of Biochemical and Molecular Toxicology, 2019, 33, e22390.	1.4	3
205	The RNA-binding ubiquitin ligase MKRN1 functions in ribosome-associated quality control of poly(A) translation. Genome Biology, 2019, 20, 216.	3.8	29
206	Non-catalytic Roles of Tet2 Are Essential to Regulate Hematopoietic Stem and Progenitor Cell Homeostasis. Cell Reports, 2019, 28, 2480-2490.e4.	2.9	66
207	Expression and clinical significance of CPS1 in glioblastoma multiforme. Current Research in Translational Medicine, 2019, 67, 123-128.	1.2	15
208	Druggable Transcriptional Networks in the Human Neurogenic Epigenome. Pharmacological Reviews, 2019, 71, 520-538.	7.1	11
209	Rectal cancer sub-clones respond differentially to neoadjuvant therapy. Neoplasia, 2019, 21, 1051-1062.	2.3	21
210	A fungal ABC transporter FgAtm1 regulates iron homeostasis via the transcription factor cascade FgAreA-HapX. PLoS Pathogens, 2019, 15, e1007791.	2.1	29
211	The impact of tomato fruits containing multi-walled carbon nanotube residues on human intestinal epithelial cell barrier function and intestinal microbiome composition. Nanoscale, 2019, 11, 3639-3655.	2.8	20
212	miR-22 Regulates Invasion, Gene Expression and Predicts Overall Survival in Patients with Clear Cell Renal Cell Carcinoma. Kidney Cancer, 2019, 3, 119-132.	0.2	9
213	Transcriptome analysis reveals that fertilization with cryopreserved sperm downregulates genes relevant for early embryo development in the horse. PLoS ONE, 2019, 14, e0213420.	1.1	22
214	MicroRNAs associated with lung squamous cell carcinoma: New prognostic biomarkers and therapeutic targets. Journal of Cellular Biochemistry, 2019, 120, 18956-18966.	1.2	33
215	Identification of key pathways and genes changes in pancreatic cancer cells (BXPC-3) after cross-talk with primary pancreatic stellate cells using bioinformatics analysis. Neoplasma, 2019, 66, 681-693.	0.7	7
216	Molecular mechanisms involved in drug-induced liver injury caused by urate-lowering Chinese herbs: A network pharmacology study and biology experiments. PLoS ONE, 2019, 14, e0216948.	1.1	20
217	Identifying the Antiproliferative Effect of Astragalus Polysaccharides on Breast Cancer: Coupling Network Pharmacology With Targetable Screening From the Cancer Genome Atlas. Frontiers in Oncology, 2019, 9, 368.	1.3	27
218	Array expression meta-analysis of cancer stem cell genes identifies upregulation of PODXL especially in DCC low expression meningiomas. PLoS ONE, 2019, 14, e0215452.	1.1	6
219	Transcriptomic analysis between Normal and high-intake feeding geese provides insight into adipose deposition and susceptibility to fatty liver in migratory birds. BMC Genomics, 2019, 20, 372.	1.2	15

#	Article	IF	CITATIONS
220	Development of a Cx46 Targeting Strategy for Cancer Stem Cells. Cell Reports, 2019, 27, 1062-1072.e5.	2.9	27
221	Implications of the mitochondrial interactome of mammalian thioredoxin 2 for normal cellular function and disease. Free Radical Biology and Medicine, 2019, 137, 59-73.	1.3	10
222	Identification of RE1-Silencing Transcription Factor as a Promoter of Metastasis in Pancreatic Cancer. Frontiers in Oncology, 2019, 9, 291.	1.3	6
223	The Transcriptomic Toolbox: Resources for Interpreting Large Gene Expression Data within a Precision Medicine Context for Metabolic Disease Atherosclerosis. Journal of Personalized Medicine, 2019, 9, 21.	1.1	6
224	Reconstruction and analysis of circRNA‑miRNA‑mRNA network in the pathology of cervical cancer. Oncology Reports, 2019, 41, 2209-2225.	1.2	58
225	De novo whole transcriptome profiling of Edwardsiella tarda isolated from infected fish (Labeo) Tj ETQq1 1 0.784	314 rgBT 1.0	/Oyerlock 1(
226	Exomic and transcriptomic alterations of hereditary gingival fibromatosis. Oral Diseases, 2019, 25, 1374-1383.	1.5	6
227	Genome-scale integrated analysis to identify prospective molecular mechanisms and therapeutic targets in isocitrate dehydrogenase 2 R140Q-mutated acute myeloid leukemia. Oncology Reports, 2019, 41, 2876-2888.	1.2	4
228	Six novel immunoglobulin genes as biomarkers for better prognosis in triple-negative breast cancer by gene co-expression network analysis. Scientific Reports, 2019, 9, 4484.	1.6	32
229	The Epstein-Barr virus EBNA1 protein modulates the alternative splicing of cellular genes. Virology Journal, 2019, 16, 29.	1.4	23
230	Genome-wide DNA methylation analysis of pituitaries during the initiation of puberty in gilts. PLoS ONE, 2019, 14, e0212630.	1.1	6
231	Widespread PERK-dependent repression of ER targets in response to ER stress. Scientific Reports, 2019, 9, 4330.	1.6	39
232	Defining the <scp>RNA</scp> interactome by total <scp>RNA</scp> â€associated protein purification. Molecular Systems Biology, 2019, 15, e8689.	3.2	114
233	Dynamic evolutionary history and gene content of sex chromosomes across diverse songbirds. Nature Ecology and Evolution, 2019, 3, 834-844.	3.4	68
234	Analysis of polymorphisms in genes associated with the FA/BRCA pathway in three patients with multiple primary malignant neoplasms. Artificial Cells, Nanomedicine and Biotechnology, 2019, 47, 1101-1112.	1.9	9
235	The bifunctional protein GlmU is a key factor in biofilm formation induced by alkylating stress in Mycobacterium smegmatis. Research in Microbiology, 2019, 170, 171-181.	1.0	18
236	ZEB1-AS1 initiates a miRNA-mediated ceRNA network to facilitate gastric cancer progression. Cancer Cell International, 2019, 19, 27.	1.8	25
237	Chromatin changes in Anopheles gambiae induced by Plasmodium falciparum infection. Epigenetics and Chromatin, 2019, 12, 5.	1.8	32

#	Article	IF	CITATIONS
238	Comparative acetylome analysis reveals the potential roles of lysine acetylation for DON biosynthesis in Fusarium graminearum. BMC Genomics, 2019, 20, 841.	1.2	13
239	Significant random signatures reveals new biomarker for breast cancer. BMC Medical Genomics, 2019, 12, 160.	0.7	2
240	Proteomics of Cytochrome c Oxidase-Negative versus -Positive Muscle Fiber Sections in Mitochondrial Myopathy. Cell Reports, 2019, 29, 3825-3834.e4.	2.9	17
241	7-IncRNA Assessment Model for Monitoring and Prognosis of Breast Cancer Patients: Based on Cox Regression and Co-expression Analysis. Frontiers in Oncology, 2019, 9, 1348.	1.3	34
242	Computational Inference of Gene Co-Expression Networks for the identification of Lung Carcinoma Biomarkers: An Ensemble Approach. Genes, 2019, 10, 962.	1.0	4
243	Parasympathetic Effect Induces Cell Cycle Activation in Upper Limbs of Paraplegic Patients with Spinal Cord Injury. International Journal of Molecular Sciences, 2019, 20, 5982.	1.8	4
244	Integrative Analysis of ceRNA Network Reveals Functional IncRNAs in Intrahepatic Cholangiocarcinoma. BioMed Research International, 2019, 2019, 1-9.	0.9	12
245	Exploring the changing landscape of cell-to-cell variation after CTCF knockdown via single cell RNA-seq. BMC Genomics, 2019, 20, 1015.	1.2	13
246	Monocytes and Monocyte-Derived Antigen-Presenting Cells Have Distinct Gene Signatures in Experimental Model of Multiple Sclerosis. Frontiers in Immunology, 2019, 10, 2779.	2.2	18
247	In Silico Methods for Studying T Cell Biology. International Review of Cell and Molecular Biology, 2019, 342, 265-304.	1.6	1
248	Bichirs employ similar genetic pathways for limb regeneration as are used in lungfish and salamanders. Gene, 2019, 690, 68-74.	1.0	9
249	Identification of genes associated with cancer progression and prognosis in lung adenocarcinoma: Analyses based on microarray from Oncomine and The Cancer Genome Atlas databases. Molecular Genetics & Enomic Medicine, 2019, 7, e00528.	0.6	42
250	Proteomics turns functional. Journal of Proteomics, 2019, 198, 36-44.	1.2	74
251	HOPS-dependent endosomal fusion required for efficient cytosolic delivery of therapeutic peptides and small proteins. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 512-521.	3.3	41
252	A novel form of JARID2 is required for differentiation in lineageâ€committed cells. EMBO Journal, 2019, 38, .	3.5	19
253	RNA sequencing data integration reveals an miRNA interactome of osteoarthritis cartilage. Annals of the Rheumatic Diseases, 2019, 78, 270-277.	0.5	130
254	An accurate regression of developmental stages for breast cancer based on transcriptomic biomarkers. Biomarkers in Medicine, 2019, 13, 5-15.	0.6	13
255	GLIS Rearrangement is a Genomic Hallmark of Hyalinizing Trabecular Tumor of the Thyroid Gland. Thyroid, 2019, 29, 161-173.	2.4	69

#	Article	IF	CITATIONS
256	Revisiting the role of dihydroorotate dehydrogenase as a therapeutic target for cancer., 2019, 195, 111-131.		128
257	The Mouse Microbiome Is Required for Sex-Specific Diurnal Rhythms of Gene Expression and Metabolism. Cell Metabolism, 2019, 29, 362-382.e8.	7.2	178
258	Symptom-based network classification identifies distinct clinical subgroups of liver diseases with common molecular pathways. Computer Methods and Programs in Biomedicine, 2019, 174, 41-50.	2.6	15
259	Transcriptomic analysis reveals that BMP4 sensitizes glioblastoma tumor-initiating cells to mechanical cues. Matrix Biology, 2020, 85-86, 112-127.	1.5	11
260	Transcriptomic and Proteomic Profiling of Human Mesenchymal Stem Cell Derived from Umbilical Cord in the Study of Preterm Birth. Proteomics - Clinical Applications, 2020, 14, e1900024.	0.8	6
261	Unsupervised Feature Extraction Applied to Bioinformatics. Unsupervised and Semi-supervised Learning, 2020, , .	0.4	48
262	Genomic regions influencing intramuscular fat in divergently selected rabbit lines. Animal Genetics, 2020, 51, 58-69.	0.6	21
263	Hypothalamic transcriptome of tame and aggressive silver foxes ( <scp><i>Vulpes vulpes</i></scp> ) identifies gene expression differences shared across brain regions. Genes, Brain and Behavior, 2020, 19, e12614.	1.1	24
264	Effect of Starch Isolation Method on Structural and Physicochemical Properties of Acorn Kernel Starch. Starch/Staerke, 2020, 72, 1900122.	1.1	19
265	A genomewide association study in divergently selected lines in rabbits reveals novel genomic regions associated with litter size traits. Journal of Animal Breeding and Genetics, 2020, 137, 123-138.	0.8	12
266	Metallothionein-2 is associated with the amelioration of asthmatic pulmonary function by acupuncture through protein phosphorylation. Biomedicine and Pharmacotherapy, 2020, 123, 109785.	2.5	5
267	Omic approaches to decipher the molecular mechanisms of fibrosis, and design new anti-fibrotic strategies. Seminars in Cell and Developmental Biology, 2020, 101, 161-169.	2.3	11
268	Proteome-wide observation of the phenomenon of life on the edge of solubility. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1015-1020.	3.3	115
269	Informative top-k class associative rule for cancer biomarker discovery on microarray data. Expert Systems With Applications, 2020, 146, 113169.	4.4	10
270	Cross-disorder analysis of endometriosis and its comorbid diseases reveals shared genes and molecular pathways and proposes putative biomarkers of endometriosis. Reproductive BioMedicine Online, 2020, 40, 305-318.	1.1	8
271	To Elucidate the Inhibition of Excessive Autophagy of <i>Rhodiola crenulata</i> on Exhaustive Exercise-Induced Skeletal Muscle Injury by Combined Network Pharmacology and Molecular Docking. Biological and Pharmaceutical Bulletin, 2020, 43, 296-305.	0.6	17
272	Comprehensive analysis of biological networks and the eukaryotic initiation factor 4Aâ€3 gene as pivotal in hepatocellular carcinoma. Journal of Cellular Biochemistry, 2020, 121, 4094-4107.	1.2	11
273	Prediction of Radiosensitivity in Head and Neck Squamous Cell Carcinoma Based on Multiple Omics Data. Frontiers in Genetics, 2020, 11, 960.	1.1	8

#	Article	IF	CITATIONS
274	Inhibition of aquaporin-1 prevents myocardial remodeling by blocking the transmembrane transport of hydrogen peroxide. Science Translational Medicine, 2020, 12, .	5.8	39
275	<p>Integrated Network Pharmacology Analysis and Pharmacological Evaluation to Explore the Active Components and Mechanism of <em>Abelmoschus manihot</em> (L.) Medik. on Renal Fibrosis</p> . Drug Design, Development and Therapy, 2020, Volume 14, 4053-4067.	2.0	10
276	PyGNA: a unified framework for geneset network analysis. BMC Bioinformatics, 2020, 21, 476.	1.2	0
277	Tet2 regulates Barx2 expression in undifferentiated and early differentiated mouse embryonic stem cells. Biochemical and Biophysical Research Communications, 2020, 533, 1212-1218.	1.0	1
278	Selection of suitable bioinformatic tools in micro-RNA research. Gene Reports, 2020, 21, 100893.	0.4	3
279	Identification of Differentially Expressed IncRNAs and mRNAs in Children with Acquired Aplastic Anemia by RNA Sequencing. BioMed Research International, 2020, 2020, 1-9.	0.9	1
280	Human forebrain endothelial cell therapy for psychiatric disorders. Molecular Psychiatry, 2020, 26, 4864-4883.	4.1	6
281	Proteomic Profiling of the Human Fetal Multipotent Mesenchymal Stromal Cells Secretome. Molecules, 2020, 25, 5283.	1.7	4
282	Identification of Characteristic Genomic Markers in Human Hepatoma HuH-7 and Huh7.5.1-8 Cell Lines. Frontiers in Genetics, 2020, 11, 546106.	1.1	24
283	Novel Genomic Regions Associated with Intramuscular Fatty Acid Composition in Rabbits. Animals, 2020, 10, 2090.	1.0	12
284	BioLitMine: Advanced Mining of Biomedical and Biological Literature About Human Genes and Genes from Major Model Organisms. G3: Genes, Genomes, Genetics, 2020, 10, 4531-4539.	0.8	9
285	Trade-off between cost and efficiency during mRNA translation is largely driven by natural selection in angiosperms. Plant Systematics and Evolution, 2020, 306, 1.	0.3	O
286	Thermostable small-molecule inhibitor of angiogenesis and vascular permeability that suppresses a pERK-FosBſi"FosB–VCAM-1 axis. Science Advances, 2020, 6, eaaz7815.	4.7	16
287	Construct a circRNA/miRNA/mRNA regulatory network to explore potential pathogenesis and therapy options of clear cell renal cell carcinoma. Scientific Reports, 2020, 10, 13659.	1.6	56
288	Development and validation of a four-microRNA signature for placenta accreta spectrum: an integrated competing endogenous RNA network analysis. Annals of Translational Medicine, 2020, 8, 919-919.	0.7	15
289	Integrating Pharmacology and Gut Microbiota Analysis to Explore the Mechanism of Citri Reticulatae Pericarpium Against Reserpine-Induced Spleen Deficiency in Rats. Frontiers in Pharmacology, 2020, 11, 586350.	1.6	28
290	Prediction of transcription factors binding events based on epigenetic modifications in different human cells. Epigenomics, 2020, 12, 1443-1456.	1.0	20
291	Discriminating miRNA Profiles between Endometrioid Well- and Poorly-Differentiated Tumours and Endometrioid and Serous Subtypes of Endometrial Cancers. International Journal of Molecular Sciences, 2020, 21, 6071.	1.8	10

#	Article	IF	CITATIONS
292	Systematic analysis reveals cis and trans determinants affecting C-to-U RNA editing in Arabidopsis thaliana. BMC Genetics, 2020, 21, 98.	2.7	15
293	Microbial regulation of a lincRNA–miRNA–mRNA network in the mouse hippocampus. Epigenomics, 2020, 12, 1377-1387.	1.0	13
294	GC usage of SARS-CoV-2 genes might adapt to the environment of human lung expressed genes. Molecular Genetics and Genomics, 2020, 295, 1537-1546.	1.0	37
295	Identification of common differentially expressed genes in Turner (45,X) and Klinefelter (47,XXY) syndromes using bioinformatics analysis. Molecular Genetics & Enomic Medicine, 2020, 8, e1503.	0.6	9
296	Comprehensive Proteomic Analysis of Lysine Ubiquitination in Seedling Leaves of <i>Nicotiana tabacum</i> . ACS Omega, 2020, 5, 20122-20133.	1.6	7
297	Target Analysis and Mechanism of Podophyllotoxin in the Treatment of Triple-Negative Breast Cancer. Frontiers in Pharmacology, 2020, 11, 1211.	1.6	17
298	TrypOx, a Novel Eukaryotic Homolog of the Redox-Regulated Chaperone Hsp33 in Trypanosoma brucei. Frontiers in Microbiology, 2020, 11, 1844.	1.5	5
299	Genome-wide RNA-sequencing dataset reveals the prognostic value and potential molecular mechanisms of lncRNA in non-homologous end joining pathway $1$ in early stage Pancreatic Ductal Adenocarcinoma. Journal of Cancer, 2020, $11$ , 5556-5567.	1.2	4
300	Potential mechanism of RRM2 for promoting Cervical Cancer based on weighted gene co-expression network analysis. International Journal of Medical Sciences, 2020, 17, 2362-2372.	1.1	13
301	MiR-302b as a Combinatorial Therapeutic Approach to Improve Cisplatin Chemotherapy Efficacy in Human Triple-Negative Breast Cancer. Cancers, 2020, 12, 2261.	1.7	12
302	Systematic Pharmacology and GEO Database Mining Revealed the Therapeutic Mechanism of Xuefu Zhuyu Decoration for Atherosclerosis Cardiovascular Disease. Frontiers in Cardiovascular Medicine, 2020, 7, 592201.	1.1	8
303	RNA-seq profile of African American men with a clinically localized prostate cancer. Prostate International, 2021, 9, 125-131.	1.2	8
304	Characterization of Lysine Monomethylome and Methyltransferase in Model Cyanobacterium Synechocystis sp. PCC 6803. Genomics, Proteomics and Bioinformatics, 2020, 18, 289-304.	3.0	6
305	Facultative protein selenation regulates redox sensitivity, adipose tissue thermogenesis, and obesity. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10789-10796.	3.3	30
306	Chinese Medicine for Psoriasis Vulgaris Based on Syndrome Pattern: A Network Pharmacological Study. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-16.	0.5	4
307	The extracellular matrix protein TasA is a developmental cue that maintains a motile subpopulation within $\langle i \rangle$ Bacillus subtilis $\langle i \rangle$ biofilms. Science Signaling, 2020, 13, .	1.6	39
308	Analysis of genes associated with prognosis of lung adenocarcinoma based on GEO and TCGA databases. Medicine (United States), 2020, 99, e20183.	0.4	26
309	Amplification of transglutaminase 2 enhances tumor-promoting inflammation in gastric cancers. Experimental and Molecular Medicine, 2020, 52, 854-864.	3.2	22

#	Article	IF	CITATIONS
310	Mutation severity spectrum of rare alleles in the human genome is predictive of disease type. PLoS Computational Biology, 2020, 16, e1007775.	1.5	11
311	Identification of Hub Genes in Type 2 Diabetes Mellitus Using Bioinformatics Analysis. Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy, 2020, Volume 13, 1793-1801.	1.1	14
312	Changes in the host transcriptome and microbial metatranscriptome of the ileum of dairy calves subjected to artificial dosing of exogenous rumen contents. Physiological Genomics, 2020, 52, 333-346.	1.0	1
313	G9a regulates tumorigenicity and stemness through genome-wide DNA methylation reprogramming in non-small cell lung cancer. Clinical Epigenetics, 2020, 12, 88.	1.8	28
314	Identification of the core ontologies and signature genes of polycystic ovary syndrome (PCOS): A bioinformatics analysis. Informatics in Medicine Unlocked, 2020, 18, 100304.	1.9	13
315	Identification of small RNAs during cold acclimation in Arabidopsis thaliana. BMC Plant Biology, 2020, 20, 298.	1.6	26
316	PODXL might be a new prognostic biomarker in various cancers: a meta-analysis and sequential verification with TCGA datasets. BMC Cancer, 2020, 20, 620.	1.1	12
317	Phosphoproteomic Analysis of Neonatal Regenerative Myocardium Revealed Important Roles of Checkpoint Kinase 1 via Activating Mammalian Target of Rapamycin C1/Ribosomal Protein S6 Kinase b-1 Pathway. Circulation, 2020, 141, 1554-1569.	1.6	39
318	Role of miRNAâ€542â€5p in the tumorigenesis of osteosarcoma. FEBS Open Bio, 2020, 10, 627-636.	1.0	12
319	Identify potential clinical significance of long noncoding RNA forkhead box P4 antisense RNA 1 in patients with early stage pancreatic ductal adenocarcinoma. Cancer Medicine, 2020, 9, 2062-2076.	1.3	12
320	Tris(4-hydroxyphenyl)ethane (THPE), a trisphenol compound, is antiestrogenic and can retard uterine development in CD-1 mice. Environmental Pollution, 2020, 260, 113962.	3.7	8
321	Integrating Network Pharmacology and Experimental Models to Investigate the Efficacy of Coptidis and Scutellaria Containing Huanglian Jiedu Decoction on Hepatocellular Carcinoma. The American Journal of Chinese Medicine, 2020, 48, 161-182.	1.5	43
322	A Network Pharmacology-Based Study of the Molecular Mechanisms of Shaoyao-Gancao Decoction in Treating Parkinson's Disease. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 131-144.	2,2	19
323	Effects of A2E-Induced Oxidative Stress on Retinal Epithelial Cells: New Insights on Differential Gene Response and Retinal Dystrophies. Antioxidants, 2020, 9, 307.	2.2	46
324	Specific histone modifications associate with alternative exon selection during mammalian development. Nucleic Acids Research, 2020, 48, 4709-4724.	6.5	19
325	O2-Tuned Protein Synthesis Machinery in Escherichia coli-Based Cell-Free System. Frontiers in Bioengineering and Biotechnology, 2020, 8, 312.	2.0	11
326	The Sodium Channel B4-Subunits are Dysregulated in Temporal Lobe Epilepsy Drug-Resistant Patients. International Journal of Molecular Sciences, 2020, 21, 2955.	1.8	11
327	Transcriptome Profile of Yeast Strain Used for Biological Wine Aging Revealed Dynamic Changes of Gene Expression in Course of Flor Development. Frontiers in Microbiology, 2020, 11, 538.	1.5	11

#	Article	IF	CITATIONS
328	Development of a risk scoring system for evaluating the prognosis of patients with Her2-positive breast cancer. Cancer Cell International, 2020, 20, 121.	1.8	14
329	Gene interaction network approach to elucidate the multidrug resistance mechanisms in the pathogenic bacterial strain <i>Proteus mirabilis</i> I>. Journal of Cellular Physiology, 2021, 236, 468-479.	2.0	24
330	Molecular signatures identified by integrating gene expression and methylation in non-seminoma and seminoma of testicular germ cell tumours. Epigenetics, 2021, 16, 162-176.	1.3	12
331	Inhibition of cathepsin S attenuates myocardial ischemia/reperfusion injury by suppressing inflammation and apoptosis. Journal of Cellular Physiology, 2021, 236, 1309-1320.	2.0	21
332	Statistical methods with exhaustive search in the identification of gene–gene interactions for colorectal cancer. Genetic Epidemiology, 2021, 45, 222-234.	0.6	5
333	Whole genome analyses reveal significant convergence in obsessive-compulsive disorder between humans and dogs. Science Bulletin, 2021, 66, 187-196.	4.3	8
334	Integrated analysis of phosphoproteome and ubiquitylome in epididymal sperm of buffalo ( <i>Bubalus) Tj ETQq0</i>	00rgBT/	Overlock 10
335	IDDB: a comprehensive resource featuring genes, variants and characteristics associated with infertility. Nucleic Acids Research, 2021, 49, D1218-D1224.	6.5	25
337	Identification of fibronectin 1 (FN1) and complement component 3 (C3) as immune infiltration-related biomarkers for diabetic nephropathy using integrated bioinformatic analysis. Bioengineered, 2021, 12, 5386-5401.	1.4	21
338	The novel potential multidrug-resistance biomarkers for Pseudomonas aeruginosa lung infections using transcriptomics data analysis. Informatics in Medicine Unlocked, 2021, 22, 100509.	1.9	3
339	An Integrative Transcriptomic Analysis of Systemic Juvenile Idiopathic Arthritis for Identifying Potential Genetic Markers and Drug Candidates. International Journal of Molecular Sciences, 2021, 22, 712.	1.8	6
341	Bioinformatics analysis identifies COL1A1, THBS2 and SPP1 as potential predictors of patient prognosis and immunotherapy response in gastric cancer. Bioscience Reports, 2021, 41, .	1.1	16
342	OUP accepted manuscript. Cerebral Cortex, 2021, 31, 4554-4575.	1.6	9
343	Comprehensive investigation of the clinical significance of long non-coding RNA HOXA-AS2 in acute myeloid leukemia using genome-wide RNA sequencing dataset. Journal of Cancer, 2021, 12, 2151-2164.	1.2	4
344	Cryptotanshinone Is a Intervention for ER-Positive Breast Cancer: An Integrated Approach to the Study of Natural Product Intervention Mechanisms. Frontiers in Pharmacology, 2020, 11, 592109.	1.6	3
345	Identification of a novel snoRNA expression signature associated with overall survival in patients with lung adenocarcinoma: A comprehensive analysis based on RNA sequencing dataset. Mathematical Biosciences and Engineering, 2021, 18, 7837-7860.	1.0	5
346	The regulatory genome of the malaria vector <i>Anopheles gambiae</i> : integrating chromatin accessibility and gene expression. NAR Genomics and Bioinformatics, 2021, 3, Iqaa113.	1.5	12
347	LPA signaling acts as a cell-extrinsic mechanism to initiate cilia disassembly and promote neurogenesis. Nature Communications, 2021, 12, 662.	5.8	25

#	Article	IF	CITATIONS
348	Germline copy number variations in BRCA1/2 negative families: Role in the molecular etiology of hereditary breast cancer in Tunisia. PLoS ONE, 2021, 16, e0245362.	1.1	9
349	Transcriptome Characterization of Short Distance Transport Stress in Beef Cattle Blood. Frontiers in Genetics, 2021, 12, 616388.	1.1	16
350	Toxicant exposure during pregnancy increases protective proteins in the dam and a sexually dimorphic response in the fetus. Toxicology and Applied Pharmacology, 2021, 413, 115407.	1.3	0
351	Decoding the role of long noncoding RNAs in the healthy aging of centenarians. Briefings in Bioinformatics, 2021, 22, .	3.2	12
352	Genetic diversity and population structure of Tibetan sheep breeds determined by whole genome resequencing. Tropical Animal Health and Production, 2021, 53, 174.	0.5	3
355	Alterations of RNA splicing patterns in esophagus squamous cell carcinoma. Cell and Bioscience, 2021, 11, 36.	2.1	12
356	circRNA-miRNA-mRNA network in age-related macular degeneration: From construction to identification. Experimental Eye Research, 2021, 203, 108427.	1.2	17
358	Proteome-Wide Analysis of Lysine 2-Hydroxyisobutyrylated Proteins in Fusarium oxysporum. Frontiers in Microbiology, 2021, 12, 623735.	1.5	5
362	Computational prediction of CRISPR-impaired non-coding regulatory regions. Biological Chemistry, 2021, 402, 973-982.	1.2	1
364	Five candidate biomarkers associated with the diagnosis and prognosis of cervical cancer. Bioscience Reports, 2021, 41, .	1.1	9
365	Identification of Pivotal MicroRNAs and Target Genes Associated with Persistent Atrial Fibrillation Based on Bioinformatics Analysis. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-13.	0.7	5
366	LINC01816 promotes the migration, invasion and epithelial‑mesenchymal transition of thyroid carcinoma cells by sponging miR‑34c‑5p and regulating CRABP2 expression levels. Oncology Reports, 2021, 45, .	1.2	10
367	NFIB promotes the migration and progression of kidney renal clear cell carcinoma by regulating PINK1 transcription. PeerJ, 2021, 9, e10848.	0.9	5
368	Sigma-1 Receptor (S1R) Interaction with Cholesterol: Mechanisms of S1R Activation and Its Role in Neurodegenerative Diseases. International Journal of Molecular Sciences, 2021, 22, 4082.	1.8	24
369	Identification and Functional Analysis of Long Non-coding RNAs in Human Pulmonary Microvascular Endothelial Cells Subjected to Cyclic Stretch. Frontiers in Physiology, 2021, 12, 655971.	1.3	4
370	Transcriptome analysis of liver elucidates key immune-related pathways in Nile tilapia Oreochromis niloticus following infection with tilapia lake virus. Fish and Shellfish Immunology, 2021, 111, 208-219.	1.6	20
371	Haploinsufficiency of PRR12 causes a spectrum of neurodevelopmental, eye, and multisystem abnormalities. Genetics in Medicine, 2021, 23, 1234-1245.	1.1	6
372	Identification and characterization of heat-responsive microRNAs at the booting stage in two rice varieties, 9311 and Nagina 22. Genome, 2021, 64, 969-984.	0.9	3

#	Article	IF	CITATIONS
373	Identification of a novel autophagy signature for predicting survival in patients with lung adenocarcinoma. Peerl, 2021, 9, e11074.	0.9	5
374	Integrative Systems Biology Approaches to Identify Potential Biomarkers and Pathways of Cervical Cancer. Journal of Personalized Medicine, 2021, 11, 363.	1.1	9
375	EnRank: An Ensemble Method to Detect Pulmonary Hypertension Biomarkers Based on Feature Selection and Machine Learning Models. Frontiers in Genetics, 2021, 12, 636429.	1.1	6
378	NSrp70 is a lymphocyte-essential splicing factor that controls thymocyte development. Nucleic Acids Research, 2021, 49, 5760-5778.	6.5	5
379	Identifying Genes Devoted to the Cell Death Process in the Gene Regulatory Network of Ustilago maydis. Frontiers in Microbiology, 2021, 12, 680290.	1.5	6
380	A review of the biological activity and pharmacology of cryptotanshinone, an important active constituent in Danshen. Biomedicine and Pharmacotherapy, 2021, 137, 111332.	2.5	47
381	Machine Learning Assisted Prediction of Prognostic Biomarkers Associated With COVID-19, Using Clinical and Proteomics Data. Frontiers in Genetics, 2021, 12, 636441.	1.1	17
383	DNA Methylation, Deamination, and Translesion Synthesis Combine to Generate Footprint Mutations in Cancer Driver Genes in B-Cell Derived Lymphomas and Other Cancers. Frontiers in Genetics, 2021, 12, 671866.	1.1	4
384	Identification of Hypertension Subgroups through Topological Analysis of Symptom-Based Patient Similarity. Chinese Journal of Integrative Medicine, 2021, 27, 656-665.	0.7	5
385	An 8-gene DNA methylation signature predicts the recurrence risk of cervical cancer. Journal of International Medical Research, 2021, 49, 030006052110184.	0.4	6
386	A phase-separated nuclear GBPL circuit controls immunity in plants. Nature, 2021, 594, 424-429.	13.7	79
387	Loss of inner-envelope K+/H+ exchangers impairs plastid rRNA maturation and gene expression. Plant Cell, 2021, 33, 2479-2505.	3.1	19
388	PD-1 Coexpression Gene Analysis and the Regulatory Network in Endometrial Cancer Based on Bioinformatics Analysis. BioMed Research International, 2021, 2021, 1-7.	0.9	1
389	Potential role of chimeric genes in pathway-related gene co-expression modules. World Journal of Surgical Oncology, 2021, 19, 149.	0.8	7
390	Upregulated CD58 is associated with clinicopathological characteristics and poor prognosis of patients with pancreatic ductal adenocarcinoma. Cancer Cell International, 2021, 21, 327.	1.8	6
391	Transcriptomics Analysis Uncovers Transient Ceftazidime Tolerance in <i>Burkholderia</i> Biofilms. ACS Infectious Diseases, 2021, 7, 2324-2336.	1.8	2
392	Comprehensive analysis of lncRNA biomarkers in kidney renal clear cell carcinoma by lncRNA-mediated ceRNA network. PLoS ONE, 2021, 16, e0252452.	1,1	4
393	Genomic Landscapes of Noncoding RNAs Regulating <i>VEGFA</i> and <i>VEGFC</i> Expression in Endothelial Cells. Molecular and Cellular Biology, 2021, 41, e0059420.	1.1	12

#	Article	IF	CITATIONS
394	Sex-Specific Age-Related Changes in Methylation of Certain Genes. Sovremennye Tehnologii V Medicine, 2021, 13, 26.	0.4	2
395	Identification of TAZ-Dependent Breast Cancer Vulnerabilities Using a Chemical Genomics Screening Approach. Frontiers in Cell and Developmental Biology, 2021, 9, 673374.	1.8	5
396	Integrative Analysis of Next-Generation Sequencing for Next-Generation Cancer Research toward Artificial Intelligence. Cancers, 2021, 13, 3148.	1.7	15
397	A 13-Gene Metabolic Prognostic Signature Is Associated With Clinical and Immune Features in Stomach Adenocarcinoma. Frontiers in Oncology, 2021, 11, 612952.	1.3	17
398	Genome Wide Prediction, Mapping and Development of Genomic Resources of Mastitis Associated Genes in Water Buffalo. Frontiers in Veterinary Science, 2021, 8, 593871.	0.9	8
399	Binding patterns of RNA-binding proteins to repeat-derived RNA sequences reveal putative functional RNA elements. NAR Genomics and Bioinformatics, 2021, 3, lqab055.	1.5	5
400	Integrative Analysis of Genome, 3D Genome, and Transcriptome Alterations of Clinical Lung Cancer Samples. Genomics, Proteomics and Bioinformatics, 2021, 19, 741-753.	3.0	3
401	Bioinformatics Accelerates the Major Tetrad: A Real Boost for the Pharmaceutical Industry. International Journal of Molecular Sciences, 2021, 22, 6184.	1.8	16
402	A SARS-CoV-2 â€"human metalloproteome interaction map. Journal of Inorganic Biochemistry, 2021, 219, 111423.	1.5	23
403	ldentification of Small RNAs During High Light Acclimation in Arabidopsis thaliana. Frontiers in Plant Science, 2021, 12, 656657.	1.7	12
404	Genome-wide association for plasma urea concentration in sheep. Livestock Science, 2021, 248, 104483.	0.6	4
406	Identification of potential diagnostic and prognostic biomarkers for LUAD based on TCGA and GEO databases. Bioscience Reports, 2021, 41, .	1.1	26
407	Circular RNA expression profile in transgenic diabetic mouse kidneys. Cellular and Molecular Biology Letters, 2021, 26, 25.	2.7	5
408	Establishment of a fluorescent reporter of RNA-polymerase II activity to identify dormant cells. Nature Communications, 2021, 12, 3318.	5.8	2
409	<i>Stat3</i> loss in mesenchymal progenitors causes Job syndrome–like skeletal defects by reducing Wnt $\hat{I}^2$ -catenin signaling. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	16
410	Variation in Gene Expression between Two Sorghum bicolor Lines Differing in Innate Immunity Response. Plants, 2021, 10, 1536.	1.6	3
411	Identification and Validation of Potential Biomarkers and Pathways for Idiopathic Pulmonary Fibrosis by Comprehensive Bioinformatics Analysis. BioMed Research International, 2021, 2021, 1-15.	0.9	6
412	Regulation of Inc-TLCD2-1 on Radiation Sensitivity of Colorectal Cancer and Comprehensive Analysis of Its Mechanism. Frontiers in Oncology, 2021, 11, 714159.	1.3	7

#	Article	IF	CITATIONS
413	Development of a fixed module repertoire for the analysis and interpretation of blood transcriptome data. Nature Communications, 2021, 12, 4385.	5.8	29
415	Unraveling the molecular crosstalk between Atherosclerosis and COVID-19 comorbidity. Computers in Biology and Medicine, 2021, 134, 104459.	3.9	18
417	Reelin Alleviates Mesenchymal Stem Cell Senescence and Reduces Pathological α-Synuclein Expression in an In Vitro Model of Parkinson's Disease. Genes, 2021, 12, 1066.	1.0	2
418	Characterization of a functional endothelial super-enhancer that regulates ADAMTS18 and angiogenesis. Nucleic Acids Research, 2021, 49, 8078-8096.	6.5	13
419	Identification of a 15 DNA Damage Repair–Related Gene Signature as a Prognostic Predictor for Lung Adenocarcinoma. Combinatorial Chemistry and High Throughput Screening, 2021, 24, .	0.6	2
420	Network Pharmacology-Based Investigation on the Anti-Osteoporosis Mechanism of Astragaloside IV. Natural Product Communications, 2021, 16, 1934578X2110295.	0.2	2
421	Autophagy-Related Three-Gene Prognostic Signature for Predicting Survival in Esophageal Squamous Cell Carcinoma. Frontiers in Oncology, 2021, $11,650891$ .	1.3	9
422	Eukaryotic initiation factor EIF-3.G augments mRNA translation efficiency to regulate neuronal activity. ELife, 2021, 10, .	2.8	8
423	Zebrafish intestinal transcriptome highlights subdued inflammatory responses to dietary soya bean and efficacy of yeast βâ€glucan. Journal of Fish Diseases, 2021, 44, 1619-1637.	0.9	7
424	HOXA9 promotes MYC-mediated leukemogenesis by maintaining gene expression for multiple anti-apoptotic pathways. ELife, 2021, 10, .	2.8	13
425	Genetic alterations and functional networks of m6A RNA methylation regulators in pancreatic cancer based on data mining. Journal of Translational Medicine, 2021, 19, 323.	1.8	3
426	<i>In silico</i> predictions of protein interactions between Zika virus and human host. PeerJ, 2021, 9, e11770.	0.9	3
427	Quantitative Tyrosine Phosphoproteome Profiling of AXL Receptor Tyrosine Kinase Signaling Network. Cancers, 2021, 13, 4234.	1.7	1
428	ldentPMP: identification of moonlighting proteins in plants using sequence-based learning models. PeerJ, 2021, 9, e11900.	0.9	3
429	Regulation of the HTRA2 Protease Activity by an Inhibitory Antibody-Derived Peptide Ligand and the Influence on HTRA2-Specific Protein Interaction Networks in Retinal Tissues. Biomedicines, 2021, 9, 1013.	1.4	7
430	Proteomic and phosphoproteomic profiles of Sertoli cells in buffalo. Theriogenology, 2021, 170, 1-14.	0.9	3
431	Comprehensive investigation of RNAâ€sequencing dataset reveals the hub genes and molecular mechanisms of coronavirus disease 2019 acute respiratory distress syndrome. IET Systems Biology, 2021, 15, 205-218.	0.8	4
432	Piwi–piRNA complexes induce stepwise changes in nuclear architecture at target loci. EMBO Journal, 2021, 40, e108345.	3.5	8

#	Article	IF	CITATIONS
433	Comparative Genomic Analysis of the DUF34 Protein Family Suggests Role as a Metal Ion Chaperone or Insertase. Biomolecules, 2021, 11, 1282.	1.8	5
436	Bacterial lysis, autophagy and innate immune responses during adjunctive phage therapy in a child. EMBO Molecular Medicine, 2021, 13, e13936.	3.3	38
437	METTL3 involves the progression of osteoarthritis probably by affecting ECM degradation and regulating the inflammatory response. Life Sciences, 2021, 278, 119528.	2.0	43
438	Genomic introgression from a distant congener in the Levant fritillary butterfly, <i>Melitaea acentria</i> . Molecular Ecology, 2021, 30, 4819-4832.	2.0	7
439	Identifying novel transcript biomarkers for hepatocellular carcinoma (HCC) using RNA-Seq datasets and machine learning. BMC Cancer, 2021, 21, 962.	1.1	10
440	Progesterone receptor antagonists reverse stem cell expansion and the paracrine effectors of progesterone action in the mouse mammary gland. Breast Cancer Research, 2021, 23, 78.	2.2	7
441	Network Pharmacology and Experimental Evidence: PI3K/AKT Signaling Pathway is Involved in the Antidepressive Roles of Chaihu Shugan San. Drug Design, Development and Therapy, 2021, Volume 15, 3425-3441.	2.0	25
444	Systems biology analysis of lung fibrosis-related genes in the bleomycin mouse model. Scientific Reports, 2021, 11, 19269.	1.6	7
445	Computational workflow for functional characterization of COVID-19 through secondary data analysis. STAR Protocols, 2021, 2, 100873.	0.5	2
446	Identification and Functional Characterization of Two Noncoding RNAs Transcribed from Putative Active Enhancers in Hepatocellular Carcinoma. Molecules and Cells, 2021, 44, 658-669.	1.0	4
447	Screening of Mycobacterium tuberculosis genes as putative drug targets for treatment of HIV-TB and lung cancer-TB comorbidities: An in silico analysis. Gene Reports, 2021, 24, 101215.	0.4	0
448	Hypothalamus–pituitary axis transcriptomic modification dependent on growth rate in geese ( Anser) Tj ETQq1	10.7843	14 rgBT /Ov
449	Quantitative Proteomic Analysis for High- and Low-Aflatoxin-Yield Aspergillus flavus Strains Isolated From Natural Environments. Frontiers in Microbiology, 2021, 12, 741875.	1.5	4
450	Identification and validation of circulating miRNAs as potential new biomarkers for severe liver disease in patients with leptospirosis. PLoS ONE, 2021, 16, e0257805.	1.1	2
452	Rare variants in the endocytic pathway are associated with Alzheimer's disease, its related phenotypes, and functional consequences. PLoS Genetics, 2021, 17, e1009772.	1.5	1
453	GeneTrail: A Framework for the Analysis of High-Throughput Profiles. Frontiers in Molecular Biosciences, 2021, 8, 716544.	1.6	1
454	Polydatin Ameliorates Osteoporosis via Suppression of the Mitogen-Activated Protein Kinase Signaling Pathway. Frontiers in Cell and Developmental Biology, 2021, 9, 730362.	1.8	4
455	Upregulation of Low-Density Lipoprotein Receptor of the Steroidogenesis Pathway in the Cumulus Cells Is Associated with the Maturation of Oocytes and Achievement of Pregnancy. Cells, 2021, 10, 2389.	1.8	6

#	Article	IF	Citations
456	HandyCNV: Standardized Summary, Annotation, Comparison, and Visualization of Copy Number Variant, Copy Number Variation Region, and Runs of Homozygosity. Frontiers in Genetics, 2021, 12, 731355.	1.1	9
457	Tissue environment, not ontogeny, defines murine intestinal intraepithelial T lymphocytes. ELife, 2021, 10, .	2.8	14
458	Small RNA-Seq Analysis Reveals miRNA Expression of Short Distance Transportation Stress in Beef Cattle Blood. Animals, 2021, 11, 2850.	1.0	1
459	Identification of novel candidate genes for age at first calving in Nellore cows using a SNP chip specifically developed for Bos taurus indicus cattle. Theriogenology, 2021, 173, 156-162.	0.9	7
460	Prediction of microRNAs in Pseudomonas syringae pv. tomato DC3000 and their potential target prediction in Solanum lycopersicum. Gene Reports, 2021, 25, 101360.	0.4	3
461	Whole blood gene expression signature in patients with obstructive sleep apnea and effect of continuous positive airway pressure treatment. Respiratory Physiology and Neurobiology, 2021, 294, 103746.	0.7	3
462	Systematic analysis of the molecular mechanisms mediated by coffee in Parkinson's disease based on network pharmacology approach. Journal of Functional Foods, 2021, 87, 104764.	1.6	7
463	Subtype-WESLR: identifying cancer subtype with weighted ensemble sparse latent representation of multi-view data. Briefings in Bioinformatics, 2022, 23, .	3.2	15
464	Protein Phosphorylation in Depolarized Synaptosomes: Dissecting Primary Effects of Calcium from Synaptic Vesicle Cycling. Molecular and Cellular Proteomics, 2021, 20, 100061.	2.5	11
465	The Lymph Proteome, Peptidome, and Degradome. , 2013, , 65-79.		1
466	Functional Analysis of Legume Genome Arrays. Methods in Molecular Biology, 2013, 1069, 59-66.	0.4	1
467	The Extracellular Matrix Goes -Omics: Resources and Tools. Biology of Extracellular Matrix, 2020, , 1-16.	0.3	6
468	Transcriptator: Computational Pipeline to Annotate Transcripts and Assembled Reads from RNA-Seq Data. Lecture Notes in Computer Science, 2015, , 156-169.	1.0	2
469	Ubiquitome analysis reveals the involvement of lysine ubiquitination in the spermatogenesis process of adult buffalo ( <i>Bubalus bubalis</i> ) testis. Bioscience Reports, 2020, 40, .	1.1	6
470	Bursal transcriptome profiling of different inbred chicken lines reveals key differentially expressed genes at 3 days post-infection with very virulent infectious bursal disease virus. Journal of General Virology, 2018, 99, 21-35.	1.3	10
478	Heritable Gut Microbiome Associated with <i>Salmonella enterica</i> Serovar Pullorum Infection in Chickens. MSystems, 2021, 6, .	1.7	15
479	NK cell defects in X-linked pigmentary reticulate disorder. JCI Insight, 2019, 4, .	2.3	17
481	Probing instructions for expression regulation in gene nucleotide compositions. PLoS Computational Biology, 2018, 14, e1005921.	1.5	11

#	Article	IF	CITATIONS
482	Global Identification of EVI1 Target Genes in Acute Myeloid Leukemia. PLoS ONE, 2013, 8, e67134.	1.1	60
483	SiBIC: A Web Server for Generating Gene Set Networks Based on Biclusters Obtained by Maximal Frequent Itemset Mining. PLoS ONE, 2013, 8, e82890.	1.1	1
484	Multiple Sporadic Colorectal Cancers Display a Unique Methylation Phenotype. PLoS ONE, 2014, 9, e91033.	1.1	9
485	Energy Metabolism in Mycobacterium gilvum PYR-GCK: Insights from Transcript Expression Analyses Following Two States of Induction. PLoS ONE, 2014, 9, e99464.	1.1	4
486	Genomic Responses during Acute Human Anaphylaxis Are Characterized by Upregulation of Innate Inflammatory Gene Networks. PLoS ONE, 2014, 9, e101409.	1.1	22
487	Gene Expression Profiling of Peri-Implant Healing of PLGA-Li+ Implants Suggests an Activated Wnt Signaling Pathway In Vivo. PLoS ONE, 2014, 9, e102597.	1.1	14
488	Integrated Analysis of Transcriptome in Cancer Patient-Derived Xenografts. PLoS ONE, 2015, 10, e0124780.	1.1	9
489	A Methodology for the Development of RESTful Semantic Web Services for Gene Expression Analysis. PLoS ONE, 2015, 10, e0134011.	1.1	7
490	Elucidation of Relevant Neuroinflammation Mechanisms Using Gene Expression Profiling in Patients with Amyotrophic Lateral Sclerosis. PLoS ONE, 2016, 11, e0165290.	1.1	25
491	Atomistic simulations and network-based modeling of the Hsp90-Cdc37 chaperone binding with Cdk4 client protein: A mechanism of chaperoning kinase clients by exploiting weak spots of intrinsically dynamic kinase domains. PLoS ONE, 2017, 12, e0190267.	1.1	32
492	Efficient progressive minimum k-core search. Proceedings of the VLDB Endowment, 2019, 13, 362-375.	2.1	20
493	Micro <scp>RNA</scp> â€483 amelioration of experimental pulmonary hypertension. EMBO Molecular Medicine, 2020, 12, e11303.	3.3	35
494	Quantitative Proteomics Analysis Revealed Compromised Chicken Dendritic Cells Function at Early Stage of Very Virulent Infectious Bursal Disease Virus Infection. Avian Diseases, 2019, 63, 275.	0.4	4
495	ERG induces a mesenchymal-like state associated with chemoresistance in leukemia cells. Oncotarget, 2014, 5, 351-362.	0.8	30
496	A class of genes in the HER2 regulon that is poised for transcription in breast cancer cell lines and expressed in human breast tumors. Oncotarget, 2015, 6, 1286-1301.	0.8	8
497	Extracting tumor tissue immune status from expression profiles: correlating renal cancer prognosis with tumor-associated immunome. Oncotarget, 2015, 6, 33191-33205.	0.8	3
498	Development of a Cx46 Targeting Strategy for Cancer Stem Cells. SSRN Electronic Journal, 0, , .	0.4	1
499	Function Analysis of Human Protein Interactions Based on a Novel Minimal Loop Algorithm. Current Bioinformatics, 2019, 14, 164-173.	0.7	5

#	Article	IF	Citations
500	Chronic Obstructive Pulmonary Disease Molecular Subtyping and Pathway Deviation-Based Candidate Gene Identification. Cell Journal, 2018, 20, 326-332.	0.2	7
501	Transglutaminase 2 mediates hypoxia-induced selective mRNA translation via polyamination of 4EBPs. Life Science Alliance, 2020, 3, e201900565.	1.3	6
502	Transcriptome of Teak (Tectona grandis, L.f) in Vegetative to Generative Stages Development. Journal of Plant Sciences, 2014, 10, 1-14.	0.2	11
503	Gene expression profiling reveals key genes and pathways related to the development of non-alcoholic fatty liver disease. Annals of Hepatology, 2016, 15, 190-9.	0.6	28
504	Genome wide association study of fatty acid composition in Duroc swine. Asian-Australasian Journal of Animal Sciences, 2018, 31, 1127-1133.	2.4	13
505	Tunable protein synthesis by transcript isoforms in human cells. ELife, 2016, 5, .	2.8	238
506	KLHL41 stabilizes skeletal muscle sarcomeres by nonproteolytic ubiquitination. ELife, 2017, 6, .	2.8	40
507	Pathway-GPS and SIGORA: identifying relevant pathways based on the over-representation of their gene-pair signatures. Peerl, 2013, 1, e229.	0.9	64
508	Identification of NUF2 and FAM83D as potential biomarkers in triple-negative breast cancer. PeerJ, 2020, 8, e9975.	0.9	13
509	iProbiotics: a machine learning platform for rapid identification of probiotic properties from whole-genome primary sequences. Briefings in Bioinformatics, 2022, 23, .	3.2	23
510	A New Murine Liver Fibrosis Model Induced by Polyhexamethylene Guanidine-Phosphate. Biomolecules and Therapeutics, 2022, 30, 126-136.	1.1	6
511	Dysregulated expression of microRNAs in aqueous humor from intraocular tuberculosis patients. Molecular Biology Reports, 2022, 49, 97-107.	1.0	4
512	Investigation of anti-osteoporosis mechanisms of Rehmanniae Radix Preparata based on network pharmacology and experimental verification. Journal of Orthopaedic Surgery and Research, 2021, 16, 599.	0.9	11
513	Effect of SARS-CoV-2 infection on host competing endogenous RNA and miRNA network. Peerl, 2021, 9, e12370.	0.9	4
514	Novel chemotherapeutic agent FX-9 activates NF- $\hat{P}$ B signaling and induces G1 phase arrest by activating CDKN1A in a human prostate cancer cell line. BMC Cancer, 2021, 21, 1088.	1.1	0
515	Reduced cue-induced reinstatement of cocaine-seeking behavior in Plcb1 +/â^' mice. Translational Psychiatry, 2021, 11, 521.	2.4	4
516	Combined Metabolic Activators Decrease Liver Steatosis by Activating Mitochondrial Metabolism in Hamsters Fed with a High-Fat Diet. Biomedicines, 2021, 9, 1440.	1.4	8
517	OnTheFly2.0: a text-mining web application for automated biomedical entity recognition, document annotation, network and functional enrichment analysis. NAR Genomics and Bioinformatics, 2021, 3, lqab090.	1.5	10

#	Article	IF	CITATIONS
518	Integrating Statistical and Machine-Learning Approach for Meta-Analysis of Bisphenol A-Exposure Datasets Reveals Effects on Mouse Gene Expression within Pathways of Apoptosis and Cell Survival. International Journal of Molecular Sciences, 2021, 22, 10785.	1.8	4
519	Bioinformatics Prediction and Analysis of MicroRNAs and Their Targets as Biomarkers for Prostate Cancer: A Preliminary Study. Molecular Biotechnology, 2022, 64, 401-412.	1.3	5
520	Cardiac-specific CGI-58 deficiency activates the ER stress pathway to promote heart failure in mice. Cell Death and Disease, 2021, 12, 1003.	2.7	4
521	Identification of Significant Genes in Lung Cancer of Nonsmoking Women via Bioinformatics Analysis. BioMed Research International, 2021, 2021, 1-12.	0.9	2
522	RUNX2 and LAMC2: promising pancreatic cancer biomarkers identified by an integrative data mining of pancreatic adenocarcinoma tissues. Aging, 2021, 13, 22963-22984.	1.4	10
524	MicroRNA-146a Serves as a Biomarker for Adverse Prognosis of ST-Segment Elevation Myocardial Infarction. Cardiovascular Therapeutics, 2021, 2021, 1-13.	1.1	10
526	Identification of Hub mRNAs and IncRNAs in Atrial Fibrillation Using Weighted Co-expression Network Analysis With RNA-Seq Data. Frontiers in Cell and Developmental Biology, 2021, 9, 722671.	1.8	3
527	Standards for Proteomics Data Dissemination and Experiments Reporting. Translational Bioinformatics, 2014, , 41-68.	0.0	0
528	Leveraging Naked Mole Rat (Heterocephalus glaber) Comparative Genomics to Identify Canine Genes Modulating Susceptibility to Tumorigenesis and Cancer Phenotypes. Journal of Veterinary Science & Technology, 2015, 07, .	0.3	2
532	WTFgenes:ÂWhat's The Function of these genes? Static sites for model-based gene set analysis. F1000Research, 0, 6, 423.	0.8	0
535	De Novo Transcriptome Profiling of Buasbuas (Premna pubescens. Blume). Biotechnology, 2018, 17, 75-85.	0.5	0
544	Identification of Candidate Genes Responsible for Age-Related Macular Degeneration Using Microarray Data., 2019,, 969-1001.		0
547	Human cancer cells compensate the genes unfavorable for translation by N6-methyladenosine modification and enhance their translation efficiency. Translational Cancer Research, 2019, 8, 499-508.	0.4	2
549	Applications of PCA Based Unsupervised FE to Bioinformatics. Unsupervised and Semi-supervised Learning, 2020, , 119-211.	0.4	1
557	Pathway-targeting gene matrix for Drosophila gene set enrichment analysis. PLoS ONE, 2021, 16, e0259201.	1.1	6
560	YQFC: a web tool to compare quantitative biological features between two yeast gene lists. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	1
563	Rapid evolution of expression levels in hepatocellular carcinoma. International Journal of Computational Biology and Drug Design, 2020, 13, 454.	0.3	0
564	The evolutionarily conserved kinase SnRK1 orchestrates resource mobilization during Arabidopsis seedling establishment. Plant Cell, 2022, 34, 616-632.	3.1	42

#	Article	IF	CITATIONS
565	Biomarker Gene Identification Using a Quantum Inspired Clustering Approach. Advances in Intelligent Systems and Computing, 2020, , 43-56.	0.5	1
566	Regulatory network of miRNA, IncRNA, transcription factor and target immune response genes in bovine mastitis. Scientific Reports, 2021, 11, 21899.	1.6	16
567	Screening for the Key Proteins Associated with Rete Testis Invasion in Clinical Stage I Seminoma via Label-Free Quantitative Mass Spectrometry. Cancers, 2021, 13, 5573.	1.7	4
568	Comparative Analysis of Dental Pulp and Periodontal Stem Cells: Differences in Morphology, Functionality, Osteogenic Differentiation and Proteome. Biomedicines, 2021, 9, 1606.	1.4	15
569	Identification of molecular subtyping system and four-gene prognostic signature with immune-related genes for uveal melanoma. Experimental Biology and Medicine, 2022, 247, 246-262.	1.1	3
570	A gene toolbox for monitoring autophagy transcription. Cell Death and Disease, 2021, 12, 1044.	2.7	46
571	Estimation of Hub Genes and Infiltrating Immune Cells in Non-Smoking Females with Lung Adenocarcinoma by Integrated Bioinformatic Analysis. Medical Science Monitor, 2020, 26, e922680.	0.5	2
573	A TMT-based quantitative proteomic analysis provides insights into the protein changes in the seeds of high- and low- protein content soybean cultivars. Journal of Plant Biotechnology, 2020, 47, 209-217.	0.1	4
575	Re-construction of Co-expression Network of Genes Involved in Bacterial Cell Wall Synthesis and Their Role in Penicillin Resistance. Avicenna Journal of Clinical Microbiology and Infection, 2020, 7, 65-71.	0.2	3
576	EFNB2 acts as the target of miR-557 to facilitate cell proliferation, migration and invasion in pancreatic ductal adenocarcinoma by bioinformatics analysis and verification. American Journal of Translational Research (discontinued), 2018, 10, 3514-3528.	0.0	11
577	Single-cell RNA sequencing to characterize the response of pancreatic cancer to anti-PD-1 immunotherapy. Translational Oncology, 2022, 15, 101262.	1.7	6
578	Discovery of TGFBR1 (ALK5) as a potential drug target of quercetin glycoside derivatives (QGDs) by reverse molecular docking and molecular dynamics simulation. Biophysical Chemistry, 2022, 281, 106731.	1.5	4
579	Cellular and molecular level host-pathogen interactions in Francisella tularensis: A microbial gene network study. Computational Biology and Chemistry, 2022, 96, 107601.	1.1	10
580	Identifying the Mechanisms of R <i>osa Roxburghii</i> Tratt on Treating Gastric Cancer: Combining the Targetable Screening From the Cancer Genome Atlas With Network Pharmacology. Natural Product Communications, 2021, 16, 1934578X2110596.	0.2	0
581	Verification of the Potential Targets of the Herbal Prescription Sochehwan for Drug Repurposing Processes as Deduced by Network Pharmacology. Processes, 2021, 9, 2034.	1.3	1
582	Systematic analysis of the lysine malonylome in Sanghuangporus sanghuang. BMC Genomics, 2021, 22, 840.	1.2	4
583	Insilico Functional Analysis of Genome-Wide Dataset From 17,000 Individuals Identifies Candidate Malaria Resistance Genes Enriched in Malaria Pathogenic Pathways. Frontiers in Genetics, 2021, 12, 676960.	1.1	1
584	Integrated Strategy From In Vitro, In Situ, In Vivo to In Silico for Predicting Active Constituents and Exploring Molecular Mechanisms of Tongfengding Capsule for Treating Gout by Inhibiting Inflammatory Responses. Frontiers in Pharmacology, 2021, 12, 759157.	1.6	4

#	Article	IF	CITATIONS
585	Genome-wide Identification and Analysis of Splicing QTLs in Multiple Sclerosis by RNA-Seq Data. Frontiers in Genetics, 2021, 12, 769804.	1.1	2
586	Transcriptomic Analysis Reveals that Activating Transcription Factor 3/c-Jun/Lgals3 Axis Is Associated with Central Diabetes Insipidus after Hypothalamic Injury. Neuroendocrinology, 2022, 112, 874-893.	1.2	5
587	Revealing the efficacy-toxicity relationship of Fuzi in treating rheumatoid arthritis by systems pharmacology. Scientific Reports, 2021, 11, 23083.	1.6	8
589	Transcriptome Analysis of Host Inflammatory Responses to the Ectoparasitic Mite Sarcoptes scabiei var. hominis. Frontiers in Immunology, 2021, 12, 778840.	2.2	4
590	Integrated omics analysis reveals sirtuin signaling is central to hepatic response to a high fructose diet. BMC Genomics, 2021, 22, 870.	1.2	7
591	Using the Symptom Patient Similarity Network to Explore the Difference between the Chinese and Western Medicine Pathways of Ischemic Stroke and its Comorbidities. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-12.	0.5	0
592	A Systems Biology Approach for Detecting Active Molecular Subpathways Related to Alzheimer's Disease. , 2021, , 1-19.		0
593	Frequency and Spectrum of Mutations Induced by Gamma Rays Revealed by Phenotype Screening and Whole-Genome Re-Sequencing in Arabidopsis thaliana. International Journal of Molecular Sciences, 2022, 23, 654.	1.8	10
594	Machine Learning Identifies Six Genetic Variants and Alterations in the Heart Atrial Appendage as Key Contributors to PD Risk Predictivity. Frontiers in Genetics, 2021, 12, 785436.	1.1	4
595	The effect and mechanism of Jiao-tai-wan in the treatment of diabetes mellitus with depression based on network pharmacology and experimental analysis. Molecular Medicine, 2021, 27, 154.	1.9	11
597	Identification of differentially methylated genes in first-trimester placentas with trisomy 16. Scientific Reports, 2022, 12, 1166.	1.6	2
598	Milk exosomes-mediated miR-31-5p delivery accelerates diabetic wound healing through promoting angiogenesis. Drug Delivery, 2022, 29, 214-228.	2.5	88
599	MOET: a web-based gene set enrichment tool at the Rat Genome Database for multiontology and multispecies analyses. Genetics, 2022, 220, .	1.2	7
600	Systematic Understanding of Mechanism of Danggui Shaoyao San against Ischemic Stroke Using a Network Pharmacology Approach. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-20.	0.5	0
602	Identification of target genes and prognostic evaluation for colorectal cancer using integrated bioinformatics analysis. International Journal of Transgender Health, 2022, 15, 160-173.	1.1	0
603	The transcription factor hepatocyte nuclear factor 4A acts in the intestine to promote white adipose tissue energy storage. Nature Communications, 2022, 13, 224.	5.8	15
605	The DNA dioxygenase Tet1 regulates H3K27 modification and embryonic stem cell biology independent of its catalytic activity. Nucleic Acids Research, 2022, 50, 3169-3189.	6.5	27
606	Anhydroicaritin Inhibits EMT in Breast Cancer by Enhancing GPX1 Expression: A Research Based on Sequencing Technologies and Bioinformatics Analysis. Frontiers in Cell and Developmental Biology, 2021, 9, 764481.	1.8	4

#	Article	IF	CITATIONS
607	Artificial intelligence analysis to explore synchronize exercise, cobalamin, and magnesium as new actors to therapeutic of migraine symptoms: a randomized, placebo-controlled trial. Neurological Sciences, 2022, 43, 4413-4424.	0.9	11
608	Changes in Brassica oleracea Leaves Infected With Xanthomonas campestris pv. campestris by Proteomics Analysis. Frontiers in Plant Science, 2021, 12, 781984.	1.7	2
610	Uncovering the Pathogenesis of Orofacial Clefts Using Bioinformatics Analysis. Journal of Craniofacial Surgery, 2022, Publish Ahead of Print, .	0.3	0
611	Identification of genes and pathways leading to poor prognosis of non-small cell lung cancer using integrated bioinformatics analysis. Translational Cancer Research, 2022, 11, 710-724.	0.4	1
612	Study on Immunomodulatory Effect of Belamcandae Rhizoma and Ephedrae Herba on Bronchitis Based on Network Pharmacology and Experimental Verification. Hans Journal of Medicinal Chemistry, 2022, 10, 53-69.	0.0	0
613	Identification of molecular signatures and pathways common to blood cells and brain tissue based RNA-Seq datasets of bipolar disorder: Insights from comprehensive bioinformatics approach. Informatics in Medicine Unlocked, 2022, 29, 100881.	1.9	6
615	Identifying Potential New Gene Expression-Based Biomarkers in the Peripheral Blood Mononuclear Cells of Hepatitis B-Related Hepatocellular Carcinoma. Canadian Journal of Gastroenterology and Hepatology, 2022, 2022, 1-13.	0.8	2
616	Comprehensive bioinformatics analysis of functional molecules in colorectal cancer. Journal of Gastrointestinal Oncology, 2022, 13, 231-245.	0.6	6
617	Analysis of Gene Expression Microarray Data Reveals Androgen-Responsive Genes of Muscles in Polycystic Ovarian Syndrome Patients. Processes, 2022, 10, 387.	1.3	0
618	Development of a Novel Immune Subtyping System Expanded with Immune Landscape and an 11-Gene Signature for Predicting Prostate Cancer Survival. Journal of Oncology, 2022, 2022, 1-18.	0.6	0
619	A Pan-Cancer In Silico Analysis of the COVID-19 Internalization Protease: Transmembrane Proteaseserine-2. Frontiers in Genetics, 2022, 13, 805880.	1.1	2
620	MadR mediates acyl CoA-dependent regulation of mycolic acid desaturation in mycobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	O
621	LIMK2 Is a Novel Prognostic Biomarker and Correlates With Tumor Immune Cell Infiltration in Lung Squamous Cell Carcinoma. Frontiers in Immunology, 2022, 13, 788375.	2.2	6
622	Microbial and molecular differences according to the location of head and neck cancers. Cancer Cell International, 2022, 22, 135.	1.8	13
623	Integrative epigenomic and transcriptomic analyses reveal metabolic switching by intermittent fasting in brain. GeroScience, 2022, 44, 2171-2194.	2.1	10
624	Expansion of Schizophrenia Gene Network Knowledge Using Machine Learning Selected Signals From Dorsolateral Prefrontal Cortex and Amygdala RNA-seq Data. Frontiers in Psychiatry, 2022, 13, 797329.	1.3	9
625	Network Pharmacological Study on Mechanism of the Therapeutic Effect of Modified Duhuo Jisheng Decoction in Osteoporosis. Frontiers in Endocrinology, 2022, 13, 860649.	1.5	2
626	Differential Expression of Zinc-Dependent HDAC Subtypes and their Involvement in Unique Pathways Associated with Carcinogenesis. Asian Pacific Journal of Cancer Prevention, 2022, 23, 877-883.	0.5	4

#	Article	IF	CITATIONS
627	miR-32 promotes MYC-driven prostate cancer. Oncogenesis, 2022, 11, 11.	2.1	4
628	Whole-Genome Sequencing of Vero E6 (VERO C1008) and Comparative Analysis of Four Vero Cell Sublines. Frontiers in Genetics, 2022, 13, 801382.	1.1	5
629	Gene Regulatory Networks of Epidermal and Neural Fate Choice in a Chordate. Molecular Biology and Evolution, 2022, 39, .	3.5	4
630	DAVID: a web server for functional enrichment analysis and functional annotation of gene lists (2021Âupdate). Nucleic Acids Research, 2022, 50, W216-W221.	6.5	1,694
632	Contribution of STIM-Activated TRPC-ORAI Channels in Pulmonary Hypertension Induced by Chronic Sustained and Intermittent Hypoxia. Current Vascular Pharmacology, 2022, 20, 272-283.	0.8	2
633	In-Silico Functional Annotation of Plasmodium falciparum Hypothetical Proteins to Identify Novel Drug Targets. Frontiers in Genetics, 2022, 13, 821516.	1.1	3
634	Study on the mechanism of Cortex Lycii on lung cancer based on network pharmacology combined with experimental validation. Journal of Ethnopharmacology, 2022, 293, 115280.	2.0	2
635	A polygenic stacking classifier revealed the complicated platelet transcriptomic landscape of adult immune thrombocytopenia. Molecular Therapy - Nucleic Acids, 2022, 28, 477-487.	2.3	4
636	Systems pharmacology, proteomics and in vivo studies identification of mechanisms of cerebral ischemia injury amelioration by Huanglian Jiedu Decoction. Journal of Ethnopharmacology, 2022, 293, 115244.	2.0	9
637	Cysteine is highly enriched in the canonical N-linked glycosylation motif of bovine spermatozoa N-Glycoproteome. Theriogenology, 2022, 184, 1-12.	0.9	3
638	Metagenome-genome-wide association studies reveal human genetic impact on the oral microbiome. Cell Discovery, 2021, 7, 117.	3.1	31
639	Tracing the Origin and Evolutionary Fate of Recent Gene Retrocopies in Natural Populations of the House Mouse. Molecular Biology and Evolution, 2022, 39, .	3.5	6
640	Development of a Machine Learning Model to Distinguish between Ulcerative Colitis and Crohn's Disease Using RNA Sequencing Data. Diagnostics, 2021, 11, 2365.	1.3	11
641	m6A Regulator Expression Segregates Meningiomas Into Biologically Distinct Subtypes. Frontiers in Oncology, 2021, 11, 760892.	1.3	3
642	Metformin alleviates the calcification of aortic valve interstitial cells through activating the PI3K/AKT pathway in an AMPK dependent way. Molecular Medicine, 2021, 27, 156.	1.9	12
643	Dual Host and Pathogen RNA-Seq Analysis Unravels Chicken Genes Potentially Involved in Resistance to Highly Pathogenic Avian Influenza Virus Infection. Frontiers in Immunology, 2021, 12, 800188.	2.2	7
644	Treatment of microglia with Anti-PrP monoclonal antibodies induces neuronal apoptosis in vitro. Heliyon, 2021, 7, e08644.	1.4	2
645	Influence of Escherichia coli on Expression of Selected Human Drug Addiction Genes. Life, 2021, 11, 1346.	1.1	0

#	Article	IF	CITATIONS
646	Mouse Organ-Specific Proteins and Functions. Cells, 2021, 10, 3449.	1.8	2
647	GENPPI: standalone software for creating protein interaction networks from genomes. BMC Bioinformatics, 2021, 22, 596.	1.2	1
648	Computational Systems Pharmacology, Molecular Docking and Experiments Reveal the Protective Mechanism of Li-Da-Qian Mixture in the Treatment of Glomerulonephritis. Journal of Inflammation Research, 2021, Volume 14, 6939-6958.	1.6	3
649	Proteolytic Profiling of Streptococcal Pyrogenic Exotoxin B (SpeB) by Complementary HPLC-MS Approaches. International Journal of Molecular Sciences, 2022, 23, 412.	1.8	7
650	The effect and apoptosis mechanism of 6-methoxyflavone in HeLa cells. Biomarkers, 2022, 27, 470-482.	0.9	1
651	PAGER Web APP: An Interactive, Online Gene Set and Network Interpretation Tool for Functional Genomics. Frontiers in Genetics, 2022, 13, 820361.	1.1	2
652	ROR activation by Nobiletin enhances antitumor efficacy via suppression of lîºB/NF-κB signaling in triple-negative breast cancer. Cell Death and Disease, 2022, 13, 374.	2.7	23
653	Global Transcriptomic Profiling Identifies Differential Gene Expression Signatures Between Inflammatory and Noninflammatory Aortic Aneurysms. Arthritis and Rheumatology, 2022, 74, 1376-1386.	2.9	4
721	Alcoholâ€associated fibrosis in females is mediated by femaleâ€specific activation of lysine demethylases KDM5B and KDM5C. Hepatology Communications, 2022, 6, 2042-2057.	2.0	10
722	FUNAGE-Pro: comprehensive web server for gene set enrichment analysis of prokaryotes. Nucleic Acids Research, 2022, 50, W330-W336.	6.5	17
723	Effect of Humantenine on mRNA m6A Modification and Expression in Human Colon Cancer Cell Line HCT116. Genes, 2022, 13, 781.	1.0	9
724	Network- and enrichment-based inference of phenotypes and targets from large-scale disease maps. Npj Systems Biology and Applications, 2022, 8, 13.	1.4	7
725	Transcriptome Analysis Using RNA Sequencing for Finding Genes Related to Fiber in Cotton: A Review. , $0,  ,  .$		0
726	Radiobiological effects of wound fluid on breast cancer cell lines and human-derived tumor spheroids in 2D and microfluidic culture. Scientific Reports, 2022, 12, 7668.	1.6	3
727	Extrachromosomal Circular DNA from TCGA Tumors Is Generated from Common Genomic Loci, Is Characterized by Self-Homology and DNA Motifs near Circle Breakpoints. Cancers, 2022, 14, 2310.	1.7	4
728	Identification of hub genes and role of CDKN2A as a biomarker in cervical cancer: An in-silico approach. , 2022, 33, 201048.		2
729	Network pharmacology of iridoid glycosides from Eucommia ulmoides Oliver against osteoporosis. Scientific Reports, 2022, 12, 7430.	1.6	11
730	Hydroxyproline stimulates inflammation and reprograms macrophage signaling in a rat kidney stone model. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2022, 1868, 166442.	1.8	8

#	ARTICLE	IF	CITATIONS
731	Anti-inflammatory properties of Fangji Huangqi tang: Novel application based on integrated network pharmacology combined with in vitro validation. Phytomedicine Plus, 2022, 2, 100296.	0.9	0
732	A Potential Prognostic Marker PRDM1 in Pancreatic Adenocarcinoma. Journal of Oncology, 2022, 2022, 1-10.	0.6	0
733	Incidence and immunomic features of apyretic COVID-19 in patients affected by solid tumors: a prospective cohort study. Journal of Translational Medicine, 2022, 20, 230.	1.8	0
734	Signal requirement for cortical potential of transplantable human neuroepithelial stem cells. Nature Communications, 2022, $13$ , .	5.8	5
735	An Epistatic Network Describes oppA and glgB as Relevant Genes for Mycobacterium tuberculosis. Frontiers in Molecular Biosciences, 0, 9, .	1.6	1
736	elF6 as a Promising Diagnostic and Prognostic Biomarker for Poorer Survival of Cutaneous Melanoma. Frontiers in Oncology, 0, $12$ , .	1.3	1
737	Survival-Associated Metabolic Genes and Risk Scoring System in HER2-Positive Breast Cancer. Frontiers in Endocrinology, 0, 13, .	1.5	4
738	SARS CoV-2 (Delta Variant) Infection Kinetics and Immunopathogenesis in Domestic Cats. Viruses, 2022, 14, 1207.	1.5	5
739	Protective Effects and Mechanisms of Yinchen Linggui Zhugan Decoction in HFD-Induced Nonalcoholic Fatty Liver Disease Rats Based on Network Pharmacology and Experimental Verification. Frontiers in Pharmacology, 0, 13, .	1.6	7
740	Exploring key molecular signatures of immune responses and pathways associated with tuberculosis in comorbid diabetes mellitus: a systems biology approach. Beni-Suef University Journal of Basic and Applied Sciences, 2022, $11$ , .	0.8	0
741	Long non-coding RNAs act as novel therapeutic targets by regulating molecular networks associated with ischemic stroke. Journal of King Saud University - Science, 2022, 34, 102119.	1.6	2
743	Endothelin system expression in the kidney following cisplatin-induced acute kidney injury in male and female mice. Canadian Journal of Physiology and Pharmacology, 2022, 100, 868-879.	0.7	1
744	Secukinumab for the treatment of adult-onset pityriasis rubra pilaris: a single-arm clinical trial with transcriptomic analysis. British Journal of Dermatology, 2022, 187, 650-658.	1.4	19
745	MAGE: An Open-Source Tool for Meta-Analysis of Gene Expression Studies. Biology, 2022, 11, 895.	1.3	1
746	Identification of HnRNP Family as Prognostic Biomarkers in Five Major Types of Gastrointestinal Cancer. Current Gene Therapy, 2022, 22, 449-461.	0.9	2
747	Oncogenic ZMYND11-MBTD1 fusion protein anchors the NuA4/TIP60 histone acetyltransferase complex to the coding region of active genes. Cell Reports, 2022, 39, 110947.	2.9	5
748	Bioinformatics and Experimental Analyses Reveal NFIC as an Upstream Transcriptional Regulator for Ischemic Cardiomyopathy. Genes, 2022, 13, 1051.	1.0	4
750	Screening membraneless organelle participants with machine-learning models that integrate multimodal features. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	34

#	Article	IF	CITATIONS
751	Posterior cingulate cortex reveals an expression profile of resilience in cognitively intact elders. Brain Communications, 2022, 4, .	1.5	10
752	Predicting functional riboSNitches in the context of alternative splicing. Gene, 2022, 837, 146694.	1.0	0
753	Traditional herbal formula Jiao-tai-wan improves chronic restrain stress-induced depression-like behaviors in mice. Biomedicine and Pharmacotherapy, 2022, 153, 113284.	2.5	7
754	A Honeybee Stinger Inspired Self-Interlocking Microneedle Patch and its Application in Myocardial Infarction Treatment. SSRN Electronic Journal, 0, , .	0.4	0
755	JunB Is Critical for Survival of T Helper Cells. Frontiers in Immunology, 0, 13, .	2.2	6
756	One-Week Dynamic Changes in Cardiac Proteomes After Cardiac Radioablation in Experimental Rat Model. Frontiers in Cardiovascular Medicine, 0, 9, .	1.1	3
757	Sinensetin protects against pulmonary fibrosis via inhibiting Wnt/ $\hat{l}^2$ -Catenin signaling pathway. Tissue and Cell, 2022, , 101866.	1.0	6
758	A genome-wide screen for resilient responses in growing pigs. Genetics Selection Evolution, 2022, 54, .	1.2	2
759	Regular combined training and vitamins modulated the apoptosis process in diabetic rats: Bioinformatics analysis of heart failure's differential genes expression network correlated with antiâ€apoptotic process. Journal of Food Biochemistry, 2022, 46, .	1.2	2
760	Predicting for anti-(mutant) SARS-CoV-2 and anti-inflammation compounds of Lianhua Qingwen Capsules in treating COVID-19. Chinese Medicine, 2022, 17, .	1.6	2
761	Co-inhibition of ATM and ROCK synergistically improves cell proliferation in replicative senescence by activating FOXM1 and E2F1. Communications Biology, 2022, 5, .	2.0	5
762	Comparative Analysis of Gene Correlation Networks of Breast Cancer Patients Based on Mutations in TP53. Biomolecules, 2022, 12, 979.	1.8	1
763	System-wide analyses reveal essential roles of N-terminal protein modification in bacterial membrane integrity. IScience, 2022, 25, 104756.	1.9	3
764	Loss-of-function of the hippo transducer TAZ reduces mammary tumor growth through a myeloid-derived suppressor cell-dependent mechanism. Cancer Gene Therapy, 0, , .	2.2	0
765	A network pharmacology-based study on the mechanism of astragaloside IV alleviating renal fibrosis through the AKT1/GSK-31² pathway. Journal of Ethnopharmacology, 2022, 297, 115535.	2.0	14
766	Pattern Discovery in Protein Networks Reveals High-Confidence Predictions of Novel Interactions. Proceedings of the AAAI Conference on Artificial Intelligence, 2014, 28, 2938-2945.	3.6	2
767	Gene Identification and Potential Drug Therapy for Drug-Resistant Melanoma with Bioinformatics and Deep Learning Technology. Disease Markers, 2022, 2022, 1-13.	0.6	1
768	Identification of Differential Expression Genes between Volume and Pressure Overloaded Hearts Based on Bioinformatics Analysis. Genes, 2022, 13, 1276.	1.0	0

#	ARTICLE	IF	CITATIONS
769	PROM1, CXCL8, RUNX1, NAV1 and TP73 genes as independent markers predictive of prognosis or response to treatment in two cohorts of high-grade serous ovarian cancer patients. PLoS ONE, 2022, 17, e0271539.	1.1	3
770	TMT-based quantitative N-glycoproteomic analysis reveals glycoprotein protection can improve the quality of frozen bovine sperm. International Journal of Biological Macromolecules, 2022, 218, 168-180.	3.6	2
771	Coupled Analysis of Single-Cell Transcriptome and TCR Sequencing Uncovers the Role of TRAV1-2 & lt;sup>+/J33 & lt;sup>+ MAIT Cells in Immune Reconstitution of Hiv-Infected Patients Under Antiretroviral Therapy. SSRN Electronic Journal, 0, , .	0.4	0
773	Identifying the Antitumor Effects of Curcumin on Lung Adenocarcinoma Using Comprehensive Bioinformatics Analysis. Drug Design, Development and Therapy, 0, Volume 16, 2365-2382.	2.0	4
774	Mechanism of Danhong Injection in the Treatment of Arrhythmia Based on Network Pharmacology, Molecular Docking, and In Vitro Experiments. BioMed Research International, 2022, 2022, 1-14.	0.9	3
775	Transcript and metabolite network perturbations in lignin biosynthetic mutants of Arabidopsis. Plant Physiology, 2022, 190, 2828-2846.	2.3	9
776	Potential of ATP5MG to Treat Metabolic Syndrome-Associated Cardiovascular Diseases. Frontiers in Cardiovascular Medicine, $0, 9, .$	1.1	2
777	Expression profile analysis to identify potential gene changes induced by dexamethasone in the trabecular meshwork. International Journal of Ophthalmology, 2022, 15, 1240-1248.	0.5	3
778	Proteomics and Biochemical Analyses of Secreted Proteins Revealed a Novel Mechanism by Which ADAM12S Regulates the Migration of Gastric Cancer Cells. Journal of Proteome Research, 0, , .	1.8	2
779	An expanded role for the transcription factor WRINKLED1 in the biosynthesis of triacylglycerols during seed development. Frontiers in Plant Science, 0, 13, .	1.7	9
780	Identification of G6PC as a potential prognostic biomarker in hepatocellular carcinoma based on bioinformatics analysis. Medicine (United States), 2022, 101, e29548.	0.4	3
781	Analysis of protective effects of <i>Rosa Roxburghii</i> Tratt fruit polyphenols on lipopolysaccharideâ€induced acute lung injury through network pharmacology and metabolomics. Food Science and Nutrition, 2022, 10, 4258-4269.	1.5	5
782	Multiple roles of apolipoprotein B mRNA editing enzyme catalytic subunit 3B (APOBEC3B) in human tumors: a pan-cancer analysis. BMC Bioinformatics, 2022, 23, .	1.2	1
783	A landscape of gene regulation in the parasitic amoebozoa Entamoeba spp. PLoS ONE, 2022, 17, e0271640.	1.1	1
784	Shotgun proteomic profiling of dormant, â€~non-culturable' Mycobacterium tuberculosis. PLoS ONE, 2022, 17, e0269847.	1,1	3
786	A cholesterogenic gene signature for predicting the prognosis of young breast cancer patients. PeerJ, 0, 10, e13922.	0.9	2
787	Mechanism Study of Cinnamomi Ramulus and Paris polyphylla Sm. Drug Pair in the Treatment of Adenomyosis by Network Pharmacology and Experimental Validation. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-14.	0.5	1
788	Network Pharmacology-Based Investigation on Therapeutic Mechanisms of the Angelica dahurica Radix and Ligusticum chuanxiong Rhizoma Herb Pair for Anti-Migraine Effect. Plants, 2022, 11, 2196.	1.6	0

#	Article	IF	CITATIONS
789	Synthesis and discovery of mitochondria-targeting oleanolic acid derivatives for potential PI3K inhibition. FÃ-toterapÃ-â, 2022, 162, 105291.	1.1	2
790	Effect of acute Cu exposure on immune response mechanisms of golden cuttlefish (Sepia esculenta). Fish and Shellfish Immunology, 2022, 130, 252-260.	1.6	4
791	Monoamine Oxidase-Dependent Pro-Survival Signaling in Diabetic Hearts Is Mediated by miRNAs. Cells, 2022, 11, 2697.	1.8	10
792	Cross-Talk of Protein Expression and Lysine Acetylation in Response to TMV Infection in <i>Nicotiana benthamiana</i> . ACS Omega, 2022, 7, 32496-32511.	1.6	0
793	Investigation of chicken housekeeping genes using next-generation sequencing data. Frontiers in Genetics, $0,13,1$	1.1	5
794	The oncogenic transcription factor FOXQ1 is a differential regulator of Wnt target genes. Journal of Cell Science, 2022, $135$ , .	1.2	10
795	A Novel Strategy for Identifying NSCLC MicroRNA Biomarkers and Their Mechanism Analysis Based on a Brand-New CeRNA-Hub-FFL Network. International Journal of Molecular Sciences, 2022, 23, 11303.	1.8	0
796	Autotaxin is a potential link between genetic risk factors and immunological disturbances of plasmacytoid dendritic cells in systematic lupus erythematosus. Lupus, 2022, 31, 1578-1585.	0.8	2
797	Exploration of immune response mechanisms in cadmium and copper co-exposed juvenile golden cuttlefish (Sepia esculenta) based on transcriptome profiling. Frontiers in Immunology, $0,13,13$	2.2	10
798	Transcriptome profiling combined with network analysis deepens the understanding of immune response mechanisms in blood of pacific oyster Crassostrea gigas infected by Vibrio alginolyticus. Frontiers in Marine Science, 0, 9, .	1.2	0
799	A honeybee stinger-inspired self-interlocking microneedle patch and its application in myocardial infarction treatment. Acta Biomaterialia, 2022, 153, 386-398.	4.1	12
800	Label-free quantitative SWATH-MS proteomic analysis of adult myocardial slices in vitro after biomimetic electromechanical stimulation. Scientific Reports, 2022, 12, .	1.6	0
801	Machine learning-assisted elucidation of CD81 $\hat{a}$ CD44 interactions in promoting cancer stemness and extracellular vesicle integrity. ELife, 0, 11, .	2.8	12
803	Developmental defects and behavioral changes in a diet-induced inflammation model of zebrafish. Frontiers in Immunology, 0, $13$ , .	2.2	3
804	Construction of miRNA–mRNA networks for the identification of lung cancer biomarkers in liquid biopsies. Clinical and Translational Oncology, 2023, 25, 643-652.	1.2	0
805	The E3 ubiquitin ligase RNF115 regulates phagosome maturation and host response to bacterial infection. EMBO Journal, 2022, 41, .	3.5	11
806	Genome of the endangered Guatemalan Beaded Lizard, <i>Heloderma charlesbogerti</i> , reveals evolutionary relationships of squamates and declines in effective population sizes. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	2
807	Single-cell RNA sequencing reveals TCR+ macrophages in HPV-related head and neck squamous cell carcinoma. Frontiers in Immunology, $0,13,13$	2.2	5

#	Article	IF	CITATIONS
808	Prevention of Testicular Damage by Indole Derivative MMINA via Upregulated StAR and CatSper Channels with Coincident Suppression of Oxidative Stress and Inflammation: In Silico and In Vivo Validation. Antioxidants, 2022, $11$ , 2063.	2.2	2
809	The potential immunotoxicity of emamectin benzoate on the human THPâ€1 macrophages. Environmental Toxicology, 2023, 38, 500-510.	2.1	6
810	Changes in subcutaneous adipose tissue microRNA expression in response to exercise training in African women with obesity. Scientific Reports, 2022, 12, .	1.6	2
811	Landscape and evolutionary dynamics of Helitron transposons in plant genomes as well as construction of online database HelDB. Journal of Systematics and Evolution, 2023, 61, 919-931.	1.6	1
812	Transcriptomics and genetic engineering., 2023,, 43-65.		0
813	Network pharmacology to uncover potential anti-inflammatory and immunomodulatory constituents in Curcuma longa rhizome as complementary treatment in COVID-19. Pharmacia, 2022, 69, 995-1003.	0.4	1
814	Transcriptome Analysis Reveals the Anti-Tumor Mechanism of Eucalyptol Treatment on Neuroblastoma Cell Line SH-SY5Y. Neurochemical Research, 2022, 47, 3854-3862.	1.6	3
815	Multiple Genes of Candida albicans Influencing Echinocandin Susceptibility in Caspofungin-Adapted Mutants. Antimicrobial Agents and Chemotherapy, 0, , .	1.4	5
816	Modeling and cleaning RNA-seq data significantly improve detection of differentially expressed genes. BMC Bioinformatics, 2022, 23, .	1.2	3
818	Establishment of transgenic pigs overexpressing human PKD2-D511V mutant. Frontiers in Genetics, 0, 13,	1.1	0
819	Ferroptosis related genes participate in the pathogenesis of spinal cord injury via HIF-1 signaling pathway. Brain Research Bulletin, 2023, 192, 192-202.	1.4	8
821	Time-dependent immune injury induced by short-term exposure to nanoplastics in the Sepia esculenta larvae. Fish and Shellfish Immunology, 2023, 132, 108477.	1.6	0
822	Transcriptome analysis preliminary reveals the immune response mechanism of golden cuttlefish (Sepia esculenta) larvae exposed to Cd. Fish and Shellfish Immunology, 2023, 132, 108494.	1.6	0
823	Isoliquiritigenin from licorice flavonoids attenuates NLRP3-mediated pyroptosis by SIRT6 in vascular endothelial cells. Journal of Ethnopharmacology, 2023, 303, 115952.	2.0	9
824	$HNF4\hat{l}\pm$ Acts as Upstream Functional Regulator of Intestinal Wnt3 and Paneth Cell Fate. Cellular and Molecular Gastroenterology and Hepatology, 2023, 15, 593-612.	2.3	5
825	Sex differences in the oral microbiome, host traits, and their causal relationships. IScience, 2023, 26, 105839.	1.9	9
827	A novel post-developmental role of the Hox genes underlies normal adult behavior. Proceedings of the National Academy of Sciences of the United States of America, 2022, $119$ , .	3.3	3
828	<i>TERT</i> silencing alters the expression of <i>ARG1, GLUL, VIM</i> , <i>NES</i> genes and hsa-miR-29b-3p in the T98G cell line. Nucleosides, Nucleotides and Nucleic Acids, 2023, 42, 464-477.	0.4	1

#	Article	IF	CITATIONS
829	Revealing the neurobiology underlying interpersonal neural synchronization with multimodal data fusion. Neuroscience and Biobehavioral Reviews, 2023, 146, 105042.	2.9	7
830	Modelling metastatic colonization of cholangiocarcinoma organoids in decellularized lung and lymph nodes. Frontiers in Oncology, 0, $12$ , .	1.3	3
831	End-to-end sequence-structure-function meta-learning predicts genome-wide chemical-protein interactions for dark proteins. PLoS Computational Biology, 2023, 19, e1010851.	1.5	5
832	Transcript shortening via alternative polyadenylation promotes gene expression during fracture healing. Bone Research, 2023, $11$ , .	5.4	5
833	<i>N</i> <sup>6</sup> â€methyladenine profiling of lowâ€input multiplex clinical samples on transcriptome reveals RNA modifications implicated in type 2 diabetes and acute myocardial infarction. Clinical and Translational Medicine, 2023, 13, .	1.7	1
834	Modification and Expression of mRNA m6A in the Lateral Habenular of Rats after Long-Term Exposure to Blue Light during the Sleep Period. Genes, 2023, 14, 143.	1.0	3
835	Sequencing-based network analysis provides a core set of genes for understanding hemolymph immune response mechanisms against Poly I:C stimulation in Amphioctopus fangsiao. Fish and Shellfish Immunology, 2023, 133, 108544.	1.6	1
836	The Mechanism of Quercetin in the Treatment of Lung Squamous Cell Carcinoma Based on a Protein-Protein Interaction Network. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-14.	0.5	O
837	Neuroprotective effect of hyperoside in MPP+/MPTP -induced dopaminergic neurodegeneration. Metabolic Brain Disease, 2023, 38, 1035-1050.	1.4	1
838	Characterization of a lipid droplet and endoplasmic reticulum stress related gene risk signature to evaluate the clinical and biological value in hepatocellular carcinoma. Lipids in Health and Disease, 2022, 21, .	1.2	1
839	Prognostic Genomic Markers of Pathological Stage in Oral Squamous Cell Carcinoma. Head and Neck Pathology, 2023, 17, 409-421.	1.3	2
840	Integrated Profiles of Transcriptome and mRNA m6A Modification Reveal the Intestinal Cytotoxicity of Aflatoxin B1 on HCT116 Cells. Genes, 2023, 14, 79.	1.0	3
841	Study on the Mechanism of Astragalus Polysaccharides on Cervical Cancer Based on Network Pharmacology. Combinatorial Chemistry and High Throughput Screening, 2023, 26, .	0.6	0
842	PARP1 Inhibition and Effect on Burn Injury-Induced Inflammatory Response and Cardiac Function. Journal of the American College of Surgeons, 2023, 236, 783-802.	0.2	0
843	Assessing the epithelial-to-mesenchymal plasticity in a small cell lung carcinoma (SCLC) and lung fibroblasts co-culture model. Frontiers in Molecular Biosciences, $0,10,10$	1.6	4
844	Determining human-coronavirus protein-protein interaction using machine intelligence. Medicine in Novel Technology and Devices, 2023, 18, 100228.	0.9	0
845	Circ-calm4 regulates hypoxia-induced pulmonary artery smooth muscle autophagy by binding Purb. Journal of Molecular and Cellular Cardiology, 2023, 176, 41-54.	0.9	5
846	Study of the inflammatory activating process in the early stage of Fusobacterium nucleatum infected PDLSCs. International Journal of Oral Science, 2023, 15, .	3.6	5

#	Article	IF	Citations
847	798. Sequencing-based genome-wide association study for resilience indicators in growing pigs. , 2022, , .		O
848	Detecting Active Molecular Subpathways Related to Alzheimer's Disease: A Systems Biology Approach. , 2023, , 1-19.		0
849	The Effect of BSCL2 Gene on Fat Deposition Traits in Pigs. Animals, 2023, 13, 641.	1.0	1
850	Proteomics profiling of vitreous humor reveals complement and coagulation components, adhesion factors, and neurodegeneration markers as discriminatory biomarkers of vitreoretinal eye diseases. Frontiers in Immunology, $0,14,.$	2.2	11
851	Can biomarkers identified from the uterine fluid transcriptome be used to establish a noninvasive endometrial receptivity prediction tool? A proof-of-concept study. Reproductive Biology and Endocrinology, 2023, 21, .	1.4	3
852	Soluble Klotho protects against glomerular injury through regulation of ER stress response. Communications Biology, 2023, 6, .	2.0	4
853	Genomic diversity and signals of selection processes in wild and farm-reared red-legged partridges (Alectoris rufa). Genomics, 2023, 115, 110591.	1.3	2
854	High content predictive models and new alternative methods (NAMs) in the context of adverse outcome pathways (AOPs) to assess arsenic toxicology. , 2023, , 883-898.		1
855	A Zeb1/MtCK1 metabolic axis controls osteoclast activation and skeletal remodeling. EMBO Journal, 2023, 42, .	3.5	3
856	Network Pharmacology Study to reveal the mechanism of Zuogui Pill for treating osteoporosis. Current Computer-Aided Drug Design, 2023, 19, .	0.8	0
857	Estrogen Mediates the Sexual Dimorphism of GT1b-Induced Central Pain Sensitization. Cells, 2023, 12, 808.	1.8	2
858	Proteolytic regulation of a galectin-3/Lrp1 axis controls osteoclast-mediated bone resorption. Journal of Cell Biology, 2023, 222, .	2.3	5
860	Ellagitannin Punicalagin Disrupts the Pathways Related to Bacterial Growth and Affects Multiple Pattern Recognition Receptor Signaling by Acting as a Selective Histone Deacetylase Inhibitor. Journal of Agricultural and Food Chemistry, 2023, 71, 5016-5026.	2.4	4
861	Using a whole genome coâ€expression network to inform the functional characterisation of predicted genomic elements from <i>Mycobacterium tuberculosis</i> transcriptomic data. Molecular Microbiology, 2023, 119, 381-400.	1.2	1
862	Network pharmacology predicts combinational effect of novel herbal pair consist of Ephedrae herba and Coicis semen on adipogenesis in 3T3-L1 cells. PLoS ONE, 2023, 18, e0282875.	1.1	3
863	Pharmacogenomic and Statistical Analysis. Methods in Molecular Biology, 2023, , 305-330.	0.4	0
864	Inhibitors of the Oncogenic PA2G4-MYCN Protein-Protein Interface. Cancers, 2023, 15, 1822.	1.7	0
865	Proteome Dynamics of Persulfidation in Leaf Tissue under Light/Dark Conditions and Carbon Deprivation. Antioxidants, 2023, 12, 789.	2.2	3

#	Article	IF	CITATIONS
866	Upregulation of Biomarker Limd1 Was Correlated with Immune Infiltration in Doxorubicin-Related Cardiotoxicity. Mediators of Inflammation, 2023, 2023, 1-23.	1.4	0
867	Preliminary Exploration of Metabolic Mechanisms in Copper-Exposed Sepia esculenta Based on Transcriptome Analysis. Metabolites, 2023, 13, 471.	1.3	0
868	Functional Annotation Routines Used by ABRF Bioinformatics Core Facilities - Observations, Comparisons, and Considerations. Journal of Biomolecular Techniques, 2023, 34, 3fc1f5fe.0b74b9db.	0.8	0
869	HD-ZIP III-dependent local promotion of brassinosteroid synthesis suppresses vascular cell division in Arabidopsis root apical meristem. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	2
870	Comparison of the molecular mechanisms of Fuzi Lizhong Pill and Huangqin decoction in the treatment of the cold and heat syndromes of ulcerative colitis based on network pharmacology. Computers in Biology and Medicine, 2023, 159, 106870.	3.9	1
871	Screening of Drosophila microRNA-degradation sequences reveals Argonaute1 mRNA's role in regulating miR-999. Nature Communications, 2023, 14, .	5.8	11
872	A modified Fangji Huangqi decoction ameliorates pulmonary artery hypertension via phosphatidylinositide 3-kinases/protein kinase B-mediated regulation of proliferation and apoptosis of smooth muscle cells in vitro and in vivo. Journal of Ethnopharmacology, 2023, 314, 116544.	2.0	1
893	Detecting Active Molecular Subpathways Related to Alzheimer's Disease: A Systems Biology Approach. , 2023, , 91-109.		0
930	Wound Healing from Bench to Bedside: A PPPM Bridge Between Physical Therapies and Chronic Inflammation. Advances in Predictive, Preventive and Personalised Medicine, 2023, , 221-232.	0.6	0
938	Evolutionary Graph-Clustering vs Evolutionary Cluster-Detection Approaches forÂCommunity Identification inÂPPI Networks. Lecture Notes in Business Information Processing, 2024, , 98-113.	0.8	0
946	Introduction to sample preparation for proteomics and mass spectrometry. , 2024, , 7-32.		0