## KOBAS 2.0: a web server for annotation and identificati diseases

Nucleic Acids Research 39, W316-W322

DOI: 10.1093/nar/gkr483

**Citation Report** 

#	Article	IF	CITATIONS
1	AutismKB: an evidence-based knowledgebase of autism genetics. Nucleic Acids Research, 2012, 40, D1016-D1022.	6.5	157
2	A Deep Exploration of the Transcriptome and "Excretory/Secretory―Proteome of Adult Fascioloides magna. Molecular and Cellular Proteomics, 2012, 11, 1340-1353.	2.5	35
3	Transcriptome analysis reveals the time of the fourth round of genome duplication in common carp (Cyprinus carpio). BMC Genomics, 2012, 13, 96.	1.2	101
4	TranSeqAnnotator: large-scale analysis of transcriptomic data. BMC Bioinformatics, 2012, 13, S24.	1.2	6
5	Detecting recurrent gene mutation in interaction network context using multi-scale graph diffusion. BMC Bioinformatics, 2013, 14, 29.	1.2	31
6	Global characterization of signalling networks associated with tamoxifen resistance in breast cancer. FEBS Journal, 2013, 280, 5237-5257.	2.2	36
7	Getting the most out of parasitic helminth transcriptomes using HelmDB: Implications for biology and biotechnology. Biotechnology Advances, 2013, 31, 1109-1119.	6.0	23
8	Superparamagnetic iron oxide nanoparticles alter expression of obesity and T2D-associated risk genes in human adipocytes. Scientific Reports, 2013, 3, 2173.	1.6	36
9	The predicted secretome and transmembranome of the poultry red mite Dermanyssus gallinae. Parasites and Vectors, 2013, 6, 259.	1.0	32
10	Protein profiling of striatum and substantia nigra from hemiparkinsonian rat model by offgel-HPLC-MS/MS. , 2013, , .		0
11	Directed Multistep Biocatalysis Using Tailored Permeabilized Cells. Advances in Biochemical Engineering/Biotechnology, 2013, 137, 185-234.	0.6	15
12	Deep sequencing analysis of the transcriptomes of peanut aerial and subterranean young pods identifies candidate genes related to early embryo abortion. Plant Biotechnology Journal, 2013, 11, 115-127.	4.1	75
13	Functional Annotation of the Human Chromosome 7 "Missing―Proteins: A Bioinformatics Approach. Journal of Proteome Research, 2013, 12, 2504-2510.	1.8	17
14	EDdb: A web resource for eating disorder and its application to identify an extended adipocytokine signaling pathway related to eating disorder. Science China Life Sciences, 2013, 56, 1086-1096.	2.3	36
15	Unlocking the Puzzling Biology of the Black Périgord Truffle <i>Tuber melanosporum</i> . Journal of Proteome Research, 2013, 12, 5349-5356.	1.8	24
16	Phylogeny, Functional Annotation, and Protein Interaction Network Analyses of theXenopus tropicalisBasic Helix-Loop-Helix Transcription Factors. BioMed Research International, 2013, 2013, 1-15.	0.9	3
17	TSGene: a web resource for tumor suppressor genes. Nucleic Acids Research, 2013, 41, D970-D976.	6.5	295
18	Evolution of the Eye Transcriptome under Constant Darkness in Sinocyclocheilus Cavefish. Molecular Biology and Evolution, 2013, 30, 1527-1543.	3.5	83

#	Article	IF	CITATIONS
19	Photobacterium profundum under Pressure: A MS-Based Label-Free Quantitative Proteomics Study. PLoS ONE, 2013, 8, e60897.	1.1	29
20	Integrative Analysis of Porcine microRNAome during Skeletal Muscle Development. PLoS ONE, 2013, 8, e72418.	1.1	36
21	Transcriptome Analysis Reveals Common and Distinct Mechanisms for Sheepgrass (Leymus chinensis) Responses to Defoliation Compared to Mechanical Wounding. PLoS ONE, 2014, 9, e89495.	1.1	29
22	Comparative Transcriptional Analysis of Asexual and Sexual Morphs Reveals Possible Mechanisms in Reproductive Polyphenism of the Cotton Aphid. PLoS ONE, 2014, 9, e99506.	1.1	19
23	De Novo Transcriptome Sequencing Analysis and Comparison of Differentially Expressed Genes (DEGs) in Macrobrachium rosenbergii in China. PLoS ONE, 2014, 9, e109656.	1.1	15
24	Transcriptome Sequencing and De Novo Analysis of Cytoplasmic Male Sterility and Maintenance in JA-CMS Cotton. PLoS ONE, 2014, 9, e112320.	1.1	26
25	Screening for key genes associated with invasive ductal carcinoma of the breast via microarray data analysis. Genetics and Molecular Research, 2014, 13, 7919-7925.	0.3	7
26	Assessment of Subnetwork Detection Methods for Breast Cancer. Cancer Informatics, 2014, 13s6, CIN.S17641.	0.9	8
27	Small RNAs as important regulators for the hybrid vigour of super-hybrid rice. Journal of Experimental Botany, 2014, 65, 5989-6002.	2.4	30
28	Identification of a Missense Variant in LNPEP that Confers Psoriasis Risk. Journal of Investigative Dermatology, 2014, 134, 359-365.	0.3	46
29	The Transcriptomes of the Crucian Carp Complex (Carassius auratus) Provide Insights into the Distinction between Unisexual Triploids and Sexual Diploids. International Journal of Molecular Sciences, 2014, 15, 9386-9406.	1.8	12
30	Transcriptome Profiles of the Protoscoleces of Echinococcus granulosus Reveal that Excretory-Secretory Products Are Essential to Metabolic Adaptation. PLoS Neglected Tropical Diseases, 2014, 8, e3392.	1.3	28
31	Next Generation Sequencing Reveals Regulation of Distinct Aedes microRNAs during Chikungunya Virus Development. PLoS Neglected Tropical Diseases, 2014, 8, e2616.	1.3	62
32	Comparative Transcriptional Profiling of Three Super-Hybrid Rice Combinations. International Journal of Molecular Sciences, 2014, 15, 3799-3815.	1.8	7
33	HumanViCe: host ceRNA network in virus infected cells in human. Frontiers in Genetics, 2014, 5, 249.	1.1	41
34	RNA Sequencing Analysis Reveals Transcriptomic Variations in Tobacco (Nicotiana tabacum) Leaves Affected by Climate, Soil, and Tillage Factors. International Journal of Molecular Sciences, 2014, 15, 6137-6160.	1.8	17
35	Comparative Transcriptome Analysis of Leaves and Roots in Response to Sudden Increase in Salinity in <i>Brassica napus</i> by RNA-seq. BioMed Research International, 2014, 2014, 1-19.	0.9	48
36	Comparative Transcriptomics in East African Cichlids Reveals Sex- and Species-Specific Expression and New Candidates for Sex Differentiation in Fishes. Genome Biology and Evolution, 2014, 6, 2567-2585.	1.1	61

#	ARTICLE Transcriptome de novo assembly and differentially expressed genes related to cytoplasmic male	IF	CITATIONS
37	sterility in kenaf (Hibiscus cannabinus L.). Molecular Breeding, 2014, 34, 1879-1891.	1.0	33
38	Bovine serum albumin in saliva mediates grazing response in Leymus chinensis revealed by RNA sequencing. BMC Genomics, 2014, 15, 1126.	1.2	12
39	MORPHIN: a web tool for human disease research by projecting model organism biology onto a human integrated gene network. Nucleic Acids Research, 2014, 42, W147-W153.	6.5	16
40	Phosphoproteomic Profiling Identifies Focal Adhesion Kinase as a Mediator of Docetaxel Resistance in Castrate-Resistant Prostate Cancer. Molecular Cancer Therapeutics, 2014, 13, 190-201.	1.9	42
41	Network-based detection of disease modules and potential drug targets in intractable epilepsy. , 2014, , .		2
42	Heterosis in Early Maize Ear Inflorescence Development: A Genome-Wide Transcription Analysis for Two Maize Inbred Lines and Their Hybrid. International Journal of Molecular Sciences, 2014, 15, 13892-13915.	1.8	25
43	iPathCons and iPathDB: an improved insect pathway construction tool and the database. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	1.4	14
44	Arginine Deiminase in Staphylococcus epidermidis Functions To Augment Biofilm Maturation through pH Homeostasis. Journal of Bacteriology, 2014, 196, 2277-2289.	1.0	82
45	Proteomic analysis of rat proximal tubule cells following stretch-induced apoptosis in an in vitro model of kidney obstruction. Journal of Proteomics, 2014, 100, 125-135.	1.2	8
46	Transcriptome and Gene Expression Analysis of an Oleaginous Diatom Under Different Salinity Conditions. Bioenergy Research, 2014, 7, 192-205.	2.2	55
47	Deep transcriptome sequencing of rhizome and aerial-shoot in Sorghum propinquum. Plant Molecular Biology, 2014, 84, 315-327.	2.0	26
48	Genome-Wide Identification of Embryogenesis-Associated microRNAs in Radish (Raphanus sativus L.) by High-Throughput Sequencing. Plant Molecular Biology Reporter, 2014, 32, 900-915.	1.0	30
49	gsGator: an integrated web platform for cross-species gene set analysis. BMC Bioinformatics, 2014, 15, 13.	1.2	7
50	Principles and methods of integrative genomic analyses in cancer. Nature Reviews Cancer, 2014, 14, 299-313.	12.8	337
51	Quantitative proteomics in resected renal cancer tissue for biomarker discovery and profiling. British Journal of Cancer, 2014, 110, 1622-1633.	2.9	61
52	Systems genetics: From GWAS to disease pathways. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2014, 1842, 1903-1909.	1.8	67
53	Protannotator: A Semiautomated Pipeline for Chromosome-Wise Functional Annotation of the "Missing―Human Proteome. Journal of Proteome Research, 2014, 13, 76-83.	1.8	13
54	Comparative transcriptome profiling of potassium starvation responsiveness in two contrasting watermelon genotypes. Planta, 2014, 239, 397-410.	1.6	62

#	Article	IF	CITATIONS
55	Genomeâ€ <scp>w</scp> ide patterns of largeâ€ <scp>s</scp> ize presence/ <scp>a</scp> bsence variants in sorghum. Journal of Integrative Plant Biology, 2014, 56, 24-37.	4.1	22
56	An evidence-based knowledgebase of pulmonary arterial hypertension to identify genes and pathways relevant to pathogenesis. Molecular BioSystems, 2014, 10, 732-740.	2.9	16
57	Proteomic changes in brain tissues of marine medaka (Oryzias melastigma) after chronic exposure to two antifouling compounds: Butenolide and 4,5-dichloro-2-n-octyl-4-isothiazolin-3-one (DCOIT). Aquatic Toxicology, 2014, 157, 47-56.	1.9	29
58	RNAseq analysis of cassava reveals similar plant responses upon infection with pathogenic and non-pathogenic strains of Xanthomonas axonopodis pv. manihotis. Plant Cell Reports, 2014, 33, 1901-1912.	2.8	46
59	Quantitative phosphoproteomic profiling of fiber differentiation and initiation in a fiberless mutant of cotton. BMC Genomics, 2014, 15, 466.	1.2	33
60	In-depth Proteomics Characterization of Embryogenesis of the Honey Bee Worker (Apis mellifera) Tj ETQq1 1 0.	784314 rg 2.5	BT (Overlock
61	Hydrogen peroxide primes heart regeneration with a derepression mechanism. Cell Research, 2014, 24, 1091-1107.	5.7	115
62	Molecular Mechanism of Acute Radiation Enteritis Revealed Using Proteomics and Biological Signaling Network Analysis in Rats. Digestive Diseases and Sciences, 2014, 59, 2704-2713.	1.1	18
63	New Insights into Clostridia Through Comparative Analyses of Their 40 Genomes. Bioenergy Research, 2014, 7, 1481-1492.	2.2	16
64	Abundant and Selective RNA-Editing Events in the Medicinal Mushroom <i>Ganoderma lucidum</i> . Genetics, 2014, 196, 1047-1057.	1.2	28
65	Biocomputional construction of a gene network under acid stress in Synechocystis sp. PCC 6803. Research in Microbiology, 2014, 165, 420-428.	1.0	6
66	Root proteome of rice studied by iTRAQ provides integrated insight into aluminum stress tolerance mechanisms in plants. Journal of Proteomics, 2014, 98, 189-205.	1.2	116
67	Evolutionary conservation of the mature oocyte proteome. EuPA Open Proteomics, 2014, 3, 27-36.	2.5	18
68	Gene expression and metabolic pathways related to cell growth and lipid synthesis in diatom Nitzschia ZJU2 after two rounds of mutagenesis by γ-rays. RSC Advances, 2014, 4, 28463-28470.	1.7	8
69	Transcriptome analysis of grain-filling caryopses reveals the potential formation mechanism of the rice sugary mutant. Gene, 2014, 546, 318-326.	1.0	9
70	Profiling the tyrosine phosphoproteome of different mouse mammary tumour models reveals distinct, model-specific signalling networks and conserved oncogenic pathways. Breast Cancer Research, 2014, 16, 437.	2.2	13
71	RNA-seq analysis of synovial fibroblasts in human rheumatoid arthritis. Molecular Medicine Reports, 2014, 10, 241-247.	1.1	20
72	Proteome of human plasma very low-density lipoprotein and low-density lipoprotein exhibits a link with coagulation and lipid metabolism. Thrombosis and Haemostasis, 2014, 112, 518-530.	1.8	82

#	Article	IF	CITATIONS
73	Protein functional analysis data in support of comparative proteomics of the pathogenic black yeast Exophiala dermatitidis under different temperature conditions. Data in Brief, 2015, 5, 372-375.	0.5	2
74	Gonadal transcriptomic analysis and differentially expressed genes in the testis and ovary of the Pacific white shrimp (Litopenaeus vannamei). BMC Genomics, 2015, 16, 1006.	1.2	72
75	Different combinations of atomic interactions predict proteinâ€small molecule and protein―DNA/RNA affinities with similar accuracy. Proteins: Structure, Function and Bioinformatics, 2015, 83, 2100-2114.	1.5	17
76	Identification of bolting-related microRNAs and their targets reveals complex miRNA-mediated flowering-time regulatory networks in radish (Raphanus sativus L.). Scientific Reports, 2015, 5, 14034.	1.6	63
77	dbEMT: an epithelial-mesenchymal transition associated gene resource. Scientific Reports, 2015, 5, 11459.	1.6	117
78	Transcriptome analysis provides insights into the regulatory function of alternative splicing in antiviral immunity in grass carp (Ctenopharyngodon idella). Scientific Reports, 2015, 5, 12946.	1.6	73
79	Molecular portraits revealing the heterogeneity of breast tumor subtypes defined using immunohistochemistry markers. Scientific Reports, 2015, 5, 14499.	1.6	29
80	Analysis of key genes of jasmonic acid mediated signal pathway for defense against insect damages by comparative transcriptome sequencing. Scientific Reports, 2015, 5, 16500.	1.6	35
81	An evidence-based knowledgebase of metastasis suppressors to identify key pathways relevant to cancer metastasis. Scientific Reports, 2015, 5, 15478.	1.6	19
82	Exploring molecular variation in Schistosoma japonicum in China. Scientific Reports, 2015, 5, 17345.	1.6	33
83	Transcriptome-wide analysis of chromium-stress responsive microRNAs to explore miRNA-mediated regulatory networks in radish (Raphanus sativus L). Scientific Reports, 2015, 5, 14024.	1.6	76
84	Screening of biomarkers in cervical squamous cell carcinomas via gene expression profiling. Molecular Medicine Reports, 2015, 12, 6985-6989.	1.1	3
85	Reporter pathway analysis from transcriptome data: Metabolite-centric versus Reaction-centric approach. Scientific Reports, 2015, 5, 14563.	1.6	19
86	p38 MAPK regulates PKAα and CUB-serine protease in Amphibalanus amphitrite cyprids. Scientific Reports, 2015, 5, 14767.	1.6	5
87	Transcriptomic profiling of host-parasite interactions in the microsporidian Trachipleistophora hominis. BMC Genomics, 2015, 16, 983.	1.2	30
88	Transcriptome profile analysis of cell proliferation molecular processes during multicellular trichome formation induced by tomato Wo v gene in tobacco. BMC Genomics, 2015, 16, 868.	1.2	42
89	MGDB: a comprehensive database of genes involved in melanoma. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav097.	1.4	11
90	Nitric oxide inhibits larval settlement in <i>Amphibalanus amphitrite</i> cyprids by repressing muscle locomotion and molting. Proteomics, 2015, 15, 3854-3864.	1.3	13

#	Article	IF	CITATIONS
91	Transcriptome comparison in the pituitary–adrenal axis between Beagle and Chinese Field dogs after chronic stress exposure. Animal Genetics, 2015, 46, 522-534.	0.6	8
92	Integrating herb effect similarity for network-based herb target prediction. , 2015, , .		0
93	Identification of long non-coding RNA involved in osteogenic differentiation from mesenchymal stem cells using RNA-Seq data. Genetics and Molecular Research, 2015, 14, 18268-18279.	0.3	41
94	Deep sequencing revealed molecular signature of horizontal gene transfer of plant like transcripts inÂthe mosquito Anopheles culicifacies: an evolutionary puzzle. F1000Research, 2015, 4, 1523.	0.8	9
95	Insights on predominant edible bamboo shoot proteins. African Journal of Biotechnology, 2015, 14, 1511-1518.	0.3	10
96	Translational Arrest Due to Cytoplasmic Redox Stress Delays Adaptation to Growth on Methanol and Heterologous Protein Expression in a Typical Fed-Batch Culture of Pichia pastoris. PLoS ONE, 2015, 10, e0119637.	1.1	12
97	Increased Expression of Interferon Signaling Genes in the Bone Marrow Microenvironment of Myelodysplastic Syndromes. PLoS ONE, 2015, 10, e0120602.	1.1	18
98	Comprehensive Analysis of Temporal Alterations in Cellular Proteome of Bacillus subtilis under Curcumin Treatment. PLoS ONE, 2015, 10, e0120620.	1.1	4
99	De Novo Characterization of Fall Dormant and Nondormant Alfalfa (Medicago sativa L.) Leaf Transcriptome and Identification of Candidate Genes Related to Fall Dormancy. PLoS ONE, 2015, 10, e0122170.	1.1	36
100	Transcriptome Analysis and Its Application in Identifying Genes Associated with Fruiting Body Development in Basidiomycete Hypsizygus marmoreus. PLoS ONE, 2015, 10, e0123025.	1.1	54
101	From Glacier to Sauna: RNA-Seq of the Human Pathogen Black Fungus Exophiala dermatitidis under Varying Temperature Conditions Exhibits Common and Novel Fungal Response. PLoS ONE, 2015, 10, e0127103.	1.1	32
102	Pancreas-Specific Sirt1-Deficiency in Mice Compromises Beta-Cell Function without Development of Hyperglycemia. PLoS ONE, 2015, 10, e0128012.	1.1	25
103	Transcriptome and Molecular Pathway Analysis of the Hepatopancreas in the Pacific White Shrimp Litopenaeus vannamei under Chronic Low-Salinity Stress. PLoS ONE, 2015, 10, e0131503.	1.1	85
104	Transcriptomic Profiling Reveals Complex Molecular Regulation in Cotton Genic Male Sterile Mutant Yu98-8A. PLoS ONE, 2015, 10, e0133425.	1.1	8
105	Proteomics of Aggregatibacter actinomycetemcomitans Outer Membrane Vesicles. PLoS ONE, 2015, 10, e0138591.	1.1	46
106	Single Base-Resolution Methylome of the Dizygotic Sheep. PLoS ONE, 2015, 10, e0142034.	1.1	5
107	Comparative Transcriptome Analysis in the Hepatopancreas Tissue of Pacific White Shrimp Litopenaeus vannamei Fed Different Lipid Sources at Low Salinity. PLoS ONE, 2015, 10, e0144889.	1.1	23
108	Fundamental Roles of the Golgi-Associated Toxoplasma Aspartyl Protease, ASP5, at the Host-Parasite Interface. PLoS Pathogens, 2015, 11, e1005211.	2.1	108

		CITATION REPORT	
#	Article	IF	CITATIONS
109	Analysis of mechanical ventilation and lipopolysaccharide-induced acute lung injury using DNA microarray analysis. Molecular Medicine Reports, 2015, 11, 4239-4245.	1.1	4
110	Genome-Wide Expression Profiling of Anoxia/Reoxygenation in Rat Cardiomyocytes Uncovers the Ro of MitoKATPin Energy Homeostasis. Oxidative Medicine and Cellular Longevity, 2015, 2015, 1-14.	ole 1.9	11

Genome-Wide Identification of Genes Probably Relevant to the Uniqueness of Tea Plant ( $\langle i \rangle$  Camellia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf

112	Suppression of endogenous gene silencing by bidirectional cytoplasmic RNA decay in <i>Arabidopsis</i> . Science, 2015, 348, 120-123.	6.0	140
113	Comparative Transcriptome Analysis between the Cytoplasmic Male Sterile Line NJCMS1A and Its Maintainer NJCMS1B in Soybean (Glycine max (L.) Merr.). PLoS ONE, 2015, 10, e0126771.	1.1	53
114	De novo RNA-Seq Analysis of the Venus Clam, Cyclina sinensis, and the Identification of Immune-Related Genes. PLoS ONE, 2015, 10, e0123296.	1.1	15
115	Transcriptome profile analysis of cell proliferation molecular processes during multicellular trichome formation induced by tomato Wo v gene in tobacco. Genomics Data, 2015, 6, 173-174.	1.3	4
116	Comparative analysis of blood and saliva expression profiles in chronic and refractory periodontitis patients. BMC Oral Health, 2015, 15, 166.	0.8	11
117	Proteomics Analyses of <i>Bacillus subtilis</i> after Treatment with Plumbagin, a Plant-Derived Naphthoquinone. OMICS A Journal of Integrative Biology, 2015, 19, 12-23.	1.0	22
118	Predicting of disease genes for gestational diabetes mellitus based on network and functional consistency. European Journal of Obstetrics, Gynecology and Reproductive Biology, 2015, 186, 91-96.	0.5	6
119	Hepatic Proteomic Responses in Marine Medaka ( <i>Oryzias melastigma</i> ) Chronically Exposed to Antifouling Compound Butenolide [5-octylfuran-2(5H)-one] or 4,5-Dichloro-2- <i>N</i> -Octyl-4-Isothiazolin-3-One (DCOIT). Environmental Science & Technology, 2015, 49, 1851-1859.	4.6	41
120	Enrichment or depletion? The impact of stool pretreatment on metaproteomic characterization of the human gut microbiota. Proteomics, 2015, 15, 3474-3485.	1.3	63
121	Genome-wide identification, classification and functional analyses of the bHLH transcription factor family in the pig, Sus scrofa. Molecular Genetics and Genomics, 2015, 290, 1415-1433.	1.0	4
122	<i>Treponema pallidum</i> Putative Novel Drug Target Identification and Validation: Rethinking Syphilis Therapeutics with Plant-Derived Terpenoids. OMICS A Journal of Integrative Biology, 2015, 19, 104-114.	1.0	6
123	A comprehensive proteomic analysis of totarol induced alterations in Bacillus subtilis by multipronged quantitative proteomics. Journal of Proteomics, 2015, 114, 247-262.	1.2	26
124	Comparative analysis of the silk gland transcriptomes between the domestic and wild silkworms. BMC Genomics, 2015, 16, 60.	1.2	84
125	Pedican: an online gene resource for pediatric cancers with literature evidence. Scientific Reports, 2015, 5, 11435.	1.6	8
126	Transcriptomic changes during maize roots development responsive to Cadmium (Cd) pollution using comparative RNAseq-based approach. Biochemical and Biophysical Research Communications, 2015, 464, 1040-1047.	1.0	37

#	Article	IF	Citations
127	Transcriptome Analysis of Invasive Plants in Response to Mineral Toxicity of Reclaimed Coal-Mine Soil in the Appalachian Region. Environmental Science & Technology, 2015, 49, 10320-10329.	4.6	16
128	Nonuniform gene expression pattern detected along the longitudinal axis in the matured rice leaf. Scientific Reports, 2015, 5, 8015.	1.6	10
129	Unsaturated fatty acids as high-affinity ligands of the C-terminal Per-ARNT-Sim domain from the Hypoxia-inducible factor 31±. Scientific Reports, 2015, 5, 12698.	1.6	17
130	Genome-Wide Identification of Klebsiella pneumoniae Fitness Genes during Lung Infection. MBio, 2015, 6, e00775.	1.8	168
131	Comparative transcriptome analysis reveals defense-related genes and pathways against downy mildew in Vitis amurensis grapevine. Plant Physiology and Biochemistry, 2015, 95, 1-14.	2.8	66
132	Transcriptomic dissection of sexual differences in Bemisia tabaci, an invasive agricultural pest worldwide. Scientific Reports, 2014, 4, 4088.	1.6	27
133	Transcriptome analysis reveals the oxidative stress response in Saccharomyces cerevisiae. RSC Advances, 2015, 5, 22923-22934.	1.7	22
134	Global gene expression patterns of grass carp following compensatory growth. BMC Genomics, 2015, 16, 184.	1.2	37
135	Pistillody mutant reveals key insights into stamen and pistil development in wheat (Triticum aestivum) Tj ETQq0	0 0 rgBT /( 1.2	Overlock 10 T
135 136	Pistillody mutant reveals key insights into stamen and pistil development in wheat (Triticum aestivum) Tj ETQqO Global analysis of the Gossypium hirsutum L. Transcriptome during leaf senescence by RNA-Seq. BMC Plant Biology, 2015, 15, 43.	0 Q. <u>rg</u> BT /( 1.6	Overlock 10 T
	Global analysis of the Gossypium hirsutum L. Transcriptome during leaf senescence by RNA-Seq. BMC	1,2	20
136	Global analysis of the Gossypium hirsutum L. Transcriptome during leaf senescence by RNA-Seq. BMC Plant Biology, 2015, 15, 43. Comparative metabolic and transcriptional analysis of a doubled diploid and its diploid citrus rootstock (C. junos cv. Ziyang xiangcheng) suggests its potential value for stress resistance	1.6	85
136 137	<ul> <li>Global analysis of the Gossypium hirsutum L. Transcriptome during leaf senescence by RNA-Seq. BMC Plant Biology, 2015, 15, 43.</li> <li>Comparative metabolic and transcriptional analysis of a doubled diploid and its diploid citrus rootstock (C. junos cv. Ziyang xiangcheng) suggests its potential value for stress resistance improvement. BMC Plant Biology, 2015, 15, 89.</li> <li>Comparative Analysis of Testis Transcriptomes from Triploid and Fertile Diploid Cyprinid Fish1. Biology</li> </ul>	1.6 1.6	85 120
136 137 138	<ul> <li>Global analysis of the Gossypium hirsutum L. Transcriptome during leaf senescence by RNA-Seq. BMC Plant Biology, 2015, 15, 43.</li> <li>Comparative metabolic and transcriptional analysis of a doubled diploid and its diploid citrus rootstock (C. junos cv. Ziyang xiangcheng) suggests its potential value for stress resistance improvement. BMC Plant Biology, 2015, 15, 89.</li> <li>Comparative Analysis of Testis Transcriptomes from Triploid and Fertile Diploid Cyprinid Fish1. Biology of Reproduction, 2015, 92, 95.</li> <li>Insights from the Metagenome of an Acid Salt Lake: The Role of Biology in an Extreme Depositional</li> </ul>	1.6 1.6 1.2	85 120 32
136 137 138 139	Global analysis of the Gossypium hirsutum L. Transcriptome during leaf senescence by RNA-Seq. BMC Plant Biology, 2015, 15, 43.         Comparative metabolic and transcriptional analysis of a doubled diploid and its diploid citrus rootstock (C. junos cv. Ziyang xiangcheng) suggests its potential value for stress resistance improvement. BMC Plant Biology, 2015, 15, 89.         Comparative Analysis of Testis Transcriptomes from Triploid and Fertile Diploid Cyprinid Fish1. Biology of Reproduction, 2015, 92, 95.         Insights from the Metagenome of an Acid Salt Lake: The Role of Biology in an Extreme Depositional Environment. PLoS ONE, 2015, 10, e0122869.         Transcription profiling of the chilling requirement for bud break in apples: a putative role for FLC-like	1.6 1.6 1.2 1.1	20 85 120 32 44
136 137 138 139 140	Clobal analysis of the Cossypium hirsutum L. Transcriptome during leaf senescence by RNA-Seq. BMC         Plant Biology, 2015, 15, 43.         Comparative metabolic and transcriptional analysis of a doubled diploid and its diploid citrus rootstock (C. junos cv. Ziyang xiangcheng) suggests its potential value for stress resistance improvement. BMC Plant Biology, 2015, 15, 89.         Comparative Analysis of Testis Transcriptomes from Triploid and Fertile Diploid Cyprinid Fish1. Biology of Reproduction, 2015, 92, 95.         Insights from the Metagenome of an Acid Salt Lake: The Role of Biology in an Extreme Depositional Environment. PLoS ONE, 2015, 10, e0122869.         Transcription profiling of the chilling requirement for bud break in apples: a putative role for FLC-like genes. Journal of Experimental Botany, 2015, 66, 2659-2672.	1.2 1.6 1.2 1.1 2.4	20 85 120 32 44 78

145	Palladin expression is a conserved characteristic of the desmoplastic tumor microenvironment and contributes to altered gene expression. Cytoskeleton, 2015, 72, 402-411.	1.0	16
-----	---	-----	----

#	Article	IF	CITATIONS
146	Identifying new targets in leukemogenesis using computational approaches. Saudi Journal of Biological Sciences, 2015, 22, 610-622.	1.8	8
147	Proteome Analysis Unravels Mechanism Underling the Embryogenesis of the Honeybee Drone and Its Divergence with the Worker ( <i>Apis mellifera lingustica</i> ). Journal of Proteome Research, 2015, 14, 4059-4071.	1.8	22
148	Proteome of tolerance fine-tuning in the human pathogen black yeast Exophiala dermatitidis. Journal of Proteomics, 2015, 128, 39-57.	1.2	19
149	Resistance gene analogs involved in tolerant cassava–geminivirus interaction that shows a recovery phenotype. Virus Genes, 2015, 51, 393-407.	0.7	17
150	SILAC-based quantitative proteomics identified lysosome as a fast response target to PDT agent Gd-N induced oxidative stress in human ovarian cancer IGROV1 cells. Molecular BioSystems, 2015, 11, 3059-3067.	2.9	6
151	MicroRNA-regulation of Anopheles gambiae immunity to Plasmodium falciparum infection and midgut microbiota. Developmental and Comparative Immunology, 2015, 49, 170-178.	1.0	59
152	Profiling the RNA editomes of wild-type <i>C. elegans</i> and ADAR mutants. Genome Research, 2015, 25, 66-75.	2.4	70
153	Genomic and transcriptomic analysis of NDM-1 Klebsiella pneumoniae in spaceflight reveal mechanisms underlying environmental adaptability. Scientific Reports, 2014, 4, 6216.	1.6	36
155	SOX9 regulates ERBB signalling in pancreatic cancer development. Gut, 2015, 64, 1790-1799.	6.1	71
156	Transcript analysis of a goat mesenteric lymph node by deep next-generation sequencing. Genetics and Molecular Research, 2016, 15, .	0.3	1
157	XGSA: A statistical method for cross-species gene set analysis. Bioinformatics, 2016, 32, i620-i628.	1.8	18
158	RNA interference-mediated silencing of speckle-type POZ protein promotes apoptosis of renal cell cancer cells. OncoTargets and Therapy, 2016, 9, 2393.	1.0	11
159	RNA sequencing analysis to capture the transcriptome landscape during skin ulceration syndrome progression in sea cucumber Apostichopus japonicus. BMC Genomics, 2016, 17, 459.	1.2	40
160	Dynamic transcriptome profiling of Bean Common Mosaic Virus (BCMV) infection in Common Bean (Phaseolus vulgaris L.). BMC Genomics, 2016, 17, 613.	1.2	30
161	Isobaric Tags for Relative and Absolute Quantitation (iTRAQ)-Based Comparative Proteome Analysis of the Response of Ramie under Drought Stress. International Journal of Molecular Sciences, 2016, 17, 1607.	1.8	15
162	Functional Genomic Analysis of Aspergillus flavus Interacting with Resistant and Susceptible Peanut. Toxins, 2016, 8, 46.	1.5	33
163	Transcriptome Analysis to Understand the Toxicity of Latrodectus tredecimguttatus Eggs. Toxins, 2016, 8, 378.	1.5	13
164	Genome-Wide Transcriptional and Post-transcriptional Regulation of Innate Immune and Defense Responses of Bovine Mammary Gland to Staphylococcus aureus. Frontiers in Cellular and Infection Microbiology 2016 6, 193	1.8	96

#	Article	IF	CITATIONS
165	The Global Reciprocal Reprogramming between Mycobacteriophage SWU1 and Mycobacterium Reveals the Molecular Strategy of Subversion and Promotion of Phage Infection. Frontiers in Microbiology, 2016, 7, 41.	1.5	8
166	Transcriptomes of Arbuscular Mycorrhizal Fungi and Litchi Host Interaction after Tree Girdling. Frontiers in Microbiology, 2016, 7, 408.	1.5	36
167	Dual Identification and Analysis of Differentially Expressed Transcripts of Porcine PK-15 Cells and Toxoplasma gondii during in vitro Infection. Frontiers in Microbiology, 2016, 7, 721.	1.5	60
168	Transcriptomic and Proteomic Analysis of Oenococcus oeni Adaptation to Wine Stress Conditions. Frontiers in Microbiology, 2016, 7, 1554.	1.5	62
169	Proteome Profile and Quantitative Proteomic Analysis of Buffalo (Bubalusbubalis) Follicular Fluid during Follicle Development. International Journal of Molecular Sciences, 2016, 17, 618.	1.8	33
170	Transcriptome Sequencing and De Novo Assembly of Golden Cuttlefish Sepia esculenta Hoyle. International Journal of Molecular Sciences, 2016, 17, 1749.	1.8	15
171	Transcriptome Analysis of mRNA and miRNA in Somatic Embryos of Larix leptolepis Subjected to Hydrogen Treatment. International Journal of Molecular Sciences, 2016, 17, 1951.	1.8	17
172	Comparative Transcriptomic Analysis of Grape Berry in Response to Root Restriction during Developmental Stages. Molecules, 2016, 21, 1431.	1.7	21
173	Systematic Identification and Characterization of Long Non-Coding RNAs in the Silkworm, Bombyx mori. PLoS ONE, 2016, 11, e0147147.	1.1	155
174	Comparative RNA-Seq Analysis Reveals That Regulatory Network of Maize Root Development Controls the Expression of Genes in Response to N Stress. PLoS ONE, 2016, 11, e0151697.	1.1	29
175	Comparative Analysis of Transcriptomes among Bombyx mori Strains and Sexes Reveals the Genes Regulating Melanic Morph and the Related Phenotypes. PLoS ONE, 2016, 11, e0155061.	1.1	3
176	Quantitative Determination of Flexible Pharmacological Mechanisms Based On Topological Variation in Mice Anti-Ischemic Modular Networks. PLoS ONE, 2016, 11, e0158379.	1.1	8
177	Time-Course Study of the Transcriptome of Peripheral Blood Mononuclear Cells (PBMCs) from Sheep Infected with Fasciola hepatica. PLoS ONE, 2016, 11, e0159194.	1.1	29
178	Comparative Transcriptome Analysis Reveals Substantial Tissue Specificity in Human Aortic Valve. Evolutionary Bioinformatics, 2016, 12, EBO.S37594.	0.6	6
179	Transcriptome Analysis Identifies Candidate Genes Related to Triacylglycerol and Pigment Biosynthesis and Photoperiodic Flowering in the Ornamental and Oil-Producing Plant, Camellia reticulata (Theaceae). Frontiers in Plant Science, 2016, 7, 163.	1.7	29
180	Transcriptomic Analysis Identifies Differentially Expressed Genes (DEGs) Associated with Bolting and Flowering in Radish (Raphanus sativus L.). Frontiers in Plant Science, 2016, 7, 682.	1.7	26
181	Suppression Substractive Hybridization and NGS Reveal Differential Transcriptome Expression Profiles in Wayfaring Tree (Viburnum lantana L.) Treated with Ozone. Frontiers in Plant Science, 2016, 7, 713.	1.7	12
182	Transcriptome- Assisted Label-Free Quantitative Proteomics Analysis Reveals Novel Insights into Piper nigrum—Phytophthora capsici Phytopathosystem. Frontiers in Plant Science, 2016, 7, 785.	1.7	29

#	Article	IF	CITATIONS
183	Transcriptome Profiling Revealed Stress-Induced and Disease Resistance Genes Up-Regulated in PRSV Resistant Transgenic Papaya. Frontiers in Plant Science, 2016, 7, 855.	1.7	28
184	Comparative Transcriptome Analysis Reveals Heat-Responsive Genes in Chinese Cabbage (Brassica rapa) Tj ETQq1	1,0.7843 1.7	14 rgBT /0\ 46
185	Identification of microRNAs and Their Target Genes Explores miRNA-Mediated Regulatory Network of Cytoplasmic Male Sterility Occurrence during Anther Development in Radish (Raphanus sativus L.). Frontiers in Plant Science, 2016, 7, 1054.	1.7	40
186	Identification of Drought Tolerant Mechanisms in Maize Seedlings Based on Transcriptome Analysis of Recombination Inbred Lines. Frontiers in Plant Science, 2016, 7, 1080.	1.7	98

188	Transcriptome Analysis of Pepper (Capsicum annuum) Revealed a Role of 24-Epibrassinolide in Response to Chilling. Frontiers in Plant Science, 2016, 7, 1281.	1.7	51
189	Transcriptome Analysis of Cadmium-Treated Roots in Maize (Zea mays L.). Frontiers in Plant Science, 2016, 7, 1298.	1.7	59
190	Comparative Analysis of miRNAs and Their Target Transcripts between a Spontaneous Late-Ripening Sweet Orange Mutant and Its Wild-Type Using Small RNA and Degradome Sequencing. Frontiers in Plant Science, 2016, 7, 1416.	1.7	23
191	Insights from the Cold Transcriptome and Metabolome of Dendrobium officinale: Global Reprogramming of Metabolic and Gene Regulation Networks during Cold Acclimation. Frontiers in Plant Science, 2016, 7, 1653.	1.7	75
192	Tomato FK506 Binding Protein 12KD (FKBP12) Mediates the Interaction between Rapamycin and Target of Rapamycin (TOR). Frontiers in Plant Science, 2016, 7, 1746.	1.7	40
193	Comparative Transcriptomics of Strawberries (Fragaria spp.) Provides Insights into Evolutionary Patterns. Frontiers in Plant Science, 2016, 7, 1839.	1.7	33
194	Genome-wide identification and characterization of long non-coding RNAs in developmental skeletal muscle of fetal goat. BMC Genomics, 2016, 17, 666.	1.2	117
195	Methanogenic paraffin degradation proceeds via alkane addition to fumarate by <i>â€~Smithella'</i> spp. mediated by a syntrophic coupling with hydrogenotrophic methanogens. Environmental Microbiology, 2016, 18, 2604-2619.	1.8	71
196	Comparative metabolomic analysis reveals a reactive oxygen speciesâ€dominated dynamic model underlying chilling environment adaptation and tolerance in rice. New Phytologist, 2016, 211, 1295-1310.	3.5	118
197	Deciphering the transcriptomic response of Fusarium verticillioides in relation to nitrogen availability and the development of sugarcane pokkah boeng disease. Scientific Reports, 2016, 6, 29692.	1.6	23
198	Identification of conserved and novel microRNAs in Porphyridium purpureum via deep sequencing and bioinformatics. BMC Genomics, 2016, 17, 612.	1.2	12
199	Analysis of Annotation and Differential Expression Methods used in RNA-seq Studies in Crustacean Systems. Integrative and Comparative Biology, 2016, 56, 1067-1079.	0.9	20
200	FARNA: knowledgebase of inferred functions of non-coding RNA transcripts. Nucleic Acids Research, 2017, 45, gkw973.	6.5	30

#	Article	IF	CITATIONS
201	Evolutionary study of Yersinia genomes deciphers emergence of human pathogenic species. Scientific Reports, 2016, 6, 36116.	1.6	14
202	Suppressive subtractive hybridization reveals different gene expression between high and low virulence strains of Cladosporium cladosporioides. Microbial Pathogenesis, 2016, 100, 276-284.	1.3	1
203	De novo Transcriptome Analysis Reveals Distinct Defense Mechanisms by Young and Mature Leaves of Hevea brasiliensis (Para Rubber Tree). Scientific Reports, 2016, 6, 33151.	1.6	40
204	Genome-wide Investigation of microRNAs and Their Targets in Brassica rapa ssp. pekinensis Root with Plasmodiophora brassicae Infection. Horticultural Plant Journal, 2016, 2, 209-216.	2.3	16
205	The C-terminal motif of SiAGO1b is required for the regulation of growth, development and stress responses in foxtail millet ( <i>Setaria italica</i> (L.) P. Beauv). Journal of Experimental Botany, 2016, 67, 3237-3249.	2.4	33
206	High-throughput transcriptome sequencing reveals the combined effects of key e-waste contaminants, decabromodiphenyl ether (BDE-209) and lead, in zebrafish larvae. Environmental Pollution, 2016, 214, 324-333.	3.7	33
207	Effect of interleukin- $1\hat{l}^2$ and tumor necrosis factor $\hat{l}\pm$ gene silencing on mouse gastric cancer cell proliferation and migration. Oncology Letters, 2016, 11, 2559-2565.	0.8	6
208	Biological findings from the PheWAS catalog: focus on connective tissue-related disorders (pelvic) Tj ETQq1 1 779-795.	0.784314 rgE 1.8	3T /Overlock 14
209	Molecular exploration of algal interaction between the diatom Phaeodactylum tricornutum and the dinoflagellate Alexandrium tamarense. Algal Research, 2016, 17, 132-141.	2.4	29
210	The chemical toxicity of cesium in Indian mustard (Brassica juncea L.) seedlings. Journal of Environmental Radioactivity, 2016, 160, 93-101.	0.9	13
211	The phytopathogenic virulent effector protein Ripl induces apoptosis in budding yeast Saccharomyces cerevisiae. Toxicon, 2016, 121, 109-118.	0.8	8
212	Draft genome sequence and annotation ofLactobacillus acetotoleransBM-LA14527, a beer-spoilage bacteria. FEMS Microbiology Letters, 2016, 363, fnw201.	0.7	45
213	Transcriptome profiling of developmental leaf senescence in sorghum (Sorghum bicolor). Plant Molecular Biology, 2016, 92, 555-580.	2.0	36
214	De novo transcriptome assembly and development of SSR markers of oaks Quercus austrocochinchinensis and Q. kerrii (Fagaceae). Tree Genetics and Genomes, 2016, 12, 1.	0.6	20
215	RNA sequencing reveals differential thermal regulation mechanisms between sexes of Glanville fritillary butterfly in the Tianshan Mountains, China. Molecular Biology Reports, 2016, 43, 1423-1433.	1.0	3
216	New insights into the mechanisms of acetic acid resistance in Acetobacter pasteurianus using iTRAQ-dependent quantitative proteomic analysis. International Journal of Food Microbiology, 2016, 238, 241-251.	2.1	40
217	Comparative RNA-Seq profiling of berry development between table grape â€~Kyoho' and its early-ripenin mutant 'Fengzao'. BMC Genomics, 2016, 17, 795.	g <sub>1.2</sub>	47
218	Long noncoding RNA expression profile of infantile hemangioma identified by microarray analysis. Tumor Biology, 2016, 37, 15977-15987.	0.8	26

ARTICLE IF CITATIONS Multi-omics analysis reveals regulators of the response to PDGF-BB treatment in pulmonary artery 219 1.2 24 smooth muscle cells. BMC Genomics, 2016, 17, 781. Identification of 2-oxohistidine Interacting Proteins Using E. coli Proteome Chips. Molecular and 2.5 Cellular Proteomics, 2016, 15, 3581-3593. Root transcriptome sequencing and differentially expressed drought-responsive genes in the 221 0.6 12 Platycladus orientalis (L.). Tree Genetics and Genomes, 2016, 12, 1. Identification of novel biomarkers associated with poor patient outcomes in invasive breast 0.8 carcinoma. Tumor Biology, 2016, 37, 13855-13870. Transcriptome analysis of Dlm mutants reveals the potential formation mechanism of lesion mimic in 223 0.8 6 wheat. European Journal of Plant Pathology, 2016, 146, 987-997. The transcriptome response of <i>Heliconius melpomene</i> larvae to a novel host plant. Molecular Ecology, 2016, 25, 4850-4865. 224 39 Expression patterns of miR-146a and miR-146b in mastitis infected dairy cattle. Molecular and Cellular 225 0.9 33 Probes, 2016, 30, 342-344. Chromatin Immunoprecipitation Sequencing Technology Reveals Global Regulatory Roles of Low-Cell-Density Quorum-Sensing Regulator AphA in the Pathogen Vibrio alginolyticus. Journal of 1.0 40 Bacteriology, 2016, 198, 2985-2999. 227 Applications of Quantitative Proteomics in Plant Research., 2016, , 1-29. 5 Proteome profiling reveals insights into cold-tolerant growth in sea buckthorn. Proteome Science, 2016, 14, 14. COMAN: a web server for comprehensive metatranscriptomics analysis. BMC Genomics, 2016, 17, 622. 229 1.2 34 Transcriptomic analysis of different stages of pigeon ovaries by RNAâ€sequencing. Molecular 1.0 Reproduction and Development, 2016, 83, 640-648. Survive or die? A molecular insight into salt-dependant signaling network. Environmental and 231 2.0 16 Experimental Botany, 2016, 132, 140-153. Extremotolerant tardigrade genome and improved radiotolerance of human cultured cells by 5.8 270 tardigrade-unique protein. Nature Communications, 2016, 7, 12808. The genome and transcriptome of Trichormus sp. NMC-1: insights into adaptation to extreme 233 33 1.6 environments on the Qinghai-Tibet Plateau. Scientific Reports, 2016, 6, 29404. Comprehensive proteomic analysis of developing protein bodies in maize (<i>Zea mays</i>) endosperm 234 2.4 28 provides novel insights into its biogenesis. Journal of Experimental Botany, 2016, 67, 6323-6335. High hydrostatic pressure adaptive strategies in an obligate piezophile Pyrococcus yayanosii. 235 1.6 53 Scientific Reports, 2016, 6, 27289. Metagenomic analysis and functional characterization of the biogas microbiome using high 6.2 248 throughput shotgun sequencing and a novel binning strategy. Biotechnology for Biofuels, 2016, 9, 26.

#	Article	IF	CITATIONS
237	Exploring the intrinsic differences among breast tumor subtypes defined using immunohistochemistry markers based on the decision tree. Scientific Reports, 2016, 6, 35773.	1.6	17
238	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
239	A combination of genome-wide association and transcriptome analysis reveals candidate genes controlling harvest index-related traits in Brassica napus. Scientific Reports, 2016, 6, 36452.	1.6	59
240	Comparative analysis of the integument transcriptomes of the black dilute mutant and the wild-type silkworm Bombyx mori. Scientific Reports, 2016, 6, 26114.	1.6	18
241	Identification and Characterization of miRNAs in Chondrus crispus by High-Throughput Sequencing and Bioinformatics Analysis. Scientific Reports, 2016, 6, 26397.	1.6	7
242	Transcriptome sequencing of Crucihimalaya himalaica (Brassicaceae) reveals how Arabidopsis close relative adapt to the Qinghai-Tibet Plateau. Scientific Reports, 2016, 6, 21729.	1.6	47
243	Metabolic engineering of cottonseed oil biosynthesis pathway via RNA interference. Scientific Reports, 2016, 6, 33342.	1.6	31
244	Differential Gene Expression Analysis of the <i>Epacromius coerulipes</i> (Orthoptera: Acrididae) Transcriptome. Journal of Insect Science, 2016, 16, 42.	0.6	8
245	REGene: a literature-based knowledgebase of animal regeneration that bridge tissue regeneration and cancer. Scientific Reports, 2016, 6, 23167.	1.6	16
246	Identification of microRNAs regulating Escherichia coli F18 infection in Meishan weaned piglets. Biology Direct, 2016, 11, 59.	1.9	15
247	Dissection of early transcriptional responses to water stress in Arundo donax L. by unigene-based RNA-seq. Biotechnology for Biofuels, 2016, 9, 54.	6.2	32
248	MiR-130a regulates neurite outgrowth and dendritic spine density by targeting MeCP2. Protein and Cell, 2016, 7, 489-500.	4.8	30
249	Resolution of Novel Pancreatic Ductal Adenocarcinoma Subtypes by Global Phosphotyrosine Profiling. Molecular and Cellular Proteomics, 2016, 15, 2671-2685.	2.5	29
250	In depth understanding the molecular response to the enhanced secretion of fatty acids in S accharomyces cerevisiae due to one-step gene deletion of acyl-CoA synthetases. Process Biochemistry, 2016, 51, 1162-1174.	1.8	6
251	Gene expression comparison of resistant and susceptible Atlantic salmon fry challenged with Infectious Pancreatic Necrosis virus reveals a marked contrast in immune response. BMC Genomics, 2016, 17, 279.	1.2	78
252	Comparative transcript profiling of resistant and susceptible peanut post-harvest seeds in response to aflatoxin production by Aspergillus flavus. BMC Plant Biology, 2016, 16, 54.	1.6	41
253	DESM: portal for microbial knowledge exploration systems. Nucleic Acids Research, 2016, 44, D624-D633.	6.5	12
254	Global transcriptome profiling analysis reveals insight into saliva-responsive genes in alfalfa. Plant Cell Reports, 2016, 35, 561-571.	2.8	29

#	Article	IF	CITATIONS
255	Phytophthora infestans specific phosphorylation patterns and new putative control targets. Fungal Biology, 2016, 120, 631-644.	1.1	0
256	Characterization and refinement of growth related quantitative trait loci in European sea bass (Dicentrarchus labrax) using a comparative approach. Aquaculture, 2016, 455, 8-21.	1.7	16
257	iTRAQ protein profile analysis provides integrated insight into mechanisms of tolerance to TMV in tobacco (Nicotiana tabacum). Journal of Proteomics, 2016, 132, 21-30.	1.2	35
258	Hyperlipidemia, Disease Associations, and Top 10 Potential Drug Targets: A Network View. OMICS A Journal of Integrative Biology, 2016, 20, 152-168.	1.0	16
259	Transcriptome analyses of insect cells to facilitate baculovirus-insect expression. Protein and Cell, 2016, 7, 373-382.	4.8	12
260	A Chronic Obstructive Pulmonary Disease Susceptibility Gene, <i>FAM13A</i> , Regulates Protein Stability of β-Catenin. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 185-197.	2.5	101
261	Host cell interactome of PA protein of H5N1 influenza A virus in chicken cells. Journal of Proteomics, 2016, 136, 48-54.	1.2	24
262	Critical Genomic Networks and Vasoreactive Variants in Idiopathic Pulmonary Arterial Hypertension. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 464-475.	2.5	69
263	Cardiac concentric hypertrophy promoted by activated Met receptor is mitigated in vivo by inhibition of Erk1,2 signalling with Pimasertib. Journal of Molecular and Cellular Cardiology, 2016, 93, 84-97.	0.9	12
264	Genomic structural variation contributes to phenotypic change of industrial bioethanol yeast <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2016, 16, fov118.	1.1	21
265	Identification and characterization of microRNAs in Eucheuma denticulatum by high-throughput sequencing and bioinformatics analysis. RNA Biology, 2016, 13, 343-352.	1.5	11
266	TNF-alpha â^'308G/A and â^'238G/A polymorphisms and its protein network associated with type 2 diabetes mellitus. Saudi Journal of Biological Sciences, 2017, 24, 1195-1203.	1.8	25
267	Dataset of the proteome of purified outer membrane vesicles from the human pathogen Aggregatibacter actinomycetemcomintans. Data in Brief, 2017, 10, 426-431.	0.5	6
268	Linking genomic responses of gonads with reproductive impairment in marine medaka (Oryzias) Tj ETQq1 1 0.78 (DIM). Aquatic Toxicology, 2017, 183, 135-143.	34314 rgBT 1.9	/Overlock 1 12
269	DGE-seq analysis of MUR3-related Arabidopsis mutants provides insight into how dysfunctional xyloglucan affects cell elongation. Plant Science, 2017, 258, 156-169.	1.7	22
270	Transcriptome-wide identification and functional investigation of circular RNA in the teleost large yellow croaker (Larimichthys crocea). Marine Genomics, 2017, 32, 71-78.	0.4	38
271	Decoding the role of the nuclear receptor SHP in regulating hepatic stellate cells and liver fibrogenesis. Scientific Reports, 2017, 7, 41055.	1.6	12
272	Histopathology combined with transcriptome analyses reveals the mechanism of resistance to Meloidogyne incognita in Cucumis metuliferus. Journal of Plant Physiology, 2017, 212, 115-124.	1.6	27

#	ARTICLE	IF	CITATIONS
273	Divergent adaptation to Qinghai-Tibetan Plateau implicated from transciptome study of Gymnocypris dobula and Schizothorax nukiangensis. Biochemical Systematics and Ecology, 2017, 71, 97-105.	0.6	4
274	Chilling Affects Phytohormone and Post-Embryonic Development Pathways during Bud Break and Fruit Set in Apple (Malus domestica Borkh.). Scientific Reports, 2017, 7, 42593.	1.6	22
275	Transcriptome data analysis of grass carp ( Ctenopharyngodon idella ) infected by reovirus provides insights into two immune-related genes. Fish and Shellfish Immunology, 2017, 64, 68-77.	1.6	35
276	Transcriptomic and virulence factors analyses of <i>Cryptococcus neoformans</i> hypoxia response. Apmis, 2017, 125, 236-248.	0.9	7
277	Deep Illumina sequencing reveals conserved and novel microRNAs in grass carp in response to grass carp reovirus infection. BMC Genomics, 2017, 18, 195.	1.2	18
278	Genomic complexity and targeted genes in anaplastic thyroid cancer cell lines. Endocrine-Related Cancer, 2017, 24, 209-220.	1.6	19
279	Anatomical and transcriptional dynamics of early floral development of mulberry (Morus alba). Tree Genetics and Genomes, 2017, 13, 1.	0.6	9
280	Gene discovery and marker resource development by transcriptome sequencing from a shortâ€rotation coppice willow, <i><scp>S</scp>alix suchowensis</i> . Plant Breeding, 2017, 136, 279-286.	1.0	2
281	Proteome analysis of human embryonic stem cells organelles. Journal of Proteomics, 2017, 162, 108-118.	1.2	12
282	Transcriptomic analyses reveal biosynthetic genes related to rosmarinic acid in Dracocephalum tanguticum. Scientific Reports, 2017, 7, 74.	1.6	27
283	Ethylene Signaling Is Important for Isoflavonoid-Mediated Resistance to <i>Rhizoctonia solani</i> in Roots of <i>Medicago truncatula</i> . Molecular Plant-Microbe Interactions, 2017, 30, 691-700.	1.4	40
284	Using scale and feather traits for module construction provides a functional approach to chicken epidermal development. Functional and Integrative Genomics, 2017, 17, 641-651.	1.4	2
285	Signalome-wide assessment of host cell response to hepatitis C virus. Nature Communications, 2017, 8, 15158.	5.8	14
286	iTRAQ-based proteomic analysis reveals key proteins affecting muscle growth and lipid deposition in pigs. Scientific Reports, 2017, 7, 46717.	1.6	77
287	Dynamics of the Interaction between Cotton Bollworm Helicoverpa armigera and Nucleopolyhedrovirus as Revealed by Integrated Transcriptomic and Proteomic Analyses. Molecular and Cellular Proteomics, 2017, 16, 1009-1028.	2.5	40
288	Comparative transcriptomic analysis of <i>Bombyx mori</i> fat body tissue following dietary restriction. Archives of Insect Biochemistry and Physiology, 2017, 95, e21388.	0.6	5
289	RNA Sequencing Exposes Adaptive and Immune Responses to Intrauterine Growth Restriction in Fetal Sheep Islets. Endocrinology, 2017, 158, 743-755.	1.4	29
290	Comparative transcriptomic and proteomic analyses provide insights into the key genes involved in high-altitude adaptation in the Tibetan pig. Scientific Reports, 2017, 7, 3654.	1.6	38

#	Article	IF	CITATIONS
291	Characteristics and Expression Profile of <i>KRT71</i> Screened by Suppression Subtractive Hybridization cDNA Library in Curly Fleece Chinese Tan Sheep. DNA and Cell Biology, 2017, 36, 552-564.	0.9	11
292	Transcriptomics analysis of hulless barley during grain development with a focus on starch biosynthesis. Functional and Integrative Genomics, 2017, 17, 107-117.	1.4	14
293	Expression Profiling of mRNAs and Long Non-Coding RNAs in Aged Mouse Olfactory Bulb. Scientific Reports, 2017, 7, 2079.	1.6	12
294	Comparative transcriptome analysis of sweet corn seedlings under low-temperature stress. Crop Journal, 2017, 5, 396-406.	2.3	21
295	Transcriptomic analysis of short-fruit 1 (sf1) reveals new insights into the variation of fruit-related traits in Cucumis sativus. Scientific Reports, 2017, 7, 2950.	1.6	26
296	Similarity in gene-regulatory networks suggests that cancer cells share characteristics of embryonic neural cells. Journal of Biological Chemistry, 2017, 292, 12842-12859.	1.6	46
297	Understanding the mechanisms of dormancy in an invasive alien Sycamore lace bug, Corythucha ciliata through transcript and metabolite profiling. Scientific Reports, 2017, 7, 2631.	1.6	31
298	Global identification, structural analysis and expression characterization of bHLH transcription factors in wheat. BMC Plant Biology, 2017, 17, 90.	1.6	51
299	Different exogenous sugars affect the hormone signal pathway and sugar metabolism in "Red Globe― (Vitis vinifera L.) plantlets grown in vitro as shown by transcriptomic analysis. Planta, 2017, 246, 537-552.	1.6	15
300	The effect of histone deacetylase inhibitor trichostatin A on porcine mesenchymal stem cell transcriptome. Biochimie, 2017, 139, 56-73.	1.3	8
301	Insights into the prevalence and underlying causes of clonal variation through transcriptomic analysis in Pichia pastoris. Applied Microbiology and Biotechnology, 2017, 101, 5045-5058.	1.7	28
302	Acute Ischemia Induced by High-Density Culture Increases Cytokine Expression and Diminishes the Function and Viability of Highly Purified Human Islets of Langerhans. Transplantation, 2017, 101, 2705-2712.	0.5	24
303	Comparative transcriptomics provide insight into the morphogenesis and evolution of fistular leaves in Allium. BMC Genomics, 2017, 18, 60.	1.2	24
304	Analysis on pathogenic and virulent characteristics of the Cronobacter sakazakii strain BAA-894 by whole genome sequencing and its demonstration in basic biology science. Microbial Pathogenesis, 2017, 109, 280-286.	1.3	46
305	Comparative Proteomic Analysis of Posterior Silk Glands of Wild and Domesticated Silkworms Reveals Functional Evolution during Domestication. Journal of Proteome Research, 2017, 16, 2495-2507.	1.8	28
306	Early and late gene expression profiles of the ovine mucosa in response to Haemonchus contortus infection employing Illumina RNA-seq technology. Parasitology International, 2017, 66, 681-692.	0.6	13
307	Identification of salt-stress responsive microRNAs from Solanum lycopersicum and Solanum pimpinellifolium. Plant Growth Regulation, 2017, 83, 129-140.	1.8	23
308	Transcriptome comparative analysis between the cytoplasmic male sterile line and fertile line in soybean (Glycine max (L.) Merr.). Genes and Genomics, 2017, 39, 1117-1127.	0.5	7

#	Article	IF	CITATIONS
309	Mutual regulation of tumour vessel normalization and immunostimulatory reprogramming. Nature, 2017, 544, 250-254.	13.7	555
310	Different expression patterns of sperm motility-related genes in testis of diploid and tetraploid cyprinid fishâ€. Biology of Reproduction, 2017, 96, 907-920.	1.2	21
311	Comparative analysis of the liver transcriptome of Pelteobagrus vachellii with an alternative feeding time. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 22, 131-138.	0.4	12
312	Characterization of Leaf Transcriptome in Banksia hookeriana. Genomics, Proteomics and Bioinformatics, 2017, 15, 49-56.	3.0	14
313	Genome-wide transcriptome profiling of Carica papaya L. embryogenic callus. Physiology and Molecular Biology of Plants, 2017, 23, 357-368.	1.4	26
314	DES-ncRNA: A knowledgebase for exploring information about human micro and long noncoding RNAs based on literature-mining. RNA Biology, 2017, 14, 963-971.	1.5	21
315	Integrating Sequence-based GWAS and RNA-Seq Provides Novel Insights into the Genetic Basis of Mastitis and Milk Production in Dairy Cattle. Scientific Reports, 2017, 7, 45560.	1.6	81
316	Genome-wide identification, classification, and functional analysis of the basic helix–loop–helix transcription factors in the cattle, Bos Taurus. Mammalian Genome, 2017, 28, 176-197.	1.0	11
317	Transcriptomic profile of tobacco in response to Phytophthora nicotianae infection. Scientific Reports, 2017, 7, 401.	1.6	26
318	A metagenomic study of the preventive effect of <i>Lactobacillus rhamnosus</i> GG on intestinal polyp formation in Apc <sup>Min/+</sup> mice. Journal of Applied Microbiology, 2017, 122, 770-784.	1.4	23
319	Making a queen: an epigenetic analysis of the robustness of the honeybee ( <i><scp>A</scp>pis) Tj ETQq0 0 0 rg</i>	BT/Overlo 2.0	ock 10 Tf 50 3
320	Global transcriptional response of solventâ€sensitive and solventâ€tolerant <i>Pseudomonas putida</i> strains exposed to toluene. Environmental Microbiology, 2017, 19, 645-658.	1.8	36
321	Network-Based Approach to Identify Potential Targets and Drugs that Promote Neuroprotection and Neurorepair in Acute Ischemic Stroke. Scientific Reports, 2017, 7, 40137.	1.6	38
322	De Novo Peptide Sequencing: Deep Mining of High-Resolution Mass Spectrometry Data. Methods in Molecular Biology, 2017, 1549, 119-134.	0.4	10
323	Comparative interactomics for virus–human protein–protein interactions: <scp>DNA</scp> viruses versus <scp>RNA</scp> viruses. FEBS Open Bio, 2017, 7, 96-107.	1.0	42
324	A Systematic Bioinformatics Approach to Identify High Quality Mass Spectrometry Data and Functionally Annotate Proteins and Proteomes. Methods in Molecular Biology, 2017, 1549, 163-176.	0.4	3
325	Gene expression profile identifies potential biomarkers for human intervertebral disc degeneration. Molecular Medicine Reports, 2017, 16, 8665-8672.	1.1	27
326	Comparative analysis of tree peony petal development by transcriptome sequencing. Acta Physiologiae Plantarum, 2017, 39, 1.	1.0	10

#	Article	IF	CITATIONS
327	Transcriptomic responses to drought and salt stress in desert tree Prosopis juliflora. Plant Gene, 2017, 12, 114-122.	1.4	13
328	Bioinformatic analysis of retinal gene function and expression in diabetic rats. Experimental and Therapeutic Medicine, 2017, 14, 2485-2492.	0.8	20
329	Changes of host DNA methylation in domestic chickens infected with Salmonella enterica. Journal of Genetics, 2017, 96, 545-550.	0.4	7
330	Transcriptome profiling and functional analysis of sheep fed with high zinc-supplemented diet: A nutrigenomic approach. Animal Feed Science and Technology, 2017, 234, 195-204.	1.1	11
331	Time-Resolved Transposon Insertion Sequencing Reveals Genome-Wide Fitness Dynamics during Infection. MBio, 2017, 8, .	1.8	42
332	Identification of genes associated with castration-resistant prostate cancer by gene expression profile analysis. Molecular Medicine Reports, 2017, 16, 6803-6813.	1.1	13
333	Quantitative proteome analysis of bovine mammary gland reveals protein dynamic changes involved in peak and late lactation stages. Biochemical and Biophysical Research Communications, 2017, 494, 292-297.	1.0	16
334	Annotation of nerve cord transcriptome in earthworm Eisenia fetida. Genomics Data, 2017, 14, 91-105.	1.3	17
335	Gill transcriptomes reveal involvement of cytoskeleton remodeling and immune defense in ammonia stress response in the banana shrimp Fenneropenaeus merguiensis. Fish and Shellfish Immunology, 2017, 71, 319-328.	1.6	51
336	Panax ginseng genome examination for ginsenoside biosynthesis. GigaScience, 2017, 6, 1-15.	3.3	150
337	Genome-wide gene expression analysis of amphioxus ( <i>Branchiostoma belcheri</i> ) following lipopolysaccharide challenge using strand-specific RNA-seq. RNA Biology, 2017, 14, 1799-1809.	1.5	18
338	The molecular mechanism and post-transcriptional regulation characteristic of Tetragenococcus halophilus acclimation to osmotic stress revealed by quantitative proteomics. Journal of Proteomics, 2017, 168, 1-14.	1.2	23
339	Transcriptome analysis of the response of Burmese python to digestion. GigaScience, 2017, 6, 1-18.	3.3	17
340	Transcriptome profiling of the Plutella xylostella (Lepidoptera: Plutellidae) ovary reveals genes involved in oogenesis. Gene, 2017, 637, 90-99.	1.0	18
341	Identification of circular RNA in the Bombyx mori silk gland. Insect Biochemistry and Molecular Biology, 2017, 89, 97-106.	1.2	39
342	Transcriptome analysis of the spleen of the darkbarbel catfish Pelteobagrus vachellii in response to Aeromonas hydrophila infection. Fish and Shellfish Immunology, 2017, 70, 498-506.	1.6	27
343	Differential gene expression profiling analysis in Pleurotus ostreatus during interspecific antagonistic interactions with Dichomitus squalens and Trametes versicolor. Fungal Biology, 2017, 121, 1025-1036.	1.1	11
344	Brain Membrane Proteome and Phosphoproteome Reveal Molecular Basis Associating with Nursing and Foraging Behaviors of Honeybee Workers. Journal of Proteome Research, 2017, 16, 3646-3663.	1.8	23

#	Article	IF	Citations
345	Identification of hub genes, key miRNAs and potential molecular mechanisms of colorectal cancer. Oncology Reports, 2017, 38, 2043-2050.	1.2	41
346	Comparative RNA-Seq Analysis Uncovers a Complex Regulatory Network for Soybean Cyst Nematode Resistance in Wild Soybean (Glycine soja). Scientific Reports, 2017, 7, 9699.	1.6	46
347	Genomic and transcriptomic analysis of the toluene degrading black yeast Cladophialophora immunda. Scientific Reports, 2017, 7, 11436.	1.6	37
348	Dynamic transcriptome and phytohormone profiling along the time of light exposure in the mesocotyl of rice seedling. Scientific Reports, 2017, 7, 11961.	1.6	55
349	Desiccation tolerance in bryophytes: The dehydration and rehydration transcriptomes in the desiccation-tolerant bryophyte Bryum argenteum. Scientific Reports, 2017, 7, 7571.	1.6	50
350	Expression changes in pelvic organ prolapse: a systematic review and in silico study. Scientific Reports, 2017, 7, 7668.	1.6	12
351	Genotype-specific physiological and transcriptomic responses to drought stress in Setaria italica (an) Tj ETQq0 0	0 rgBT /O 1.6	verlock 10 Tf
352	Integrated Analysis of Copy Number Variations and Gene Expression Profiling in Hepatocellular carcinoma. Scientific Reports, 2017, 7, 10570.	1.6	33
353	Circulating Long Noncoding RNAs as Potential Biomarkers of Sepsis: A Preliminary Study. Genetic Testing and Molecular Biomarkers, 2017, 21, 649-657.	0.3	35
354	Virulent and pathogenic features on the Cronobacter sakazakii polymyxin resistant pmr mutant strain s-3. Microbial Pathogenesis, 2017, 110, 359-364.	1.3	31
355	Comparative transcripome data for commercial maturity and physiological maturity of â€~Royal Gala' apple fruit under room temperature storage condition. Scientia Horticulturae, 2017, 225, 386-393.	1.7	8
356	In vivo gene expression profiling of the entomopathogenic fungus Beauveria bassiana elucidates its infection stratagems in Anopheles mosquito. Science China Life Sciences, 2017, 60, 839-851.	2.3	33
357	Genome re-sequencing analysis uncovers pathogenecity-related genes undergoing positive selection in Magnaporthe oryzae. Science China Life Sciences, 2017, 60, 880-890.	2.3	11
	DEC TOMATO: A Knowledge Evaluation Custom Featured On Tomate Creation Crimitific Departs 2017, 7		

358	5968.	1.6	8
359	Clinical Significance and Effect of IncRNA HOXA11-AS in NSCLC: A Study Based on Bioinformatics, In Vitro and in Vivo Verification. Scientific Reports, 2017, 7, 5567.	1.6	47
360	A systems approach to a spatio-temporal understanding of the drought stress response in maize. Scientific Reports, 2017, 7, 6590.	1.6	68
361	Promising significance of the association of miR-204-5p expression with clinicopathological features of hepatocellular carcinoma. Medicine (United States), 2017, 96, e7545.	0.4	16
362	Genomic landscape of copy number variation and copy neutral loss of heterozygosity events in equine sarcoids reveals increased instability of the sarcoid genome. Biochimie, 2017, 140, 122-132.	1.3	5

#	Article	IF	CITATIONS
363	Populus simonii × Populus nigra WRKY70 is involved in salt stress and leaf blight disease responses. Tree Physiology, 2017, 37, 827-844.	1.4	54
364	Drought and salt stress in Chrysopogon zizanioides leads to common and specific transcriptomic responses and may affect essential oil composition and benzylisoquinoline alkaloids metabolism. Current Plant Biology, 2017, 11-12, 12-22.	2.3	14
365	Comparative transcriptomic analysis of Tibetan Gynaephora to explore the genetic basis of insect adaptation to divergent altitude environments. Scientific Reports, 2017, 7, 16972.	1.6	15
366	DISTAG/TBCCd1 Is Required for Basal Cell Fate Determination in <i>Ectocarpus</i> . Plant Cell, 2017, 29, 3102-3122.	3.1	22
367	Genome-wide analysis of circular RNAs in prenatal and postnatal pituitary glands of sheep. Scientific Reports, 2017, 7, 16143.	1.6	50
368	Gene expression profile changes in the jejunum of weaned piglets after oral administration of Lactobacillus or an antibiotic. Scientific Reports, 2017, 7, 15816.	1.6	17
369	Expression Profiles of Long Noncoding RNA in UVA-Induced Human Skin Fibroblasts. Skin Pharmacology and Physiology, 2017, 30, 315-323.	1.1	9
370	DNA methylation alterations induced by transient exposure of MCF-7 cells to maghemite nanoparticles. Nanomedicine, 2017, 12, 2637-2649.	1.7	4
371	Diet-induced reconstruction of mucosal microbiota associated with alterations of epithelium lectin expression and regulation in the maintenance of rumen homeostasis. Scientific Reports, 2017, 7, 3941.	1.6	5
372	Noncoding and coding transcriptome analysis reveals the regulation roles of long noncoding RNAs in fruit development of hot pepper (Capsicum annuum L.). Plant Growth Regulation, 2017, 83, 141-156.	1.8	30
373	Transcript profiling of native Korean grapevine species Vitis flexuosa exposed to dehydration and rehydration treatment. Horticulture Environment and Biotechnology, 2017, 58, 66-77.	0.7	2
374	Integrated analysis of transcriptome and metabolites reveals an essential role of metabolic flux in starch accumulation under nitrogen starvation in duckweed. Biotechnology for Biofuels, 2017, 10, 167.	6.2	42
375	Transcriptome dynamics of Camellia sinensis in response to continuous salinity and drought stress. Tree Genetics and Genomes, 2017, 13, 1.	0.6	67
376	Exploring the genetic architecture and improving genomic prediction accuracy for mastitis and milk production traits in dairy cattle by mapping variants to hepatic transcriptomic regions responsive to intra-mammary infection. Genetics Selection Evolution, 2017, 49, 44.	1.2	53
377	NFPscanner: a webtool for knowledge-based deciphering of biomedical networks. BMC Bioinformatics, 2017, 18, 262.	1.2	0
378	Exploring the key genes and signaling transduction pathways related to the survival time of glioblastoma multiforme patients by a novel survival analysis model. BMC Genomics, 2017, 18, 950.	1.2	31
379	CNV discovery for milk composition traits in dairy cattle using whole genome resequencing. BMC Genomics, 2017, 18, 265.	1.2	87
380	Genome-wide identification of genes probably relevant to the adaptation of schizothoracins (Teleostei: Cypriniformes) to the uplift of the Qinghai-Tibet Plateau. BMC Genomics, 2017, 18, 310.	1.2	10

#	ARTICLE	IF	CITATIONS
381	Differences in responses of grass carp to different types of grass carp reovirus (GCRV) and the mechanism of hemorrhage revealed by transcriptome sequencing. BMC Genomics, 2017, 18, 452.	1.2	58
382	Genome-wide comparative transcriptome analysis of CMS-D2 and its maintainer and restorer lines in upland cotton. BMC Genomics, 2017, 18, 454.	1.2	38
383	Transcriptome profiling of Elymus sibiricus, an important forage grass in Qinghai-Tibet plateau, reveals novel insights into candidate genes that potentially connected to seed shattering. BMC Plant Biology, 2017, 17, 78.	1.6	16
384	Analysis of differentially expressed genes and adaptive mechanisms of Prunus triloba Lindl. under alkaline stress. Hereditas, 2017, 154, 10.	0.5	12
385	Comparative proteomic studies of a Scrippsiella acuminata bloom with its laboratory-grown culture using a 15N-metabolic labeling approach. Harmful Algae, 2017, 67, 26-35.	2.2	5
386	Quantitative trait loci for morphometric traits in multiple families of common carp (Cyprinus carpio). Science China Life Sciences, 2017, 60, 287-297.	2.3	10
387	iTRAQ analysis of the tobacco leaf proteome reveals that RNA-directed DNA methylation (RdDM) has important roles in defense against geminivirus-betasatellite infection. Journal of Proteomics, 2017, 152, 88-101.	1.2	37
388	Hormone-sensitive lipase deficiency alters gene expression and cholesterol content of mouse testis. Reproduction, 2017, 153, 175-185.	1.1	22
389	Comparative transcriptomic analyses of male and female adult Toxocara canis. Gene, 2017, 600, 85-89.	1.0	12
390	Donor Graft MicroRNAs: A Newly Identified Player in the Development of New-onset Diabetes After Liver Transplantation. American Journal of Transplantation, 2017, 17, 255-264.	2.6	30
391	Population genomics identifies the origin and signatures of selection of Korean weedy rice. Plant Biotechnology Journal, 2017, 15, 357-366.	4.1	51
392	Bioinformatics analysis of gene expression profile data to screen key genes involved in pulmonary sarcoidosis. Gene, 2017, 596, 98-104.	1.0	40
393	New Insight Into Early Somatic Embryogenesis of Mangosteen (Garcinia mangostana) Through de Novo and Comparative Transcriptome Analyses. Tropical Plant Biology, 2017, 10, 30-44.	1.0	8
394	Transcriptome analysis of peach [Prunus persica (L.) Batsch] stigma in response to low-temperature stress with digital gene expression profiling. Journal of Plant Biochemistry and Biotechnology, 2017, 26, 141-148.	0.9	17
395	Illumina-based de novo transcriptome sequencing and analysis of Chinese forest musk deer. Journal of Genetics, 2017, 96, 1033-1040.	0.4	11
396	Comparative transcriptome and proteome profiling of two Citrus sinensis cultivars during fruit development and ripening. BMC Genomics, 2017, 18, 984.	1.2	41
397	Transcriptome analysis reveals key roles of AtLBR-2 in LPS-induced defense responses in plants. BMC Genomics, 2017, 18, 995.	1.2	15
398	Gene expression profiling analysis of keloids with and without hydrocortisone treatment. Experimental and Therapeutic Medicine, 2017, 14, 5283-5288.	0.8	4

#	Article	IF	CITATIONS
399	Transcriptomic profile of tobacco in response to Tomato zonate spot orthotospovirus infection. Virology Journal, 2017, 14, 153.	1.4	9
400	Identification and analysis of key genes in osteosarcoma using bioinformatics. Oncology Letters, 2018, 15, 2789-2794.	0.8	29
401	Transcriptomic Studies in Non-Model Plants: Case of Pisum sativum L. and Medicago lupulina L. , 2017, ,		1
402	Transcriptome Analysis of the Cf-12-Mediated Resistance Response to Cladosporium fulvum in Tomato. Frontiers in Plant Science, 2016, 7, 2012.	1.7	25
403	Transcriptome Analyses Reveal Candidate Genes Potentially Involved in Al Stress Response in Alfalfa. Frontiers in Plant Science, 2017, 8, 26.	1.7	27
404	Differential Gene Expression Analysis in Polygonum minus Leaf upon 24 h of Methyl Jasmonate Elicitation. Frontiers in Plant Science, 2017, 8, 109.	1.7	25
405	Global Transcriptome Analysis and Identification of Differentially Expressed Genes in Strawberry after Preharvest Application of Benzothiadiazole and Chitosan. Frontiers in Plant Science, 2017, 8, 235.	1.7	59
406	Transcriptome Analysis of Genes Associated with the Artemisinin Biosynthesis by Jasmonic Acid Treatment under the Light in Artemisia annua. Frontiers in Plant Science, 2017, 8, 971.	1.7	69
407	Root Transcriptomic Analysis Revealing the Importance of Energy Metabolism to the Development of Deep Roots in Rice (Oryza sativa L.). Frontiers in Plant Science, 2017, 8, 1314.	1.7	27
408	Identification of Genes under Positive Selection Reveals Differences in Evolutionary Adaptation between Brown-Algal Species. Frontiers in Plant Science, 2017, 8, 1429.	1.7	17
409	Transcriptomic Analysis of Seed Coats in Yellow-Seeded Brassica napus Reveals Novel Genes That Influence Proanthocyanidin Biosynthesis. Frontiers in Plant Science, 2017, 8, 1674.	1.7	55
410	Arbuscular Mycorrhizal Fungus Enhances Lateral Root Formation in Poncirus trifoliata (L.) as Revealed by RNA-Seq Analysis. Frontiers in Plant Science, 2017, 8, 2039.	1.7	36
411	pathDIP: an annotated resource for known and predicted human gene-pathway associations and pathway enrichment analysis. Nucleic Acids Research, 2017, 45, D419-D426.	6.5	105
412	De Novo Assembly and Analysis of Polygonatum sibiricum Transcriptome and Identification of Genes Involved in Polysaccharide Biosynthesis. International Journal of Molecular Sciences, 2017, 18, 1950.	1.8	36
413	RNA Sequencing and Coexpression Analysis Reveal Key Genes Involved in α-Linolenic Acid Biosynthesis in Perilla frutescens Seed. International Journal of Molecular Sciences, 2017, 18, 2433.	1.8	27
414	The Fungal bZIP Transcription Factor AtfB Controls Virulence-Associated Processes in Aspergillus parasiticus. Toxins, 2017, 9, 287.	1.5	30
415	Integrative analysis of IncRNAs and miRNAs with coding RNAs associated with ceRNA crosstalk network in triple negative breast cancer. OncoTargets and Therapy, 2017, Volume 10, 5883-5897.	1.0	49
416	Fine Mapping and Transcriptome Analysis Reveal Candidate Genes Associated with Hybrid Lethality in Cabbage (Brassica Oleracea). Genes, 2017, 8, 147.	1.0	15

				1
#	Article	IF		CITATIONS
417	Transcription Factors Responding to Pb Stress in Maize. Genes, 2017, 8, 231.	1.	0	35
418	Novel Insights into Antiviral Gene Regulation of Red Swamp Crayfish, Procambarus clarkii, Infected with White Spot Syndrome Virus. Genes, 2017, 8, 320.	1.	0	30
419	Comparative Genomics of Mycoplasma bovis Strains Reveals That Decreased Virulence with Increasing Passages Might Correlate with Potential Virulence-Related Factors. Frontiers in Cellular and Infection Microbiology, 2017, 7, 177.	1,	8	39
420	Thioredoxin A Is Essential for Motility and Contributes to Host Infection of Listeria monocytogenes via Redox Interactions. Frontiers in Cellular and Infection Microbiology, 2017, 7, 287.	1.	8	46
421	Involvement of MicroRNAs in Probiotics-Induced Reduction of the Cecal Inflammation by Salmonella Typhimurium. Frontiers in Immunology, 2017, 8, 704.	2.	2	40
422	Identification of Novel Long Non-coding and Circular RNAs in Human Papillomavirus-Mediated Cervical Cancer. Frontiers in Microbiology, 2017, 8, 1720.	1.	5	44
423	Weighted gene co-expression network analysis of expression data of monozygotic twins identifies specific modules and hub genes related to BMI. BMC Genomics, 2017, 18, 872.	1.	2	53
424	Abnormal expression of mRNA, microRNA alteration and aberrant DNA methylation patterns in rectal adenocarcinoma. PLoS ONE, 2017, 12, e0174461.	1.	1	21
425	Genomic and transcriptomic analyses reveal adaptation mechanisms of an Acidithiobacillus ferrivorans strain YL15 to alpine acid mine drainage. PLoS ONE, 2017, 12, e0178008.	1.	1	34
426	Comparative transcriptomes analysis of the wing disc between two silkworm strains with different size of wings. PLoS ONE, 2017, 12, e0179560.	1.	1	7
427	Circular RNA profile of infantile hemangioma by microarray analysis. PLoS ONE, 2017, 12, e0187581.	1.	1	18
428	Antigenic and immunosuppressive properties of a trimeric recombinant transmembrane envelope protein gp41 of HIV-1. PLoS ONE, 2017, 12, e0173454.	1.	1	7
429	Evolution of beak morphology in the Ground Tit revealed by comparative transcriptomics. Frontiers in Zoology, 2017, 14, 58.	0	.9	18
430	Metagenomic mining pectinolytic microbes and enzymes from an apple pomace-adapted compost microbial community. Biotechnology for Biofuels, 2017, 10, 198.	6.	.2	27
431	Associations among dietary non-fiber carbohydrate, ruminal microbiota and epithelium G-protein-coupled receptor, and histone deacetylase regulations in goats. Microbiome, 2017, 5, 123.	4.	.9	74
432	Characterization of the peripheral blood transcriptome and adaptive evolution of the MHC I and TLR gene families in the wolf (Canis lupus). BMC Genomics, 2017, 18, 584.	1.	2	21
433	Potential role of upregulated microRNA-146b and â^'21 in renal fibrosis. Molecular Medicine Reports, 2017, 16, 2863-2867.	1.	1	6
434	Overexpression of CKAP4 is Associated with Poor Prognosis in Clear Cell Renal Cell Carcinoma and Functions via Cyclin B Signaling. Journal of Cancer, 2017, 8, 4018-4026.	1.	2	11
_				

#	Article	IF	CITATIONS
435	Transcriptome analysis of avian reovirus-mediated changes in gene expression of normal chicken fibroblast DF-1 cells. BMC Genomics, 2017, 18, 911.	1.2	16
436	Genome-wide analysis of circular RNAs in prenatal and postnatal muscle of sheep. Oncotarget, 2017, 8, 97165-97177.	0.8	32
437	Transcriptome-wide analysis of immune-responsive microRNAs against poly (I:C) challenge in <i>Branchiostoma belcheri</i> by deep sequencing and bioinformatics. Oncotarget, 2017, 8, 73590-73602.	0.8	11
438	iTRAQ-based quantitative proteomic analysis reveals important metabolic pathways for arsenic-induced liver fibrosis in rats. Scientific Reports, 2018, 8, 3267.	1.6	14
439	Transcriptome profiling of rubber tree (Hevea brasiliensis) discovers candidate regulators of the cold stress response. Genes and Genomics, 2018, 40, 1181-1197.	0.5	34
440	Transcriptome changes induced by abiotic stresses in Artemisia annua. Scientific Reports, 2018, 8, 3423.	1.6	36
441	Isolation of Exosome-Like Nanoparticles and Analysis of MicroRNAs Derived from Coconut Water Based on Small RNA High-Throughput Sequencing. Journal of Agricultural and Food Chemistry, 2018, 66, 2749-2757.	2.4	69
442	Comparative Transcriptome Analysis Reveals Growth-Related Genes in Juvenile Chinese Sea Cucumber, Russian Sea Cucumber, and Their Hybrids. Marine Biotechnology, 2018, 20, 193-205.	1.1	25
443	Comparative transcriptomic analysis provides insights into antibacterial mechanisms of Branchiostoma belcheri under Vibrio parahaemolyticus infection. Fish and Shellfish Immunology, 2018, 76, 196-205.	1.6	17
444	Comparative transcriptomic analysis of white and red Chinese bayberry ( Myrica rubra ) fruits reveals flavonoid biosynthesis regulation. Scientia Horticulturae, 2018, 235, 9-20.	1.7	19
445	Transcriptome, Biochemical and Growth Responses of the Marine Phytoplankter Phaeodactylum Tricornutum Bohlin (Bacillariophyta) to Copepod Grazer Presence. Cellular Physiology and Biochemistry, 2018, 46, 1091-1111.	1.1	9
446	The transcriptome properties of reeds under cadmium stress in Liaohe Estuary wetland. South African Journal of Botany, 2018, 116, 200-206.	1.2	2
447	GA3 application in grapes (Vitis vinifera L.) modulates different sets of genes at cluster emergence, full bloom, and berry stage as revealed by RNA sequence-based transcriptome analysis. Functional and Integrative Genomics, 2018, 18, 439-455.	1.4	14
448	Comparative transcriptome analysis of genes involved in anthocyanin synthesis in blueberry. Plant Physiology and Biochemistry, 2018, 127, 561-572.	2.8	76
449	Tocopherols inhibit esophageal carcinogenesis through attenuating NF-κB activation and CXCR3-mediated inflammation. Oncogene, 2018, 37, 3909-3923.	2.6	20
450	Cellular response to persistent foot-and-mouth disease virus infection is linked to specific types of alterations in the host cell transcriptome. Scientific Reports, 2018, 8, 5074.	1.6	21
451	Transcriptome analysis of Jatropha curcas L. flower buds responded to the paclobutrazol treatment. Plant Physiology and Biochemistry, 2018, 127, 276-286.	2.8	30
452	The phosphorylated redox proteome of Chlamydomonas reinhardtii: Revealing novel means for regulation of protein structure and function. Redox Biology, 2018, 17, 35-46.	3.9	29

#	Article	IF	CITATIONS
453	Impact of the Anticancer Drug NT157 on Tyrosine Kinase Signaling Networks. Molecular Cancer Therapeutics, 2018, 17, 931-942.	1.9	15
454	Adrenergic receptor stimulation suppresses oxidative metabolism in isolated rat islets and Min6 cells. Molecular and Cellular Endocrinology, 2018, 473, 136-145.	1.6	13
455	Comprehensive Analysis of DNA Methylation and Gene Expression Datasets IdentifiedMMP9andTWIST1as Important Pathogenic Genes of Lung Adenocarcinoma. DNA and Cell Biology, 2018, 37, 336-346.	0.9	5
456	Transcriptomic characterization and potential marker development of contrasting sugarcane cultivars. Scientific Reports, 2018, 8, 1683.	1.6	46
457	The expression and significance of microRNA in different stages of colorectal cancer. Medicine (United States), 2018, 97, e9635.	0.4	16
458	Brain of the blind: transcriptomics of the golden-line cavefish brain. Environmental Epigenetics, 2018, 64, 765-773.	0.9	8
459	Pla2g6 Deficiency in Zebrafish Leads to Dopaminergic Cell Death, Axonal Degeneration, Increased β-Synuclein Expression, and Defects in Brain Functions and Pathways. Molecular Neurobiology, 2018, 55, 6734-6754.	1.9	17
460	Leukemia-propagating cells demonstrate distinctive gene expression profiles compared with other cell fractions from patients with de novo Philadelphia chromosome-positive ALL. Annals of Hematology, 2018, 97, 799-811.	0.8	0
461	The transcriptomic changes of Huipizhi Heidou ( Glycine max ), a nematode-resistant black soybean during Heterodera glycines race 3 infection. Journal of Plant Physiology, 2018, 220, 96-104.	1.6	16
462	Integrated analysis of transcriptomic and metabolomic data reveals critical metabolic pathways involved in rotenoid biosynthesis in the medicinal plant Mirabilis himalaica. Molecular Genetics and Genomics, 2018, 293, 635-647.	1.0	21
463	Systems Biology Modeling to Study Pathogen–Host Interactions. Methods in Molecular Biology, 2018, 1734, 97-112.	0.4	13
464	Proteomics reveals key proteins participating in growth difference between fall dormant and non-dormant alfalfa in terminal buds. Journal of Proteomics, 2018, 173, 126-138.	1.2	9
465	Comparative Analysis of Gene Expression Profiles of Human Dental Fluorosis and Kashin-Beck Disease. Scientific Reports, 2018, 8, 170.	1.6	6
466	Discovery of microRNA-target modules of African rice (Oryza glaberrima) under salinity stress. Scientific Reports, 2018, 8, 570.	1.6	44
467	Genome-wide characterization of differentially expressed genes provides insights into regulatory network of heat stress response in radish (Raphanus sativus L.). Functional and Integrative Genomics, 2018, 18, 225-239.	1.4	33
468	Systematic analysis of the regulatory roles of microRNAs in postnatal maturation and metergasis of liver of breeder cocks. Scientific Reports, 2018, 8, 61.	1.6	0
469	Dynamic transcriptome landscape of Asian domestic honeybee (Apis cerana) embryonic development revealed by high-quality RNA sequencing. BMC Developmental Biology, 2018, 18, 11.	2.1	23
470	Transcriptome profiling of lentil (Lens culinaris) through the first 24 hours of Ascochyta lentis infection reveals key defence response genes. BMC Genomics, 2018, 19, 108.	1.2	53

#	Article	IF	CITATIONS
471	Divergent transcriptomic responses underlying the ranaviruses-amphibian interaction processes on interspecies infection of Chinese giant salamander. BMC Genomics, 2018, 19, 211.	1.2	15
472	Long-term smoking alters abundance of over half of the proteome in bronchoalveolar lavage cell in smokers with normal spirometry, with effects on molecular pathways associated with COPD. Respiratory Research, 2018, 19, 40.	1.4	26
473	Transcriptome analysis reveals enrichment of genes associated with auditory system in swimbladder of channel catfish. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 27, 30-39.	0.4	8
474	Catechin supplemented in a FOS diet induces weight loss by altering cecal microbiota and gene expression of colonic epithelial cells. Food and Function, 2018, 9, 2962-2969.	2.1	29
475	Comparative transcriptomic analysis identifies genes responsible for fruit count and oil yield in the oil tea plant Camellia chekiangoleosa. Scientific Reports, 2018, 8, 6637.	1.6	16
476	The plant hormone abscisic acid regulates the growth and metabolism of endophytic fungus Aspergillus nidulans. Scientific Reports, 2018, 8, 6504.	1.6	34
477	Two-dimensional analysis provides molecular insight into flower scent of Lilium â€~Siberia'. Scientific Reports, 2018, 8, 5352.	1.6	24
478	trans-10,cis-12 conjugated linoleic acid alters lipid metabolism of goat mammary epithelial cells by regulation of de novo synthesis and the AMPK signaling pathway. Journal of Dairy Science, 2018, 101, 5571-5581.	1.4	18
479	Induction of hepatocytes-derived insulin-producing cells using small molecules and identification of microRNA profiles during this procedure. Biochemical and Biophysical Research Communications, 2018, 498, 646-653.	1.0	6
480	High-Concentrate Diet-Induced Change of Cellular Metabolism Leads to Decreases of Immunity and Imbalance of Cellular Activities in Rumen Epithelium. Cellular Physiology and Biochemistry, 2018, 45, 2145-2157.	1.1	3
481	An ex vivo abomasal ovine model to study the immediate immune response in the context of Haemonchus contortus larval-stage. Veterinary Parasitology, 2018, 254, 105-113.	0.7	5
482	An ex vivo ruminal ovine model to study the immediate immune response in the context of bacterial lipopolysaccharide. Functional and Integrative Genomics, 2018, 18, 277-285.	1.4	4
483	Regulation of trichome development in tobacco by JcZFP8 , a C2H2 zinc finger protein gene from Jatropha curcas L Gene, 2018, 658, 47-53.	1.0	17
484	Transcriptome analysis of sugar beet root maggot ( Tetanops myopaeformis ) genes modulated by the Beta vulgaris host. Insect Science, 2018, 25, 222-234.	1.5	2
485	Identification and comparison of long nonâ€coding RNAs in the silk gland between domestic and wild silkworms. Insect Science, 2018, 25, 604-616.	1.5	37
486	Large-scale label-free proteomics analysis of occupational poisoned patients of 1-bromopropane, workers exposed to 1-bromopropane and healthy individuals. Human and Experimental Toxicology, 2018, 37, 3-12.	1.1	1
487	Adding biological meaning to human protein-protein interactions identified by yeast two-hybrid screenings: A guide through bioinformatics tools. Journal of Proteomics, 2018, 171, 127-140.	1.2	9
488	Sequencing, de novo assembly and characterization of the spotted scat Scatophagus argus (Linnaeus) Tj ETQq1 Limnology, 2018, 36, 1329-1341.	1 0.78431 0.6	4 rgBT /Ove 15

#	Article	IF	Citations
489	Drought and salt stress in Macrotyloma uniflorum leads to common and specific transcriptomic responses and reveals importance of raffinose family oligosaccharides in stress tolerance. Gene Reports, 2018, 10, 7-16.	0.4	10
490	Transcriptional profile of the human skin pathogenic fungus Mucor irregularis in response to low oxygen. Medical Mycology, 2018, 56, 631-644.	0.3	11
491	Dynamic transcriptomic analysis in hircine longissimus dorsi muscle from fetal to neonatal development stages. Functional and Integrative Genomics, 2018, 18, 43-54.	1.4	25
492	Transcriptional memory contributes to drought tolerance in coffee (Coffea canephora) plants. Environmental and Experimental Botany, 2018, 147, 220-233.	2.0	47
493	Effects of starch-coating of magnetite nanoparticles on cellular uptake, toxicity and gene expression profiles in adult zebrafish. Science of the Total Environment, 2018, 622-623, 930-941.	3.9	40
494	The NADPH organizers NoxO1 and p47phox are both mediators of diabetes-induced vascular dysfunction in mice. Redox Biology, 2018, 15, 12-21.	3.9	40
495	Comparative transcriptome analysis provides insights of antiâ€insect molecular mechanism of <i>Cassia obtusifolia</i> trypsin inhibitor against <i>Pieris rapae</i> . Archives of Insect Biochemistry and Physiology, 2018, 97, e21427.	0.6	7
496	Metatranscriptomics analysis of cyanobacterial aggregates during cyanobacterial bloom period in Lake Taihu, China. Environmental Science and Pollution Research, 2018, 25, 4811-4825.	2.7	20
497	Transcriptome Analysis Reveals the Mechanism of Fungicidal of Thymol Against Fusarium oxysporum f. sp. niveum. Current Microbiology, 2018, 75, 410-419.	1.0	30
498	Alternative polyadenylation is involved in auxinâ€based plant growth and development. Plant Journal, 2018, 93, 246-258.	2.8	38
499	Genome-wide identification and characterization of putative IncRNAs in the diamondback moth, Plutella xylostella (L.). Genomics, 2018, 110, 35-42.	1.3	53
500	Identification and prediction of novel non-coding and coding RNA-associated competing endogenous RNA networks in colorectal cancer. World Journal of Gastroenterology, 2018, 24, 5259-5270.	1.4	30
501	A homozygous G insertion in MPLKIP leads to TTDN1 with the hypergonadotropic hypogonadism symptom. BMC Medical Genetics, 2018, 19, 214.	2.1	5
502	Identification of cordycepin biosynthesis-related genes through de novo transcriptome assembly and analysis in <i>Cordyceps cicadae</i> . Royal Society Open Science, 2018, 5, 181247.	1.1	21
503	Expression profiles of circular RNAs in sheep skeletal muscle. Asian-Australasian Journal of Animal Sciences, 2018, 31, 1550-1557.	2.4	54
504	Development of polymorphic microsatellite markers by using de novo transcriptome assembly of Calanthe masuca and C. sinica (Orchidaceae). BMC Genomics, 2018, 19, 800.	1.2	3
505	Transcriptome Analysis of Gene Expression Patterns Potentially Associated with Premature Senescence in Nicotiana tabacum L Molecules, 2018, 23, 2856.	1.7	12
506	Transcriptome and Resistance-Related Genes Analysis of Botrytis cinerea B05.10 Strain to Different Selective Pressures of Cyprodinil and Fenhexamid. Frontiers in Microbiology, 2018, 9, 2591.	1.5	8

#	Article	IF	CITATIONS
507	Plasma microRNA expression signature involving miR-548q, miR-630 and miR-940 as biomarkers for nasopharyngeal carcinoma detection. Cancer Biomarkers, 2018, 23, 579-587.	0.8	16
508	Improving Cell Survival in Injected Embryos Allows Primed Pluripotent Stem Cells to Generate Chimeric Cynomolgus Monkeys. Cell Reports, 2018, 25, 2563-2576.e9.	2.9	22
509	The Chrysanthemum nankingense Genome Provides Insights into the Evolution and Diversification of Chrysanthemum Flowers and Medicinal Traits. Molecular Plant, 2018, 11, 1482-1491.	3.9	148
510	Identification of Potential Key Genes Associated with Adipogenesis through Integrated Analysis of Five Mouse Transcriptome Datasets. International Journal of Molecular Sciences, 2018, 19, 3557.	1.8	14
511	Identification of browning-related microRNAs and their targets reveals complex miRNA-mediated browning regulatory networks in Luffa cylindrica. Scientific Reports, 2018, 8, 16242.	1.6	11
512	Comparative Transcriptome Analysis of Temperature-Induced Green Discoloration in Garlic. International Journal of Genomics, 2018, 2018, 1-8.	0.8	4
513	A genome-wide detection of selection signatures in conserved and commercial pig breeds maintained in Poland. BMC Genetics, 2018, 19, 95.	2.7	31
514	Genome-wide association study of Mycobacterium avium subspecies Paratuberculosis infection in Chinese Holstein. BMC Genomics, 2018, 19, 972.	1.2	20
515	Transcriptome reprogramming during severe dehydration contributes to physiological and metabolic changes in the resurrection plant Haberlea rhodopensis. BMC Plant Biology, 2018, 18, 351.	1.6	40
516	RNA sequencing reveals the expression profiles of circRNA and indicates that circDDX17 acts as a tumor suppressor in colorectal cancer. Journal of Experimental and Clinical Cancer Research, 2018, 37, 325.	3.5	183
517	Cardiac function evaluation for a novel one-step detoxification product of Aconiti Lateralis Radix Praeparata. Chinese Medicine, 2018, 13, 62.	1.6	12
518	Investigation into the underlying molecular mechanisms of white adipose tissue through comparative transcriptome analysis of multiple tissues. Molecular Medicine Reports, 2018, 19, 959-966.	1.1	4
519	Identification of Two Novel Wheat Drought Tolerance-Related Proteins by Comparative Proteomic Analysis Combined with Virus-Induced Gene Silencing. International Journal of Molecular Sciences, 2018, 19, 4020.	1.8	16
520	RNA sequencing and anthocyanin synthesis-related genes expression analyses in white-fruited Vaccinium uliginosum. BMC Genomics, 2018, 19, 930.	1.2	8
521	Differences in Root Physiological and Proteomic Responses to Dibutyl Phthalate Exposure between Low- and High-DBP-Accumulation Cultivars of <i>Brassica parachinensis</i> . Journal of Agricultural and Food Chemistry, 2018, 66, 13541-13551.	2.4	13
522	Differential responses of Lasiopodomys mandarinus and Lasiopodomys brandtii to chronic hypoxia: a cross-species brain transcriptome analysis. BMC Genomics, 2018, 19, 901.	1.2	14
523	An integrated omics analysis reveals molecular mechanisms that are associated with differences in seed oil content between Glycine max and Brassica napus. BMC Plant Biology, 2018, 18, 328.	1.6	23
524	Comparative transcriptomics identifies genes differentially expressed in the intestine of a new fast-growing strain of common carp with higher unsaturated fatty acid content in muscle. PLoS ONE, 2018, 13, e0206615.	1.1	14

#	Article	IF	CITATIONS
525	Genome-wide identification and functional prediction of tobacco lncRNAs responsive to root-knot nematode stress. PLoS ONE, 2018, 13, e0204506.	1.1	21
526	ROBO2 is a stroma suppressor gene in the pancreas and acts via TGF-Î <sup>2</sup> signalling. Nature Communications, 2018, 9, 5083.	5.8	41
527	Analysis of transcripts and splice isoforms in red clover (Trifolium pratense L.) by single-molecule long-read sequencing. BMC Plant Biology, 2018, 18, 300.	1.6	94
528	Microarray analysis of the molecular mechanisms associated with age and body mass index in human meniscal injury. Molecular Medicine Reports, 2018, 19, 93-102.	1.1	4
529	Early Responses to Severe Drought Stress in the Arabidopsis thaliana Cell Suspension Culture Proteome. Proteomes, 2018, 6, 38.	1.7	24
530	Long non-coding RNA AFAP1-AS1 plays an oncogenic role in promoting cell migration in non-small cell lung cancer. Cellular and Molecular Life Sciences, 2018, 75, 4667-4681.	2.4	42
531	MicroRNA-transcription factor network analysis reveals miRNAs cooperatively suppress RORA in oral squamous cell carcinoma. Oncogenesis, 2018, 7, 79.	2.1	29
532	<scp>RNA</scp> â€seq analysis reveals different gene ontologies and pathways in rheumatoid arthritis and Kashin–Beck disease. International Journal of Rheumatic Diseases, 2018, 21, 1686-1694.	0.9	8
533	Integrated analysis of long noncoding <scp>RNA</scp> associatedâ€competing endogenous <scp>RNA</scp> as prognostic biomarkers in clear cell renal carcinoma. Cancer Science, 2018, 109, 3336-3349.	1.7	33
534	Transgenerational transmission of maternal stimulatory experience in domesticated birds. FASEB Journal, 2018, 32, 7002-7017.	0.2	10
535	Genome-wide identification of the interactions between key genes and pathways provide new insights into the toxicity of bisphenol F and S during early development in zebrafish. Chemosphere, 2018, 213, 559-567.	4.2	27
536	Comprehensive analysis of multi Ewing sarcoma microarray datasets identifies several prognosis biomarkers. Molecular Medicine Reports, 2018, 18, 4229-4238.	1.1	3
537	Identification of key genes and associated pathways in KIT/PDGFRA wild‑type gastrointestinal stromal tumors through bioinformatics analysis. Molecular Medicine Reports, 2018, 18, 4499-4515.	1.1	5
538	Integrated genomic analyses in PDX model reveal a cyclin-dependent kinase inhibitor Palbociclib as a novel candidate drug for nasopharyngeal carcinoma. Journal of Experimental and Clinical Cancer Research, 2018, 37, 233.	3.5	23
539	Comparative transcriptome analysis of red swamp crayfish (Procambarus clarkia) hepatopancreas in response to WSSV and Aeromonas hydrophila infection. Fish and Shellfish Immunology, 2018, 83, 397-405.	1.6	33
540	Chronic Adrenergic Signaling Causes Abnormal RNA Expression of Proliferative Genes in Fetal Sheep Islets. Endocrinology, 2018, 159, 3565-3578.	1.4	13
541	Transcriptome Sequencing and Metabolism Analysis Reveals the role of Cyanidin Metabolism in Dark-red Onion (Allium cepa L.) Bulbs. Scientific Reports, 2018, 8, 14109.	1.6	23
542	Changes in gene and genotype frequencies during the development of the grass carp <scp><i>Ctenopharyngodon idella</i></scp> . Journal of Fish Biology, 2018, 93, 1113-1120.	0.7	0

#	Article	IF	CITATIONS
543	Which Genes in a Typical Intertidal Seagrass (Zostera japonica) Indicate Copper-, Lead-, and Cadmium Pollution?. Frontiers in Plant Science, 2018, 9, 1545.	1.7	11
544	Identification of a sixâ€gene signature with prognostic value for patients with endometrial carcinoma. Cancer Medicine, 2018, 7, 5632-5642.	1.3	39
545	Intestinal toxicity of deoxynivalenol is limited by supplementation with Lactobacillus plantarum JM113 and consequentially altered gut microbiota in broiler chickens. Journal of Animal Science and Biotechnology, 2018, 9, 74.	2.1	65
546	Transcriptomic Analysis of Betula halophila in Response to Salt Stress. International Journal of Molecular Sciences, 2018, 19, 3412.	1.8	17
547	Identification of Five Genes as a Potential Biomarker for Predicting Progress and Prognosis in Adrenocortical Carcinoma. Journal of Cancer, 2018, 9, 4484-4495.	1.2	39
548	AutismKB 2.0: a knowledgebase for the genetic evidence of autism spectrum disorder. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	37
549	Characterization of Duck (Anas platyrhynchos) Short Tandem Repeat Variation by Population-Scale Genome Resequencing. Frontiers in Genetics, 2018, 9, 520.	1.1	3
550	Comparative Genome-Wide Survey of Single Nucleotide Variation Uncovers the Genetic Diversity and Potential Biomedical Applications among Six Macaca Species. International Journal of Molecular Sciences, 2018, 19, 3123.	1.8	3
551	Comparative transcriptome analysis of Eimeria maxima (Apicomplexa: Eimeriidae) suggests DNA replication activities correlating with its fecundity. BMC Genomics, 2018, 19, 699.	1.2	12
552	Effects of sugarcane aphid herbivory on transcriptional responses of resistant and susceptible sorghum. BMC Genomics, 2018, 19, 774.	1.2	40
553	Comparative transcriptome analysis of the wild-type model apomict Hieracium praealtum and its loss of parthenogenesis (lop) mutant. BMC Plant Biology, 2018, 18, 206.	1.6	14
554	PGD: Pineapple Genomics Database. Horticulture Research, 2018, 5, 66.	2.9	25
555	Systematic transcriptomic analysis provides insights into lotus (Nelumbo nucifera) seed development. Plant Growth Regulation, 2018, 86, 339-350.	1.8	21
556	The acute transcriptomic response of coral-algae interactions to pH fluctuation. Marine Genomics, 2018, 42, 32-40.	0.4	9
557	Genome-wide methylation analysis identifies novel prognostic methylation markers in colon adenocarcinoma. Biomedicine and Pharmacotherapy, 2018, 108, 288-296.	2.5	14
558	Global identification of circular RNAs in chronic myeloid leukemia reveals hsa_circ_0080145 regulates cell proliferation by sponging miR-29b. Biochemical and Biophysical Research Communications, 2018, 504, 660-665.	1.0	39
559	Proteomic Analysis of Rapeseed Root Response to Waterlogging Stress. Plants, 2018, 7, 71.	1.6	23
560	Transcriptomic analyses of cacao cell suspensions in light and dark provide target genes for controlled flavonoid production. Scientific Reports. 2018. 8. 13575.	1.6	14

#	Article	IF	CITATIONS
561	Characterization of Laguncularia racemosa transcriptome and molecular response to oil pollution. Aquatic Toxicology, 2018, 205, 36-50.	1.9	5
562	Comparative transcriptome analysis to identify putative genes involved in thymol biosynthesis pathway in medicinal plant Trachyspermum ammi L Scientific Reports, 2018, 8, 13405.	1.6	24
563	Genome-wide transcriptome analysis of the salt stress tolerance mechanism in Rosa chinensis. PLoS ONE, 2018, 13, e0200938.	1.1	30
564	DES-Mutation: System for Exploring Links of Mutations and Diseases. Scientific Reports, 2018, 8, 13359.	1.6	13
565	Discovery and Characterization of a High-Affinity Small Peptide Ligand, H1, Targeting FGFR2IIIc for Skin Wound Healing. Cellular Physiology and Biochemistry, 2018, 49, 1074-1089.	1.1	14
566	DNA methylation footprints during soybean domestication and improvement. Genome Biology, 2018, 19, 128.	3.8	61
567	Identification of SNPs and Candidate Genes Associated With Salt Tolerance at the Seedling Stage in Cotton (Gossypium hirsutum L.). Frontiers in Plant Science, 2018, 9, 1011.	1.7	50
568	Transcriptome analysis and physiological responses of the potato plantlets in vitro under red, blue, and white light conditions. 3 Biotech, 2018, 8, 394.	1.1	9
569	Serum miRNAs miR-140-3p and miR-23b-3p as potential biomarkers for osteoporosis and osteoporotic fracture in postmenopausal Mexican-Mestizo women. Gene, 2018, 679, 19-27.	1.0	61
570	Coregulation of ribosomal RNA with hundreds of genes contributes to phenotypic variation. Genome Research, 2018, 28, 1555-1565.	2.4	16
571	Network and Pathway-Based Prioritization and Analyses of Genes Related to Chronic Obstructive Pulmonary Disease. Cytologia, 2018, 83, 251-258.	0.2	0
572	Molecular alterations during larval development of Haemonchus contortus in vitro are under tight post-transcriptional control. International Journal for Parasitology, 2018, 48, 763-772.	1.3	30
573	Differential transcriptome patterns associated with early seedling development in a wild and a domesticated common bean (Phaseolus vulgaris L.) accession. Plant Science, 2018, 274, 153-162.	1.7	9
574	Toxicity and Transcriptome Sequencing (RNA-seq) Analyses of Adult Zebrafish in Response to Exposure Carboxymethyl Cellulose Stabilized Iron Sulfide Nanoparticles. Scientific Reports, 2018, 8, 8083.	1.6	44
575	De novo characterization of Phenacoccus solenopsis transcriptome and analysis of gene expression profiling during development and hormone biosynthesis. Scientific Reports, 2018, 8, 7573.	1.6	15
576	A Five-microRNA Signature for Survival Prognosis in Pancreatic Adenocarcinoma based on TCGA Data. Scientific Reports, 2018, 8, 7638.	1.6	51
577	Circular RNAs are differentially expressed in liver ischemia/reperfusion injury model. Journal of Cellular Biochemistry, 2018, 119, 7397-7405.	1.2	12
578	Precise control of SCRaMbLE in synthetic haploid and diploid yeast. Nature Communications, 2018, 9, 1933.	5.8	118

#	Article	IF	Citations
π 579	Transcriptomic and metabolomic analyses reveal that bacteria promote plant defense during infection	1.6	61
077	of soybean cyst nematode in soybean. BMC Plant Biology, 2018, 18, 86.	1.0	01
580	Transcriptome analysis reveals the genetic foundation for the dynamics of starch and lipid production in Ettlia oleoabundans. Algal Research, 2018, 33, 142-155.	2.4	21
581	MiRâ€181a/b induce the growth, invasion, and metastasis of neuroblastoma cells through targeting ABI1. Molecular Carcinogenesis, 2018, 57, 1237-1250.	1.3	24
582	Transcriptomic response and perturbation of toxicity pathways in zebrafish larvae after exposure to graphene quantum dots (GQDs). Journal of Hazardous Materials, 2018, 357, 146-158.	6.5	42
583	Genome-wide DNA methylation profile of prepubertal porcine testis. Reproduction, Fertility and Development, 2018, 30, 349.	0.1	16
584	Genome-Wide Identification of Drought Response Genes in Soybean Seedlings and Development of Biomarkers for Early Diagnoses. Plant Molecular Biology Reporter, 2018, 36, 350-362.	1.0	5
585	Deletion of the GCW13 gene derepresses Gap1-dependent uptake of amino acids in Pichia pastoris grown on methanol as the sole carbon source. Biochemical and Biophysical Research Communications, 2018, 501, 226-231.	1.0	4
586	Dietary restriction alters the fatbody transcriptome during immune responses in Bombyx mori. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2018, 223, 50-57.	0.7	4
587	The transcriptome of the rat subfornical organ is altered in response to early postnatal overnutrition. IBRO Reports, 2018, 5, 17-23.	0.3	7
588	Combined QTL mapping, physiological and transcriptomic analyses to identify candidate genes involved in Brassica napus seed aging. Molecular Genetics and Genomics, 2018, 293, 1421-1435.	1.0	22
589	Transcriptomic Profiling of Fruit Development in Black Raspberry Rubus coreanus. International Journal of Genomics, 2018, 2018, 1-13.	0.8	7
590	Transcriptome analysis reveals heat tolerance of Tribolium castaneum (Herbst) (Coleoptera:) Tj ETQq1 1 0.7843	14 <u>rg</u> BT /C	Overlock 10 Tr
591	Comparative phenotype and microRNAome in developing anthers of wild-type and male-sterile Lycium barbarum L Plant Science, 2018, 274, 349-359.	1.7	12
593	In vitro characterization of neonatal, juvenile, and adult porcine islet oxygen demand, β ell function, and transcriptomes. Xenotransplantation, 2018, 25, e12432.	1.6	20
594	Comparative transcriptome analysis of the swimbladder reveals expression signatures in response to low oxygen stress in channel catfish, <i>lctalurus punctatus</i> . Physiological Genomics, 2018, 50, 636-647.	1.0	22
595	Comparative iTRAQ proteomics revealed proteins associated with horn development in yak. Proteome Science, 2018, 16, 14.	0.7	11
596	Transcriptome Analysis Reveals Multiple Hormones, Wounding and Sugar Signaling Pathways Mediate Adventitious Root Formation in Apple Rootstock. International Journal of Molecular Sciences, 2018, 19, 2201.	1.8	48
597	Metalloproteinase Adamts16 Is Required for Proper Closure of the Optic Fissure. , 2018, 59, 1167.		21

#	Article	IF	CITATIONS
598	Integrated Modules Analysis to Explore the Molecular Mechanisms of Phlegm-Stasis Cementation Syndrome with Ischemic Heart Disease. Frontiers in Physiology, 2018, 9, 7.	1.3	21
599	Brain Transcriptome Profiling Analysis of Nile Tilapia (Oreochromis niloticus) Under Long-Term Hypersaline Stress. Frontiers in Physiology, 2018, 9, 219.	1.3	27
600	Liver Transcriptome and miRNA Analysis of Silver Carp (Hypophthalmichthys molitrix) Intraperitoneally Injected With Microcystin-LR. Frontiers in Physiology, 2018, 9, 381.	1.3	17
601	The Novel Secreted Meloidogyne incognita Effector MilSE6 Targets the Host Nucleus and Facilitates Parasitism in Arabidopsis. Frontiers in Plant Science, 2018, 9, 252.	1.7	40
602	Maize Stem Response to Long-Term Attack by Sesamia nonagrioides. Frontiers in Plant Science, 2018, 9, 522.	1.7	10
603	Integration of the Pokeweed miRNA and mRNA Transcriptomes Reveals Targeting of Jasmonic Acid-Responsive Genes. Frontiers in Plant Science, 2018, 9, 589.	1.7	10
604	Characterization of long non-coding RNA and messenger RNA profiles in follicular fluid from mature and immature ovarian follicles of healthy women and women with polycystic ovary syndrome. Human Reproduction, 2018, 33, 1735-1748.	0.4	65
605	Genome-Wide Identification and Characterization of WD40 Protein Genes in the Silkworm, Bombyx mori. International Journal of Molecular Sciences, 2018, 19, 527.	1.8	17
606	Messenger RNA Sequencing and Pathway Analysis Provide Novel Insights Into the Susceptibility to Salmonella enteritidis Infection in Chickens. Frontiers in Genetics, 2018, 9, 256.	1.1	20
607	Transcriptome Analysis of a Premature Leaf Senescence Mutant of Common Wheat (Triticum aestivum) Tj ETQq1	1 0.78431 1.8	4 rgBT /Ove
608	Comparative transcriptome analysis of field- and chamber-grown samples of Colobanthus quitensis (Kunth) Bartl, an Antarctic flowering plant. Scientific Reports, 2018, 8, 11049.	1.6	27
609	Comprehensive analysis of NAC transcription factors uncovers their roles during fiber development and stress response in cotton. BMC Plant Biology, 2018, 18, 150.	1.6	61
610	Roxithromycin regulates intestinal microbiota and alters colonic epithelial gene expression. Applied Microbiology and Biotechnology, 2018, 102, 9303-9316.	1.7	7
611	De novo transcriptome assembly based on RNA-seq and dynamic expression of key enzyme genes in loganin biosynthetic pathway of Cornus officinalis. Tree Genetics and Genomes, 2018, 14, 1.	0.6	6
612	Transcriptome analysis of chrysanthemum (Dendranthema grandiflorum) in response to low temperature stress. BMC Genomics, 2018, 19, 319.	1.2	55
613	Growth Hormone Overexpression Disrupts Reproductive Status Through Actions on Leptin. Frontiers in Endocrinology, 2018, 9, 131.	1.5	29
614	Genetic Architecture of Feeding Behavior and Feed Efficiency in a Duroc Pig Population. Frontiers in Genetics, 2018, 9, 220.	1.1	105
615	Csn5 Is Required for the Conidiogenesis and Pathogenesis of the Alternaria alternata Tangerine Pathotype. Frontiers in Microbiology, 2018, 9, 508.	1.5	24

#	Article	IF	CITATIONS
616	Host Interaction Analysis of PA-N155 and PA-N182 in Chicken Cells Reveals an Essential Role of UBA52 for Replication of H5N1 Avian Influenza Virus. Frontiers in Microbiology, 2018, 9, 936.	1.5	13
617	Identification and annotation of breed-specific single nucleotide polymorphisms in Bos taurus genomes. PLoS ONE, 2018, 13, e0198419.	1.1	8
618	De Novo Sequencing and Assembly Analysis of Transcriptome in Pinus bungeana Zucc. ex Endl Forests, 2018, 9, 156.	0.9	7
619	Genome-Wide Identification of circRNAs in Pathogenic Basidiomycetous Yeast Cryptococcus neoformans Suggests Conserved circRNA Host Genes over Kingdoms. Genes, 2018, 9, 118.	1.0	15
620	The molecular events of IAA inhibiting citrus fruitlet abscission revealed by digital gene expression profiling. Plant Physiology and Biochemistry, 2018, 130, 192-204.	2.8	24
621	Comparative transcriptome analysis provides global insight into gene expression differences between two orchid cultivars. PLoS ONE, 2018, 13, e0200155.	1.1	12
622	Comparative microRNA-seq Analysis Depicts Candidate miRNAs Involved in Skin Color Differentiation in Red Tilapia. International Journal of Molecular Sciences, 2018, 19, 1209.	1.8	38
623	Common microRNA–mRNA Interactions in Different Newcastle Disease Virus-Infected Chicken Embryonic Visceral Tissues. International Journal of Molecular Sciences, 2018, 19, 1291.	1.8	22
624	Quantitative Changes in the Transcription of Phytohormone-Related Genes: Some Transcription Factors Are Major Causes of the Wheat Mutant dmc Not Tillering. International Journal of Molecular Sciences, 2018, 19, 1324.	1.8	22
625	Comparative Proteomic Analysis of Rana chensinensis Oviduct. Molecules, 2018, 23, 1384.	1.7	6
626	Transcriptome Analysis of Epithelioma Papulosum Cyprini Cells Infected by Reovirus Isolated from Allogynogenetic Silver Crucian Carp. Viruses, 2018, 10, 135.	1.5	3
627	Tissue expression and variation analysis of three bovine adipokine genes revealed their effect on growth traits in native Chinese cattle. Reproduction in Domestic Animals, 2018, 53, 1227-1234.	0.6	7
628	CDK13 RNA Over-Editing Mediated by ADAR1 Associates with Poor Prognosis of Hepatocellular Carcinoma Patients. Cellular Physiology and Biochemistry, 2018, 47, 2602-2612.	1.1	23
629	Identification and differential regulation of microRNAs during thyroid hormone-dependent metamorphosis in Microhyla fissipes. BMC Genomics, 2018, 19, 507.	1.2	9
630	Transcriptome characterization and differential expression analysis of disease-responsive genes in alfalfa leaves infected by Pseudopeziza medicaginis. Euphytica, 2018, 214, 1.	0.6	3
631	An early ABA-induced stomatal closure, Na+ sequestration in leaf vein and K+ retention in mesophyll confer salt tissue tolerance in Cucurbita species. Journal of Experimental Botany, 2018, 69, 4945-4960.	2.4	77
632	Identification and Characterization of CircRNAs of Two Pig Breeds as a New Biomarker in Metabolism-Related Diseases. Cellular Physiology and Biochemistry, 2018, 47, 2458-2470.	1.1	56
633	Transcriptome analysis unravels spatiotemporal modulation of phytohormone-pathway expression underlying gibberellin-induced parthenocarpic fruit set in San Pedro-type fig (Ficus carica L.). BMC Plant Biology, 2018, 18, 100.	1.6	15

#	Article	IF	CITATIONS
634	Bioinformatics Approaches for Genomics and Post Genomics Applications of Anticancer Plants. , 2018, , 283-317.		3
635	Landscape of copy number variations in Bos taurus: individual – and inter-breed variability. BMC Genomics, 2018, 19, 410.	1.2	25
636	Identification of a 5‑lncRNA signature‑based risk scoring system for survival prediction in colorectal cancer. Molecular Medicine Reports, 2018, 18, 279-291.	1.1	7
637	A comprehensive review of web-based resources of non-coding RNAs for plant science research. International Journal of Biological Sciences, 2018, 14, 819-832.	2.6	23
638	Identification and characterization of long noncoding RNAs and mRNAs expression profiles related to postnatal liver maturation of breeder roosters using Ribo-zero RNA sequencing. BMC Genomics, 2018, 19, 498.	1.2	6
639	Analysis of the <i>Gliâ€D2</i> locus identifies a genetic target for simultaneously improving the breadmaking and healthâ€related traits of common wheat. Plant Journal, 2018, 95, 414-426.	2.8	19
640	Analysis of microRNA profile of Anopheles sinensis by deep sequencing and bioinformatic approaches. Parasites and Vectors, 2018, 11, 172.	1.0	7
641	Feasibility and transcriptomic analysis of betalain production by biomembrane surface fermentation of Penicillium novae-zelandiae. AMB Express, 2018, 8, 4.	1.4	2
642	Transcriptomic insights into citrus segment membrane's cell wall components relating to fruit sensory texture. BMC Genomics, 2018, 19, 280.	1.2	14
643	Proteomic profiling of lung immune cells reveals dysregulation of phagocytotic pathways in female-dominated molecular COPD phenotype. Respiratory Research, 2018, 19, 39.	1.4	24
644	Integrated microRNA and mRNA sequencing analysis of ageâ€related changes to mouse thymic epithelial cells. IUBMB Life, 2018, 70, 678-690.	1.5	15
645	Transcriptome-based identification of genes related to resistance against Botrytis elliptica in Lilium regale. Canadian Journal of Plant Science, 2018, 98, 1058-1071.	0.3	17
646	Comparative transcriptome analysis reveals the gene expression profiling in bighead carp (Aristichthys nobilis) in response to acute nitrite toxicity. Fish and Shellfish Immunology, 2018, 79, 244-255.	1.6	25
647	Specific expression network analysis of diabetic nephropathy kidney tissue revealed key methylated sites. Journal of Cellular Physiology, 2018, 233, 7139-7147.	2.0	22
648	Transcriptome profiling using Illumina- and SMRT-based RNA-seq of hot pepper for in-depth understanding of genes involved in CMV infection. Gene, 2018, 666, 123-133.	1.0	62
649	MicroRNA Expression Analysis of Naked Silkworms. Journal of Economic Entomology, 2018, 111, 2876-2883.	0.8	4
650	Transcriptomic Analyses of Root Restriction Effects on Phytohormone Content and Signal Transduction during Grape Berry Development and Ripening. International Journal of Molecular Sciences, 2018, 19, 2300.	1.8	12
651	Label-free quantitative proteomics of rat hypothalamus under fever induced by LPS and PGE2. Journal of Proteomics, 2018, 187, 182-199.	1.2	14

#	ARTICLE Transcriptome analysis in Malus halliana roots in response to iron deficiency reveals insight into	IF	CITATIONS
652 653	sugar regulation. Molecular Genetics and Genomics, 2018, 293, 1523-1534. A genome-wide association study uncovers novel genomic regions and candidate genes of yield-related traits in upland cotton. Theoretical and Applied Genetics, 2018, 131, 2413-2425.	1.0	15
654	In Vivo Analysis of miR-34a Regulated Glucose Metabolism Related Genes in Megalobrama amblycephala. International Journal of Molecular Sciences, 2018, 19, 2417.	1.8	7
655	Three-IncRNA signature is a potential prognostic biomarker for pancreatic adenocarcinoma. Oncotarget, 2018, 9, 24248-24259.	0.8	30
656	Transcriptomics reveals the molecular processes of light-induced rapid darkening of the non-obligate cave dweller Oreolalax rhodostigmatus (Megophryidae, Anura) and their genetic basis of pigmentation strategy. BMC Genomics, 2018, 19, 422.	1.2	11
657	High-density genetic map construction and QTL mapping for fiber strength on Chr24 across multiple environments in a CCRI70 recombinant inbred lines population. Euphytica, 2018, 214, 1.	0.6	9
658	Ganoderma lucidum polysaccharide alleviating colorectal cancer by alteration of special gut bacteria and regulation of gene expression of colonic epithelial cells. Journal of Functional Foods, 2018, 47, 127-135.	1.6	64
659	Global transcriptome analysis of grapevine (Vitis vinifera L.) leaves under salt stress reveals differential response at early and late stages of stress in table grape cv. Thompson Seedless. Plant Physiology and Biochemistry, 2018, 129, 168-179.	2.8	36
660	Genome-wide screening differential long non-coding RNAs expression profiles discloses its roles involved in OHSS development. Journal of Assisted Reproduction and Genetics, 2018, 35, 1473-1482.	1.2	5
661	Comparative transcriptome sequencing of the intestine reveals differentially expressed genes in <i>Pelteobagrus vachellii</i> . Aquaculture Research, 2018, 49, 2560-2571.	0.9	3
662	Improved de novo genome assembly and analysis of the Chinese cucurbit Siraitia grosvenorii, also known as monk fruit or luo-han-guo. GigaScience, 2018, 7, .	3.3	32
663	Construction and analysis for differentially expressed long non-coding RNAs and MicroRNAs mediated competing endogenous RNA network in colon cancer. PLoS ONE, 2018, 13, e0192494.	1.1	39
664	Involvement of an ABI-like protein and a Ca2+-ATPase in drought tolerance as revealed by transcript profiling of a sweetpotato somatic hybrid and its parents Ipomoea batatas (L.) Lam. and I. triloba L PLoS ONE, 2018, 13, e0193193.	1.1	13
665	Detection of genomic structural variations in Guizhou indigenous pigs and the comparison with other breeds. PLoS ONE, 2018, 13, e0194282.	1.1	11
666	RNA sequencing and differential expression reveals the effects of serial oestrus synchronisation on ovarian genes in dairy goats. Reproduction, Fertility and Development, 2018, 30, 1622.	0.1	4
667	Transcriptomic analysis of differentially expressed genes in the molting gland (Y-organ) of the blackback land crab, Gecarcinus lateralis, during molt-cycle stage transitions. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 28, 37-53.	0.4	18
668	Transcriptome analysis of nitric oxide-responsive genes in upland cotton (Gossypium hirsutum). PLoS ONE, 2018, 13, e0192367.	1.1	23
669	The UbL-UBA Ubiquilin4 protein functions as a tumor suppressor in gastric cancer by p53-dependent and p53-independent regulation of p21. Cell Death and Differentiation, 2019, 26, 516-530.	5.0	42

# 670	ARTICLE Influence of isopropylmalate synthase <i>Os<scp>IPMS</scp>1</i> on seed vigour associated with amino acid and energy metabolism in rice. Plant Biotechnology Journal, 2019, 17, 322-337.	IF 4.1	CITATIONS
671	Global analysis of tissue-differential gene expression patterns and functional regulation of rapid antler growth. Mammal Research, 2019, 64, 235-248.	0.6	10
672	Identification of a fiveâ€gene signature with prognostic value in colorectal cancer. Journal of Cellular Physiology, 2019, 234, 3829-3836.	2.0	22
673	Chemoprevention of elite tea variety CFTâ€1 rich in EGCG against chemically induced liver cancer in rats. Food Science and Nutrition, 2019, 7, 2647-2665.	1.5	12
674	An improved genome assembly of the fluke Schistosoma japonicum. PLoS Neglected Tropical Diseases, 2019, 13, e0007612.	1.3	50
675	RNAi based transcriptome suggests genes potentially regulated by HSF1 in the Pacific oyster Crassostrea gigas under thermal stress. BMC Genomics, 2019, 20, 639.	1.2	18
676	Hybrid-Transcriptome Sequencing and Associated Metabolite Analysis Reveal Putative Genes Involved in Flower Color Difference in Rose Mutants. Plants, 2019, 8, 267.	1.6	14
677	Genome-Wide Identification and Characterization of Long Noncoding RNAs of Brown to White Adipose Tissue Transformation in Goats. Cells, 2019, 8, 904.	1.8	20
678	Comparative Transcriptome Analyses Reveal the Role of Conserved Function in Electric Organ Convergence Across Electric Fishes. Frontiers in Genetics, 2019, 10, 664.	1.1	4
679	Genome-Wide Association Study of Growth and Feeding Traits in Pekin Ducks. Frontiers in Genetics, 2019, 10, 702.	1.1	19
680	Construction and Investigation of a IncRNA-Associated ceRNA Regulatory Network in Cholangiocarcinoma. Frontiers in Oncology, 2019, 9, 649.	1.3	32
681	Identification of differentially expressed genes and signaling pathways in chronic obstructive pulmonary disease via bioinformatic analysis. FEBS Open Bio, 2019, 9, 1880-1899.	1.0	16
682	Comparative metagenomic sequencing analysis of cecum microbiotal diversity and function in broilers and layers. 3 Biotech, 2019, 9, 316.	1.1	30
683	Circular RNA expression profiles in cisplatin-induced acute kidney injury in mice. Epigenomics, 2019, 11, 1191-1207.	1.0	19
684	Identification of CFTR as a novel key gene in chromophobe renal cell carcinoma through bioinformatics analysis. Oncology Letters, 2019, 18, 1767-1774.	0.8	5
685	Transcriptomic characterisation of the optimised rat model of Walker 256 breast cancer cellâ€induced bone pain. Clinical and Experimental Pharmacology and Physiology, 2019, 46, 1201-1215.	0.9	2
686	iTRAQ-based quantitative analysis reveals proteomic changes in Chinese cabbage (Brassica rapa L.) in response to Plasmodiophora brassicae infection. Scientific Reports, 2019, 9, 12058.	1.6	17
687	Global transcriptome and gene co-expression network analyses on the development of distyly in Primula oreodoxa. Heredity, 2019, 123, 784-794.	1.2	15

#	Article	IF	CITATIONS
688	Cytokeratin 18 regulates the transcription and alternative splicing of apoptotic‑related genes and pathways in HeLa cells. Oncology Reports, 2019, 42, 301-312.	1.2	11
689	De novo Assembly and Characterization of the Floral Transcriptomes of Two Varieties of Melastoma malabathricum. Frontiers in Genetics, 2019, 10, 521.	1.1	4
690	Inactivated Mycobacterium vaccine induces innate immunity against M. ulcerans ecovar Liflandii (MuLiflandii ASM001) infection in Dabry's sturgeon (Acipenser dabryanus). Aquaculture, 2019, 512, 734312.	1.7	2
691	De novo transcriptome sequencing and gene expression profiling of Magnolia wufengensis in response to cold stress. BMC Plant Biology, 2019, 19, 321.	1.6	42

692 Comparative transcriptome analysis of translucent flesh disorder in mangosteen (Garcinia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Td

693	Screening of key genes and prediction of therapeutic agents in Arsenic-induced lung carcinoma. Cancer Biomarkers, 2019, 25, 351-360.	0.8	7
694	Single-Locus and Multi-Locus Genome-Wide Association Studies for Intramuscular Fat in Duroc Pigs. Frontiers in Genetics, 2019, 10, 619.	1.1	47
695	Transcriptome analysis provides new insights into the growth superiority of a novel backcross variety, Megalobrama amblycephala ♀ × (M. amblycephala ♀ × Culter alburnus â™,) â™,. Aqı 734317.	ua <b>duf</b> ture,	20149, 512,
696	Quantitative proteomic analysis reveals the ethanologenic metabolism regulation of Ethanoligenens harbinense by exogenous ethanol addition. Biotechnology for Biofuels, 2019, 12, 166.	6.2	14
697	Identifying microRNAs and Their Editing Sites in Macaca mulatta. Cells, 2019, 8, 682.	1.8	10
698	Cloudy with a Chance of Insights: Context Dependent Gene Regulation and Implications for Evolutionary Studies. Genes, 2019, 10, 492.	1.0	21
699	Comparative proteomic analysis of sex-biased proteins in ovary and testis at different stages of Spodoptera litura. Journal of Proteomics, 2019, 206, 103439.	1.2	1
700	Comparative transcriptome analysis of cultivated and wild seeds of Salvia hispanica (chia). Scientific Reports, 2019, 9, 9761.	1.6	27
701	Comparative proteomic analysis of Tibetan pig spermatozoa at high and low altitudes. BMC Genomics, 2019, 20, 569.	1.2	14
702	Frequent intra- and inter-species introgression shapes the landscape of genetic variation in bread wheat. Genome Biology, 2019, 20, 136.	3.8	148
703	Genome-Wide Identification of Circular RNAs Revealed the Dominant Intergenic Region Circularization Model in Apostichopus japonicus. Frontiers in Genetics, 2019, 10, 603.	1.1	16
704	Genome Resequencing Reveals Congenital Causes of Embryo and Nestling Death in Crested Ibis (Nipponia nippon). Genome Biology and Evolution, 2019, 11, 2125-2135.	1.1	4
705	Epithelial-mesenchymal transition markers screened in a cell-based model and validated in lung adenocarcinoma. BMC Cancer, 2019, 19, 680.	1.1	31

#	Article	IF	CITATIONS
706	A pollution gradient contributes to the taxonomic, functional, and resistome diversity of microbial communities in marine sediments. Microbiome, 2019, 7, 104.	4.9	100
707	Transcriptome analysis of oriental river Prawn(Macrobrachium nipponense)Hepatopancreas in response to ammonia exposure. Fish and Shellfish Immunology, 2019, 93, 223-231.	1.6	36
708	Eye Degeneration and Loss of otx5b Expression in the Cavefish Sinocyclocheilus tileihornes. Journal of Molecular Evolution, 2019, 87, 199-208.	0.8	10
709	Immunotoxicity and transcriptome analysis of zebrafish embryos in response to glufosinate-ammonium exposure. Chemosphere, 2019, 236, 124423.	4.2	49
710	Transcriptome profiling of Gerbera hybrida reveals that stem bending is caused by water stress and regulation of abscisic acid. BMC Genomics, 2019, 20, 600.	1.2	14
711	Generation of Tβ4 knock-in Cashmere goat using CRISPR/Cas9. International Journal of Biological Sciences, 2019, 15, 1743-1754.	2.6	17
712	Metagenomic sequencing reveals microbial gene catalogue of phosphinothricin-utilized soils in South China. Gene, 2019, 711, 143942.	1.0	22
713	Identification of Key Genes and Circular RNAs in Human Gastric Cancer. Medical Science Monitor, 2019, 25, 2488-2504.	0.5	40
714	The construction and analysis of the aberrant lncRNA-miRNA-mRNA network in non-small cell lung cancer. Journal of Thoracic Disease, 2019, 11, 1772-1778.	0.6	43
715	A Maternal Effect on Queen Production in Honeybees. Current Biology, 2019, 29, 2208-2213.e3.	1.8	22
716	De novo transcriptome analysis of Tibetan medicinal plant Dysphania schraderiana. Genetics and Molecular Biology, 2019, 42, 480-487.	0.6	8
717	<p>Candidate tumor suppressor gene IRF6 is involved in human breast cancer pathogenesis via modulating PI3K-regulatory subunit PIK3R2 expression</p> . Cancer Management and Research, 2019, Volume 11, 5557-5572.	0.9	14
718	Digital gene expression analyses of mammary glands from meat ewes naturally infected with clinical mastitis. Royal Society Open Science, 2019, 6, 181604.	1.1	8
719	Identification and Analysis of IncRNAs by Whole-Transcriptome Sequencing in Porcine Preadipocytes Induced by BMP2. Cytogenetic and Genome Research, 2019, 158, 133-144.	0.6	4
720	Precise Prediction of Calpain Cleavage Sites and Their Aberrance Caused by Mutations in Cancer. Frontiers in Genetics, 2019, 10, 715.	1.1	26
721	Gene clustering, enrichment and survival analysis of differentially expressed genes in Low Grade Glioma between different genders by big data analysis. , 2019, , .		4
722	Conjoint Analysis of Genome-Wide IncRNA and mRNA Expression of Heteromorphic Leavesin Response to Environmental Heterogeneityin Populus euphratica. International Journal of Molecular Sciences, 2019, 20, 5148.	1.8	16
723	Search for Nutritional Fitness Traits in a Biological Pest Control Agent Harmonia axyridis Using Comparative Transcriptomics. Frontiers in Physiology, 2019, 10, 1148.	1.3	6

#	Article	IF	CITATIONS
724	Integration of Transcriptomics and Metabolomics for Pepper (Capsicum annuum L.) in Response to Heat Stress. International Journal of Molecular Sciences, 2019, 20, 5042.	1.8	47
725	The capping pheromones and putative biosynthetic pathways in worker and drone larvae of honey bees Apis mellifera. Apidologie, 2019, 50, 793-803.	0.9	5
726	Dynamic changes of root proteome reveal diverse responsive proteins in maize subjected to cadmium stress. Journal of Integrative Agriculture, 2019, 18, 2193-2204.	1.7	9
727	An Overview of Genes From Cyberlindnera americana, a Symbiont Yeast Isolated From the Gut of the Bark Beetle Dendroctonus rhizophagus (Curculionidae: Scolytinae), Involved in the Detoxification Process Using Genome and Transcriptome Data. Frontiers in Microbiology, 2019, 10, 2180.	1.5	11
728	Transcription Analysis of the Stress and Immune Response Genes to Temperature Stress in Ostrinia furnacalis. Frontiers in Physiology, 2019, 10, 1289.	1.3	34
729	Identification of Candidate Adaxial–Abaxial-Related Genes Regulating Petal Expansion During Flower Opening in Rosa chinensis "Old Blush― Frontiers in Plant Science, 2019, 10, 1098.	1.7	12
730	Bioinformatic Identification of miR-622 Key Target Genes and Experimental Validation of the miR-622-RNF8 Axis in Breast Cancer. Frontiers in Oncology, 2019, 9, 1114.	1.3	20
731	Modulation of Proteome Profile in AβPP/PS1 Mice Hippocampus, Medial Prefrontal Cortex, and Striatum by Palm Oil Derived Tocotrienol-Rich Fraction. Journal of Alzheimer's Disease, 2019, 72, 229-246.	1.2	12
732	Tumor Vessel Normalization, Immunostimulatory Reprogramming, and Improved Survival in Glioblastoma with Combined Inhibition of PD-1, Angiopoietin-2, and VEGF. Cancer Immunology Research, 2019, 7, 1910-1927.	1.6	74
733	Gene expression profiling by mRNA sequencing reveals dysregulation of core genes in Rictor deficient T-ALL mouse model. Leukemia Research, 2019, 87, 106229.	0.4	0
734	AGRP and ESPL1 as Biomarkers of Brain-Metastasis in Lung Adenocarcinoma. Journal of Physics: Conference Series, 2019, 1302, 042040.	0.3	0
735	The hepatoprotective effects of Salvia plebeia R. Br. extract in zebrafish (Danio rerio). Fish and Shellfish Immunology, 2019, 95, 399-410.	1.6	24
736	Transcript-Level Analysis in Combination with Real-Time PCR Elucidates Heat Adaptation Mechanism of Tribolium castaneum (Herbst) (Coleoptera: Tenebrionidae) Larvae. Journal of Economic Entomology, 2019, 112, 2984-2992.	0.8	2
737	PacBio single-molecule long-read sequencing shed new light on the complexity of the Carex breviculmis transcriptome. BMC Genomics, 2019, 20, 789.	1.2	25
738	Auxin regulation involved in gynoecium morphogenesis of papaya flowers. Horticulture Research, 2019, 6, 119.	2.9	12
739	Study of the Differentially Expressed Genes in the Pomacea canaliculata Transcriptome after Treatment with Pedunsaponin A. Metabolites, 2019, 9, 268.	1.3	2
740	Root Transcriptomic Analysis Reveals Global Changes Induced by Systemic Infection of Solanum lycopersicum with Mild and Severe Variants of Potato Spindle Tuber Viroid. Viruses, 2019, 11, 992.	1.5	21
741	Transcriptome analysis reveals a positive effect of brassinosteroids on the photosynthetic capacity of wucai under low temperature. BMC Genomics, 2019, 20, 810.	1.2	29

#	Article	IF	CITATIONS
742	Lower Circulating Branchedâ€Chain Amino Acid Concentrations Among Vegetarians are Associated with Changes in Gut Microbial Composition and Function. Molecular Nutrition and Food Research, 2019, 63, e1900612.	1.5	29
743	Time-coursed transcriptome analysis identifies key expressional regulation in growth cessation and dormancy induced by short days in Paulownia. Scientific Reports, 2019, 9, 16602.	1.6	12
744	Exploring the Molecular Mechanism underlying the Stable Purple-Red Leaf Phenotype in Lagerstroemia indica cv. Ebony Embers. International Journal of Molecular Sciences, 2019, 20, 5636.	1.8	23
745	Analysis of high-throughput sequencing for cecal microbiota diversity and function in hens under different rearing systems. 3 Biotech, 2019, 9, 438.	1.1	14
746	Phosphoproteomics Profiling of Cotton ( <i>Gossypium hirsutum</i> L) Roots in Response to <i>Verticillium dahliae</i> Inoculation. ACS Omega, 2019, 4, 18434-18443.	1.6	10
747	Lymph node metastasis in lung squamous cell carcinoma and identification of metastasisâ€related genes based on the Cancer Genome Atlas. Cancer Medicine, 2019, 8, 6280-6294.	1.3	11
748	Differential quantitative proteomics reveals the functional difference of two <i>yigP</i> locus products, UbiJ and EsrE. Journal of Basic Microbiology, 2019, 59, 1125-1133.	1.8	5
749	MicroRNAs and their regulatory networks in Chinese Gushi chicken abdominal adipose tissue during postnatal late development. BMC Genomics, 2019, 20, 778.	1.2	23
750	Hepatic PKA inhibition accelerates the lipid accumulation in liver. Nutrition and Metabolism, 2019, 16, 69.	1.3	10
751	Long non-coding RNA HCP5 serves as a ceRNA sponging miR-17-5p and miR-27a/b to regulate the pathogenesis of childhood obesity via the MAPK signaling pathway. Journal of Pediatric Endocrinology and Metabolism, 2019, 32, 1327-1339.	0.4	19
752	Candidate genes in red pigment biosynthesis of a red-fleshed radish cultivar (Raphanus sativus L.) as revealed by transcriptome analysis. Biochemical Systematics and Ecology, 2019, 86, 103933.	0.6	3
753	Novel Pituitary Actions of Epidermal Growth Factor: Receptor Specificity and Signal Transduction for UTS1, EGR1, and MMP13 Regulation by EGF. International Journal of Molecular Sciences, 2019, 20, 5172.	1.8	6
754	Deletion of Gcw13 represses autophagy in Pichia pastoris cells grown in methanol medium with sufficient amino acids. Biotechnology Letters, 2019, 41, 1423-1431.	1.1	1
755	Deep learning-based model for predicting progression in patients with head and neck squamous cell carcinoma. Cancer Biomarkers, 2019, 27, 19-28.	0.8	15
756	The Interaction between Phagocytes and Streptococcus agalactiae (GBS) Mediated by the Activated Complement System is the Key to GBS Inducing Acute Bacterial Meningitis of Tilapia. Animals, 2019, 9, 818.	1.0	15
757	Plasma extracellular vesicle‑packaged microRNAs as candidate diagnostic biomarkers for early‑stage breast cancer. Molecular Medicine Reports, 2019, 20, 3991-4002.	1.1	17
758	A time-dependent genome-wide SNP-SNP interaction analysis of chicken body weight. BMC Genomics, 2019, 20, 771.	1.2	9
759	Pneumonia: host susceptibility and shared genetics with pulmonary function and other traits. Clinical and Experimental Immunology, 2019, 198, 367-380.	1.1	6

#	Article	IF	CITATIONS
760	A SNP Mutation of SiCRC Regulates Seed Number Per Capsule and Capsule Length of cs1 Mutant in Sesame. International Journal of Molecular Sciences, 2019, 20, 4056.	1.8	7
761	Comprehensive analysis of differentially expressed profiles and reconstruction of a competing endogenous RNA network in papillary renal cell carcinoma. Molecular Medicine Reports, 2019, 19, 4685-4696.	1.1	11
762	SNV discovery and functional candidate gene identification for milk composition based on whole genome resequencing of Holstein bulls with extremely high and low breeding values. PLoS ONE, 2019, 14, e0220629.	1,1	8
763	Transcriptome Analysis of Elm (Ulmus pumila) Fruit to Identify Phytonutrients Associated Genes and Pathways. Forests, 2019, 10, 738.	0.9	7
764	Transcriptomic analysis of Chlorimuron-ethyl degrading bacterial strain Klebsiella jilinsis 2N3. Ecotoxicology and Environmental Safety, 2019, 183, 109581.	2.9	23
765	Identification of markers predictive for response to induction chemotherapy in patients with sinonasal undifferentiated carcinoma. Oral Oncology, 2019, 97, 56-61.	0.8	16
766	In silico evidence of de novo interactions between ribosomal and Epstein - Barr virus proteins. BMC Molecular and Cell Biology, 2019, 20, 34.	1.0	3
767	Reconstruction of the full-length transcriptome atlas using PacBio Iso-Seq provides insight into the alternative splicing in Gossypium australe. BMC Plant Biology, 2019, 19, 365.	1.6	43
768	Comparative transcriptome analysis reveals potential fruiting body formation mechanisms in Morchella importuna. AMB Express, 2019, 9, 103.	1.4	29
769	Transcriptome Analysis Reveals Differential Expression of Genes Regulating Hepatic Triglyceride Metabolism in Pekin Ducks During Dietary Threonine Deficiency. Frontiers in Genetics, 2019, 10, 710.	1.1	9
770	Dual RNA-seq uncovers the immune response of Larimichthys crocea to the secY gene of Pseudomonas plecoglossicida from the perspective of host-pathogen interactions. Fish and Shellfish Immunology, 2019, 93, 949-957.	1.6	19
771	Right Atrial Mechanisms of AtrialÂFibrillation in a Rat Model of RightÂHeartÂDisease. Journal of the American College of Cardiology, 2019, 74, 1332-1347.	1.2	72
772	RNA-seq analysis of local tissue of Carassius auratus gibelio with pharyngeal myxobolosis: Insights into the pharyngeal mucosal immune response in a fish-parasite dialogue. Fish and Shellfish Immunology, 2019, 94, 99-112.	1.6	22
773	The Reason for Growth Inhibition of Ulmus pumila â€~Jinye': Lower Resistance and Abnormal Development of Chloroplasts Slow Down the Accumulation of Energy. International Journal of Molecular Sciences, 2019, 20, 4227.	1.8	12
774	High-Throughput RNA Sequencing Reveals NDUFC2-AS lncRNA Promotes Adipogenic Differentiation in Chinese Buffalo (Bubalus bubalis L). Genes, 2019, 10, 689.	1.0	32
775	Differential Regulation of Anthocyanins in Green and Purple Turnips Revealed by Combined De Novo Transcriptome and Metabolome Analysis. International Journal of Molecular Sciences, 2019, 20, 4387.	1.8	66
776	Paternal chronic folate supplementation induced the transgenerational inheritance of acquired developmental and metabolic changes in chickens. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191653.	1.2	19
777	Parental Exposure to Perfluorobutanesulfonate Impairs Offspring Development through Inheritance of Paternal Methylome. Environmental Science & 2019, 100, 2019, 53, 12018-12025.	4.6	22

#	Article	IF	CITATIONS
778	Effects and transcriptional responses in the hepatopancreas of red claw crayfish Cherax quadricarinatus under cold stress. Journal of Thermal Biology, 2019, 85, 102404.	1.1	40
779	Identification of novel genes associated with duck OASL in response to influenza A virus. Journal of Integrative Agriculture, 2019, 18, 1451-1459.	1.7	2
780	Large-Scale Analysis of the Mycoplasma bovis Genome Identified Non-essential, Adhesion- and Virulence-Related Genes. Frontiers in Microbiology, 2019, 10, 2085.	1.5	21
781	Transcriptomic analysis reveals potential mechanisms of toxicity in a combined exposure to dibutyl phthalate and diisobutyl phthalate in zebrafish (Danio rerio) ovary. Aquatic Toxicology, 2019, 216, 105290.	1.9	46
782	Gene Expression Profiles and microRNA Regulation Networks in Tiller Primordia, Stem Tips, and Young Spikes of Wheat Guomai 301. Genes, 2019, 10, 686.	1.0	6
783	Comparative proteomic analysis provides new insights into the specialization of shoots and stolons in bermudagrass (Cynodon dactylon L.). BMC Genomics, 2019, 20, 708.	1.2	6
784	The Draft Genome of the Endangered Sichuan Partridge (Arborophila rufipectus) with Evolutionary Implications. Genes, 2019, 10, 677.	1.0	8
785	Transcriptome Sequencing and Metabolome Analysis Reveal Genes Involved in Pigmentation of Green-Colored Cotton Fibers. International Journal of Molecular Sciences, 2019, 20, 4838.	1.8	33
786	Effects of Essential Oil Citral on the Growth, Mycotoxin Biosynthesis and Transcriptomic Profile of Alternaria alternata. Toxins, 2019, 11, 553.	1.5	45
787	A comparative morphological and transcriptomic study on autotetraploid Stevia rebaudiana (bertoni) and its diploid. Plant Physiology and Biochemistry, 2019, 143, 154-164.	2.8	18
788	Protective Role of Leaf Variegation in Pittosporum tobira under Low Temperature: Insights into the Physio-Biochemical and Molecular Mechanisms. International Journal of Molecular Sciences, 2019, 20, 4857.	1.8	4
789	Comparative transcript profiling and cytological observation of the newly bred recessive genic male sterility non-heading Chinese cabbage (Brassica rapa ssp. chinensis) line WS24-3A. Genes and Genomics, 2019, 41, 1475-1492.	0.5	3
790	RNA-seq revealed the signatures of immunity and metabolism in the Litopenaeus vannamei intestine in response to dietary succinate. Fish and Shellfish Immunology, 2019, 95, 16-24.	1.6	9
791	Transcriptome Sequencing of Peripheral Blood Mononuclear Cells from Elite Controller-Long Term Non Progressors. Scientific Reports, 2019, 9, 14265.	1.6	29
792	Multiomics analyses reveal that NOD-like signaling pathway plays an important role against Streptococcus agalactiae in the spleen of tilapia. Fish and Shellfish Immunology, 2019, 95, 336-348.	1.6	22
793	Impact of high or low levels of phosphorus and high sodium in soils on productivity and stress tolerance of Arundo donax plants. Plant Science, 2019, 289, 110260.	1.7	13
795	Identification and validation of four hub genes involved in the plaque deterioration of atherosclerosis. Aging, 2019, 11, 6469-6489.	1.4	13
796	Transcriptomic and physiological changes in western mosquitofish (Gambusia affinis) after exposure to norgestrel. Ecotoxicology and Environmental Safety, 2019, 171, 579-586.	2.9	10

#	Article	IF	CITATIONS
797	Weighted gene co‑expression network analysis for identifying hub genes in association with prognosis in Wilms tumor. Molecular Medicine Reports, 2019, 19, 2041-2050.	1.1	13
798	Diversifying selection signatures among divergently selected subpopulations of Polish Red cattle. Journal of Applied Genetics, 2019, 60, 87-95.	1.0	12
799	Ioxynil and diethylstilbestrol disrupt vascular and heart development in zebrafish. Environment International, 2019, 124, 511-520.	4.8	30
800	Study of the whole genome, methylome and transcriptome of Cordyceps militaris. Scientific Reports, 2019, 9, 898.	1.6	17
801	Proteomic analysis of adult Galeruca daurica (Coleoptera: Chrysomelidae) at different stages during summer diapause. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 29, 351-357.	0.4	6
802	Integrative Analysis of Transcriptome and GWAS Data to Identify the Hub Genes Associated With Milk Yield Trait in Buffalo. Frontiers in Genetics, 2019, 10, 36.	1.1	52
803	RNA-Seq Analyses of Midgut and Fat Body Tissues Reveal the Molecular Mechanism Underlying Spodoptera litura Resistance to Tomatine. Frontiers in Physiology, 2019, 10, 8.	1.3	20
804	Identification and characterization of circular RNAs during the sea buckthorn fruit development. RNA Biology, 2019, 16, 354-361.	1.5	30
805	Transcriptomic analysis of the life-extending effect exerted by black rice anthocyanin extract in D. melanogaster through regulation of aging pathways. Experimental Gerontology, 2019, 119, 33-39.	1.2	15
806	Non‑canonical Wnt signaling contributes to ventilator‑induced lung injury through upregulation of WISP1 expression. International Journal of Molecular Medicine, 2019, 43, 1217-1228.	1.8	4
807	Hormone and RNA-seq analyses reveal the mechanisms underlying differences in seed vigour at different maize ear positions. Plant Molecular Biology, 2019, 99, 461-476.	2.0	11
808	Dual RNA-seq reveals the effect of the flgM gene of Pseudomonas plecoglossicida on the immune response of Epinephelus coioides. Fish and Shellfish Immunology, 2019, 87, 515-523.	1.6	39
809	Regulation of Growth and Flavonoid Formation of Tea Plants ( <i>Camellia sinensis</i> ) by Blue and Green Light. Journal of Agricultural and Food Chemistry, 2019, 67, 2408-2419.	2.4	56
810	Spaceflight/microgravity inhibits the proliferation of hematopoietic stem cells by decreasing Kitâ€Ras/cAMPâ€CREB pathway networks as evidenced by RNAâ€Seq assays. FASEB Journal, 2019, 33, 5903-5913	0.2	25
811	A largeâ€scale circular <scp>RNA</scp> profiling reveals universal molecular mechanisms responsive to drought stress in maize and Arabidopsis. Plant Journal, 2019, 98, 697-713.	2.8	99
812	Investigating proteome and transcriptome response of Cryptococcus podzolicus Y3 to citrinin and the mechanisms involved in its degradation. Food Chemistry, 2019, 283, 345-352.	4.2	18
813	Transcriptomic Analysis Reveals a Comprehensive Calcium- and Phytohormone-Dominated Signaling Response in Leymus chinensis Self-Incompatibility. International Journal of Molecular Sciences, 2019, 20, 2356.	1.8	16
814	Robust and cost-saving static solid cultivation method for lipid production using the chlamydospores of Phanerochaete chrysosporium. Biotechnology for Biofuels, 2019, 12, 123.	6.2	13

	CIAIO	N REPORT	
#	Article	lF	CITATIONS
815	Metagenomic insights into functional traits variation and coupling effects on the anammox community during reactor start-up. Science of the Total Environment, 2019, 687, 50-60.	3.9	53
816	Transcriptome analysis reveals differentially expressed genes and pathways for oviduct development and defense in prelaying and laying hens. American Journal of Reproductive Immunology, 2019, 82, e13159.	1.2	11
817	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. Science, 2019, 364, .	6.0	266
818	Biological adaptations in the Arctic cervid, the reindeer ( <i>Rangifer tarandus</i> ). Science, 2019, 364,	6.0	58
819	Effects of dietary supplementation with lysozyme on the structure and function of the cecal microbiota in broiler chickens. PLoS ONE, 2019, 14, e0216748.	1.1	20
820	The Impact of cDNA Normalization on Long-Read Sequencing of a Complex Transcriptome. Frontiers in Genetics, 2019, 10, 654.	1.1	8
821	Cecal CircRNAs Are Associated With the Response to Salmonella Enterica Serovar Enteritidis Inoculation in the Chicken. Frontiers in Immunology, 2019, 10, 1186.	2.2	10
822	Comparative analysis of peripheral blood reveals transcriptomic adaptations to extreme environments on the Qinghai-Tibetan Plateau in the gray wolf (Canis lupus chanco). Organisms Diversity and Evolution, 2019, 19, 543-556.	0.7	5
823	Synchronous profiling and analysis of mRNAs and ncRNAs in the dermal papilla cells from cashmere goats. BMC Genomics, 2019, 20, 512.	1.2	17
824	A liver-specific IncRNA, FAM99B, suppresses hepatocellular carcinoma progression through inhibition of cell proliferation, migration, and invasion. Journal of Cancer Research and Clinical Oncology, 2019, 145, 2027-2038.	1.2	21
825	Multi-omics analysis of the development and fracture resistance for maize internode. Scientific Reports, 2019, 9, 8183.	1.6	10
826	Identification of key genes and pathways of thyroid cancer by integrated bioinformatics analysis. Journal of Cellular Physiology, 2019, 234, 23647-23657.	2.0	41
827	Alliin protects against inflammatory bowel disease by preserving the gene expression in colonic epithelial cells rather than altering gut microbiota. Journal of Functional Foods, 2019, 59, 309-318.	1.6	3
828	Transcriptomic and proteomic response of Manihot esculenta to Tetranychus urticae infestation at different densities. Experimental and Applied Acarology, 2019, 78, 273-293.	0.7	13
829	Comparative transcriptomic and proteomic analysis of yellow shell and black shell pearl oysters, Pinctada fucata martensii. BMC Genomics, 2019, 20, 469.	1.2	25
830	The complexity of alternative splicing and landscape of tissue-specific expression in lotus (Nelumbo) Tj ETQq 2019, 26, 301-311.	1 1 0.784314 1.5	rgBT /Overlo 28
831	Developmental and transcriptomic features characterize defects of silk gland growth and silk production in silkworm naked pupa mutant. Insect Biochemistry and Molecular Biology, 2019, 111, 103175.	1.2	17
832	CRKL regulates alternative splicing of cancer-related genes in cervical cancer samples and HeLa cell. BMC Cancer, 2019, 19, 499.	1.1	26

#	Article	IF	CITATIONS
833	Screening of key miRNAs and evaluation of their diagnostic and prognostic values in nasopharyngeal carcinoma. Oncology Letters, 2019, 17, 5803-5810.	0.8	5
834	Classical swine fever virus-Shimen infection upregulates SH3GLB1 expression in porcine alveolar macrophages. Biotechnology and Biotechnological Equipment, 2019, 33, 93-97.	0.5	0
835	Integrative Analyses of Long Non-coding RNA and mRNA Involved in Piglet lleum Immune Response to Clostridium perfringens Type C Infection. Frontiers in Cellular and Infection Microbiology, 2019, 9, 130.	1.8	40
836	An 11â€IncRNA expression could be potential prognostic biomarkers in head and neck squamous cell carcinoma. Journal of Cellular Biochemistry, 2019, 120, 18094-18103.	1.2	5
837	Differential color development and response to light deprivation of fig (Ficus carica L) syconia peel and female flower tissues: transcriptome elucidation. BMC Plant Biology, 2019, 19, 217.	1.6	23
838	Title is missing!. Turkish Journal of Fisheries and Aquatic Sciences, 2019, 19, .	0.4	0
839	Correlation between pri-miR-124 (rs531564) polymorphism and congenital heart disease susceptibility in Chinese population at two different altitudes: a case-control and in silico study. Environmental Science and Pollution Research, 2019, 26, 21983-21992.	2.7	10
840	Physiological responses of the abalone Haliotis discus hannai to daily and seasonal temperature variations. Scientific Reports, 2019, 9, 8019.	1.6	14
841	Ruminal microbiome-host crosstalk stimulates the development of the ruminal epithelium in a lamb model. Microbiome, 2019, 7, 83.	4.9	116
842	Quantitative trait locus mapping for plant height and branch number in an upland cotton recombinant inbred line with an SNP-based high-density genetic map. Euphytica, 2019, 215, 1.	0.6	4
843	Increased chalcopyrite bioleaching capabilities of extremely thermoacidophilic <i>Metallosphaera sedula</i> inocula by mixotrophic propagation. Journal of Industrial Microbiology and Biotechnology, 2019, 46, 1113-1127.	1.4	21
844	Determination of the Key Resistance Gene Analogs Involved in Ascochyta rabiei Recognition in Chickpea. Frontiers in Plant Science, 2019, 10, 644.	1.7	23
845	Cill transcriptome alterations in Macrobrachium rosenbergii under copper exposure. Chemosphere, 2019, 233, 796-808.	4.2	21
846	Potential Molecular Mechanisms of AURKB in the Oncogenesis and Progression of Osteosarcoma Cells: A Label-Free Quantitative Proteomics Analysis. Technology in Cancer Research and Treatment, 2019, 18, 153303381985326.	0.8	6
847	Transcriptome analysis reveals immune-related gene expression changes with age in giant panda (Ailuropoda melanoleuca) blood. Aging, 2019, 11, 249-262.	1.4	17
848	Comparative transcriptomics sheds light on differential adaptation and species diversification between two Melastoma species and their F1 hybrid. AoB PLANTS, 2019, 11, plz019.	1.2	5
849	Transcriptome Analysis of Yamame (Oncorhynchus masou) in Normal Conditions after Heat Stress. Biology, 2019, 8, 21.	1.3	2
850	modEnrichr: a suite of gene set enrichment analysis tools for model organisms. Nucleic Acids Research, 2019, 47, W183-W190.	6.5	62

#	Article	IF	CITATIONS
851	Weighted gene co-expression network analysis to explain the relationship between plasma total carotenoids and lipid profile. Genes and Nutrition, 2019, 14, 16.	1.2	9
852	Transcriptome analysis of differentially expressed genes during anther development stages on male sterility and fertility in Cucumis melo L. line. Gene, 2019, 707, 65-77.	1.0	11
853	Proteomic profiles of buffalo spermatozoa and seminal plasma. Theriogenology, 2019, 134, 74-82.	0.9	24
854	g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019) Tj ETQq1 1 0.784	314 rgBT , 6.5	Overlock 10
855	Whole-genome resequencing reveals genetic indels of feathered-leg traits in domestic chickens. Journal of Genetics, 2019, 98, 1.	0.4	12
856	Expanding dynamics of the virulence-related gene variations in the toxigenic Vibrio cholerae serogroup O1. BMC Genomics, 2019, 20, 360.	1.2	9
857	Genome-wide characterization of drought stress responsive long non-coding RNAs in Tibetan wild barley. Environmental and Experimental Botany, 2019, 164, 124-134.	2.0	31
858	Insights on acetate-ethanol fermentation by hydrogen-producing Ethanoligenens under acetic acid accumulation based on quantitative proteomics. Environment International, 2019, 129, 1-9.	4.8	23
859	Transcriptome Analysis of a Multiple-Branches Mutant Terminal Buds in Betula platyphylla × B. pendula. Forests, 2019, 10, 374.	0.9	3
860	Gender specific differences of immune competence in the sea cucumber Apostichopus japonicus before and after spawning. Fish and Shellfish Immunology, 2019, 90, 73-79.	1.6	12
861	In Silico Investigation of the Anti-Tumor Mechanisms of Epigallocatechin-3-Gallate. Molecules, 2019, 24, 1445.	1.7	17
862	Analysis of microRNAs, phased small interfering RNAs and their potential targets in Rosarugosa Thunb BMC Genomics, 2019, 19, 983.	1.2	13
863	Transcriptional alterations in Caenorhabditis elegans following exposure to an anthelmintic fraction of the plant Picria fel-terrae Lour Parasites and Vectors, 2019, 12, 181.	1.0	2
864	Acute exposure to triphenyl phosphate (TPhP) disturbs ocular development and muscular organization in zebrafish larvae. Ecotoxicology and Environmental Safety, 2019, 179, 119-126.	2.9	42
865	The genomes of pecan and Chinese hickory provide insights into Carya evolution and nut nutrition. GigaScience, 2019, 8, .	3.3	88
866	Tristetraprolin specifically regulates the expression and alternative splicing of immune response genes in HeLa cells. BMC Immunology, 2019, 20, 13.	0.9	34
867	Usnic acid modifies <scp>MRSA</scp> drug resistance through downâ€regulation of proteins involved in peptidoglycan and fatty acid biosynthesis. FEBS Open Bio, 2019, 9, 2025-2040.	1.0	11
868	Alternative Sigma Factor RpoX Is a Part of the RpoE Regulon and Plays Distinct Roles in Stress Responses, Motility, Biofilm Formation, and Hemolytic Activities in the Marine Pathogen Vibrio alginolyticus. Applied and Environmental Microbiology, 2019, 85, .	1.4	18

#	Article	IF	CITATIONS
869	Computational inference of the transcriptional regulatory network of Candida glabrata. FEMS Yeast Research, 2019, 19, .	1.1	0
870	Comparative transcriptome profiling of low light tolerant and sensitive rice varieties induced by low light stress at active tillering stage. Scientific Reports, 2019, 9, 5753.	1.6	31
871	Comparative genomics reveal pathogenicityâ€related loci in <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> biovar 3. Molecular Plant Pathology, 2019, 20, 923-942.	2.0	28
872	A transcriptional and functional analysis of heat hardening in two invasive fruit fly species, <i>Bactrocera dorsalis</i> and <i>Bactrocera correcta</i> . Evolutionary Applications, 2019, 12, 1147-1163.	1.5	26
873	Circular RNAs exhibit extensive intraspecific variation in maize. Planta, 2019, 250, 69-78.	1.6	11
874	Development and validation of a TP53-associated immune prognostic model for hepatocellular carcinoma. EBioMedicine, 2019, 42, 363-374.	2.7	257
875	Digital gene expression profiling in larvae of Tribolium castaneum at different periods post UV-B exposure. Ecotoxicology and Environmental Safety, 2019, 174, 514-523.	2.9	10
876	Transcriptomic Analysis of Coding Genes and Non-Coding RNAs Reveals Complex Regulatory Networks Underlying the Black Back and White Belly Coat Phenotype in Chinese Wuzhishan Pigs. Genes, 2019, 10, 201.	1.0	6
877	Genome of <i>Crucihimalaya himalaica</i> , a close relative of <i>Arabidopsis</i> , shows ecological adaptation to high altitude. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7137-7146.	3.3	108
878	Hybrid sequencing reveals insight into heat sensing and signaling of bread wheat. Plant Journal, 2019, 98, 1015-1032.	2.8	73
879	Genome-wide analysis reveals the genomic features of the turkey vulture (Cathartes aura) as a scavenger. Molecular Genetics and Genomics, 2019, 294, 679-692.	1.0	10
880	The Molecular Basis of Freshwater Adaptation in Prawns: Insights from Comparative Transcriptomics of Three <i>Macrobrachium</i> Species. Genome Biology and Evolution, 2019, 11, 1002-1018.	1.1	23
881	Distinct genomeâ€wide alternative polyadenylation during the response to silicon availability in the marine diatom <i>Thalassiosira pseudonana</i> . Plant Journal, 2019, 99, 67-80.	2.8	9
882	Identification and expression analysis of candidate chemosensory receptors based on the antennal transcriptome of Lissorhoptrus oryzophilus. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 30, 133-142.	0.4	9
883	Metabolism disruption analysis of zebrafish larvae in response to BPA and BPA analogs based on RNA-Seq technique. Ecotoxicology and Environmental Safety, 2019, 174, 181-188.	2.9	30
884	High-throughput sequencing of small RNAs and analysis of differentially expressed microRNAs associated with high-fat diet-induced hepatic insulin resistance in mice. Genes and Nutrition, 2019, 14, 6.	1.2	16
885	Comprehensive analysis of a ceRNA network reveals potential prognostic cytoplasmic lncRNAs involved in HCC progression. Journal of Cellular Physiology, 2019, 234, 18837-18848.	2.0	103
886	The up-regulation of two identified wound healing specific proteins-HSP70 and lysozyme in regenerated Eisenia fetida through transcriptome analysis. Journal of Ethnopharmacology, 2019, 237, 64-73.	2.0	15

#	Article	IF	CITATIONS
887	Proteomics and phosphoproteomics study of LCMT1 overexpression and oxidative stress: overexpression of LCMT1 arrests H <sub>2</sub> O <sub>2</sub> -induced lose of cells viability. Redox Report, 2019, 24, 1-9.	1.4	12
888	Mapping Gene Markers for Apple Fruit Ring Rot Disease Resistance Using a Multi-omics Approach. G3: Genes, Genomes, Genetics, 2019, 9, 1663-1678.	0.8	27
889	Differential Alternative Splicing Genes in Response to Boron Deficiency in Brassica napus. Genes, 2019, 10, 224.	1.0	12
890	Transcriptome Analysis Reveals Cotton (Gossypium hirsutum) Genes That Are Differentially Expressed in Cadmium Stress Tolerance. International Journal of Molecular Sciences, 2019, 20, 1479.	1.8	32
891	Comparative transcriptome analysis uncovers the regulatory functions of long noncoding RNAs in fruit development and color changes of Fragaria pentaphylla. Horticulture Research, 2019, 6, 42.	2.9	28
892	Neonicotinoid Insecticides Alter the Transcriptome of Soybean and Decrease Plant Resistance. International Journal of Molecular Sciences, 2019, 20, 783.	1.8	20
893	Gene expression analysis of the tibetan grassland caterpillars (Lepidoptera: Lymantriinae: Gynaephora) in response to high-altitude stress. AIP Conference Proceedings, 2019, , .	0.3	0
894	GenTree, an integrated resource for analyzing the evolution and function of primate-specific coding genes. Genome Research, 2019, 29, 682-696.	2.4	67
895	In vitro expansion affects the response of human bone marrow stromal cells to irradiation. Stem Cell Research and Therapy, 2019, 10, 82.	2.4	8
896	Ganoderma lucidum polysaccharide improves rat DSS-induced colitis by altering cecal microbiota and gene expression of colonic epithelial cells. Food and Nutrition Research, 2019, 63, .	1.2	85
897	Elymus nutans genes for seed shattering and candidate gene-derived EST-SSR markers for germplasm evaluation. BMC Plant Biology, 2019, 19, 102.	1.6	14
898	Key Maize Drought-Responsive Genes and Pathways Revealed by Comparative Transcriptome and Physiological Analyses of Contrasting Inbred Lines. International Journal of Molecular Sciences, 2019, 20, 1268.	1.8	78
899	Prostaglandin�D2 expression is prognostic in high‑grade serous ovarian cancer. Oncology Reports, 2019, 41, 2254-2264.	1.2	12
900	Comparative transcriptome analysis of salt-sensitive and salt-tolerant maize reveals potential mechanisms to enhance salt resistance. Genes and Genomics, 2019, 41, 781-801.	0.5	50
901	New Zealand Tree and Giant Wētĕ(Orthoptera) Transcriptomics Reveal Divergent Selection Patterns in Metabolic Loci. Genome Biology and Evolution, 2019, 11, 1293-1306.	1.1	6
902	Studies Into β-Glucan Recognition in Fish Suggests a Key Role for the C-Type Lectin Pathway. Frontiers in Immunology, 2019, 10, 280.	2.2	56
903	Transcriptome analysis of rare minnow (Gobiocypris rarus) infected by the grass carp reovirus. Fish and Shellfish Immunology, 2019, 89, 337-344.	1.6	27
904	Repeated pregnant mare serum gonadotropinâ€mediated oestrous synchronization alters gene expression in the ovaries and reduces reproductive performance in dairy goats. Reproduction in Domestic Animals, 2019, 54, 873-881.	0.6	11

#	Article	IF	CITATIONS
905	Highâ€quality draft genome sequence of <i>Gaiella occulta</i> isolated from a 150 meter deep mineral water borehole and comparison with the genome sequences of other deepâ€branching lineages of the phylum <i>Actinobacteria</i> . MicrobiologyOpen, 2019, 8, e00840.	1.2	38
906	RNA sequencing revealing the role of AMP-activated protein kinase signaling in mice myocardial ischemia reperfusion injury. Gene, 2019, 703, 91-101.	1.0	11
908	Nitric oxide-dependent regulation of sweet pepper fruit ripening. Journal of Experimental Botany, 2019, 70, 4557-4570.	2.4	84
909	RNA N6-methyladenosine demethylase FTO promotes breast tumor progression through inhibiting BNIP3. Molecular Cancer, 2019, 18, 46.	7.9	416
910	Molecular insights into cancer drug resistance from a proteomics perspective. Expert Review of Proteomics, 2019, 16, 413-429.	1.3	17
911	Physiological and Growth Response of Pepper (Capsicum annum L.) Seedlings to Supplementary Red/Blue Light Revealed through Transcriptomic Analysis. Agronomy, 2019, 9, 139.	1.3	15
912	Genetic compensation triggered by mutant mRNA degradation. Nature, 2019, 568, 193-197.	13.7	734
913	Gene expression profiles at different stages for formation of pearl sac and pearl in the pearl oyster Pinctada fucata. BMC Genomics, 2019, 20, 240.	1.2	26
914	Data Mining and Validation of AMPK Pathway as a Novel Candidate Role Affecting Intramuscular Fat Content in Pigs. Animals, 2019, 9, 137.	1.0	12
915	Comparative Genomics Reveals the Genetic Mechanisms of Musk Secretion and Adaptive Immunity in Chinese Forest Musk Deer. Genome Biology and Evolution, 2019, 11, 1019-1032.	1.1	17
916	De novo transcriptome and phytochemical analyses reveal differentially expressed genes and characteristic secondary metabolites in the original oolong tea (Camellia sinensis) cultivar â€~Tieguanyin' compared with cultivar â€~Benshan'. BMC Genomics, 2019, 20, 265.	1.2	46
917	Weighted gene coexpression network analysis identifies specific transcriptional modules and hub genes related to intramuscular fat traits in chicken breast muscle. Journal of Cellular Biochemistry, 2019, 120, 13625-13639.	1.2	11
918	Transcriptome analysis reveals novel insights in air-breathing magur catfish (Clarias magur) in response to high environmental ammonia. Gene, 2019, 703, 35-49.	1.0	25
919	Colonic Mucosal Transcriptomic Changes in Patients with Long-Duration Ulcerative Colitis Revealed Colitis-Associated Cancer Pathways. Journal of Crohn's and Colitis, 2019, 13, 755-763.	0.6	65
920	Alliin alters gut microbiota and gene expression of colonic epithelial tissues. Journal of Food Biochemistry, 2019, 43, e12795.	1.2	13
921	Comprehensive analysis of dysregulated IncRNAs, miRNAs and mRNAs with associated ceRNA network in esophageal squamous cell carcinoma. Gene, 2019, 696, 206-218.	1.0	29
922	The selective NLRP3 inflammasome inhibitor MCC950 alleviates cholestatic liver injury and fibrosis in mice. International Immunopharmacology, 2019, 70, 147-155.	1.7	61
923	Host cell interactome of PB1 N40 protein of H5N1 influenza A virus in chicken cells. Journal of Proteomics, 2019, 197, 34-41.	1.2	14

#	Article	IF	CITATIONS
924	CircFunBase: a database for functional circular RNAs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	108
925	Oxygen Perfusion (Persufflation) of Human Pancreata Enhances Insulin Secretion and Attenuates Islet Proinflammatory Signaling. Transplantation, 2019, 103, 160-167.	0.5	23
926	Whole Genome Messenger RNA Profiling Identifies a Novel Signature to Predict Gastric Cancer Survival. Clinical and Translational Gastroenterology, 2019, 10, e00004.	1.3	35
927	Transcriptome, proteome and draft genome of Euglena gracilis. BMC Biology, 2019, 17, 11.	1.7	98
928	Fine mapping of the major QTL for seed coat color in Brassica rapa var. Yellow Sarson by use of NIL populations and transcriptome sequencing for identification of the candidate genes. PLoS ONE, 2019, 14, e0209982.	1.1	12
929	Transcriptomic analysis of cultivated cotton Gossypium hirsutum provides insights into host responses upon whitefly-mediated transmission of cotton leaf curl disease. PLoS ONE, 2019, 14, e0210011.	1.1	28
930	A genome-wide scan for diversifying selection signatures in selected horse breeds. PLoS ONE, 2019, 14, e0210751.	1.1	52
931	Co-Expression Network Analysis and Hub Gene Selection for High-Quality Fiber in Upland Cotton (Gossypium hirsutum) Using RNA Sequencing Analysis. Genes, 2019, 10, 119.	1.0	29
932	Long-term and high dose dexamethasone injection decreases the expression of Immunoglobulin Heavy (Light) Chain Variable Region Genes (IGH(L)Vs) in the mouse spleen. Gene, 2019, 695, 42-50.	1.0	6
933	Transcriptomic information from the ovaries of red swamp crayfish (Procambarus clarkii) provides new insights into development of ovaries and embryos. Aquaculture, 2019, 505, 333-343.	1.7	12
934	Comparative transcriptome analysis of genes involved in anthocyanin biosynthesis in the pink-white and red fruits of Chinese bayberry (Morella rubra). Scientia Horticulturae, 2019, 250, 278-286.	1.7	15
935	DAFâ€16 stabilizes the aging transcriptome and is activated in midâ€aged <i>Caenorhabditis elegans</i> to cope with internal stress. Aging Cell, 2019, 18, e12896.	3.0	53
936	Dual RNA-Seq reveals the role of a transcriptional regulator gene in pathogen-host interactions between Pseudomonas plecoglossicida and Epinephelus coioides. Fish and Shellfish Immunology, 2019, 87, 778-787.	1.6	31
937	The Specific Inhibition of SOD1 Selectively Promotes Apoptosis of Cancer Cells via Regulation of the ROS Signaling Network. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-21.	1.9	22
938	Somatic proteome of Haemonchus contortus. International Journal for Parasitology, 2019, 49, 311-320.	1.3	38
939	Comparative Proteomic Analysis Provides New Insights Into Low Nitrogen-Promoted Primary Root Growth in Hexaploid Wheat. Frontiers in Plant Science, 2019, 10, 151.	1.7	15
940	Integrated analysis of competing endogenous RNA networks revealing five prognostic biomarkers associated with colorectal cancer. Journal of Cellular Biochemistry, 2019, 120, 11256-11264.	1.2	18
941	Transcriptomic analysis identifies critical signaling components involved in the self-incompatibility response in Chinese cabbage. Scientia Horticulturae, 2019, 248, 189-199.	1.7	5

#	Article	IF	Citations
942	B-Box Containing Proteins BBX30 and BBX31, Acting Downstream of HY5, Negatively Regulate Photomorphogenesis in <i>Arabidopsis</i> . Plant Physiology, 2019, 180, 497-508.	2.3	69
943	<i>De novo</i> transcriptome sequencing of genome analysis provides insights into <i>Solidago canadensis</i> invasive capability via photosynthesis. Journal of Plant Interactions, 2019, 14, 572-579.	1.0	6
944	Curcumin Inhibits ERK/c-Jun Expressions and Phosphorylation against Endometrial Carcinoma. BioMed Research International, 2019, 2019, 1-13.	0.9	29
945	Global Transcriptomic Analysis of the Candida albicans Response to Treatment with a Novel Inhibitor of Filamentation. MSphere, 2019, 4, .	1.3	18
946	RNA-seq analysis provides insight into molecular adaptations of Andrias davidianus. Development Genes and Evolution, 2019, 229, 197-206.	0.4	5
947	Genome–Scale Metabolic Networks Shed Light on the Carotenoid Biosynthesis Pathway in the Brown Algae Saccharina japonica and Cladosiphon okamuranus. Antioxidants, 2019, 8, 564.	2.2	19
948	Development and Validation of Tumor-educated Blood Platelets Integrin Alpha 2b (ITGA2B) RNA for Diagnosis and Prognosis of Non-small-cell Lung Cancer through RNA-seq. International Journal of Biological Sciences, 2019, 15, 1977-1992.	2.6	40
949	Screening and characterization of long noncoding RNAs involved in the albinism of Ananas comosus var. bracteatus leaves. PLoS ONE, 2019, 14, e0225602.	1.1	5
950	Genomic Variance and Transcriptional Comparisons Reveal the Mechanisms of Leaf Color Affecting Palatability and Stressed Defense in Tea Plant. Genes, 2019, 10, 929.	1.0	14
951	Transcriptomic analysis of α-synuclein knockdown after T3 spinal cord injury in rats. BMC Genomics, 2019, 20, 851.	1.2	6
952	Candidate genes for grape white rot resistance based on SMRT and Illumina sequencing. BMC Plant Biology, 2019, 19, 501.	1.6	11
953	Comparative transcriptional analysis provides insights of possible molecular mechanisms of wing polyphenism induced by postnatal crowding in Aphis gossypii. Journal of Cotton Research, 2019, 2, .	1.0	4
954	A Multi-Omics Study of Chicken Infected by Nephropathogenic Infectious Bronchitis Virus. Viruses, 2019, 11, 1070.	1.5	21
955	Integrative analysis of hexaploid wheat roots identifies signature components during iron starvation. Journal of Experimental Botany, 2019, 70, 6141-6161.	2.4	48
956	Transcriptome landscape of Rafflesia cantleyi floral buds reveals insights into the roles of transcription factors and phytohormones in flower development. PLoS ONE, 2019, 14, e0226338.	1.1	13
957	De novo Assembly and Characterization of Patagonian Toothfish Transcriptome and Develop of EST-SSR Markers for Population Genetics. Frontiers in Marine Science, 2019, 6, .	1.2	8
958	Combined De Novo Transcriptome and Metabolome Analysis of Common Bean Response to Fusarium oxysporum f. sp. phaseoli Infection. International Journal of Molecular Sciences, 2019, 20, 6278.	1.8	63
959	Genomic Survey, Transcriptome, and Metabolome Analysis of Apocynum venetum and Apocynum hendersonii to Reveal Major Flavonoid Biosynthesis Pathways. Metabolites, 2019, 9, 296.	1.3	26

#	Article	IF	CITATIONS
960	Metabonomics-assisted label-free quantitative proteomic and transcriptomic analysis reveals novel insights into the antifungal effect of graphene oxide for controlling <i>Fusarium graminearum</i> . Environmental Science: Nano, 2019, 6, 3401-3421.	2.2	23
961	Single-molecule real-time sequencing facilitates the analysis of transcripts and splice isoforms of anthers in Chinese cabbage (Brassica rapa L. ssp. pekinensis). BMC Plant Biology, 2019, 19, 517.	1.6	16
962	Transcriptome Analysis of the Cecal Tonsil of Jingxing Yellow Chickens Revealed the Mechanism of Differential Resistance to Salmonella. Genes, 2019, 10, 979.	1.0	12
963	PacBio Long-Read Sequencing Reveals the Transcriptomic Complexity and Aux/IAA Gene Evolution in Gnetum (Gnetales). Forests, 2019, 10, 1043.	0.9	6

## 964 Identification of diapause-associated proteins in migratory locust, Locusta migratoria L. (Orthoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf

965	Transcriptome Analysis and Identification of Insecticide Tolerance-Related Genes after Exposure to Insecticide in Sitobion avenae. Genes, 2019, 10, 951.	1.0	24
966	Parallel Bud Mutation Sequencing Reveals that Fruit Sugar and Acid Metabolism Potentially Influence Stress in Malus. International Journal of Molecular Sciences, 2019, 20, 5988.	1.8	11
967	Molecular Analysis of UV-C Induced Resveratrol Accumulation in Polygonum cuspidatum Leaves. International Journal of Molecular Sciences, 2019, 20, 6185.	1.8	16
968	Single-Molecule Long-Read Sequencing Reveals the Diversity of Full-Length Transcripts in Leaves of Gnetum (Gnetales). International Journal of Molecular Sciences, 2019, 20, 6350.	1.8	8
969	Comparative transcriptomic analysis of the flower induction and development of the Lei bamboo (Phyllostachys violascens). BMC Bioinformatics, 2019, 20, 687.	1.2	14
970	The transcriptome variations of Panaxnotoginseng roots treated with different forms of nitrogen fertilizers. BMC Genomics, 2019, 20, 965.	1.2	15
971	Full-length transcriptome sequencing reveals the low-temperature-tolerance mechanism of Medicago falcata roots. BMC Plant Biology, 2019, 19, 575.	1.6	43
972	Sucrose Promotes Strawberry Fruit Ripening and Affects Ripening-Related Processes. International Journal of Genomics, 2019, 2019, 1-14.	0.8	13
973	Comparative Transcriptome Analysis of Gonads for the Identification of Sex-Related Genes in Giant Freshwater Prawns (Macrobrachium Rosenbergii) Using RNA Sequencing. Genes, 2019, 10, 1035.	1.0	23
974	Transcriptome analysis reveals an important candidate gene involved in both nodal metastasis and prognosis in lung adenocarcinoma. Cell and Bioscience, 2019, 9, 92.	2.1	46
975	Comparative Transcriptome Profiling of Resistant and Susceptible Sugarcane Cultivars in Response to Infection by Xanthomonas albilineans. International Journal of Molecular Sciences, 2019, 20, 6138.	1.8	26
976	De novo sequencing of the transcriptome reveals regulators of the floral transition in Fargesia macclureana (Poaceae). BMC Genomics, 2019, 20, 1035.	1.2	8
977	Physiological and transcriptomic responses to fishmeal-based diet and rapeseed meal-based diet in two strains of gibel carp (Carassius gibelio). Fish Physiology and Biochemistry, 2019, 45, 267-286.	0.9	12

#	Article	IF	CITATIONS
978	Short-term responses of soybean roots to individual and combinatorial effects of elevated [CO2] and water deficit. Plant Science, 2019, 280, 283-296.	1.7	17
979	Comparative Transcriptomic and Physiological Analyses of Medicago sativa L. Indicates that Multiple Regulatory Networks Are Activated during Continuous ABA Treatment. International Journal of Molecular Sciences, 2019, 20, 47.	1.8	20
980	Transcriptome analysis of differential gene expression in Dichomitus squalens during interspecific mycelial interactions and the potential link with laccase induction. Journal of Microbiology, 2019, 57, 127-137.	1.3	11
981	Proteomics turns functional. Journal of Proteomics, 2019, 198, 36-44.	1.2	74
982	Cold Acclimation of the Thermoacidophilic Red Alga Galdieria sulphuraria: Changes in Gene Expression and Involvement of Horizontally Acquired Genes. Plant and Cell Physiology, 2019, 60, 702-712.	1.5	15
983	Transcriptome analysis of spleen reveals the signal transduction of toll-like receptors after Aeromonas hydrophila infection in Schizothorax prenanti. Fish and Shellfish Immunology, 2019, 84, 816-824.	1.6	21
984	Comparative transcriptome analysis reveals molecular strategies of ghost moth Thitarodes armoricanus in response to hypoxia and anoxia. Journal of Insect Physiology, 2019, 112, 23-34.	0.9	7
985	A Competing Endogenous RNA Network Reveals Novel Potential IncRNA, miRNA, and mRNA Biomarkers in the Prognosis of Human Colon Adenocarcinoma. Journal of Surgical Research, 2019, 235, 22-33.	0.8	47
986	Comparative physiological and proteomic analyses of the chloroplasts in halophyte Sesuvium portulacastrum under differential salt conditions. Journal of Plant Physiology, 2019, 232, 141-150.	1.6	24
987	hnRNPDL extensively regulates transcription and alternative splicing. Gene, 2019, 687, 125-134.	1.0	45
988	TiO2 nanoparticles and BPA are combined to impair the development of offspring zebrafish after parental coexposure. Chemosphere, 2019, 217, 732-741.	4.2	24
989	Identification and characteristics of <i>Stagonosporopsis cucurbitacearum</i> pathogenic factors influencing pumpkin seeding survival in northâ€east China. Journal of Phytopathology, 2019, 167, 41-55.	0.5	8
990	Investigating the proteomic expression profile of tobacco (Nicotiana tabacum) leaves during four growth stages using the iTRAQ method. Analytical and Bioanalytical Chemistry, 2019, 411, 403-411.	1.9	3
991	Enriched networks â€~nucleoside/nucleotide and ribonucleoside/ribonucleotide metabolic processes' and â€~response to stimulus' potentially conferred to drought adaptation of the epiphytic orchid Dendrobium wangliangii. Physiology and Molecular Biology of Plants, 2019, 25, 31-45.	1.4	13
992	Clustered miR-2, miR-13a, miR-13b and miR-71 coordinately target Notch gene to regulate oogenesis of the migratory locust Locusta migratoria. Insect Biochemistry and Molecular Biology, 2019, 106, 39-46.	1.2	34
993	Genome-wide characterization of aberrant DNA methylation patterns and the potential clinical implications in patients with endometrial cancer. Pathology Research and Practice, 2019, 215, 137-143.	1.0	9
994	Genomic and transcriptomic insights into the survival of the subaerial cyanobacterium <i>Nostoc flagelliforme</i> in arid and exposed habitats. Environmental Microbiology, 2019, 21, 845-863.	1.8	32
995	Transcriptome-wide effect of DE-ETIOLATED1 (DET1) suppression in embryogenic callus of Carica papaya. Journal of Plant Research, 2019, 132, 181-195.	1.2	6

#	Article	IF	CITATIONS
996	Cytokinin-induced parthenocarpy of San Pedro type fig (Ficus carica L.) main crop: explained by phytohormone assay and transcriptomic network comparison. Plant Molecular Biology, 2019, 99, 329-346.	2.0	14
997	Analysis of transcripts and splice isoforms in Medicago sativa L. by single-molecule long-read sequencing. Plant Molecular Biology, 2019, 99, 219-235.	2.0	38
998	Global transcriptome analysis and differentially expressed genes in grapevine after application of the yeastâ€derived defense inducer cerevisane. Pest Management Science, 2019, 75, 2020-2033.	1.7	25
999	Transcriptomic and Metabolic Profiling Reveals â€~Green Ring' and â€~Red Ring' on Jujube Fruit upon Postharvest <i>Alternaria alternata</i> Infection. Plant and Cell Physiology, 2019, 60, 844-861.	1.5	21
1000	Transcriptome-wide identification of differentially expressed genes in Procambarus clarkii in response to chromium challenge. Fish and Shellfish Immunology, 2019, 87, 43-50.	1.6	17
1001	Quantitative Proteomics of Potato Leaves Infected with Phytophthora infestans Provides Insights into Coordinated and Altered Protein Expression during Early and Late Disease Stages. International Journal of Molecular Sciences, 2019, 20, 136.	1.8	20
1002	Identification of differentially expressed genes and biological characteristics of colorectal cancer by integrated bioinformatics analysis. Journal of Cellular Physiology, 2019, 234, 15215-15224.	2.0	47
1003	UVEOGENE: An SNP database for investigations on genetic factors associated with uveitis and their relationship with other systemic autoimmune diseases. Human Mutation, 2019, 40, 258-266.	1.1	12
1004	Genome-wide DNA methylation and transcriptomic profiles in the lifestyle strategies and asexual development of the forest fungal pathogen <i>Heterobasidion parviporum</i> . Epigenetics, 2019, 14, 16-40.	1.3	11
1005	ZWINT is the next potential target for lung cancer therapy. Journal of Cancer Research and Clinical Oncology, 2019, 145, 661-673.	1.2	23
1006	Roles of highly expressed PAICS in lung adenocarcinoma. Gene, 2019, 692, 1-8.	1.0	38
1007	Comparative transcriptome analysis reveals relationship of three major domesticated varieties of Auricularia auricula-judae. Scientific Reports, 2019, 9, 78.	1.6	16
1008	Comparative transcriptome among Euscaphis konishii Hayata tissues and analysis of genes involved in flavonoid biosynthesis and accumulation. BMC Genomics, 2019, 20, 24.	1.2	29
1009	Identification and analysis of long non-coding RNAs in response to H5N1 influenza viruses in duck (Anas platyrhynchos). BMC Genomics, 2019, 20, 36.	1.2	20
1010	Effects of amino acids on the lignocellulose degradation by Aspergillus fumigatus Z5: insights into performance, transcriptional, and proteomic profiles. Biotechnology for Biofuels, 2019, 12, 4.	6.2	22
1011	Exploring miRNAs for developing climate-resilient crops: A perspective review. Science of the Total Environment, 2019, 653, 91-104.	3.9	52
1012	The vitellogenin receptor has an essential role in vertical transmission of rice stripe virus during oogenesis in the small brown plant hopper. Pest Management Science, 2019, 75, 1370-1382.	1.7	17
1013	Long noncoding RNA MEG3 play an important role in osteosarcoma development through sponging microRNAs. Journal of Cellular Biochemistry, 2019, 120, 5151-5159.	1.2	17

#	Article	IF	CITATIONS
1014	Activation of Nrf2 by Phloretin Attenuates Palmitic Acid-Induced Endothelial Cell Oxidative Stress via AMPK-Dependent Signaling. Journal of Agricultural and Food Chemistry, 2019, 67, 120-131.	2.4	55
1015	PPIP: Automated Software for Identification of Bioactive Endogenous Peptides. Journal of Proteome Research, 2019, 18, 721-727.	1.8	2
1016	Linkages between Epithelial Microbiota and Host Transcriptome in the lleum during High-Grain Challenges: Implications for Gut Homeostasis in Goats. Journal of Agricultural and Food Chemistry, 2019, 67, 551-561.	2.4	17
1017	Identification of Back-spliced Circular RNAs. , 2019, , 247-265.		0
1019	Liver transcriptome analysis of the Sparus macrocephlus in response to Vibrio parahaemolyticus infection. Fish and Shellfish Immunology, 2019, 84, 825-833.	1.6	6
1020	Potentially critical roles of TNPO1 , RAP1B , ZDHHC17 , and PPM1B in the progression of coronary atherosclerosis through microarray data analysis. Journal of Cellular Biochemistry, 2019, 120, 4301-4311.	1.2	22
1021	A comparison of honeybee ( <i>Apis mellifera</i> ) queen, worker and drone larvae by RNAâ€Seq. Insect Science, 2019, 26, 499-509.	1.5	17
1022	Whole-genome analysis of structural variations between Xiang pigs with larger litter sizes and those with smaller litter sizes. Genomics, 2019, 111, 310-319.	1.3	11
1023	The genome-wide transcription response underlying the dorsal processes and dorsal setae of the body in Dasyaphis mirabilis (Aphididae: Calaphidinae). Oriental Insects, 2019, 53, 1-18.	0.1	1
1024	Transcriptomic reprogramming in soybean seedlings under salt stress. Plant, Cell and Environment, 2019, 42, 98-114.	2.8	111
1025	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. Briefings in Bioinformatics, 2019, 20, 1032-1056.	3.2	10
1026	Genomeâ€wide quantitative trait loci reveal the genetic basis of cotton fibre quality and yieldâ€related traits in a <i>Gossypium hirsutum</i> recombinant inbred line population. Plant Biotechnology Journal, 2020, 18, 239-253.	4.1	49
1027	Transcriptome responses to elevated CO 2 level and Wolbachia â€infection stress in Hylyphantes graminicola (Araneae: Linyphiidae). Insect Science, 2020, 27, 908-920.	1.5	1
1028	Genomic and transcriptome identification of fluconazole-resistant genes for Trichosporon asahii. Medical Mycology, 2020, 58, 393-400.	0.3	5
1029	Rapid phenotypic evolution with shallow genomic differentiation during early stages of high elevation adaptation in Eurasian Tree Sparrows. National Science Review, 2020, 7, 113-127.	4.6	36
1030	Early transcriptional responses to soybean cyst nematode HG Type 0 show genetic differences among resistant and susceptible soybeans. Theoretical and Applied Genetics, 2020, 133, 87-102.	1.8	17
1031	Whole Proteome Analysis of GA3 Response at Panicle Stage in Grape (Vitis vinifera) cv. Thompson Seedless. Journal of Plant Growth Regulation, 2020, 39, 994-1008.	2.8	0
1032	Metagenomic analysis of the biotoxicity of titanium dioxide nanoparticles to microbial nitrogen transformation in constructed wetlands. Journal of Hazardous Materials, 2020, 384, 121376.	6.5	85

#	Article	IF	CITATIONS
1033	circRNAs Are Involved in the Rice- <i>Magnaporthe oryzae</i> Interaction. Plant Physiology, 2020, 182, 272-286.	2.3	65
1034	Identification of a sixâ€gene prognostic signature for oral squamous cell carcinoma. Journal of Cellular Physiology, 2020, 235, 3056-3068.	2.0	43
1035	<i>UvCom1</i> Is an Important Regulator Required for Development and Infection in the Rice False Smut Fungus <i>Ustilaginoidea virens</i> . Phytopathology, 2020, 110, 483-493.	1.1	29
1036	Genome-wide analysis sheds light on the high-altitude adaptation of the buff-throated partridge (Tetraophasis szechenyii). Molecular Genetics and Genomics, 2020, 295, 31-46.	1.0	11
1037	Building a sequence map of the pig pan-genome from multiple de novo assemblies and Hi-C data. Science China Life Sciences, 2020, 63, 750-763.	2.3	47
1038	Proteome of cat semen obtained after urethral catheterization. Theriogenology, 2020, 141, 68-81.	0.9	15
1039	Comparative Transcriptome Analysis Reveals Different Host Cell Responses to Acute and Persistent Foot-and-Mouth Disease Virus Infection. Virologica Sinica, 2020, 35, 52-63.	1.2	7
1040	First demonstration of giant panda's immune response to canine distemper vaccine. Developmental and Comparative Immunology, 2020, 102, 103489.	1.0	13
1041	RBM4 modulates the proliferation and expression of inflammatory factors via the alternative splicing of regulatory factors in HeLa cells. Molecular Genetics and Genomics, 2020, 295, 95-106.	1.0	10
1042	Blocked synthesis of sporopollenin and jasmonic acid leads to pollen wall defects and anther indehiscence in genic male sterile wheat line 4110S at high temperatures. Functional and Integrative Genomics, 2020, 20, 383-396.	1.4	17
1043	Genomic evidence sheds light on the genetic mechanisms of musk secretion in muskrats. International Journal of Biological Macromolecules, 2020, 145, 1189-1198.	3.6	3
1044	Multigenerational effects of perfluorooctanoic acid on lipid metabolism of Caenorhabditis elegans and its potential mechanism. Science of the Total Environment, 2020, 703, 134762.	3.9	27
1045	<i>&gt;De novo</i> transcriptome characterisation of two auxinâ€related genes associated with plant growth habit in <i>Astragalus adsurgens</i> Pall. Plant Biology, 2020, 22, 3-12.	1.8	6
1046	Effects of probiotics on cecal microbiome profile altered by duck Escherichia coli 17 infection in Cherry Valley ducks. Microbial Pathogenesis, 2020, 138, 103849.	1.3	23
1047	Genome-wide analysis of long noncoding RNA and mRNA profiles in PRRSV-infected porcine alveolar macrophages. Genomics, 2020, 112, 1879-1888.	1.3	9
1048	Transcriptome analysis of golden pompano (Trachinotus ovatus) liver indicates a potential regulatory target involved in HUFA uptake and deposition. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2020, 33, 100633.	0.4	10
1049	Tissue-specific transcriptome for Dendrobium officinale reveals genes involved in flavonoid biosynthesis. Genomics, 2020, 112, 1781-1794.	1.3	50
1050	Resource Price-Aware Offloading for Edge-Cloud Collaboration: A Two-Timescale Online Control Approach. IEEE Transactions on Cloud Computing, 2022, 10, 648-661.	3.1	31

ARTICLE IF CITATIONS Identification and characterization of circular RNAs during wood formation of poplars in 1051 14 1.6 acclimation to low nitrogen availability. Planta, 2020, 251, 47. Identification of a novel anthocyanin synthesis pathway in the fungus Aspergillus sydowii H-1. BMC 1.2 Genomics, 2020, 21, 29. Structure and function analysis of various brain subregions and pituitary in grass carp 1053 (Ctenopharyngodon idellus). Comparative Biochemistry and Physiology Part D: Genomics and 7 0.4 Proteomics, 2020, 33, 100653. Label-free quantitative identification of abnormally ubiquitinated proteins as useful biomarkers for 1054 human lung squamous cell carcinomas. EPMA Journal, 2020, 11, 73-94. BcERF070, a novel ERF (ethylene-response factor) transcription factor from non-heading Chinese cabbage, affects the accumulation of ascorbic acid by regulating ascorbic acid-related genes. 1055 1.0 13 Molecular Breeding, 2020, 40, 1. A Transcriptomic Analysis of Neuropathic Pain in Rat Dorsal Root Ganglia Following Peripheral Nerve Injury. NeuroMolecular Medicine, 2020, 22, 250-263. 1.8 Identification of genes related to skeletal muscle growth and development by integrated analysis of 1057 1.2 23 transcriptome and proteome in myostatin-edited Meishan pigs. Journal of Proteomics, 2020, 213, 103628. Transcriptome and GWAS analyses reveal candidate gene for seminal root length of maize seedlings 1058 1.7 under drought stress. Plant Science, 2020, 292, 110380. Genome-wide analysis of ethylene-response factor family in adzuki bean and functional determination 1059 2.8 22 of VaERF3 under saline-alkaline stress. Plant Physiology and Biochemistry, 2020, 147, 215-222. Transcriptomic response to low pH stress in gills of the pacific white shrimp,<i>Litopenaeus vannamei</i>. Aquaculture Research, 2020, 51, 175-186. Heritability and quantitative trait locus analyses of intermuscular bones in mirror carp (Cyprinus) Tj ETQq0 0 0 rgBT,/Qverlock, 10 Tf 50 3 1061 Chloroplast morphogenesis in Chromochloris zofingiensis in the dark. Algal Research, 2020, 45, 2.4 101742. Characterization on the water deprivation-associated physiological traits as well as the related 1063 differential genes during seed filling stage in wheat (T. aestivum L.). Plant Cell, Tissue and Organ 1.2 1 Culture, 2020, 140, 605-618. Differential gene and protein expression in gastrocnemius and tibialis anterior muscle following 1064 0.3 tibial and peroneal nerve injury in rats. Gene Expression Patterns, 2020, 35, 119079. Discovery of differentially expressed genes in the intestines of Pelteobagrus vachellii within a 1065 0.9 1 light/dark cycle. Chronobiology International, 2020, 37, 339-352. A High-Quality Reference Genome Assembly of the Saltwater Crocodile, Crocodylus porosus, Reveals 1066 1.1 Patterns of Selection in Crocodylidae. Genome Biology and Evolution, 2020, 12, 3635-3646. The impact of mercury on the genome-wide transcription profile of zebrafish intestine. Journal of 1067 6.5 15 Hazardous Materials, 2020, 389, 121842. Genomic Mechanisms of Physiological and Morphological Adaptations of Limestone Langurs to Karst Habitats. Molecular Biology and Evolution, 2020, 37, 952-968.

#	Article	IF	CITATIONS
1069	Deciphering the highâ€quality genome sequence of coriander that causes controversial feelings. Plant Biotechnology Journal, 2020, 18, 1444-1456.	4.1	56
1070	The NINâ€like protein 5 (ZmNLP5) transcription factor is involved in modulating the nitrogen response in maize. Plant Journal, 2020, 102, 353-368.	2.8	41
1071	Systematic construction and validation of an immune prognostic model for lung adenocarcinoma. Journal of Cellular and Molecular Medicine, 2020, 24, 1233-1244.	1.6	52
1072	TGF-β Signaling Promotes Tissue Formation during Cardiac Valve Regeneration in Adult Zebrafish. Developmental Cell, 2020, 52, 9-20.e7.	3.1	31
1073	Bioactive ingredients obtained from Cortex Fraxini impair interactions between FAS and GPI. Free Radical Biology and Medicine, 2020, 152, 504-515.	1.3	10
1074	High-throughput transcriptome sequencing reveals the developmental toxicity mechanisms of niclosamide in zebrafish embryo. Chemosphere, 2020, 244, 125468.	4.2	29
1075	Gut Microbiome Fermentation Determines the Efficacy of Exercise for Diabetes Prevention. Cell Metabolism, 2020, 31, 77-91.e5.	7.2	223
1076	Root transcriptome analysis of Saccharum spontaneum uncovers key genes and pathways in response to low-temperature stress. Environmental and Experimental Botany, 2020, 171, 103935.	2.0	23
1077	Transcriptomic analysis of oligochaete immune responses to myxosporeans infection: Branchiura sowerbyi infected with Myxobolus cultus. Journal of Invertebrate Pathology, 2020, 169, 107283.	1.5	5
1078	Comprehensive transcriptome analysis of faba bean in response to vernalization. Planta, 2020, 251, 22.	1.6	10
1079	The dynamic transcriptome of pepper (Capsicum annuum) whole roots reveals an important role for the phenylpropanoid biosynthesis pathway in root resistance to Phytophthora capsici. Gene, 2020, 728, 144288.	1.0	25
1080	Reduced phosphorus intake throughout gestation and lactation of sows is mitigated by transcriptional adaptations in kidney and intestine. BMC Genomics, 2020, 21, 626.	1.2	7
1081	Selection signatures of Fuzhong Buffalo based on whole-genome sequences. BMC Genomics, 2020, 21, 674.	1.2	12
1082	Investigation of an Antioxidative System for Salinity Tolerance in Oenanthe javanica. Antioxidants, 2020, 9, 940.	2.2	33
1083	Multiâ€Tissue Multiâ€Omics Nutrigenomics Indicates Contextâ€Specific Effects of Docosahexaenoic Acid on Rat Brain. Molecular Nutrition and Food Research, 2020, 64, e2000788.	1.5	2
1084	An overview of the transcriptional responses of two tolerant and susceptible sugarcane cultivars to borer (Diatraea saccharalis) infestation. Functional and Integrative Genomics, 2020, 20, 839-855.	1.4	9
1085	Differential expression of genes in olive leaves and buds of ON- versus OFF-crop trees. Scientific Reports, 2020, 10, 15762.	1.6	7
1086	Sodium New Houttuyfonate Inhibits Candida albicans Biofilm Formation by Inhibiting the Ras1-cAMP-Efg1 Pathway Revealed by RNA-seq. Frontiers in Microbiology, 2020, 11, 2075.	1.5	24

#	Article	IF	CITATIONS
1087	Comparative transcriptome analysis reveals candidate genes related to cadmium accumulation and tolerance in two almond mushroom (Agaricus brasiliensis) strains with contrasting cadmium tolerance. PLoS ONE, 2020, 15, e0239617.	1.1	6
1088	Integrated phosphoproteomic and metabolomic profiling reveals perturbed pathways in the hippocampus of gut microbiota dysbiosis mice. Translational Psychiatry, 2020, 10, 346.	2.4	24
1089	Comparative transcriptomic analysis of contrasting hybrid cultivars reveal key drought-responsive genes and metabolic pathways regulating drought stress tolerance in maize at various stages. PLoS ONE, 2020, 15, e0240468.	1.1	7
1090	Combined Transcriptome and Proteome Analysis of Masson Pine (Pinus massoniana Lamb.) Seedling Root in Response to Nitrate and Ammonium Supplementations. International Journal of Molecular Sciences, 2020, 21, 7548.	1.8	11
1091	Comprehensive analysis of AGPase genes uncovers their potential roles in starch biosynthesis in lotus seed. BMC Plant Biology, 2020, 20, 457.	1.6	11
1092	Transcriptomic Analysis and Functional Characterization Reveal the Duck Interferon Regulatory Factor 1 as an Important Restriction Factor in the Replication of Tembusu Virus. Frontiers in Microbiology, 2020, 11, 2069.	1.5	8
1093	Identification of Candidate Genes Associated with Charcot-Marie-Tooth Disease by Network and Pathway Analysis. BioMed Research International, 2020, 2020, 1-13.	0.9	2
1094	Transcriptomic Analysis Reveals the Dependency of Pseudomonas aeruginosa Genes for Double-Stranded RNA Bacteriophage phiYY Infection Cycle. IScience, 2020, 23, 101437.	1.9	9
1095	Comparative transcriptome analysis reveals heat stress-responsive genes and their signalling pathways in lilies (Lilium longiflorum vs. Lilium distichum). PLoS ONE, 2020, 15, e0239605.	1.1	6
1096	Intracellular calcium current disorder and disease phenotype in OBSCN mutant iPSC-based cardiomyocytes in arrhythmogenic right ventricular cardiomyopathy. Theranostics, 2020, 10, 11215-11229.	4.6	17
1097	Quantitative Proteomic Analysis of Porcine Intestinal Epithelial Cells Infected with Porcine Deltacoronavirus Using iTRAQ-Coupled LC-MS/MS. Journal of Proteome Research, 2020, 19, 4470-4485.	1.8	16
1098	Transcriptional and physiological analyses of reduced density in apple provide insight into the regulation involved in photosynthesis. PLoS ONE, 2020, 15, e0239737.	1.1	4
1099	Aberrant RNA Splicing Events Driven by Mutations of RNA-Binding Proteins as Indicators for Skin Cutaneous Melanoma Prognosis. Frontiers in Oncology, 2020, 10, 568469.	1.3	4
1100	Uncovering the pharmacological mechanism of motherwort (Leonurus japonicus Houtt.) for treating menstrual disorders: A systems pharmacology approach. Computational Biology and Chemistry, 2020, 89, 107384.	1.1	10
1101	Evaluating the effects of ocean warming and freshening on the physiological energetics and transcriptomic response of the Antarctic limpet Nacella concinna. Science of the Total Environment, 2020, 748, 142448.	3.9	12
1102	Plasmids Related to the Symbiotic Nitrogen Fixation Are Not Only Cooperated Functionally but Also May Have Evolved over a Time Span in Family <i>Rhizobiaceae</i> . Genome Biology and Evolution, 2020, 12, 2002-2014.	1.1	14
1103	Genomic Copy Number Variation Study of Nine <i>Macaca</i> Species Provides New Insights into Their Genetic Divergence, Adaptation, and Biomedical Application. Genome Biology and Evolution, 2020, 12, 2211-2230.	1.1	6
1104	Comprehensive analysis of protein expression levels and phosphorylation levels in host skin in response to tick (Haemaphysalis longicornis) bite. Journal of Proteomics, 2020, 226, 103898.	1.2	3

#	ARTICLE Translocation of PpNPR1 is required for Î <sup>2</sup> -aminobutyric acid-triggered resistance against Rhizopus	IF 1.7	CITATIONS
1106	stolonifer in peach fruit. Scientia Horticulturae, 2020, 272, 109556. Maize YSL2 is required for iron distribution and development in kernels. Journal of Experimental Botany, 2020, 71, 5896-5910.	2.4	30
1107	Identification of biomarkers correlated with diagnosis and prognosis of endometrial cancer using bioinformatics analysis. Journal of Cellular Biochemistry, 2020, 121, 4908-4921.	1.2	7
1108	PacBio single molecule long-read sequencing provides insight into the complexity and diversity of the Pinctada fucata martensii transcriptome. BMC Genomics, 2020, 21, 481.	1.2	14
1109	The potential risks of paclobutrazol residue on yogurt fermentation from the level of chiral enantiomers. Journal of Dairy Science, 2020, 103, 7682-7694.	1.4	3
1110	Transcriptional Profiling of Normal, Stenotic, and Regurgitant Human Aortic Valves. Genes, 2020, 11, 789.	1.0	14
1111	Small RNA and degradome sequencing reveal roles of miRNAs in strobilus development in masson pine (Pinus massoniana). Industrial Crops and Products, 2020, 154, 112724.	2.5	17
1112	Transcriptome analysis of the zebrafish <i>atoh7â^'/â^'</i> Mutant, <i>lakritz</i> , highlights Atoh7â€dependent genetic networks with potential implications for human eye diseases. FASEB BioAdvances, 2020, 2, 434-448.	1.3	2
1113	Transcriptome Profiling of Abscisic Acid-Related Pathways in SNAC4/9-Silenced Tomato Fruits. Transactions of Tianjin University, 2020, 27, 473.	3.3	3
1114	Whole-exome sequencing in an Afrikaner family with bipolar disorder. Journal of Affective Disorders, 2020, 276, 69-75.	2.0	4
1115	Proteomic Analysis of Cerebrospinal Fluid in Children with Acute Enterovirus-Associated Meningoencephalitis Identifies Dysregulated Host Processes and Potential Biomarkers. Journal of Proteome Research, 2020, 19, 3487-3498.	1.8	10
1116	Construction of a Robust Sphingomonas sp. Strain for Welan Gum Production via the Expression of Global Transcriptional Regulator IrrE. Frontiers in Bioengineering and Biotechnology, 2020, 8, 674.	2.0	9
1117	The Dysregulation and Prognostic Analysis of STRIPAK Complex Across Cancers. Frontiers in Cell and Developmental Biology, 2020, 8, 625.	1.8	8
1118	Transcriptome analysis reveals key information on improving duck yolk lipid contents induced by dietary fish oil or flaxseed oil. Journal of Applied Animal Research, 2020, 48, 192-200.	0.4	0
1119	Genomeâ€wide IncRNAs identification and association analysis for coldâ€responsive genes at the booting stage in rice ( <i>Oryza sativa</i> L.). Plant Genome, 2020, 13, e20020.	1.6	12
1120	Hyperosmotic Adaptation of Pseudomonas protegens SN15-2 Helps Cells to Survive at Lethal Temperatures. Biotechnology and Bioprocess Engineering, 2020, 25, 403-413.	1.4	6
1121	Transcriptome response of Acetobacter pasteurianus Ab3 to high acetic acid stress during vinegar production. Applied Microbiology and Biotechnology, 2020, 104, 10585-10599.	1.7	15
1122	Identification of candidate genes conferring tolerance to aluminum stress in Pinus massoniana inoculated with ectomycorrhizal fungus. BMC Plant Biology, 2020, 20, 521.	1.6	20

#	Article	IF	CITATIONS
1123	Identification and Characterization of Hypothalamic Alternative Splicing Events and Variants in Ovine Fecundity-Related Genes. Animals, 2020, 10, 2111.	1.0	3
1124	Identification and Characterization of circRNAs in the Developing Stem Cambium of Poplar Seedlings. Molecular Biology, 2020, 54, 708-718.	0.4	2
1125	Overexpression Levels of LbDREB6 Differentially Affect Growth, Drought, and Disease Tolerance in Poplar. Frontiers in Plant Science, 2020, 11, 528550.	1.7	11
1126	Metabolite Support of Long-Term Storage of Sperm in the Spermatheca of Honeybee (Apis mellifera) Queens. Frontiers in Physiology, 2020, 11, 574856.	1.3	17
1127	A full-length transcriptome and gene expression analysis reveal genes and molecular elements expressed during seed development in Gnetum luofuense. BMC Plant Biology, 2020, 20, 531.	1.6	9
1128	Identification of contributing genes of Huntington's disease by machine learning. BMC Medical Genomics, 2020, 13, 176.	0.7	15
1129	Transcriptome Analysis Reveals the Potential Role of Long Non-coding RNAs in Mammary Gland of Yak During Lactation and Dry Period. Frontiers in Cell and Developmental Biology, 2020, 8, 579708.	1.8	9
1130	Regulatory Potential of Long Non-Coding RNAs (IncRNAs) in Boar Spermatozoa with Good and Poor Freezability. Life, 2020, 10, 300.	1.1	4
1131	Comparative Transcriptome Analyses of Longissimus thoracis Between Pig Breeds Differing in Muscle Characteristics. Frontiers in Genetics, 2020, 11, 526309.	1.1	15
1132	IRF-1 expressed in the inner cell mass of the porcine early blastocyst enhances the pluripotency of induced pluripotent stem cells. Stem Cell Research and Therapy, 2020, 11, 505.	2.4	9
1133	The Landscape of Immune Cells Infiltrating in Prostate Cancer. Frontiers in Oncology, 2020, 10, 517637.	1.3	63
1134	Intricate genetic variation networks control the adventitious root growth angle in apple. BMC Genomics, 2020, 21, 852.	1.2	6
1135	Landscapes of bacterial and metabolic signatures and their interaction in major depressive disorders. Science Advances, 2020, 6, .	4.7	178
1136	Salt-responsive transcriptome analysis of triticale reveals candidate genes involved in the key metabolic pathway in response to salt stress. Scientific Reports, 2020, 10, 20669.	1.6	16
1137	Knockout of STK10 promotes the migration and invasion of cervical cancer cells. Translational Cancer Research, 2020, 9, 7079-7090.	0.4	5
1138	Comprehensive profiling of extracellular RNA in HPV-induced cancers using an improved pipeline for small RNA-seq analysis. Scientific Reports, 2020, 10, 19450.	1.6	18
1139	Changes in transcriptomic and metabolomic profiles of morphotypes of Ophiocordyceps sinensis within the hemocoel of its host larvae, Thitarodes xiaojinensis. BMC Genomics, 2020, 21, 789.	1.2	10
1140	Genome-Wide Differential DNA Methylation and miRNA Expression Profiling Reveals Epigenetic Regulatory Mechanisms Underlying Nitrogen-Limitation-Triggered Adaptation and Use Efficiency Enhancement in Allotetraploid Rapeseed. International Journal of Molecular Sciences, 2020, 21, 8453.	1.8	10

#	Article	IF	CITATIONS
1141	Integrated metabolomic and transcriptomic strategies to understand the effects of dark stress on tea callus flavonoid biosynthesis. Plant Physiology and Biochemistry, 2020, 155, 549-559.	2.8	30
1142	RNA-Seq Analysis Reveals Hub Genes Involved in Chicken Intramuscular Fat and Abdominal Fat Deposition During Development. Frontiers in Genetics, 2020, 11, 1009.	1.1	25
1143	Integration of RNA-seq and RNAi provides a novel insight into the effect of pvdE gene to the pathogenic of Pseudomonas plecoglossicida and on the immune responses of orange-spotted grouper (Epinephelus coioides). Aquaculture, 2020, 529, 735695.	1.7	22
1144	Inhibition of mitochondria NADH–Ubiquinone oxidoreductase (complex I) sensitizes the radioresistant glioma U87MG cells to radiation. Biomedicine and Pharmacotherapy, 2020, 129, 110460.	2.5	10
1145	Transcriptomic Analysis of Root Restriction Effects on Phenolic Metabolites during Grape Berry Development and Ripening. Journal of Agricultural and Food Chemistry, 2020, 68, 9090-9099.	2.4	20
1146	Identification of latent core genes and pathways associated with myelodysplastic syndromes based on integrated bioinformatics analysis. Hematology, 2020, 25, 299-308.	0.7	5
1147	Investigation of the Ecological Roles of Putative Keystone Taxa during Tailing Revegetation. Environmental Science & Technology, 2020, 54, 11258-11270.	4.6	62
1148	DNA methylation and its effects on gene expression during primary to secondary growth in poplar stems. BMC Genomics, 2020, 21, 498.	1.2	23
1149	Identification of a three-long noncoding RNA prognostic model involved competitive endogenous RNA in kidney renal clear cell carcinoma. Cancer Cell International, 2020, 20, 319.	1.8	25
1150	Identification of Ear Morphology Genes in Maize (Zea mays L.) Using Selective Sweeps and Association Mapping. Frontiers in Genetics, 2020, 11, 747.	1.1	10
1151	Response to the Cold Stress Signaling of the Tea Plant (Camellia sinensis) Elicited by Chitosan Oligosaccharide. Agronomy, 2020, 10, 915.	1.3	26
1152	Transcriptomic comparison reveals modifications in gene expression, photosynthesis, and cell wall in woody plant as responses to external pH changes. Ecotoxicology and Environmental Safety, 2020, 203, 111007.	2.9	9
1153	Identification of prognosis-related genes and construction of multi-regulatory networks in pancreatic cancer microenvironment by bioinformatics analysis. Cancer Cell International, 2020, 20, 341.	1.8	4
1154	New insights into the evolutionary history of Megacodon: Evidence from a newly discovered species. Plant Diversity, 2020, 42, 198-208.	1.8	7
1155	Integrated Analyses of IncRNA and mRNA Profiles Reveal Characteristic and Functional Changes of Leukocytes in Qi-Deficiency Constitution and Pi-Qi-Deficiency Syndrome of Chronic Superficial Gastritis. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-16.	0.5	1
1156	Contribution of brain pericytes in blood–brain barrier formation and maintenance: a transcriptomic study of cocultured human endothelial cells derived from hematopoietic stem cells. Fluids and Barriers of the CNS, 2020, 17, 48.	2.4	32
1157	Time-resolved RNA-seq provided a new understanding of intestinal immune response of European eel (Anguilla anguilla) following infection with Aeromonas hydrophila. Fish and Shellfish Immunology, 2020, 105, 297-309.	1.6	8
1158	Transcriptional mechanism of differential sugar accumulation in pulp of two contrasting mango (Mangifera indica L.) cultivars. Genomics, 2020, 112, 4505-4515.	1.3	18

#	Article	IF	CITATIONS
1159	Comparative transcriptome analysis reveals ecological adaption of cold tolerance in northward invasion of Alternanthera philoxeroides. BMC Genomics, 2020, 21, 532.	1.2	10
1160	Chromosome-scale genome assembly of sweet cherry (Prunus avium L.) cv. Tieton obtained using long-read and Hi-C sequencing. Horticulture Research, 2020, 7, 122.	2.9	44
1161	Host Transcriptional Response to Persistent Infection with a Live-Attenuated Porcine Reproductive and Respiratory Syndrome Virus Strain. Viruses, 2020, 12, 817.	1.5	6
1162	Global transcriptome analysis of subterranean pod and seed in peanut (Arachis hypogaea L.) unravels the complexity of fruit development under dark condition. Scientific Reports, 2020, 10, 13050.	1.6	8
1163	Removal of sulfamethazine and Cu2+ by Sakaguchia cladiensis A5: Performance and transcriptome analysis. Science of the Total Environment, 2020, 746, 140956.	3.9	12
1164	The neonicotinoid thiacloprid causes transcriptional alteration of genes associated with mitochondria at environmental concentrations in honey bees. Environmental Pollution, 2020, 266, 115297.	3.7	24
1165	Analysis on the virulomes and resistomes of multi-drug resistance clinical Escherichia coli isolates, as well as the interactome with gut microbiome. Microbial Pathogenesis, 2020, 148, 104423.	1.3	2
1166	Genetic variation associated with the shoot biomass of upland cotton seedlings under contrasting phosphate supplies. Molecular Breeding, 2020, 40, 1.	1.0	2
1167	Comparative transcriptome analysis reveals regulatory genes involved in cold tolerance and hypoxic adaptation of high-altitude Tibetan bumblebees. Apidologie, 2020, 51, 1166-1181.	0.9	6
1168	Transcriptomic analysis reveals novel mechanisms of SARSâ€CoVâ€2 infection in human lung cells. Immunity, Inflammation and Disease, 2020, 8, 753-762.	1.3	13
1169	Identification of differentially expressed genes and pathways in isonuclear kenaf genotypes under salt stress. Physiologia Plantarum, 2021, 173, 1295-1308.	2.6	10
1170	Insights from RNA-Seq analysis of Alzheimer's data suggest upregulation of GPCRs. Gene Reports, 2020, 21, 100921.	0.4	1
1171	Morin decreases acrolein-induced cell injury in normal human hepatocyte cell line LO2. Journal of Functional Foods, 2020, 75, 104234.	1.6	10
1172	Comparative analysis of the metabolome and transcriptome between green and albino zones of variegated leaves from Hydrangea macrophylla †Maculata' infected by hydrangea ringspot virus. Plant Physiology and Biochemistry, 2020, 157, 195-210.	2.8	14
1173	The histone modification H3K4me3 marks functional genes in soybean nodules. Genomics, 2020, 112, 5282-5294.	1.3	8
1174	Metabolomic and transcriptomic analyses reveal the regulation of pigmentation in the purple variety of Dendrobium officinale. Scientific Reports, 2020, 10, 17700.	1.6	25
1175	Proteomic Analysis of UV-B-Induced Virulence-Mutant Strains of Puccinia striiformis f. sp. tritici Based on iTRAQ Technology. Frontiers in Microbiology, 2020, 11, 542961.	1.5	4
1176	A Transcriptomic Analysis Reveals Novel Patterns of Gene Expression During 3T3-L1 Adipocyte Differentiation. Frontiers in Molecular Biosciences, 2020, 7, 564339.	1.6	20

#	Article	IF	CITATIONS
1177	Transcriptome analysis reveals temperature-dependent early immune response in flounder (Paralichthys olivaceus) after Hirame novirhabdovirus (HIRRV) infection. Fish and Shellfish Immunology, 2020, 107, 367-378.	1.6	17
1178	TMT-based quantitative proteomic analysis of antitumor mechanism of Sporisorium reilianum polysaccharide WM-NP-60 against HCT116 cells. International Journal of Biological Macromolecules, 2020, 165, 1755-1764.	3.6	11
1179	Comprehensive Identification and Expression Profiling of Circular RNAs During Nodule Development in Phaseolus vulgaris. Frontiers in Plant Science, 2020, 11, 587185.	1.7	10
1180	Pulmonary toxicity and RNA sequencing analyses of mouse in response to exposure to cellulose nanofibrils. Inhalation Toxicology, 2020, 32, 388-401.	0.8	3
1181	Metagenomic Analysis Exploring Taxonomic and Functional Diversity of Soil Microbial Communities in Sugarcane Fields Applied with Organic Fertilizer. BioMed Research International, 2020, 2020, 1-11.	0.9	13
1182	Transcriptome Reveals Multi Pigmentation Genes Affecting Dorsoventral Pattern in Avian Body. Frontiers in Cell and Developmental Biology, 2020, 8, 560766.	1.8	11
1183	V <sup>V</sup> Reduction by <i>Polaromonas</i> spp. in Vanadium Mine Tailings. Environmental Science & Technology, 2020, 54, 14442-14454.	4.6	47
1184	Paper New Allele of HL6 Regulates Trichome Elongation in Rice. Rice Science, 2020, 27, 480-492.	1.7	5
1185	Genome-scale analyses and characteristics of putative pathogenicity genes of Stagonosporopsis cucurbitacearum, a pumpkin gummy stem blight fungus. Scientific Reports, 2020, 10, 18065.	1.6	6
1186	Overexpression of PLIN1 Promotes Lipid Metabolism in Bovine Adipocytes. Animals, 2020, 10, 1944.	1.0	15
1187	Genome-wide analysis of long non-coding RNAs in adult tissues of the melon fly, Zeugodacus cucurbitae (Coquillett). BMC Genomics, 2020, 21, 600.	1.2	16
1188	Deep learning-based ovarian cancer subtypes identification using multi-omics data. BioData Mining, 2020, 13, 10.	2.2	30
1189	The inflammation-resolution promoting molecule resolvin-D1 prevents atrial proarrhythmic remodelling in experimental right heart disease. Cardiovascular Research, 2021, 117, 1776-1789.	1.8	38
1190	Microbial regulation of a lincRNA–miRNA–mRNA network in the mouse hippocampus. Epigenomics, 2020, 12, 1377-1387.	1.0	13
1191	De novo transcriptome sequencing of Rhododendron molle and identification of genes involved in the biosynthesis of secondary metabolites. BMC Plant Biology, 2020, 20, 414.	1.6	9
1192	Evaluating Distribution and Prognostic Value of New Tumor-Infiltrating Lymphocytes in HCC Based on a scRNA-Seq Study With CIBERSORTx. Frontiers in Medicine, 2020, 7, 451.	1.2	15
1193	The peptidyl-prolyl isomerases FKBP15-1 and FKBP15-2 negatively affect lateral root development by repressing the vacuolar invertase VIN2 in Arabidopsis. Planta, 2020, 252, 52.	1.6	9
1194	Hemocytes transcriptomes reveal metabolism changes and detoxification mechanisms in response to ammonia stress in Octopus minor. Ecotoxicology, 2020, 29, 1441-1452.	1.1	11

~		~
$( IT \Delta$	TION	Report
		KEI OKI

#	Article	IF	CITATIONS
1195	Molecular mechanisms underlying altered neurobehavioural development of female offspring of mothers with polycystic ovary syndrome: FOS-mediated regulation of neurotrophins in placenta. EBioMedicine, 2020, 60, 102993.	2.7	15
1196	Hepatopancreas immune response during molt cycle in the mud crab, Scylla paramamosain. Scientific Reports, 2020, 10, 13102.	1.6	23
1197	Physiological Characterization and Transcriptome Analysis of Camellia oleifera Abel. during Leaf Senescence. Forests, 2020, 11, 812.	0.9	10
1198	Transcriptomic Analysis of Short-Term Salt Stress Response in Watermelon Seedlings. International Journal of Molecular Sciences, 2020, 21, 6036.	1.8	24
1199	Third-generation sequencing found LncRNA associated with heat shock protein response to heat stress in Populus qiongdaoensis seedlings. BMC Genomics, 2020, 21, 572.	1.2	15
1200	Transcriptomic analysis identifies Tollâ€ike and Nodâ€ike pathways and necroptosis in pulmonary arterial hypertension. Journal of Cellular and Molecular Medicine, 2020, 24, 11409-11421.	1.6	28
1201	Composition and Metabolic Functions of the Microbiome in Fermented Grain during Light-Flavor Baijiu Fermentation. Microorganisms, 2020, 8, 1281.	1.6	52
1202	Characterization and analysis of full-length transcriptomes from two grasshoppers, Gomphocerus licenti and Mongolotettix japonicus. Scientific Reports, 2020, 10, 14228.	1.6	5
1203	The GAMYB-like gene SIMYB33 mediates flowering and pollen development in tomato. Horticulture Research, 2020, 7, 133.	2.9	38
1204	A gene prioritization method based on a swine multi-omics knowledgebase and a deep learning model. Communications Biology, 2020, 3, 502.	2.0	36
1205	Changes in Vibrio natriegens Growth Under Simulated Microgravity. Frontiers in Microbiology, 2020, 11, 2040.	1.5	11
1206	Skim-Sequencing Based Genotyping Reveals Genetic Divergence of the Wild and Domesticated Population of Black Tiger Shrimp (Penaeus monodon) in the Indo-Pacific Region. Biology, 2020, 9, 277.	1.3	5
1207	De Novo Transcriptomic and Metabolomic Analyses Reveal the Ecological Adaptation of High-Altitude Bombus pyrosoma. Insects, 2020, 11, 631.	1.0	11
1208	Gene coâ€expression analysis reveals transcriptome divergence between wild and cultivated chickpea under drought stress. Plant Journal, 2020, 104, 1195-1214.	2.8	22
1209	Using High-Density SNP Array to Reveal Selection Signatures Related to Prolificacy in Chinese and Kazakhstan Sheep Breeds. Animals, 2020, 10, 1633.	1.0	11
1210	Transcriptomic Analysis of Streptococcus suis in Response to Ferrous Iron and Cobalt Toxicity. Genes, 2020, 11, 1035.	1.0	2
1211	IGF2BP3 May Contributes to Lung Tumorigenesis by Regulating the Alternative Splicing of PKM. Frontiers in Bioengineering and Biotechnology, 2020, 8, 679.	2.0	30
1212	A bioenergetic shift is required for spermatogonial differentiation. Cell Discovery, 2020, 6, 56.	3.1	21

#	Article	IF	CITATIONS
1213	Metabolome and transcriptome analyses of the molecular mechanisms of flower color mutation in tobacco. BMC Genomics, 2020, 21, 611.	1.2	44
1214	Stimulation of glycolysis promotes cardiomyocyte proliferation after injury in adult zebrafish. EMBO Reports, 2020, 21, e49752.	2.0	62
1215	The curvature of cucumber fruits is associated with spatial variation in auxin accumulation and expression of a YUCCA biosynthesis gene. Horticulture Research, 2020, 7, 135.	2.9	10
1216	mRNA profile provides novel insights into stress adaptation in mud crab megalopa, Scylla paramamosain after salinity stress. BMC Genomics, 2020, 21, 559.	1.2	22
1217	Carbon migration and metagenomic characteristics during anaerobic digestion of rice straw. Biotechnology for Biofuels, 2020, 13, 130.	6.2	8
1218	De novo transcriptome analysis of Lantana camara L. revealed candidate genes involved in phenylpropanoid biosynthesis pathway. Scientific Reports, 2020, 10, 13726.	1.6	17
1219	Transcriptome analysis of table grapes (Vitis vinifera L.) identified a gene network module associated with berry firmness. PLoS ONE, 2020, 15, e0237526.	1.1	13
1220	Weeping candidate genes screened using comparative transcriptomic analysis of weeping and upright progeny in an <scp>F1</scp> population of <scp><i>Prunus mume</i></scp> . Physiologia Plantarum, 2020, 170, 318-334.	2.6	9
1221	To bloom once or more times: the reblooming mechanisms of Iris germanica revealed by transcriptome profiling. BMC Genomics, 2020, 21, 553.	1.2	9
1222	Comparative Transcriptomic Analysis of the Development of Sepal Morphology in Tomato (Solanum) Tj ETQq1	1 0.78431	4 rgBT /Overlo
		1.0	-11
1223	Functional characterisation of the transcriptome from leaf tissue of the fluoroacetate-producing plant, Dichapetalum cymosum, in response to mechanical wounding. Scientific Reports, 2020, 10, 20539.	1.6	7
1223 1224		1.0	11
	plant, Dichapetalum cymosum, in response to mechanical wounding. Scientific Reports, 2020, 10, 20539. Traditional Chinese Medicine Tanreqing Inhibits Quorum Sensing Systems in Pseudomonas aeruginosa.	1.6	7
1224	plant, Dichapetalum cymosum, in response to mechanical wounding. Scientific Reports, 2020, 10, 20539. Traditional Chinese Medicine Tanreqing Inhibits Quorum Sensing Systems in Pseudomonas aeruginosa. Frontiers in Microbiology, 2020, 11, 517462. Transcriptomic analysis of gene expression of menaquinone-7 in Bacillus subtilis natto toward	1.6 1.5	7
1224 1225	<ul> <li>plant, Dichapetalum cymosum, in response to mechanical wounding. Scientific Reports, 2020, 10, 20539.</li> <li>Traditional Chinese Medicine Tanreqing Inhibits Quorum Sensing Systems in Pseudomonas aeruginosa. Frontiers in Microbiology, 2020, 11, 517462.</li> <li>Transcriptomic analysis of gene expression of menaquinone-7 in Bacillus subtilis natto toward different oxygen supply. Food Research International, 2020, 137, 109700.</li> <li>Comparative proteomic analysis reveals novel insights into the interaction between rice and</li> </ul>	1.6 1.5 2.9	7 12 10
1224 1225 1226	<ul> <li>plant, Dichapetalum cymosum, in response to mechanical wounding. Scientific Reports, 2020, 10, 20539.</li> <li>Traditional Chinese Medicine Tanreqing Inhibits Quorum Sensing Systems in Pseudomonas aeruginosa. Frontiers in Microbiology, 2020, 11, 517462.</li> <li>Transcriptomic analysis of gene expression of menaquinone-7 in Bacillus subtilis natto toward different oxygen supply. Food Research International, 2020, 137, 109700.</li> <li>Comparative proteomic analysis reveals novel insights into the interaction between rice and Xanthomonas oryzae pv. oryzae. BMC Plant Biology, 2020, 20, 563.</li> <li>Differential Gene Expression Analysis of Wheat Breeding Lines Reveal Molecular Insights in Yellow</li> </ul>	1.6 1.5 2.9 1.6	7 12 10 6
1224 1225 1226 1227	<ul> <li>plant, Dichapetalum cymosum, in response to mechanical wounding. Scientific Reports, 2020, 10, 20539.</li> <li>Traditional Chinese Medicine Tanreqing Inhibits Quorum Sensing Systems in Pseudomonas aeruginosa. Frontiers in Microbiology, 2020, 11, 517462.</li> <li>Transcriptomic analysis of gene expression of menaquinone-7 in Bacillus subtilis natto toward different oxygen supply. Food Research International, 2020, 137, 109700.</li> <li>Comparative proteomic analysis reveals novel insights into the interaction between rice and Xanthomonas oryzae pv. oryzae. BMC Plant Biology, 2020, 20, 563.</li> <li>Differential Gene Expression Analysis of Wheat Breeding Lines Reveal Molecular Insights in Yellow Rust Resistance under Field Conditions. Agronomy, 2020, 10, 1888.</li> <li>Endothelial progenitor cells promote osteogenic differentiation in co-cultured with mesenchymal</li> </ul>	1.6 1.5 2.9 1.6 1.3	11         7         12         10         6         8

#	Article	IF	CITATIONS
1231	Comparative transcriptomics reveals the molecular genetic basis of pigmentation loss in <i>Sinocyclocheilus</i> cavefishes. Ecology and Evolution, 2020, 10, 14256-14271.	0.8	14
1232	Identification of genes under positive selection reveals evolutionary adaptation of Ulva mutabilis. Acta Oceanologica Sinica, 2020, 39, 35-41.	0.4	0
1233	Transcriptome analysis reveals that exogenous ethylene activates immune and defense responses in a high late blight resistant potato genotype. Scientific Reports, 2020, 10, 21294.	1.6	23
1234	Screening and Identification of Differentially Expressed and Adipose Growth-Related Protein-Coding Genes During the Deposition of Perirenal Adipose Tissue in Rabbits. Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy, 2020, Volume 13, 4669-4680.	1.1	2
1235	Identification of diverse cell populations in skeletal muscles and biomarkers for intramuscular fat of chicken by single-cell RNA sequencing. BMC Genomics, 2020, 21, 752.	1.2	24
1236	Transcriptome Sequencing Analysis of Birch (Betula platyphylla Sukaczev) under Low-Temperature Stress. Forests, 2020, 11, 970.	0.9	7
1237	Transcriptomic Profiling of Various Developmental Stages of Aphis Aurantii to Provide a Genetic Resource for Gene Expression and SSR Analysis. Frontiers in Physiology, 2020, 11, 578939.	1.3	3
1238	The draft genome of the blood pheasant ( <i>Ithaginis cruentus</i> ): Phylogeny and highâ€altitude adaptation. Ecology and Evolution, 2020, 10, 11440-11452.	0.8	1
1239	PURα Promotes the Transcriptional Activation of PCK2 in Oesophageal Squamous Cell Carcinoma Cells. Genes, 2020, 11, 1301.	1.0	7
1240	Comparative transcriptome analyses and identification of candidate genes involved in vertebral abnormality of bighead carp Hypophthalmichthys nobilis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2020, 36, 100752.	0.4	2
1241	Comparative Genome Analysis Reveals the Molecular Basis of Niche Adaptation of Staphylococcus epidermidis Strains. Frontiers in Genetics, 2020, 11, 566080.	1.1	5
1242	Lipidomic analyses reveal enhanced lipolysis in planthoppers feeding on resistant host plants. Science China Life Sciences, 2021, 64, 1502-1521.	2.3	12
1243	Capsaicin improves glucose homeostasis by enhancing glucagonâ€like peptideâ€l secretion through the regulation of bile acid metabolism via the remodeling of the gut microbiota in male mice. FASEB Journal, 2020, 34, 8558-8573.	0.2	25
1244	Identification of a novel microRNA profile including miR-106b, miR-17, miR-20b, miR-18a and miR-93 in the metastasis of nasopharyngeal carcinoma. Cancer Biomarkers, 2020, 27, 533-539.	0.8	6
1245	Improving Gene Annotation of the Peanut Genome by Integrated Proteogenomics Workflow. Journal of Proteome Research, 2020, 19, 2226-2235.	1.8	7
1246	Epigenome-Wide Tobacco-Related Methylation Signature Identification and Their Multilevel Regulatory Network Inference for Lung Adenocarcinoma. BioMed Research International, 2020, 2020, 1-12.	0.9	5
1247	Transcriptional regulatory networks of methanol-independent protein expression in Pichia pastoris under the AOX1 promoter with trans-acting elements engineering. Bioresources and Bioprocessing, 2020, 7, .	2.0	4
1248	Development of an Early Prediction Model for Subarachnoid Hemorrhage With Genetic and Signaling Pathway Analysis. Frontiers in Genetics, 2020, 11, 391.	1.1	6

#	Article	IF	CITATIONS
1249	Third-Generation Sequencing Reveals LncRNA-Regulated HSP Genes in the Populus x canadensis Moench Heat Stress Response. Frontiers in Genetics, 2020, 11, 249.	1.1	10
1250	Genome-Wide Analysis Reveals Changes in Polled Yak Long Non-coding RNAs in Skeletal Muscle Development. Frontiers in Genetics, 2020, 11, 365.	1.1	5
1251	Review: Long non-coding RNA in livestock. Animal, 2020, 14, 2003-2013.	1.3	31
1252	Comparative Analysis of Root Transcriptome Reveals Candidate Genes and Expression Divergence of Homoeologous Genes in Response to Water Stress in Wheat. Plants, 2020, 9, 596.	1.6	11
1253	circStrn3 is involved in bone cancer pain regulation in a rat model. Acta Biochimica Et Biophysica Sinica, 2020, 52, 495-505.	0.9	7
1254	Genome-wide association analyses identify known and novel loci for teat number in Duroc pigs using single-locus and multi-locus models. BMC Genomics, 2020, 21, 344.	1.2	43
1255	Integration of sRNA, degradome, transcriptome analysis and functional investigation reveals gma-miR398c negatively regulates drought tolerance via GmCSDs and GmCCS in transgenic Arabidopsis and soybean. BMC Plant Biology, 2020, 20, 190.	1.6	29
1256	Nine hub genes related to the prognosis of HBV-positive hepatocellular carcinoma identified by protein interaction analysis. Annals of Translational Medicine, 2020, 8, 478-478.	0.7	13
1257	Direct reprogramming of mouse fibroblasts into hepatocyte-like cells by polyethyleneimine-modified nanoparticles through epigenetic activation of hepatic transcription factors. Materials Today Chemistry, 2020, 17, 100281.	1.7	4
1258	Evodiamine has therapeutic efficacy in ulcerative colitis by increasing Lactobacillus acidophilus levels and acetate production. Pharmacological Research, 2020, 159, 104978.	3.1	52
1259	RNAâ€Seq transcriptomic analyses ofAntrodia camphoratato determine antroquinonol and antrodin C biosynthetic mechanisms in thein situextractive fermentation. Journal of the Science of Food and Agriculture, 2020, 100, 4252-4262.	1.7	7
1260	Transcriptome Sequencing and Differential Expression Analysis Reveal Molecular Mechanisms for Starch Accumulation in Chestnut. Forests, 2020, 11, 388.	0.9	5
1261	Transcriptomic analysis reveals mechanism of light-sensitive albinism in tea plant Camellia sinensis â€~Huangjinju'. BMC Plant Biology, 2020, 20, 216.	1.6	24
1262	Transcriptome analysis of Catarina scallop (Argopecten ventricosus) juveniles treated with highly-diluted immunomodulatory compounds reveals activation of non-self-recognition system. PLoS ONE, 2020, 15, e0233064.	1.1	10
1263	Comparative transcriptome analysis revealing the mechanisms underlying light-induced total fatty acid and carotenoid accumulation in Crypthecodinium sp. SUN. Algal Research, 2020, 47, 101860.	2.4	2
1264	Chromosome-Level Reference Genome and Population Genomic Analysis Provide Insights into the Evolution and Improvement of Domesticated Mulberry (Morus alba). Molecular Plant, 2020, 13, 1001-1012.	3.9	59
1265	Molybdenum induces alterations in the glycerolipidome that confer drought tolerance in wheat. Journal of Experimental Botany, 2020, 71, 5074-5086.	2.4	15
1266	Evidence for a Dark Septate Endophyte (Exophiala Pisciphila, H93) Enhancing Phosphorus Absorption by Maize Seedlings. Plant and Soil, 2020, 452, 249-266.	1.8	35

CITATION REPORT ARTICLE IF CITATIONS Comparative transcriptome analysis between inbred and hybrids reveals molecular insights into yield 28 1.6 heterosis of upland cotton. BMC Plant Biology, 2020, 20, 239. Metagenomic Analyses of Microbial and Carbohydrate-Active Enzymes in the Rumen of Dairy Goats Fed 1.5 Different Rumen Dégradable Starch. Frontiers in Microbiology, 2020, 11, 1003. Transcriptome analysis of blood for the discovery of sex-related genes in ricefield eel Monopterus 0.9 5 albus. Fish Physiology and Biochemistry, 2020, 46, 1507-1518. Identifying metabolic features and engineering targets for productivity improvement in CHO cells by integrated transcriptomics and genome-scale metabolic model. Biochémical Engineering Journal, 2020, 1.8 159, 107624. Characterization of Nitrate-Dependent As(III)-Oxidizing Communities in Arsenic-Contaminated Soil and Investigation of Their Metabolic Potentials by the Combination of DNA-Stable Isotope Probing and 4.6 82 Metagenomics. Environmental Science & amp; Technology, 2020, 54, 7366-7377. The origin of domestication genes in goats. Science Advances, 2020, 6, eaaz5216. 4.7 Construction of an Immunogenomic Risk Score for Prognostication in Colon Cancer. Frontiers in 1.1 9 Genetics, 2020, 11, 499. Metatranscriptomic Characterization of Coronavirus Disease 2019 Identified a Host Transcriptional 2.9 76 Classifier Associated With Immune Signaling. Clinical Infectious Diseases, 2021, 73, 376-385. Coding and Non-coding RNAs: Molecular Basis of Forest-Insect Outbreaks. Frontiers in Cell and 9 1.8 Developmental Biology, 2020, 8, 369. Transcriptional analysis reveals physiological response to acute acidification stress of barramundi Lates calcarifer (Bloch) in coastal areas. Fish Physiology and Biochemistry, 2020, 46, 1729-1741. Transcriptome profiling of Plumbago auriculata Lam. in response to cold stress. Acta Physiologiae 1.0 5 Plantarum, 2020, 42, 1. Transcriptome analysis of different rice cultivars provides novel insights into the rice response to 1.4 bacterial leaf streak infection. Functional and Integrative Genomics, 2020, 20, 681-693. Identification of Genomic Characteristics and Selective Signals in a Du'an Goat Flock. Animals, 2020, 1.0 6 10, 994. <p&gt;Circular RNA hsa\_circ\_0131242 Promotes Triple-Negative Breast Cancer Progression by 1.0 Sponging hsa-miR-2682</p&gt;. OncoTargets and Therapy, 2020, Volume 13, 4791-4798. Insight into the Possible Formation Mechanism of the Intersex Phenotype of Lanzhou Fat-Tailed Sheep 1.0 6 Using Whole-Genome Resequencing. Animals, 2020, 10, 944.

1282	Inflammasome/NF-κB translocation inhibition via PPARγ agonist mitigates inorganic mercury induced nephrotoxicity. Ecotoxicology and Environmental Safety, 2020, 201, 110801.	2.9	14
1283	Interactions of gene expression, alternative splicing, and DNA methylation in determining nodule identity. Plant Journal, 2020, 103, 1744-1766.	2.8	26
1284	Alterations in DNA methylation profiles in cancellous bone of postmenopausal women with osteoporosis. FEBS Open Bio, 2020, 10, 1516-1531.	1.0	16

1267

1269

1270

1271

1273

1274

1275

1276

1277

1279

1280

	Сітатіо	n Report	
#	Article	IF	Citations
1285	The gut microbes, Enterococcus and Escherichia-Shigella, affect the responses of heart valve replacement patients to the anticoagulant warfarin. Pharmacological Research, 2020, 159, 104979.	3.1	24
1286	DNA methylome and transcriptome landscapes revealed differential characteristics of dioecious flowers in papaya. Horticulture Research, 2020, 7, 81.	2.9	20
1287	Transcriptomic Analysis of circRNAs and mRNAs Reveals a Complex Regulatory Network That Participate in Follicular Development in Chickens. Frontiers in Genetics, 2020, 11, 503.	1.1	15
1288	Comparative Transcriptome Profiling Analysis Uncovers Novel Heterosis-Related Candidate Genes Associated with Muscular Endurance in Mules. Animals, 2020, 10, 980.	1.0	7
1289	Pan-Genome of Wild and Cultivated Soybeans. Cell, 2020, 182, 162-176.e13.	13.5	508
1290	Full-length transcript sequencing accelerates the transcriptome research of Gymnocypris namensis, an iconic fish of the Tibetan Plateau. Scientific Reports, 2020, 10, 9668.	1.6	12
1291	A Transcriptome Analysis Reveals that Hepatic Glycolysis and Lipid Synthesis Are Negatively Associated with Feed Efficiency in DLY Pigs. Scientific Reports, 2020, 10, 9874.	1.6	8
1292	Transcriptome analysis reveals a molecular understanding of nicotinamide and butyrate sodium on meat quality of broilers under high stocking density. BMC Genomics, 2020, 21, 412.	1.2	10
1293	The reproductive toxicity and potential mechanisms of combined exposure to dibutyl phthalate and diisobutyl phthalate in male zebrafish (Danio rerio). Chemosphere, 2020, 258, 127238.	4.2	45
1294	Melatonin enhances the cadmium tolerance of mushrooms through antioxidant-related metabolites and enzymes. Food Chemistry, 2020, 330, 127263.	4.2	35
1295	Comparative transcriptomic analysis of fireflies (Coleoptera: Lampyridae) to explore the molecular adaptations to fresh water. Molecular Ecology, 2020, 29, 2676-2691.	2.0	17
1296	Upâ€regulating <scp><i>GmETO1</i></scp> improves phosphorus uptake and use efficiency by promoting root growth in soybean. Plant, Cell and Environment, 2020, 43, 2080-2094.	2.8	31
1297	Reprogramming of tumor-associated macrophages by targeting β-catenin/FOSL2/ARID5A signaling: A potential treatment of lung cancer. Science Advances, 2020, 6, eaaz6105.	4.7	110
1298	Bioinformatics Analysis of Prognostic miRNA Signature and Potential Critical Genes in Colon Cancer. Frontiers in Genetics, 2020, 11, 478.	1.1	30
1299	Interactions Among Expressed MicroRNAs and mRNAs in the Early Stages of Fowl Adenovirus Aerotype 4-Infected Leghorn Male Hepatocellular Cells. Frontiers in Microbiology, 2020, 11, 831.	1.5	9
1300	Distinct Cell Transcriptomic Landscapes Upon Henipavirus Infections. Frontiers in Microbiology, 2020, 11, 986.	1.5	2
1301	Effect of Alfalfa Hay and Starter Feeding Intervention on Gastrointestinal Microbial Community, Growth and Immune Performance of Yak Calves. Frontiers in Microbiology, 2020, 11, 994.	1.5	27
1302	HIF-1α is involved in blood–brain barrier dysfunction and paracellular migration of bacteria in pneumococcal meningitis. Acta Neuropathologica, 2020, 140, 183-208.	3.9	24

#	Article	IF	CITATIONS
1303	Blood Serum Stimulates p38-Mediated Proliferation and Changes in Global Gene Expression of Adult Human Cardiac Stem Cells. Cells, 2020, 9, 1472.	1.8	13
1304	Identification and profiling of microRNAs and differentially expressed genes during anther development between a genetic male-sterile mutant and its wildtype cotton via high-throughput RNA sequencing. Molecular Genetics and Genomics, 2020, 295, 645-660.	1.0	8
1305	Gill transcriptomes reveal expression changes of genes related with immune and ion transport under salinity stress in silvery pomfret (Pampus argenteus). Fish Physiology and Biochemistry, 2020, 46, 1255-1277.	0.9	19
1306	Rapid and strong population genetic differentiation and genomic signatures of climatic adaptation in an invasive mealybug. Diversity and Distributions, 2020, 26, 610-622.	1.9	15
1307	AllEnricher: a comprehensive gene set function enrichment tool for both model and non-model species. BMC Bioinformatics, 2020, 21, 106.	1.2	20
1308	Comparative Transcriptome Analysis Reveals Molecular Defensive Mechanism of <i>Arachis hypogaea</i> in Response to Salt Stress. International Journal of Genomics, 2020, 2020, 1-13.	0.8	20
1309	Identification of novel long non-coding RNAs involved in bisphenol A induced immunotoxicity in fish primary macrophages. Fish and Shellfish Immunology, 2020, 100, 152-160.	1.6	13
1310	Large-scale profiling of the proteome and dual transcriptome in Nile tilapia (Oreochromis niloticus) challenged with low- and high-virulence strains of Streptococcus agalactiae. Fish and Shellfish Immunology, 2020, 100, 386-396.	1.6	12
1311	Genome-Wide Detection of Key Genes and Epigenetic Markers for Chicken Fatty Liver. International Journal of Molecular Sciences, 2020, 21, 1800.	1.8	11
1312	Predictable modulation of cancer treatment outcomes by the gut microbiota. Microbiome, 2020, 8, 28.	4.9	102
1313	Integrated Analysis of miRNA-mRNA Network Reveals Different Regulatory Patterns in the Endometrium of Meishan and Duroc Sows during Mid-Late Gestation. Animals, 2020, 10, 420.	1.0	8
1314	Transcriptomic analysis identifies novel genes and pathways for salt stress responses in Suaeda salsa leaves. Scientific Reports, 2020, 10, 4236.	1.6	28
1315	Human Case Infected With Babesia venatorum: A 5-Year Follow-Up Study. Open Forum Infectious Diseases, 2020, 7, ofaa062.	0.4	8
1316	Deep Sequencing and Analysis of Transcriptomes of Pinus koraiensis Sieb. & Zucc Forests, 2020, 11, 350.	0.9	6
1317	Heat Stress Impairs the Physiological Responses and Regulates Genes Coding for Extracellular Exosomal Proteins in Rat. Genes, 2020, 11, 306.	1.0	11
1318	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. JAMA Oncology, 2020, 6, 724.	3.4	139
1319	Combined transcriptomic and metabolomic analyses uncover rearranged gene expression and metabolite metabolism in tobacco during cold acclimation. Scientific Reports, 2020, 10, 5242.	1.6	29
1320	Mammary Transcriptome Profile during Peak and Late Lactation Reveals Differentially Expression Genes Related to Inflammation and Immunity in Chinese Holstein. Animals, 2020, 10, 510.	1.0	9

## # ARTICLE

IF CITATIONS

1321 Transcriptome analysis uncovers the gene expression profile of salt-stressed potato (Solanum) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 742

1322	Somatic variants in new candidate genes identified in focal cortical dysplasia type II. Epilepsia, 2020, 61, 667-678.	2.6	16
1323	Genome‑wide integrated analysis demonstrates widespread functions of IncRNAs in mammary gland development and lactation in dairy goats. BMC Genomics, 2020, 21, 254.	1.2	20
1324	Rewiring of Microbiota Networks in Erosive Inflammation of the Stomach and Small Bowel. Frontiers in Bioengineering and Biotechnology, 2020, 8, 299.	2.0	7
1325	Chemolithoautotropic Diazotrophy Dominates the Nitrogen Fixation Process in Mine Tailings. Environmental Science & Technology, 2020, 54, 6082-6093.	4.6	63
1326	Highâ€quality genome assembly and transcriptome of <i>Ancherythroculter nigrocauda</i> , an endemic Chinese cyprinid species. Molecular Ecology Resources, 2020, 20, 882-891.	2.2	11
1327	Transcriptomic analysis of the mode of action of the candidate anti-fouling compound di(1H-indol-3-yl)methane (DIM) on a marine biofouling species, the bryozoan Bugula neritina. Marine Pollution Bulletin, 2020, 152, 110904.	2.3	3
1328	Phenotypic and Transcriptomic Analysis of Two Pinellia ternata Varieties T2 line and T2Plus line. Scientific Reports, 2020, 10, 4614.	1.6	6
1329	Fine-mapping and transcriptome analysis of a candidate gene controlling plant height in Brassica napus L Biotechnology for Biofuels, 2020, 13, 42.	6.2	25
1330	Transcriptomic Analysis Following Artificial Selection for Grasshopper Size. Insects, 2020, 11, 176.	1.0	0
1331	Genome-Wide Analysis of the DREB Subfamily in Saccharum spontaneum Reveals Their Functional Divergence During Cold and Drought Stresses. Frontiers in Genetics, 2019, 10, 1326.	1.1	28
1332	Proteome and Transcriptome Analysis of the Antioxidant Mechanism in Chicken Regulated by Eucalyptus Leaf Polyphenols Extract. Oxidative Medicine and Cellular Longevity, 2020, 2020, 1-14.	1.9	2
1333	Comfrey (Symphytum spp.) as an alternative field crop contributing to closed agricultural cycles in chicken feeding. Science of the Total Environment, 2020, 742, 140490.	3.9	6
1334	Exploration of the Effects of Different Blue LED Light Intensities on Flavonoid and Lipid Metabolism in Tea Plants via Transcriptomics and Metabolomics. International Journal of Molecular Sciences, 2020, 21, 4606.	1.8	52
1335	OncotRF: an online resource for exploration of tRNA-derived fragments in human cancers. RNA Biology, 2020, 17, 1081-1091.	1.5	39
1336	Genome-Wide Identification of Discriminative Genetic Variations in Beef and Dairy Cattle via an Information-Theoretic Approach. Genes, 2020, 11, 678.	1.0	3
1337	Characterising the mechanisms underlying genetic resistance to amoebic gill disease in Atlantic salmon using RNA sequencing. BMC Genomics, 2020, 21, 271.	1.2	23
1338	Differences in gene expression profiles at the early stage of Solanum lycopersicum infection with mild and severe variants of potato spindle tuber viroid. Virus Research, 2020, 286, 198090.	1.1	8

#	Article	IF	CITATIONS
1339	Transcriptome analyses revealed the ultraviolet B irradiation and phytohormone gibberellins coordinately promoted the accumulation of artemisinin in Artemisia annua L Chinese Medicine, 2020, 15, 67.	1.6	16
1340	Identification of QTNs and Their Candidate Genes for 100-Seed Weight in Soybean (Glycine max L.) Using Multi-Locus Genome-Wide Association Studies. Genes, 2020, 11, 714.	1.0	22
1341	Efficient System Wide Metabolic Pathway Comparisons in Multiple Microbes Using Genome to KEGG Orthology (G2KO) Pipeline Tool. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 311-322.	2.2	11
1342	Alterations of gut microbiota contribute to the progression of unruptured intracranial aneurysms. Nature Communications, 2020, 11, 3218.	5.8	56
1343	Transcription analysis of Ganoderma lucidum reveals candidate genes and pathways in response to excess exogenous indoleacetic acid (IAA). Mycoscience, 2020, 61, 226-234.	0.3	2
1344	MiR-200b in heme oxygenase-1-modified bone marrow mesenchymal stem cell-derived exosomes alleviates inflammatory injury of intestinal epithelial cells by targeting high mobility group box 3. Cell Death and Disease, 2020, 11, 480.	2.7	31
1345	Transcriptome Sequencing and Chemical Analysis Reveal the Formation Mechanism of White Florets in Carthamus tinctorius L Plants, 2020, 9, 847.	1.6	7
1346	Full-length transcriptome sequencing and modular organization analysis of oleanolic acid- and dammarane-type saponins related gene expression patterns in Panax japonicus. Genomics, 2020, 112, 4137-4147.	1.3	8
1347	Metagenomic analysis of soil microbial community under PFOA and PFOS stress. Environmental Research, 2020, 188, 109838.	3.7	55
1348	Comparative transcriptomic and physiological analyses of contrasting hybrid cultivars ND476 and ZX978 identify important differentially expressed genes and pathways regulating drought stress tolerance in maize. Genes and Genomics, 2020, 42, 937-955.	0.5	5
1349	Transcriptome Profiling Revealed Potentially Critical Roles for Digestion and Defense-Related Genes in Insects' Use of Resistant Host Plants: A Case Study with Sitobion Avenae. Insects, 2020, 11, 90.	1.0	6
1350	Gene expression profile indicates involvement of uniconazole in <i>Coix lachrymaâ€jobi</i> L. seedlings at low temperature. Food Science and Nutrition, 2020, 8, 534-546.	1.5	4
1351	Identification of Genes Related to Clinicopathological Characteristics and Prognosis of Patients with Colorectal Cancer. DNA and Cell Biology, 2020, 39, 690-699.	0.9	21
1352	A Comparative Transcriptome Analysis of Volvariella volvacea Identified the Candidate Genes Involved in Fast Growth at the Mycelial Growth Stage. Genes, 2020, 11, 161.	1.0	2
1353	Integrated Metabolomic and Transcriptomic Analysis to Characterize Cutin Biosynthesis between Low- and High-Cutin Genotypes of Capsicum chinense Jacq. International Journal of Molecular Sciences, 2020, 21, 1397.	1.8	18
1354	Porcupine Inhibitor LGK974 Downregulates the Wnt Signaling Pathway and Inhibits Clear Cell Renal Cell Carcinoma. BioMed Research International, 2020, 2020, 1-16.	0.9	15
1355	Proteomic analysis of <i>Aspergillus niger</i> 3.316 under heat stress. MicrobiologyOpen, 2020, 9, e1012.	1.2	11
1357	The biocontrol agent Streptomyces pactum increases Pseudomonas koreensis populations in the rhizosphere by enhancing chemotaxis and biofilm formation. Soil Biology and Biochemistry, 2020, 144, 107755.	4.2	39

#	Article	IF	CITATIONS
1358	Transcriptome profiles of Quercus rubra responding to increased O3 stress. BMC Genomics, 2020, 21, 160.	1.2	11
1359	Physiological and transcriptomic analysis provide novel insight into cobalt stress responses in willow. Scientific Reports, 2020, 10, 2308.	1.6	15
1360	Transcriptomic analysis at the first instar larval stage of nonmolting Bombyx mori mutant ( a42 ). Archives of Insect Biochemistry and Physiology, 2020, 104, e21663.	0.6	1
1361	Identification of key genes related to seedlessness by genome-wide detection of structural variation and transcriptome analysis in â€~Shijiwuhe' pear. Gene, 2020, 738, 144480.	1.0	2
1362	Genomic analyses reveal distinct genetic architectures and selective pressures in buffaloes. GigaScience, 2020, 9, .	3.3	18
1363	Mural Cell SDF1 Signaling Is Associated with the Pathogenesis of Pulmonary Arterial Hypertension. American Journal of Respiratory Cell and Molecular Biology, 2020, 62, 747-759.	1.4	29
1364	Identification of Candidate Chemosensory Receptors in the Antennae of the Variegated Cutworm, Peridroma saucia Hübner, Based on a Transcriptome Analysis. Frontiers in Physiology, 2020, 11, 39.	1.3	11
1365	Suppression of water-bloom cyanobacterium Microcystis aeruginosa by algaecide hydrogen peroxide maximized through programmed cell death. Journal of Hazardous Materials, 2020, 393, 122394.	6.5	55
1366	Integration of transcriptomics and metabolomics reveals the responses of earthworms to the long-term exposure of TiO2 nanoparticles in soil. Science of the Total Environment, 2020, 719, 137492.	3.9	58
1367	Comparative transcriptome analysis of inbred lines and contrasting hybrids reveals overdominance mediate early biomass vigor in hybrid cotton. BMC Genomics, 2020, 21, 140.	1.2	22
1368	Genetic Mapping Combined with a Transcriptome Analysis to Screen for Candidate Genes Responsive to Abscisic Acid Treatment in <i>Brassica napus</i> Embryos During Seed Germination. DNA and Cell Biology, 2020, 39, 533-547.	0.9	4
1369	LINC02499, a novel liverâ€specific long nonâ€coding RNA with potential diagnostic and prognostic value, inhibits hepatocellular carcinoma cell proliferation, migration, and invasion. Hepatology Research, 2020, 50, 726-740.	1.8	22
1370	The draft genome of horseshoe crab Tachypleus tridentatus reveals its evolutionary scenario and well-developed innate immunity. BMC Genomics, 2020, 21, 137.	1.2	22
1371	Comparative Transcriptome Analysis Provides Insights into the Polyunsaturated Fatty Acid Synthesis Regulation of Fat-1 Transgenic Sheep. International Journal of Molecular Sciences, 2020, 21, 1121.	1.8	3
1372	Tet1 Deficiency Leads to Premature Reproductive Aging by Reducing Spermatogonia Stem Cells and Germ Cell Differentiation. IScience, 2020, 23, 100908.	1.9	25
1373	Protein Expression Profile in Rat Silicosis Model Reveals Upregulation of PTPN2 and Its Inhibitory Effect on Epithelial-Mesenchymal Transition by Dephosphorylation of STAT3. International Journal of Molecular Sciences, 2020, 21, 1189.	1.8	12
1374	Identification of drought resistant miRNA in Macleaya cordata by high-throughput sequencing. Archives of Biochemistry and Biophysics, 2020, 684, 108300.	1.4	9
1375	Transcriptome analysis of tobacco root response to different concentrations of nitrate. Agronomy Journal, 2020, 112, 1111-1125.	0.9	1

		CITATION REPORT		
#	Article		IF	Citations
1376	A developmental landscape of 3D-cultured human pre-gastrulation embryos. Nature, 2020,	577, 537-542.	13.7	277
1377	Transcriptomic Analyses of the Hypothalamic-Pituitary-Gonadal Axis Identify Candidate Gene to Egg Production in Xinjiang Yili Geese. Animals, 2020, 10, 90.	es Related	1.0	15
1378	The chromosome 19 microRNA cluster, regulated by promoter hypomethylation, is associated tumour burden and poor prognosis in patients with hepatocellular carcinoma. Journal of Cel Physiology, 2020, 235, 6103-6112.	ed with Iular	2.0	11
1379	Maternal transcription profiles at different stages for the development of early embryo in bu Reproduction in Domestic Animals, 2020, 55, 503-514.	ıffalo.	0.6	1
1380	Whole-genome re-sequencing and transcriptome reveal cadmium tolerance related genes a pathways in Chlamydomonas reinhardtii. Ecotoxicology and Environmental Safety, 2020, 19	nd 91, 110231.	2.9	15
1381	Genome-wide analysis of circular RNAs involved in Marek's disease tumourigenesis in ch Biology, 2020, 17, 517-527.	ickens. RNA	1.5	18
1382	Comprehensive analysis of circRNAs from cashmere goat skin by next generation RNA seque (RNA-seq). Scientific Reports, 2020, 10, 516.	encing	1.6	29
1383	Plateau Grass and Greenhouse Flower? Distinct Genetic Basis of Closely Related Toad Tadpo Respectively Adapted to High Altitude and Karst Caves. Genes, 2020, 11, 123.	les	1.0	4
1384	Dynamic Transcriptomic Analysis of Breast Muscle Development From the Embryonic to Pos Periods in Chickens. Frontiers in Genetics, 2019, 10, 1308.	t-hatching	1.1	18
1385	Analysis of Differentially Expressed Transcripts in Apolygus lucorum (Meyer-Dür) Exposed Different Temperature Coefficient Insecticides. International Journal of Molecular Sciences, 658.		1.8	9
1386	Whole genome sequence of an edible and medicinal mushroom, Hericium erinaceus (Basidio	omycota,) Tj ETQq0 0	01gBT /C	)verlock 10 T 41
1387	An increase in cell membrane permeability in the in situ extractive fermentation improves th production of antroquinonol from <i>Antrodia camphorata</i> S-29. Journal of Industrial Microbiology and Biotechnology, 2020, 47, 197-207.	e	1.4	5
1388	Dynamic accumulation of fatty acids in duck (Anas platyrhynchos) breast muscle and its con with gene expression. BMC Genomics, 2020, 21, 58.	relations	1.2	17
1389	Identification of drought-responsive miRNAs in Hippophae tibetana using high-throughput s 3 Biotech, 2020, 10, 53.	equencing.	1.1	2
1390	Proteomic analysis reflects an environmental alkalinization-coupled pH-dependent mechanis regulating lignocellulases in Trichoderma guizhouense NJAU4742. Biotechnology for Biofue 13, 6.		6.2	6
1391	Comparative Transcriptome Analysis of Thitarodes Armoricanus in Response to the Entomo Fungi Paecilomyces Hepiali and Ophiocordyceps Sinensis. Insects, 2020, 11, 4.	pathogenic	1.0	18
1392	Whole-genome sequencing of wild Siberian musk deer (Moschus moschiferus) provides insi its genetic features. BMC Genomics, 2020, 21, 108.	ghts into	1.2	8
1393	Change in composition and potential functional genes of soil bacterial and fungal communi secondary succession in Quercus liaotungensis forests of the Loess Plateau, western China. Geoderma, 2020, 364, 114199.	ties with	2.3	63

#	Article	IF	CITATIONS
1394	Shading Effects on Leaf Color Conversion and Biosynthesis of the Major Secondary Metabolites in the Albino Tea Cultivar "Yujinxiang― Journal of Agricultural and Food Chemistry, 2020, 68, 2528-2538.	2.4	43
1395	Maize ZmBES1/BZR1-5 Decreases ABA Sensitivity and Confers Tolerance to Osmotic Stress in Transgenic Arabidopsis. International Journal of Molecular Sciences, 2020, 21, 996.	1.8	53
1396	Identification of gene modules and hub genes in colon adenocarcinoma associated with pathological stage based on WGCNA analysis. Cancer Genetics, 2020, 242, 1-7.	0.2	30
1397	Combining lexical and context features for automatic ontology extension. Journal of Biomedical Semantics, 2020, 11, 1.	0.9	14
1398	Comparative Transcriptome Analysis of Different Dendrobium Species Reveals Active Ingredients-Related Genes and Pathways. International Journal of Molecular Sciences, 2020, 21, 861.	1.8	23
1399	Comparative Transcriptome Analysis Provides Molecular Insights into the Interaction of Beet necrotic yellow vein virus and Beet soil-borne mosaic virus with Their Host Sugar Beet. Viruses, 2020, 12, 76.	1.5	13
1400	Transcriptome profiling reveals the molecular processes for survival of Lysinibacillus fusiformis strain 15-4 in petroleum environments. Ecotoxicology and Environmental Safety, 2020, 192, 110250.	2.9	16
1401	Comparative analysis of transcriptomes from different coloration of Chinese mitten crab Eriocheir sinensis. Fish and Shellfish Immunology, 2020, 98, 515-521.	1.6	2
1402	Identification of Potential Biomarkers Associated with Basal Cell Carcinoma. BioMed Research International, 2020, 2020, 1-10.	0.9	7
1403	Comparative transcriptome and phenotype analysis revealed the role and mechanism of <i>ompR</i> in the virulence of fish pathogenic <i>Aeromonas hydrophila</i> . MicrobiologyOpen, 2020, 9, e1041.	1.2	11
1404	Deep learning based prediction of species-specific protein S-glutathionylation sites. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140422.	1.1	17
1405	Reactive oxygen species and antimicrobial peptides are sequentially produced in silkworm midgut in response to bacterial infection. Developmental and Comparative Immunology, 2020, 110, 103720.	1.0	10
1406	Mucinous carcinoma with micropapillary features is morphologically, clinically and genetically distinct from pure mucinous carcinoma of breast. Modern Pathology, 2020, 33, 1945-1960.	2.9	19
1407	Genome-wide DNA methylation analysis reveals significant impact of long-term ambient air pollution exposure on biological functions related to mitochondria and immune response. Environmental Pollution, 2020, 264, 114707.	3.7	32
1408	Pork Meat Proteins Alter Gut Microbiota and Lipid Metabolism Genes in the Colon of Adaptive Immuneâ€Đeficient Mice. Molecular Nutrition and Food Research, 2020, 64, e1901105.	1.5	18
1409	Transcriptome analysis revealed cadmium accumulation mechanisms in hyperaccumulator Siegesbeckia orientalis L. Environmental Science and Pollution Research, 2020, 27, 18853-18865.	2.7	12
1410	Transcriptome analysis of metabolisms related to fruit cracking during ripening of a cracking-susceptible grape berry cv. Xiangfei (Vitis vinifera L.). Genes and Genomics, 2020, 42, 639-650.	0.5	15
1411	The effects of chronic cadmium exposure on Bufo gargarizans larvae: Histopathological impairment, gene expression alteration and fatty acid metabolism disorder in the liver. Aquatic Toxicology, 2020, 222, 105470.	1.9	15

#	Article	IF	CITATIONS
1412	Novel lncRNA XLOC_032768 alleviates cisplatin-induced apoptosis and inflammatory response of renal tubular epithelial cells through TNF-α. International Immunopharmacology, 2020, 83, 106472.	1.7	18
1413	Study on the virulome and resistome of a vancomycin intermediate-resistance Staphylococcus aureus. Microbial Pathogenesis, 2020, 145, 104187.	1.3	5
1414	Overexpression of HcSCL13, a Halostachys caspica GRAS transcription factor, enhances plant growth and salt stress tolerance in transgenic Arabidopsis. Plant Physiology and Biochemistry, 2020, 151, 243-254.	2.8	38
1415	Transcriptome analysis of genes and pathways associated with salt tolerance in alfalfa under non-uniform salt stress. Plant Physiology and Biochemistry, 2020, 151, 323-333.	2.8	19
1416	Lipidomic and transcriptomic analysis reveals reallocation of carbon flux from cuticular wax into plastid membrane lipids in a glossy "Newhall―navel orange mutant. Horticulture Research, 2020, 7, 41.	2.9	23
1417	Genetic and genomic analysis for cocoon yield traits in silkworm. Scientific Reports, 2020, 10, 5682.	1.6	11
1418	Gene Expression Dynamics at the Neurovascular Unit During Early Regeneration After Cerebral Ischemia/Reperfusion Injury in Mice. Frontiers in Neuroscience, 2020, 14, 280.	1.4	20
1419	Esculetin Inhibits Cancer Cell Glycolysis by Binding Tumor PGK2, GPD2, and GPI. Frontiers in Pharmacology, 2020, 11, 379.	1.6	33
1420	Ileal Transcriptome Profiles of Japanese Quail Divergent in Phosphorus Utilization. International Journal of Molecular Sciences, 2020, 21, 2762.	1.8	8
1421	Comparative analysis of the daytime and nighttime brain transcriptomes of Pelteobagrus vachellii. Aquaculture Research, 2020, 51, 2842-2851.	0.9	1
1422	Identification of differential expression genes related to anthocyanin biosynthesis in carmine radish (Raphanus sativus L.) fleshy roots using comparative RNA-Seq method. PLoS ONE, 2020, 15, e0231729.	1.1	2
1423	Red Chinese Cabbage Transcriptome Analysis Reveals Structural Genes and Multiple Transcription Factors Regulating Reddish Purple Color. International Journal of Molecular Sciences, 2020, 21, 2901.	1.8	21
1424	Biochemical and genetic basis of cadmium biosorption by Enterobacter ludwigii LY6, isolated from industrial contaminated soil. Environmental Pollution, 2020, 264, 114637.	3.7	23
1425	CircRNA Expression Profile during Yak Adipocyte Differentiation and Screen Potential circRNAs for Adipocyte Differentiation. Genes, 2020, 11, 414.	1.0	25
1426	Transcriptome signatures from discordant sibling pairs reveal changes in peripheral blood immune cell composition in Autism Spectrum Disorder. Translational Psychiatry, 2020, 10, 106.	2.4	16
1427	From Maternal Grazing to Barn Feeding During Pre-weaning Period: Altered Gastrointestinal Microbiota Contributes to Change the Development and Function of the Rumen and Intestine of Yak Calves. Frontiers in Microbiology, 2020, 11, 485.	1.5	27
1428	Transcriptome Analysis Reveals Candidate Genes for Petroselinic Acid Biosynthesis in Fruits of <i>Coriandrum sativum</i> L. Journal of Agricultural and Food Chemistry, 2020, 68, 5507-5520.	2.4	12
1429	Wholeâ€genome resequencing reveals diversity, global and local ancestry proportions in Yunling cattle. Journal of Animal Breeding and Genetics, 2020, 137, 641-650.	0.8	15

#	Article	IF	Citations
1430	Comprehensive transcriptome analyses of two <i>Oocystis</i> algae provide insights into the adaptation to Qinghai–Tibet Plateau. Journal of Systematics and Evolution, 2021, 59, 1209-1219.	1.6	9
1431	Coordinated mechanisms of leaves and roots in response to drought stress underlying full-length transcriptome profiling in Vicia sativa L. BMC Plant Biology, 2020, 20, 165.	1.6	27
1432	Combined QTL mapping and RNA-Seq profiling reveals candidate genes associated with cadmium tolerance in barley. PLoS ONE, 2020, 15, e0230820.	1.1	32
1433	Robust induction of interferon and interferon-stimulated gene expression by influenza B/Yamagata lineage virus infection of A549 cells. PLoS ONE, 2020, 15, e0231039.	1.1	8
1434	A Comparison of Co-expression Networks in Silk Gland Reveals the Causes of Silk Yield Increase During Silkworm Domestication. Frontiers in Genetics, 2020, 11, 225.	1.1	10
1435	Comparative Transcriptomic Analysis of Two Bottle Gourd Accessions Differing in Fruit Size. Genes, 2020, 11, 359.	1.0	16
1436	M6A2Target: a comprehensive database for targets of m <b>6</b> A writers, erasers and readers. Briefings in Bioinformatics, 2021, 22, .	3.2	97
1437	Effects of Shading on the Synthesis of Volatile Organic Compounds in â€ <sup>~</sup> Marselan' Grape Berries (Vitis) Tj E <sup>-</sup>	TQ <u>q1</u> 10.7	784314 rg8T
1438	Dissecting the phenotypic components and genetic architecture of maize stem vascular bundles using highâ€ŧhroughput phenotypic analysis. Plant Biotechnology Journal, 2021, 19, 35-50.	4.1	25
1439	Cold adaptation in drylands: transcriptomic insights into coldâ€stressed <i>Nostoc flagelliforme</i> and characterization of a hypothetical gene with cold and nitrogen stress tolerance. Environmental Microbiology, 2021, 23, 713-727.	1.8	11
1440	Exposure to benzo[a]pyrene triggers distinct patterns of microRNA transcriptional profiles in aquatic firefly Aquatica wuhana (Coleoptera: Lampyridae). Journal of Hazardous Materials, 2021, 401, 123409.	6.5	8
1441	Bacterial–fungal interactions revealed by genome-wide analysis of bacterial mutant fitness. Nature Microbiology, 2021, 6, 87-102.	5.9	49
1442	Microbiomic and transcriptomic insight into the pathogenesis of meningitis-like disease in cultured Pelophylax nigromaculatus. Aquaculture, 2021, 530, 735736.	1.7	8
1443	Whole genome analyses revealed genomic difference between European taurine and East Asian taurine. Journal of Animal Breeding and Genetics, 2021, 138, 56-68.	0.8	15
1444	Integrated proteomics and metabolomics analysis of tea leaves fermented by Aspergillus niger, Aspergillus tamarii and Aspergillus fumigatus. Food Chemistry, 2021, 334, 127560.	4.2	90
1445	Allopatric sibling species pair Drosophila nasuta nasuta and Drosophila nasuta albomicans exhibit expression divergence in ovarian transcriptomes. Gene, 2021, 777, 145189.	1.0	2
1446	iTRAQ and RNA-Seq analyses revealed the effects of grafting on fruit development and ripening of oriental melon (Cucumis melo L. var. makuwa). Gene, 2021, 766, 145142.	1.0	20
1447	Transcriptome analysis reveals the effects of sand substrate removal and body colour change of buruma shrimp, cipMarsupenaeus japonicus (ip, Aquaculture Research, 2021, 52, 577-588	0.9	6

#	Article	IF	CITATIONS
1448	iTRAQâ€based quantitative proteomic analysis ofSargassum fusiformein response to high temperature stress. Aquaculture Research, 2021, 52, 185-195.	0.9	3
1449	Novel pituitary actions of NKB for anorectic peptides regulation in grass carp. Aquaculture, 2021, 531, 735857.	1.7	4
1450	Endophytic Bacillus altitudinis WR10 alleviates Cu toxicity in wheat by augmenting reactive oxygen species scavenging and phenylpropanoid biosynthesis. Journal of Hazardous Materials, 2021, 405, 124272.	6.5	34
1451	Molecular and biochemical analyses of avocado (Persea americana) reveal differences in the oil accumulation pattern between the mesocarp and seed during the fruit developmental period. Scientia Horticulturae, 2021, 276, 109717.	1.7	9
1452	Long nonâ€coding <scp>RNAs</scp> associate with jasmonateâ€mediated plant defence against herbivores. Plant, Cell and Environment, 2021, 44, 982-994.	2.8	27
1453	Combining quantitative trait locus and co-expression analysis allowed identification of new candidates for oil accumulation in rapeseed. Journal of Experimental Botany, 2021, 72, 1649-1660.	2.4	12
1454	A novel tonicity-responsive microRNA miR-23a-5p modulates renal cell survival under osmotic stress through targeting heat shock protein 70 HSPA1B. American Journal of Physiology - Cell Physiology, 2021, 320, C225-C239.	2.1	6
1455	Characterizing microRNAs and their targets in different organs of Camellia sinensis var. assamica. Genomics, 2021, 113, 159-170.	1.3	10
1456	Auxin-related genes associated with leaf petiole angle at the seedling stage are involved in adaptation to low temperature in Brassica napus. Environmental and Experimental Botany, 2021, 182, 104308.	2.0	6
1457	Profiling prokaryotic community in pit mud of Chinese strong-aroma type liquor by using oligotrophic culturing. International Journal of Food Microbiology, 2021, 337, 108951.	2.1	13
1458	Mutations in Spliceosomal Genes PPIL1 and PRP17 Cause Neurodegenerative Pontocerebellar Hypoplasia with Microcephaly. Neuron, 2021, 109, 241-256.e9.	3.8	31
1459	Identification of genetic factors controlling phosphorus utilization efficiency in wheat by genome-wide association study with principal component analysis. Gene, 2021, 768, 145301.	1.0	7
1460	Transcriptional analysis for cholesterol-lowering effects of marine Lactobacillus plantarum Lp10 isolated from kelp. LWT - Food Science and Technology, 2021, 139, 110563.	2.5	7
1461	Transcriptome analysis of liver lipid metabolism disorders of the turbot Scophthalmus maximus in response to low salinity stress. Aquaculture, 2021, 534, 736273.	1.7	37
1462	Ultraprocessed foods and cardiovascular health: it's not just about the nutrients. American Journal of Clinical Nutrition, 2021, 113, 257-258.	2.2	10
1463	Increased photosystem II translation efficiency as an important photoprotective mechanism in an Arabidopsis thaliana ecotype (Tibet-0) adapted to high light environments. Environmental and Experimental Botany, 2021, 183, 104350.	2.0	7
1464	Mapping the Endothelial Cell <i>S</i> -Sulfhydrome Highlights the Crucial Role of Integrin Sulfhydration in Vascular Function. Circulation, 2021, 143, 935-948.	1.6	70
1465	Heat preadaptation improved the ability of Zygosaccharomyces rouxii to salt stress: a combined physiological and transcriptomic analysis. Applied Microbiology and Biotechnology, 2021, 105, 259-270.	1.7	19

#	Article	IF	CITATIONS
1466	Growth and transcriptome analysis of tomato under seawater stress. South African Journal of Botany, 2021, 137, 463-474.	1.2	7
1467	A highly heterogeneous mutational pattern in POEMS syndrome. Leukemia, 2021, 35, 1100-1107.	3.3	17
1468	Deciphering the molecular regulatory mechanism orchestrating ovary development of the Pacific whiteleg shrimp Litopenaeus vannamei through integrated transcriptomic analysis of reproduction-related organs. Aquaculture, 2021, 533, 736160.	1.7	10
1469	Resource allocation strategies among vegetative growth, sexual reproduction, asexual reproduction and defense during growing season of <i>Aconitum kusnezoffii</i> Reichb Plant Journal, 2021, 105, 957-977.	2.8	14
1470	Comparative microRNAs expression profiles analysis during embryonic development of common carp, Cyprinus carpio. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 37, 100754.	0.4	5
1471	Expression and functionality of allergenic genes regulated by simulated gastric juice in Anisakis pegreffii. Parasitology International, 2021, 80, 102223.	0.6	3
1472	In-depth analysis of potential PaAP2/ERF transcription factor related to fatty acid accumulation in avocado (Persea americana Mill.) and functional characterization of two PaAP2/ERF genes in transgenic tomato. Plant Physiology and Biochemistry, 2021, 158, 308-320.	2.8	5
1473	Discovery and functional understanding of MiRNAs in molluscs: a genome-wide profiling approach. RNA Biology, 2021, 18, 1702-1715.	1.5	6
1474	Identification and Validation of Key miRNAs and a microRNA-mRNA Regulatory Network Associated with Ulcerative Colitis. DNA and Cell Biology, 2021, 40, 147-156.	0.9	12
1475	Mini-metagenome analysis of psychrophilic electroactive biofilms based on single cell sorting. Science of the Total Environment, 2021, 762, 144328.	3.9	9
1476	Metagenomics combined with DNA-based stable isotope probing provide comprehensive insights of active triclosan-degrading bacteria in wastewater treatment. Journal of Hazardous Materials, 2021, 404, 124192.	6.5	18
1477	Influence of the neonicotinoid insecticide thiamethoxam on soil bacterial community composition and metabolic function. Journal of Hazardous Materials, 2021, 405, 124275.	6.5	40
1478	Coordinated regulation of starch synthesis in maize endosperm by microRNAs and DNA methylation. Plant Journal, 2021, 105, 108-123.	2.8	17
1479	Transcriptome characteristics and the expression profiles of resistance-related genes in healthy and <i>Mycocentrospora acerina</i> -infected <i>Asarum</i> sp. leaves treated with <i>Penicillium janthinellum</i> F1-6. Biocontrol Science and Technology, 2021, 31, 171-189.	0.5	0
1480	Polycyclic aromatic hydrocarbon and n-alkane pollution characteristics and structural and functional perturbations to the microbial community: a case-study of historically petroleum-contaminated soil. Environmental Science and Pollution Research, 2021, 28, 10589-10602.	2.7	23
1481	Physiological Characteristic Changes and Full-Length Transcriptome of Rose ( <i>Rosa chinensis</i> ) Roots and Leaves in Response to Drought Stress. Plant and Cell Physiology, 2021, 61, 2153-2166.	1.5	25
1482	A comprehensive integrated transcriptome and metabolome analyses to reveal key genes and essential metabolic pathways involved in CMS in kenaf. Plant Cell Reports, 2021, 40, 223-236.	2.8	5
1483	TCTP participates in hepatic metabolism by regulating gene expression involved in insulin resistance. Gene, 2021, 768, 145263.	1.0	3

#	Article	IF	CITATIONS
1484	<i>Serendipita bescii</i> promotes winter wheat growth and modulates the host root transcriptome under phosphorus and nitrogen starvation. Environmental Microbiology, 2021, 23, 1876-1888.	1.8	15
1485	An integrated network pharmacology and RNA-Seq approach for exploring the preventive effect of Lonicerae japonicae flos on LPS-induced acute lung injury. Journal of Ethnopharmacology, 2021, 264, 113364.	2.0	47
1486	Physiological and transcriptomic responses to N-deficiency and ammonium: Nitrate shift in Fugacium kawagutii (Symbiodiniaceae). Science of the Total Environment, 2021, 753, 141906.	3.9	17
1487	Comparative analysis of five different methods to design a breed-specific SNP panel for cattle. Animal Biotechnology, 2021, 32, 130-136.	0.7	23
1488	Spaceflight and simulated microgravity suppresses macrophage development via altered RAS/ERK/NFήB and metabolic pathways. Cellular and Molecular Immunology, 2021, 18, 1489-1502.	4.8	59
1489	Identifying Candidate Genes Involved in the Regulation of Early Growth Using Full-Length Transcriptome and RNA-Seq Analyses of Frontal and Parietal Bones and Vertebral Bones in Bighead Carp (Hypophthalmichthys nobilis). Frontiers in Genetics, 2020, 11, 603454.	1.1	9
1490	Role of Transportome in the Gills of Chinese Mitten Crabs in Response to Salinity Change: A Meta-Analysis of RNA-Seq Datasets. Biology, 2021, 10, 39.	1.3	13
1491	Transcriptional response of Asarum heterotropoides Fr. Schmidt var. mandshuricum (Maxim.) Kitag. leaves grown under full and partial daylight conditions. BMC Genomics, 2021, 22, 16.	1.2	1
1492	Identification of a Five-Gene Prognostic Model and Its Potential Drug Repurposing in Colorectal Cancer Based on TCGA, GTEx and GEO Databases. Frontiers in Genetics, 2020, 11, 622659.	1.1	10
1493	Identification of potential key genes and pathways associated with the Pashmina fiber initiation using RNA-Seq and integrated bioinformatics analysis. Scientific Reports, 2021, 11, 1766.	1.6	14
1494	A novel transcription factor UvCGBP1 regulates development and virulence of rice false smut fungus <i>Ustilaginoidea virens</i> . Virulence, 2021, 12, 1563-1579.	1.8	13
1495	Flow shear stress controls the initiation of neovascularization <i>via</i> heparan sulfate proteoglycans within a biomimetic microfluidic model. Lab on A Chip, 2021, 21, 421-434.	3.1	17
1496	Auxin is involved in arbuscular mycorrhizal fungi-promoted tomato growth and NADP-malic enzymes expression in continuous cropping substrates. BMC Plant Biology, 2021, 21, 48.	1.6	22
1497	<i>N</i> â€(3â€oxododecanoyl)â€ <scp><i>l</i></scp> â€homoserine lactone disrupts intestinal epithelial barrier through triggering apoptosis and collapsing extracellular matrix and tight junction. Journal of Cellular Physiology, 2021, 236, 5771-5784.	2.0	9
1498	Integrated analyses of miRNA and mRNA profiles in leukocytes and serums in traditional Chinese medicine (TCM)-defined Pi-qi-deficiency syndrome and Pi-wei damp-heat syndrome resulting from chronic atrophic gastritis. Chinese Medicine, 2021, 16, 4.	1.6	9
1500	New insights into the antibacterial and quorum sensing inhibition mechanism of Artemisia argyi leaf extracts towards Pseudomonas aeruginosa PAO1. 3 Biotech, 2021, 11, 97.	1.1	7
1501	PD-L1 correlated gene expression profiles and tumor infiltrating lymphocytes in pancreatic cancer. International Journal of Medical Sciences, 2021, 18, 3150-3157.	1.1	2
1502	Taxonomic and functional adaption of the gastrointestinal microbiome of goats kept at high altitude (4800Âm) under intensive or extensive rearing conditions. FEMS Microbiology Ecology, 2021, 97, .	1.3	12

ARTICLE IF CITATIONS Long Non-coding RNA BTG3-7:1 and JUND Co-regulate C21ORF91 to Promote Triple-Negative Breast 1503 0 1.6 Cancer Progress. Frontiers in Molecular Biosciences, 2020, 7, 605623. Gene fusion of IL7 involved in the regulation of idiopathic pulmonary fibrosis. Therapeutic Advances 1504 1.0 in Respiratory Disease, 2021, 15, 175346662199504. Three hematologic/immune system-specific expressed genes are considered as the potential biomarkers for the diagnosis of early rheumatoid arthritis through bioinformatics analysis. Journal of 1505 70 1.8 Translational Medicine, 2021, 19, 18. NGS Methodologies and Computational Algorithms for the Prediction and Analysis of. Methods in 0.4 Molecular Biology, 2021, 2362, 119-145. ATP5A1 Participates in Transcriptional and Posttranscriptional Regulation of Cancer-Associated Genes 1507 by Modulating Their Expression and Alternative Splicing Profiles in HeLa Cells. Technology in Cancer 0.8 6 Research and Treatment, 2021, 20, 153303382110391. Toxin-antitoxin HicAB regulates the formation of persister cells responsible for the acid stress resistance in Acetobacter pasteurianus. Applied Microbiology and Biotechnology, 2021, 105, 725-739. 1.7 The Effect of Dietary Lycopene Supplementation on Drip Loss during Storage of Lamb Meat by iTRAQ 1509 2.2 8 Analysis. Antioxidants, 2021, 10, 198. Evaluation on reprogramed biological processes in transgenic maize varieties using transcriptomics 1510 1.6 and metabolomics. Scientific Reports, 2021, 11, 2050. Comparative transcriptome of compatible and incompatible interaction of *<i*>Erysiphe pisi*</i*> 1511 1.3 3 garden pea reveals putative defense and pathogenicity factors. FEMS Microbiology Ecology, 2021, 97, . Deciphering the miRNA transcriptome of breast muscle from the embryonic to post-hatching periods 1.2 in chickens. BMC Genomics, 2021, 22, 64. Full-Length Transcriptome Analysis of Four Different Tissues of Cephalotaxus oliveri. International 1513 1.8 16 Journal of Molecular Sciences, 2021, 22, 787. Microarray analysis of Arabidopsis thaliana exposed to single and mixed infections with Cucumber 1514 1.4 mosaic virus and turnip viruses. Physiology and Molecular Biology of Plants, 2021, 27, 11-27. UV-B-induced molecular mechanisms of stress physiology responses in the major northern Chinese conifer<i>Pinus tabuliformis</i>Carr.. Tree Physiology, 2021, 41, 1247-1263. 1516 1.4 12 Targeted next-generation sequencing for cancer-associated gene mutation and copy number detection in 206 patients with non–small-cell lung cancer. Bioengineered, 2021, 12, 791-802. 1.4 Mdfi Promotes C2C12 Cell Differentiation and Positively Modulates Fast-to-Slow-Twitch Muscle Fiber 1518 1.8 14 Transformation. Frontiers in Cell and Developmental Biology, 2021, 9, 605875. Metagenomic analysis revealed a wide distribution of antibiotic resistance genes and biosynthesis of 1.3 antibiotics in the gut of giant pandas. BMC Microbiology, 2021, 21, 15. Effect of emodin on long nonâ€coding RNAâ€mRNA networks in rats with severe acute 1520 1.6 17 pancreatitisâ€induced acute lung injury. Journal of Cellular and Molecular Medicine, 2021, 25, 1851-1866. De novo transcriptome in roots of switchgrass (Panicum virgatum L.) reveals gene expression dynamic 1.2 and act network under alkaline salt stress. BMC Genomics, 2021, 22, 82.

#	Article	IF	CITATIONS
1522	Genome-wide identification and characterization of long non-coding RNAs conferring resistance to Colletotrichum gloeosporioides in walnut (Juglans regia). BMC Genomics, 2021, 22, 15.	1.2	27
1523	Genome-wide scan for selective footprints and genes related to cold tolerance in Chantecler chickens. Zoological Research, 2021, 42, 710-720.	0.9	15
1524	DDX41 regulates the expression and alternative splicing of genes involved in tumorigenesis and immune response. Oncology Reports, 2021, 45, 1213-1225.	1.2	16
1525	A meta-analysis of genome-wide association studies for average daily gain and lean meat percentage in two Duroc pig populations. BMC Genomics, 2021, 22, 12.	1.2	27
1526	Identification of proteins and metabolic networks associated with sucrose accumulation in sugarcane ( <i>Saccharum</i> spp. interspecific hybrids). Journal of Plant Interactions, 2021, 16, 166-178.	1.0	9
1527	Assessing genomic diversity and signatures of selection in Jiaxian Red cattle using whole-genome sequencing data. BMC Genomics, 2021, 22, 43.	1.2	42
1528	Global tissue transcriptomic analysis to improve genome annotation and unravel skin pigmentation in goldfish. Scientific Reports, 2021, 11, 1815.	1.6	15
1529	ARRB1 Drives Gallbladder Cancer Progression by Facilitating TAK1/MAPK Signaling Activation. Journal of Cancer, 2021, 12, 1926-1935.	1.2	6
1530	Attenuation of Antiviral Immune Response Caused by Perturbation of TRIM25-Mediated RIG-I Activation under Simulated Microgravity. Cell Reports, 2021, 34, 108600.	2.9	11
1531	Integrated analysis on mRNA microarray and microRNA microarray to screen immune-related biomarkers and pathways in myelodysplastic syndrome. Hematology, 2021, 26, 417-431.	0.7	4
1532	Chromosome-scale genome assembly provides insights into the evolution and flavor synthesis of passion fruit (Passiflora edulis Sims). Horticulture Research, 2021, 8, 14.	2.9	62
1533	Integrated analysis of the methylome and transcriptome of chickens with fatty liver hemorrhagic syndrome. BMC Genomics, 2021, 22, 8.	1.2	14
1534	Comparative Multi-Omics of Tender Shoots from a Novel Evergrowing Tea Cultivar Provide Insight into the Winter Adaptation Mechanism. Plant and Cell Physiology, 2021, 62, 366-377.	1.5	8
1535	Transcriptome reveals genes involving in black skin color formation of ducks. Genes and Genomics, 2021, 43, 173-182.	0.5	6
1536	Exploring the Molecular Mechanism of Blue Flower Color Formation in Hydrangea macrophylla cv. "Forever Summer― Frontiers in Plant Science, 2021, 12, 585665.	1.7	23
1537	Characterizing <i>Escherichia coli</i> 's transcriptional response to different styrene exposure modes reveals novel toxicity and tolerance insights. Journal of Industrial Microbiology and Biotechnology, 2021, 48, .	1.4	6
1538	Expanded catalog of microbial genes and metagenome-assembled genomes from the pig gut microbiome. Nature Communications, 2021, 12, 1106.	5.8	116
1540	Involvement of Circulating Exosomal MicroRNAs in Jian-Pi-Yi-Shen Formula Protection Against Adenine-Induced Chronic Kidney Disease. Frontiers in Pharmacology, 2020, 11, 622658.	1.6	5

#	Article	IF	CITATIONS
1541	An integrated analysis of lncRNA and mRNA expression profiles in the kidneys of mice with lupus nephritis. PeerJ, 2021, 9, e10668.	0.9	5
1542	Synergistic Network Pharmacology for Traditional Chinese Medicine Liangxue Tongyu Formula in Acute Intracerebral Hemorrhagic Stroke. Neural Plasticity, 2021, 2021, 1-21.	1.0	5
1543	Quantitative Proteomics Analysis of Sugarcane Ratoon Crop Chlorosis. Sugar Tech, 2021, 23, 673-681.	0.9	6
1544	Sinomenine Inhibits the Growth of Ovarian Cancer Cells Through the Suppression of Mitosis by Down-Regulating the Expression and the Activity of CDK1. OncoTargets and Therapy, 2021, Volume 14, 823-834.	1.0	6
1545	Immune profiles of male giant panda (Ailuropoda melanoleuca) during the breeding season. BMC Genomics, 2021, 22, 143.	1.2	3
1546	Investigation of carbon and energy metabolic mechanism of mixotrophy in Chromochloris zofingiensis. Biotechnology for Biofuels, 2021, 14, 36.	6.2	40
1547	The adverse effects of acrylamide exposure on the early development of marine medaka (Oryzias) Tj ETQq0 0 0 rg	gBT /Overlo 2.3	ock 10 Tf 50
1548	The Risks of miRNA Therapeutics: In a Drug Target Perspective. Drug Design, Development and Therapy, 2021, Volume 15, 721-733.	2.0	116
1549	Response of bitter and sweet Chenopodium quinoa varieties to cucumber mosaic virus: Transcriptome and small RNASeq perspective. PLoS ONE, 2021, 16, e0244364.	1.1	2
1550	Genome-Wide Identification and Characterization of Potato Long Non-coding RNAs Associated With Phytophthora infestans Resistance. Frontiers in Plant Science, 2021, 12, 619062.	1.7	9
1551	Transcriptome analysis of salt stress responsiveness in the seedlings of wild and cultivated Ricinus communis L. Journal of Biotechnology, 2021, 327, 106-116.	1.9	17
1552	An RNA-seq Analysis Reveals Differential Transcriptional Responses to Different Light Qualities in Leaf Color of Camellia sinensis cv. Huangjinya. Journal of Plant Growth Regulation, 0, , 1.	2.8	9
1553	Transcriptomic analyses show that 24-epibrassinolide (EBR) promotes cold tolerance in cotton seedlings. PLoS ONE, 2021, 16, e0245070.	1.1	13
1554	Multi-omics analysis reveals structure and function of biofilm microbial communities in a pre-denitrification biofilter. Science of the Total Environment, 2021, 757, 143908.	3.9	47
1555	Cytochrome P450 monooxygenase genes in the wild silkworm, <i>Bombyx mandarina</i> . PeerJ, 2021, 9, e10818.	0.9	6
1556	Identification and co-expression analysis of long noncoding RNAs and mRNAs involved in the deposition of intramuscular fat in Aohan fine-wool sheep. BMC Genomics, 2021, 22, 98.	1.2	14
1557	A chromosomeâ€level genome of the mud crab ( <i>Scylla paramamosain</i> estampador) provides insights into the evolution of chemical and light perception in this crustacean. Molecular Ecology Resources, 2021, 21, 1299-1317.	2.2	17
1558	Galectinâ€1–RNA interaction map reveals potential regulatory roles in angiogenesis. FEBS Letters, 2021, 595, 623-636.	1.3	13

#	Article	IF	CITATIONS
1559	Genome-wide comparative transcriptome analysis of the A4-CMS line ICPA 2043 and its maintainer ICPB 2043 during the floral bud development of pigeonpea. Functional and Integrative Genomics, 2021, 21, 251-263.	1.4	11
1560	Deciphering the transcriptomic regulation of heat stress responses in Nothofagus pumilio. PLoS ONE, 2021, 16, e0246615.	1.1	6
1561	Genomic analyses provide insights into peach local adaptation and responses to climate change. Genome Research, 2021, 31, 592-606.	2.4	30
1562	Comparative analysis of the mitochondrial proteins reveals complex structural and functional relationships in Fasciola species. Microbial Pathogenesis, 2021, 152, 104754.	1.3	3
1563	A towering genome: Experimentally validated adaptations to high blood pressure and extreme stature in the giraffe. Science Advances, 2021, 7, .	4.7	31
1564	Comparative transcriptomics and WGCNA reveal candidate genes involved in petaloid stamens in <i>Paeonia lactiflora</i> . Journal of Horticultural Science and Biotechnology, 2021, 96, 588-603.	0.9	10
1565	A proteomic analysis of skeletal tissue anomaly in the brain coral Platygyra carnosa. Marine Pollution Bulletin, 2021, 164, 111982.	2.3	6
1566	RNAseq Reveals Differential Gene Expression Contributing to Phytophthora nicotianae Adaptation to Partial Resistance in Tobacco. Agronomy, 2021, 11, 656.	1.3	1
1567	Comparative Analyses of Full-Length Transcriptomes Reveal Gnetum luofuense Stem Developmental Dynamics. Frontiers in Genetics, 2021, 12, 615284.	1.1	8
1568	Discovery of novel antagonists targeting the DNA binding domain of androgen receptor by integrated docking-based virtual screening and bioassays. Acta Pharmacologica Sinica, 2022, 43, 229-239.	2.8	14
1569	Identifying SLC27A5 as a potential prognostic marker of hepatocellular carcinoma by weighted gene co-expression network analysis and in vitro assays. Cancer Cell International, 2021, 21, 174.	1.8	10
1570	Transcriptome and metabolome profiling provide insights into molecular mechanism of pseudostem elongation in banana. BMC Plant Biology, 2021, 21, 125.	1.6	11
1572	Molecular Characterization of Donacia provosti (Coleoptera: Chrysomelidae) Larval Transcriptome by De Novo Assembly to Discover Genes Associated with Underwater Environmental Adaptations. Insects, 2021, 12, 281.	1.0	1
1573	A chromosome-level genome assembly for the Pacific oyster <i>Crassostrea gigas</i> . GigaScience, 2021, 10, .	3.3	88
1574	Transcriptome sequencing revealed the mechanism of promoting floret opening by exogenous methyl jasmonate in sorghum. 3 Biotech, 2021, 11, 181.	1.1	1
1575	Long noncoding RNA MEG3 expressed in human dental pulp regulates LPS-Induced inflammation and odontogenic differentiation in pulpitis. Experimental Cell Research, 2021, 400, 112495.	1.2	17
1577	Genome-wide differential expression analysis explores antibacterial molecular mechanisms of zebrafish intestine upon pathogenic Streptococcus agalactiae challenge. Aquaculture Reports, 2021, 19, 100639.	0.7	2
1578	Transcription factor WRKY22 regulates canker susceptibility in sweet orange (Citrus sinensis Osbeck) by enhancing cell enlargement and CsLOB1 expression. Horticulture Research, 2021, 8, 50.	2.9	35

#	Article	IF	CITATIONS
1579	Expression analysis of genes related to cold tolerance in <i> Dendroctonus valens</i> . PeerJ, 2021, 9, e10864.	0.9	9
1580	Tet1 Deficiency Leads to Premature Ovarian Failure. Frontiers in Cell and Developmental Biology, 2021, 9, 644135.	1.8	13
1581	Study on the transcriptome for breast muscle of chickens and the function of key gene RAC2 on fibroblasts proliferation. BMC Genomics, 2021, 22, 157.	1.2	7
1582	Transcriptome analysis reveals the effects of temperature on growth in tadpoles of spiny-bellied frog (Quasipaa boulengeri). Aquaculture International, 2021, 29, 925-939.	1.1	3
1583	A small molecule compound berberine as an orally active therapeutic candidate against COVIDâ€19 and SARS: A computational and mechanistic study. FASEB Journal, 2021, 35, e21360.	0.2	40
1584	Identifying the unique characteristics of the Chinese indigenous pig breeds in the Yangtze River Delta region for precise conservation. BMC Genomics, 2021, 22, 151.	1.2	9
1585	De novo transcriptome assemblies of Epicauta tibialis provide insights into the sexual dimorphism in the production of cantharidin. Archives of Insect Biochemistry and Physiology, 2021, 106, e21784.	0.6	3
1586	Transcriptomic analysis reveals the molecular mechanisms of rumen wall morphological and functional development induced by different solid diet introduction in a lamb model. Journal of Animal Science and Biotechnology, 2021, 12, 33.	2.1	19
1587	Investigating mechanisms underlying genetic resistance to Salmon Rickettsial Syndrome in Atlantic salmon using RNA sequencing. BMC Genomics, 2021, 22, 156.	1.2	15
1588	Genome-wide identification of MIKC-type genes related to stamen and gynoecium development in Liriodendron. Scientific Reports, 2021, 11, 6585.	1.6	3
1589	Prediction of hepatocellular carcinoma risk in patients with chronic liver disease from dynamic modular networks. Journal of Translational Medicine, 2021, 19, 122.	1.8	1
1590	De novo assembly, annotation and gene expression profiles of gonads of Cytorace-3, a hybrid lineage of Drosophila nasuta nasuta and D. n. albomicans. Genomics and Informatics, 2021, 19, e8.	0.4	2
1591	The oxylipin messenger 1â€octenâ€3â€ol induced rapid responses in kelp <scp><i>Macrocystis pyrifera</i></scp> . Physiologia Plantarum, 2021, 172, 1641-1652.	2.6	7
1592	Identification and validation of three core genes in p53 signaling pathway in hepatitis B virus-related hepatocellular carcinoma. World Journal of Surgical Oncology, 2021, 19, 66.	0.8	11
1593	Profile of Small RNAs, vDNA Forms and Viral Integrations in Late Chikungunya Virus Infection of Aedes albopictus Mosquitoes. Viruses, 2021, 13, 553.	1.5	13
1594	The Composition and Primary Metabolic Potential of Microbial Communities Inhabiting the Surface Water in the Equatorial Eastern Indian Ocean. Biology, 2021, 10, 248.	1.3	6
1595	Toward Systematic Understanding of Flower Bud Induction in Apple: A Multi-Omics Approach. Frontiers in Plant Science, 2021, 12, 604810.	1.7	12
1596	Metagenomic and q-PCR analysis reveals the effect of powder bamboo biochar on nitrous oxide and ammonia emissions during aerobic composting. Bioresource Technology, 2021, 323, 124567.	4.8	34

#	Article	IF	CITATIONS
1597	Interactional mechanisms of Paenibacillus polymyxa SC2 and pepper (Capsicum annuum L.) suggested by transcriptomics. BMC Microbiology, 2021, 21, 70.	1.3	20
1598	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
1599	Galactolipid and Phospholipid Profile and Proteome Alterations in Soybean Leaves at the Onset of Salt Stress. Frontiers in Plant Science, 2021, 12, 644408.	1.7	10
1600	Full-Length Transcriptome Analyses of Genes Involved in Triterpenoid Saponin Biosynthesis of Psammosilene tunicoides Hairy Root Cultures With Exogenous Salicylic Acid. Frontiers in Genetics, 2021, 12, 657060.	1.1	13
1601	Dermatopontin as a potential pathogenic factor in endometrial cancer. Oncology Letters, 2021, 21, 408.	0.8	7
1602	Immune related gene expression analysis of Macrobrachium nipponense in different hours post-infection by non-O1 Vibrio cholerae. Aquaculture Reports, 2021, 19, 100571.	0.7	4
1603	Thyroid Hormones Regulate Goblet Cell Differentiation and Fgf19-Fgfr4 Signaling. Endocrinology, 2021, 162, .	1.4	4
1604	Transcriptome-based analysis of resistance mechanism to black point caused by Bipolaris sorokiniana in wheat. Scientific Reports, 2021, 11, 6911.	1.6	7
1605	Differential MicroRNA Expression Involved in Endometrial Receptivity of Goats. Biomolecules, 2021, 11, 472.	1.8	11
1606	Transcriptomic dynamics changes related to anthocyanin accumulation in the fleshy roots of carmine radish ( <i>Raphanus sativus</i> L.) characterized using RNA-Seq. PeerJ, 2021, 9, e10978.	0.9	2
1607	Transcriptomic Analysis of Seasonal Gene Expression and Regulation during Xylem Development in "Shanxin―Hybrid Poplar (Populus davidiana × Populus bolleana). Forests, 2021, 12, 451.	0.9	5
1608	Transcriptome Analysis of Eggplant Root in Response to Root-Knot Nematode Infection. Pathogens, 2021, 10, 470.	1.2	11
1609	Identifying potential biomarkersÂofÂnonalcoholicÂfattyÂliverÂdisease via genome-wide analysis of copy number variation. BMC Gastroenterology, 2021, 21, 171.	0.8	1
1610	<i>Oar-miR-16b</i> and <i>oar-miR-27a</i> : negatively correlated with milk yield and milk protein in sheep. Animal Biotechnology, 2022, 33, 1466-1479.	0.7	3
1611	Transcriptomic and metabolomic reprogramming in cotton after Apolygus lucorum feeding implicated in enhancing recruitment of the parasitoid Peristenus spretus. Journal of Pest Science, 2022, 95, 249-262.	1.9	8
1612	Identification of key biomarkers for thyroid cancer by integrative gene expression profiles. Experimental Biology and Medicine, 2021, 246, 1617-1625.	1.1	3
1613	Genome-wide association and transcriptome analysis of root color-related genes in Gossypium arboreum L Planta, 2021, 253, 95.	1.6	8
1614	Understanding the Transcriptional Changes During Infection of Meloidogyne incognita Eggs by the Egg-Parasitic Fungus Purpureocillium lilacinum. Frontiers in Microbiology, 2021, 12, 617710.	1.5	5

ARTICLE IF CITATIONS Short-term personal PM2.5 exposure and change in DNA methylation of imprinted genes: Panel study of 1615 3.7 16 healthy young adults in Guangzhou city, China. Environmental Pollution, 2021, 275, 116601. Characteristics and expression profiles of circRNAs during abdominal adipose tissue development in 1.1 Chinese Gushi chicken's. PLoS ONE, 2021, 16, e0249288 Weighted gene co expression network analysis (WGCNA) with key pathways and hubâ€genes related to 1617 0.8 4 micro RNAs in ischemic stroke. IET Systems Biology, 2021, 15, 93-100. Transcriptional profiling of intervertebral disc in a postâ€traumatic early degeneration organ culture 1.5 model. JOR Spine, 2021, 4, e1146. Comparative transcriptomic analysis reveals the regulatory mechanism of the gibberellic acid pathway of Tartary buckwheat (Fagopyrum tataricum (L.) Gaertn.) dwarf mutants. BMC Plant Biology, 1619 1.6 5 2021, 21, 206. Nanopore long-read RNAseq reveals regulatory mechanisms of thermally variable reef environments promoting heat tolerance of scleractinian corál Pocillopora damicornis. Environmental Research, 3.7 2021, 195, 110782. Genomic and transcriptomic insights into the habitat adaptation of the diazotrophic paddyâ€field 1621 1.8 5 cyanobacterium <i>Nostoc sphaeroides</i>. Environmental Microbiology, 2021, 23, 5802-5822. A First Insight into the Gonad Transcriptome of Hong Kong Catfish (Clarias fuscus). Animals, 2021, 11, 1.0 14 1131. Integrated transcriptome and proteome analysis reveals complex regulatory mechanism of cotton in 1623 1.0 5 response to salt stress. Journal of Cotton Research, 2021, 4, . Combination of RNA-Seq transcriptomics and iTRAQ proteomics reveal the mechanism involved in 1624 1.6 fresh-cut yam yellowing. Scientific Reports, 2021, 11, 7755. Comparison of Gonadal Transcriptomes Uncovers Reproduction-Related Genes with Sexually 1625 1.0 9 Dimorphic Expression Patterns in Diodon hystrix. Animals, 2021, 11, 1042. Diet-ruminal microbiome-host crosstalk contributes to differential effects of calf starter and alfalfa hay on rumen epithelial development and pancreatic î±-amylase activity in yak calves. Journal of Dairy 1.4 Science, 2021, 104, 4326-4340. Melatonin Modulates Lipid Metabolism in Porcine Cumulus–Oocyte Complex via Its Receptors. 1627 1.8 5 Frontiers in Cell and Developmental Biology, 2021, 9, 648209. Dynamics of rumen gene expression, microbiome colonization, and their interplay in goats. BMC 1.2 Genomics, 2021, 22, 288. Whole transcriptome sequencing and integrated network analysis elucidates the effects of 1629 3,8-Di-O-methylellagic acid 2-O-glucoside derived from Sanguisorba offcinalis L., a novel 7 3.1differentiation inducer on erythroleukemia cells. Pharmacological Research, 2021, 166, 105491. A Genome-Wide Screen in Saccharomyces cerevisiae Reveals a Critical Role for Oxidative 1.8 Phosphorylation in Cellular Tolerance to Lithium Hexafluorophosphate. Cells, 2021, 10, 888. The Heat Shock Transcription Factor HsfA Is Essential for Thermotolerance and Regulates Cell Wall 1631 1.514 Integrity in Aspergillus fumigatus. Frontiers in Microbiology, 2021, 12, 656548. Comprehensive transcriptome analysis of colorectal cancer risk of hyperglycemia in humans. Journal of Gastrointestinal Oncology, 2021, 12, 602-619.

#	Article	IF	CITATIONS
1633	Identification of miRNA in Sheep Intramuscular Fat and the Role of miR-193a-5p in Proliferation and Differentiation of 3T3-L1. Frontiers in Genetics, 2021, 12, 633295.	1.1	14
1634	miRNAs derived from circulating small extracellular vesicles as diagnostic biomarkers for nasopharyngeal carcinoma. Cancer Science, 2021, 112, 2393-2404.	1.7	17
1635	SNPs with intermediate minor allele frequencies facilitate accurate breed assignment of Indian Tharparkar cattle. Gene, 2021, 777, 145473.	1.0	10
1637	Long Intergenic Non-Coding RNAs in the Mammary Parenchyma and Fat Pad of Pre-Weaning Heifer Calves: Identification and Functional Analysis. Animals, 2021, 11, 1268.	1.0	0
1639	Metabolic Control by Heat Stress Determining Cell Fate to Ferroptosis for Effective Cancer Therapy. ACS Nano, 2021, 15, 7179-7194.	7.3	91
1640	Identification of MicroRNAs as potential biomarkers for detecting ischemic stroke. Genes and Genomics, 2022, 44, 9-17.	0.5	5
1642	Title: Hypermethylation of miRNA Genes During Nodule Development. Frontiers in Molecular Biosciences, 2021, 8, 616623.	1.6	4
1643	Transcriptome analysis reveals gene responses to herbicide, tribenuron methyl, in Brassica napus L. during seed germination. BMC Genomics, 2021, 22, 299.	1.2	6
1644	Comparison and Functional Analysis of Chemosensory Protein Genes From Eucryptorrhynchus scrobiculatus Motschulsky and Eucryptorrhynchus brandti Harold. Frontiers in Physiology, 2021, 12, 661310.	1.3	1
1645	Behavioral sensitization induced by methamphetamine causes differential alterations in gene expression and histone acetylation of the prefrontal cortex in rats. BMC Neuroscience, 2021, 22, 24.	0.8	12
1646	Dynamic changes occur in the DNA gut virome of female cynomolgus macaques during aging. MicrobiologyOpen, 2021, 10, e1186.	1.2	4
1647	Comprehensive analysis of differentially expressed circRNAs and ceRNA regulatory network in porcine skeletal muscle. BMC Genomics, 2021, 22, 320.	1.2	21
1649	A novel diagnostic signature based on three circulating exosomal mircoRNAs for chronic obstructive pulmonary disease. Experimental and Therapeutic Medicine, 2021, 22, 717.	0.8	12
1650	Genome-wide detection of CNV regions and their potential association with growth and fatness traits in Duroc pigs. BMC Genomics, 2021, 22, 332.	1.2	25
1651	Single Cell RNA-Seq Analysis Identifies Differentially Expressed Genes of Treg Cell in Early Treatment-Naive Rheumatoid Arthritis By Arsenic Trioxide. Frontiers in Pharmacology, 2021, 12, 656124.	1.6	2
1652	Overexpression of vacuolar H + â€pyrophosphatase (H + â€PPase) gene from Ammopiptanthus nanus enhances drought tolerance in maize. Journal of Agronomy and Crop Science, 0, , .	1.7	3
1654	Effect of Temperature on Metronidazole Resistance in Helicobacter pylori. Frontiers in Microbiology, 2021, 12, 681911.	1.5	7
1655	Integrated Analysis of Long Noncoding RNA Expression Profiles in Acute-on-Chronic Liver Failure. BioMed Research International, 2021, 2021, 1-13.	0.9	2

#	Article	IF	CITATIONS
1656	eVITTA: a web-based visualization and inference toolbox for transcriptome analysis. Nucleic Acids Research, 2021, 49, W207-W215.	6.5	45
1657	Transcriptome analysis reveals genes expression pattern of seed response to heat stress in Brassica napus L Oil Crop Science, 2021, 6, 87-96.	0.9	14
1658	Multi-Omic Analyses Reveal Habitat Adaptation of Marine Cyanobacterium Synechocystis sp. PCC 7338. Frontiers in Microbiology, 2021, 12, 667450.	1.5	6
1659	Systems Pharmacology and In Silico Docking Analysis Uncover Association of CA2, PPARG, RXRA, and VDR with the Mechanisms Underlying the Shi Zhen Tea Formula Effect on Eczema. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-17.	0.5	1
1660	ANOX: A robust computational model for predicting the antioxidant proteins based on multiple features. Analytical Biochemistry, 2021, 631, 114257.	1.1	2
1661	Key circular RNAs identified in male osteoporosis patients by whole transcriptome sequencing. PeerJ, 2021, 9, e11420.	0.9	6
1662	Transcriptome profiling of Capsicum annuum using Illumina- and PacBio SMRT-based RNA-Seq for in-depth understanding of genes involved in trichome formation. Scientific Reports, 2021, 11, 10164.	1.6	6
1663	Revealing the developmental dynamics in male strobilus transcriptome of Gnetum luofuense using nanopore sequencing technology. Scientific Reports, 2021, 11, 10516.	1.6	6
1664	Ketogenic diet-mediated steroid metabolism reprogramming improves the immune microenvironment and myelin growth in spinal cord injury rats according to gene and co-expression network analyses. Aging, 2021, 13, 12973-12995.	1.4	7
1666	Transcriptome analysis reveals possible antitumor mechanism of Chlorella exopolysaccharide. Gene, 2021, 779, 145494.	1.0	5
1667	Exploring genetic resistance to infectious salmon anaemia virus in Atlantic salmon by genome-wide association and RNA sequencing. BMC Genomics, 2021, 22, 345.	1.2	11
1668	Genome-Wide Association Study of Kernel Traits in Aegilops tauschii. Frontiers in Genetics, 2021, 12, 651785.	1.1	4
1669	Juvenile Hormone-Sensitive Ribosomal Activity Enhances Viral Replication in Aedes aegypti. MSystems, 2021, 6, e0119020.	1.7	10
1670	Adaptive Differences in Gene Expression in Farm-Impacted Seedbeds of the Native Blue Mussel Mytilus chilensis. Frontiers in Genetics, 2021, 12, 666539.	1.1	7
1671	Identification of viral-mediated pathogenic mechanisms in neurodegenerative diseases using network-based approaches. Briefings in Bioinformatics, 2021, 22, .	3.2	7
1672	Perfluorooctane sulfonate promotes doxycycline-induced liver tumor progression in male Kras transgenic zebrafish. Environmental Research, 2021, 196, 110962.	3.7	15
1673	Diurnal transcriptomics analysis reveals the regulatory role of the circadian rhythm in super-hybrid rice LY2186. Genomics, 2021, 113, 1281-1290.	1.3	5
1674	Exogenous phytohormone application and transcriptome analysis of Mikania micrantha provides insights for a potential control strategy. Genomics, 2021, 113, 964-975.	1.3	6

#	Article	IF	CITATIONS
1675	Dynamic Expression Profiles of Circular RNAs during Brown to White Adipose Tissue Transformation in Goats (Capra hircus). Animals, 2021, 11, 1351.	1.0	7
1676	Metagenomic analyses of microbial structure and metabolic pathway in solid-phase denitrification systems for advanced nitrogen removal of wastewater treatment plant effluent: A pilot-scale study. Water Research, 2021, 196, 117067.	5.3	104
1678	Genetic diversity and evolutionary patterns of <i>Taraxacum kokâ€saghyz</i> Rodin. Ecology and Evolution, 2021, 11, 7917-7926.	0.8	7
1679	Network Pharmacology and Molecular Docking Combined to Analyze the Molecular and Pharmacological Mechanism of Pinellia ternata in the Treatment of Hypertension. Current Issues in Molecular Biology, 2021, 43, 65-78.	1.0	11
1680	Genome-Wide Transcriptional Responses of Marine Nematode Litoditis marina to Hyposaline and Hypersaline Stresses. Frontiers in Physiology, 2021, 12, 672099.	1.3	9
1681	The transcriptomic response to heat stress of a jujube (Ziziphus jujuba Mill.) cultivar is featured with changed expression of long noncoding RNAs. PLoS ONE, 2021, 16, e0249663.	1.1	6
1682	Transcriptome Analysis of <i>Myzus persicae</i> to UV-B Stress. Journal of Insect Science, 2021, 21, .	0.6	5
1683	Transcriptome Analysis Reveals the Role of Cellular Calcium Disorder in Varicella Zoster Virus-Induced Post-Herpetic Neuralgia. Frontiers in Molecular Neuroscience, 2021, 14, 665931.	1.4	17
1684	Identification of Critical Genes and Signaling Pathways in Human Monocytes Following High-Intensity Exercise. Healthcare (Switzerland), 2021, 9, 618.	1.0	2
1685	ACBP suppresses the proliferation, migration, and invasion of colorectal cancer via targeting Wnt/beta-catenin signaling pathway. Biomedicine and Pharmacotherapy, 2021, 137, 111209.	2.5	9
1686	Comparative transcriptome analysis explores candidate genes related to carotenoid accumulation in pericarp of two pummelo cultivars (Citrus grandis L. Osbeck). European Journal of Horticultural Science, 2021, 86, 156-168.	0.3	0
1687	Transcriptome Analysis Reveals the Profile of Long Non-coding RNAs During Chicken Muscle Development. Frontiers in Physiology, 2021, 12, 660370.	1.3	3
1688	Genomeâ€wide selection signal analysis of Australian Boer goat reveals artificial selection imprinting on candidate genes related to muscle development. Animal Genetics, 2021, 52, 550-555.	0.6	10
1689	Whole genome, exon mutation and transcriptomic profiling of acute myeloid leukemia: A case report. Oncology Letters, 2021, 22, 559.	0.8	1
1690	De novo transcriptome sequencing and anthocyanin metabolite analysis reveals leaf color of Acer pseudosieboldianum in autumn. BMC Genomics, 2021, 22, 383.	1.2	17
1691	Interaction Between the Intestinal Microbial Community and Transcriptome Profile in Common Carp (Cyprinus carpio L.). Frontiers in Microbiology, 2021, 12, 659602.	1.5	11
1692	DcTT8, a bHLH transcription factor, regulates anthocyanin biosynthesis in Dendrobium candidum. Plant Physiology and Biochemistry, 2021, 162, 603-612.	2.8	27
1693	Transcriptomic responses predict the toxic effect of parental co-exposure to dibutyl phthalate and diisobutyl phthalate on the early development of zebrafish offspring. Aquatic Toxicology, 2021, 235, 105838.	1.9	18

ARTICLE IF CITATIONS Combined Proteomic and Physiological Analysis of Chloroplasts Reveals Drought and Recovery 1694 3 1.6 Response Mechanisms in Nicotiana benthamiana. Plants, 2021, 10, 1127. Organ-Specific Transcriptome Analysis Identifies Candidate Genes Involved in the Stem Specialization 1.1 of Bermudagrass (Cynodon dactylón L.). Frontiers in Genetics, 2021, 12, 678673. Reconstruction of circRNA-miRNA-mRNA associated ceRNA networks reveal functional circRNAs in 1696 1.6 11 intracerebral hemorrhage. Scientific Reports, 2021, 11, 11584. Transcriptional dynamics of transposable elements when converting fibroblast cells of Macaca 1.2 mulatta to neuroepithelial stem cells. BMC Genomics, 2021, 22, 405. Genome-wide association study reveals early seedling vigour-associated quantitative trait loci in 1698 0.6 1 indica rice. Euphytica, 2021, 217, 1. Metagenomic Insights Into the Structure and Function of Intestinal Microbiota of the Hadal 1699 1.5 Amphipods. Frontiers in Microbiology, 2021, 12, 668989. Melatonin influences the early growth stage in Zoysia japonica Steud. by regulating plant oxidation 1700 1.6 8 and genes of hormones. Scientific Reports, 2021, 11, 12381. The accurate prediction and characterization of cancerlectin by a combined machine learning and GO 3.2 analysis. Briefings in Bioinformatics, 2021, 22, . Integrated Transcriptome Profiling Revealed That Elevated Long Non-Coding RNA-AC007278.2 1702 Expression Repressed CCR7 Transcription in Systemic Lupus Erythematosus. Frontiers in Immunology, 2.2 14 2021, 12, 615859. Integrated Metagenomic and Transcriptomic Analyses Reveal the Dietary Dependent Recovery of Host 1703 1.8 Metabolism From Antibiotic Exposure. Frontiers in Cell and Developmental Biology, 2021, 9, 680174. Comprehensive analysis of IncRNA biomarkers in kidney renal clear cell carcinoma by IncRNA-mediated 1704 4 1.1 ceRNA network. PLoS ONE, 2021, 16, e0252452. Reconstruction of the full-length transcriptome of cigar tobacco without a reference genome and 1.6 characterization of anion channel/transporter transcripts. BMC Plant Biology, 2021, 21, 299. Transcriptome Characterization and Expression Profiles of Disease Defense-Related Genes of Table 1706 1.9 9 Grapes in Response to Pichia anomala Induced with Chitosan. Foods, 2021, 10, 1451. KOBAS-i: intelligent prioritization and exploratory visualization of biological functions for gene enrichment analysis. Nucleic Acids Research, 2021, 49, W317-W325. 1707 6.5 727 Gapless indica rice genome reveals synergistic contributions of active transposable elements and 1708 3.9 50 segmental duplications to rice genome evolution. Molecular Plant, 2021, 14, 1745-1756. Vincristine attenuates cardiac fibrosis through the inhibition of NLRP3 inflammasome activation. 1709 1.8 Clinical Science, 2021, 135, 1409-1426. Multiple responses contribute to the enhanced drought tolerance of the autotetraploid Ziziphus 1710 2.1 20 jujuba Mill. var. spinosa. Cell and Bioscience, 2021, 11, 119. Multiomics analysis of kernel development in response to short-term heat stress at the grain 1711 2.4 formation stage in waxy maize. Journal of Experimental Botany, 2021, 72, 6291-6304.

#	Article	IF	CITATIONS
1712	A Combined Morphological and Molecular Evolutionary Analysis of Karst-Environment Adaptation for the Genus Urophysa (Ranunculaceae). Frontiers in Plant Science, 2021, 12, 667988.	1.7	2
1713	Network pharmacology analysis of pharmacological mechanisms underlying the anti-type 2 diabetes mellitus effect of guava leaf. Arabian Journal of Chemistry, 2021, 14, 103143.	2.3	6
1714	Site-directed mutagenesis of the quorum-sensing transcriptional regulator SinR affectsÂthe biosynthesis of menaquinone inÂBacillus subtilis. Microbial Cell Factories, 2021, 20, 113.	1.9	14
1715	Comparative analysis of mite genomes reveals positive selection for diet adaptation. Communications Biology, 2021, 4, 668.	2.0	6
1716	Full-Length Transcriptome Analysis Reveals Candidate Genes Involved in Terpenoid Biosynthesis in Artemisia argyi. Frontiers in Genetics, 2021, 12, 659962.	1.1	11
1717	Transcriptome Profiling Reveals a Novel Mechanism of Antiviral Immunity Upon Sacbrood Virus Infection in Honey Bee Larvae (Apis cerana). Frontiers in Microbiology, 2021, 12, 615893.	1.5	10
1718	Transcriptome Analysis of Tolerant and Susceptible Maize Genotypes Reveals Novel Insights about the Molecular Mechanisms Underlying Drought Responses in Leaves. International Journal of Molecular Sciences, 2021, 22, 6980.	1.8	36
1719	Comparative transcriptome analysis of different developmental stage of Bactrocera minax (Diptera:) Tj ETQq1 1 0. Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 38, 100818.	784314 rg 0.4	gBT /Overio 3
1720	Isolation, characterization and transcriptome analysis of porcine deltacoronavirus strain HNZK-02 from Henan Province, China. Molecular Immunology, 2021, 134, 86-99.	1.0	15
1721	Guard cells control hypocotyl elongation through HXK1, HY5, and PIF4. Communications Biology, 2021, 4, 765.	2.0	9
1722	Embryonic developmental arrest in the annual killifish Austrolebias charrua: A proteomic approach to diapause III. PLoS ONE, 2021, 16, e0251820.	1.1	6
1723	Comparative Transcriptome-Based Mining of Senescence-Related MADS, NAC, and WRKY Transcription Factors in the Rapid-Senescence Line DLS-91 of Brassica rapa. International Journal of Molecular Sciences, 2021, 22, 6017.	1.8	2
1724	Comparative transcriptome analysis of the hyperaccumulator plant Phytolacca americana in response to cadmium stress. 3 Biotech, 2021, 11, 327.	1.1	14
1725	Arginine methylation of METTL14 promotes RNA N6-methyladenosine modification and endoderm differentiation of mouse embryonic stem cells. Nature Communications, 2021, 12, 3780.	5.8	34
1727	Comparative transcriptomic analysis reveals the coordinated mechanisms of Populus × canadensis †Neva' leaves in response to cadmium stress. Ecotoxicology and Environmental Safety, 2021, 216, 112179.	2.9	21
1728	Analysis of the Coptis chinensis genome reveals the diversification of protoberberine-type alkaloids. Nature Communications, 2021, 12, 3276.	5.8	68
1729	Transcriptome in combination with experimental validation unveils hub immune-related genes in oriental river prawn Macrobrachium nipponense against Spiroplasma eriocheiris challenge. Aquaculture, 2021, 539, 736625.	1.7	4
1730	Involvement of the VEGF signaling pathway in immunosuppression and hypoxia stress: analysis of mRNA expression in lymphocytes mediating panting in Jersey cattle under heat stress. BMC Veterinary Research, 2021, 17, 209.	0.7	6

	CITATION RE	PORT	
Article		IF	Citations
Identifying a Serum Exosomal-Associated IncRNA/circRNA-miRNA-mRNA Network in Co Disease. Cardiology Research and Practice, 2021, 2021, 1-10.	pronary Heart	0.5	11
CCN1 gene polymorphisms associated with congenital heart disease susceptibility in N Chinese population from different high-altitude areas. Environmental Science and Pollo 2021, 28, 56927-56937.	Northwest ution Research,	2.7	3
Decreased Abundance of <i>Akkermansia muciniphila</i> Leads to the Impairment of and Glucose Homeostasis in Lean Type 2 Diabetes. Advanced Science, 2021, 8, e2100		5.6	68
Identification and Expression Profiling of Nonphosphorus Glycerolipid Synthase Genes Abiotic Stresses in Dendrobium catenatum. Plants, 2021, 10, 1204.	in Response to	1.6	4
MiR-337-3p lowers serum LDL-C level through targeting PCSK9 in hyperlipidemic mice. Clinical and Experimental, 2021, 119, 154768.	. Metabolism:	1.5	12
Prickle morphogenesis in rose is coupled with secondary metabolite accumulation and canonical MBW transcriptional complex. Plant Direct, 2021, 5, e00325.	governed by	0.8	13
Candidate gene screening for lipid deposition using combined transcriptomic and prot from Nanyang black pigs. BMC Genomics, 2021, 22, 441.	eomic data:	1.2	10
A Significantly High Abundance of "Candidatus Liberibacter asiaticus―in Citrus Fr Transcriptome and Anatomical Analyses. Frontiers in Microbiology, 2021, 12, 681251.		1.5	10
Petiole hormones act as regulators in the early phototropic leaf movements of grape ( revealed by comparative transcriptome profiling. Scientia Horticulturae, 2021, 283, 11	Vitis vinifera L.) 10049.	1.7	2
Proteome analysis of bermudagrass stolons and rhizomes provides new insights into t of plant stems to aboveground and underground growth. Journal of Proteomics, 2021	he adaptation , 241, 104245.	1.2	3
Genomic evolution and virulence association of <i>Clostridioides difficile</i> sequence	e type 37	2.0	19

1742	Genomic evolution and virulence association of <i>Clostridioides difficile</i> sequence type 37 (ribotype 017) in China. Emerging Microbes and Infections, 2021, 10, 1331-1345.	3.0	12
1743	Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. Genome Biology, 2021, 22, 185.	3.8	47
1744	Phytohormonal and Transcriptomic Response of Hulless Barley Leaf in Response to Powdery Mildew Infection. Agronomy, 2021, 11, 1248.	1.3	3
1745	Investigation of long non-coding RNAs as regulatory players of grapevine response to powdery and downy mildew infection. BMC Plant Biology, 2021, 21, 265.	1.6	21
1746	Therapeutic Targets and Mechanism of Xingpi Jieyu Decoction in Depression: A Network Pharmacology Study. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-15.	0.5	3
1747	Transcriptome analysis insight into ethylene metabolism and pectinase activity of apricot (Prunus) Tj ETQq1 1 0.7	′84314 rgl 1.6	BT <sub>4</sub> /Overloc

1748	Comparative Physiological and Transcriptomic Profiling Offers Insight into the Sexual Dimorphism of Hepatic Metabolism in Size-Dimorphic Spotted Scat (Scatophagus argus). Life, 2021, 11, 589.	1.1	7
1749	Tissue comparison of transcriptional response to acute acidification stress of barramundi Lates calcarifer in coastal and estuarine areas. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 38, 100830.	0.4	0

#

1731

1733

1736

1738

1740

1741

#	Article	IF	CITATIONS
1750	Insights into cold tolerance in sable (Martes zibellina) from the adaptive evolution of lipid metabolism. Mammalian Biology, 0, , 1.	0.8	2
1751	Integrated Analysis of microRNA and mRNA Transcriptome Reveals the Molecular Mechanism of Solanum lycopersicum Response to Bemisia tabaci and Tomato chlorosis virus. Frontiers in Microbiology, 2021, 12, 693574.	1.5	5
1752	A Combined Network Pharmacology and Molecular Docking Approach to Investigate Candidate Active Components and Multitarget Mechanisms of Hemerocallis Flowers on Antidepressant Effect. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-17.	0.5	3
1753	Transcriptome analysis reveals the inhibitory nature of high nitrate during adventitious roots formation in the apple rootstock. Physiologia Plantarum, 2021, 173, 867-882.	2.6	16
1754	Transcriptomic exploration of a high sucrose mutant in comparison with the low sucrose mother genotype in sugarcane during sugar accumulating stage. GCB Bioenergy, 2021, 13, 1448-1465.	2.5	11
1755	Identification of a Competing Endogenous RNA Network Related to Immune Signature in Lung Adenocarcinoma. Frontiers in Genetics, 2021, 12, 665555.	1.1	2
1756	Imbalance of TGF-β1/BMP-7 pathways induced by M2-polarized macrophages promotes hepatocellular carcinoma aggressiveness. Molecular Therapy, 2021, 29, 2067-2087.	3.7	42
1757	Transcriptome Analysis and RNA Interference Reveal GhGDH2 Regulating Cotton Resistance to Verticillium Wilt by JA and SA Signaling Pathways. Frontiers in Plant Science, 2021, 12, 654676.	1.7	15
1758	Comparative transcriptome analysis reveals genes and pathways associated with anthocyanins in strawberry. Journal of Berry Research, 2021, 11, 317-332.	0.7	7
1759	Multi-Omics Sequencing Provides Insights Into Age-Dependent Susceptibility of Grass Carp (Ctenopharyngodon idellus) to Reovirus. Frontiers in Immunology, 2021, 12, 694965.	2.2	14
1760	Impact of Transcriptome and Gut Microbiome on the Response of HIV-1 Infected Individuals to a Dendritic Cell-Based HIV Therapeutic Vaccine. Vaccines, 2021, 9, 694.	2.1	8
1761	Transcriptome Analyses Provide Insights into the Aggressive Behavior toward Conspecific and Heterospecific in Thitarodes xiaojinensis (Lepidoptera: Hepialidae). Insects, 2021, 12, 577.	1.0	1
1762	Transcriptomic and Weighted Gene Co-expression Correlation Network Analysis Reveal Resveratrol Biosynthesis Mechanisms Caused by Bud Sport in Grape Berry. Frontiers in Plant Science, 2021, 12, 690095.	1.7	3
1763	Pooled Sequencing Analysis of Geese (Anser cygnoides) Reveals Genomic Variations Associated With Feather Color. Frontiers in Genetics, 2021, 12, 650013.	1.1	6
1764	Adipose-derived stem cells therapy effectively attenuates PM2.5-induced lung injury. Stem Cell Research and Therapy, 2021, 12, 355.	2.4	9
1766	Depicting the molecular responses of adventitious rooting to waterlogging in melon hypocotyls by transcriptome profiling. 3 Biotech, 2021, 11, 351.	1.1	6
1767	Identification of QTNs and their candidate genes for flowering time and plant height in soybean using multi-locus genome-wide association studies. Molecular Breeding, 2021, 41, 1.	1.0	7
1768	Comparison of whole genome sequences of three Bacillus cereus strains reveals the food safety risks of Apostichopus japonicus in China. Aquaculture Reports, 2021, 20, 100649.	0.7	2

#	Article	IF	CITATIONS
1769	Antibiotics Attenuate Methamphetamine-Induced Hepatotoxicity by Regulating Oxidative Stress and TLR4/MyD88/Traf6 Axis. Frontiers in Pharmacology, 2021, 12, 716703.	1.6	6
1770	The N uptake-associated physiological processes at late growth stage in wheat (Triticum aestivum) under N deprivation combined with deficit irrigation condition. Plant Physiology and Biochemistry, 2021, 164, 160-172.	2.8	4
1771	Transcriptome and metabolome analyses of cold and darkness-induced pellicle cysts of Scrippsiella trochoidea. BMC Genomics, 2021, 22, 526.	1.2	9
1772	Morpho-Physiological and Transcriptome Changes in Tomato Anthers of Different Developmental Stages under Drought Stress. Cells, 2021, 10, 1809.	1.8	16
1773	A chromosome-level genome assembly of Cairina moschata and comparative genomic analyses. BMC Genomics, 2021, 22, 581.	1.2	4
1774	Metagenomics analysis revealed the distinctive ruminal microbiome and resistive profiles in dairy buffaloes. Animal Microbiome, 2021, 3, 44.	1.5	11
1775	Florigen governs shoot regeneration. Scientific Reports, 2021, 11, 13710.	1.6	4
1776	IDH2 contributes to tumorigenesis and poor prognosis by regulating m6A RNA methylation in multiple myeloma. Oncogene, 2021, 40, 5393-5402.	2.6	20
1777	Transcriptional profiling reveals multiple defense responses in downy mildew-resistant transgenic grapevine expressing a TIR-NBS-LRR gene located at the MrRUN1/MrRPV1 locus. Horticulture Research, 2021, 8, 161.	2.9	6
1778	Hybridization With an Invasive Plant of Xanthium strumarium Improves the Tolerance of Its Native Congener X. sibiricum to Cadmium. Frontiers in Plant Science, 2021, 12, 696687.	1.7	5
1779	Mechanistic insights into the inhibitory effect of theaflavins on virulence factors production in Streptococcus mutans. AMB Express, 2021, 11, 102.	1.4	7
1780	Transcriptome and Small RNA Combined Sequencing Analysis of Cold Tolerance in Non-heading Chinese Cabbage. Frontiers in Genetics, 2021, 12, 605292.	1.1	0
1781	The Welwitschia genome reveals aÂunique biology underpinning extreme longevity in deserts. Nature Communications, 2021, 12, 4247.	5.8	51
1782	Unveiling sugarcane defense response to <i>Mythimna separata</i> herbivory by a combination of transcriptome and metabolic analyses. Pest Management Science, 2021, 77, 4799-4809.	1.7	11
1783	Transcriptome analysis of differentially expressed genes in chrysanthemum MET1 RNA interference lines. Physiology and Molecular Biology of Plants, 2021, 27, 1455-1468.	1.4	3
1784	Genomic analysis of field pennycress (Thlaspi arvense) provides insights into mechanisms of adaptation to high elevation. BMC Biology, 2021, 19, 143.	1.7	23
1785	The mechanism research on the antiâ€liver fibrosis of emodin based on network pharmacology. IUBMB Life, 2021, 73, 1166-1179.	1.5	14
1786	Transcriptome analysis of signaling pathways targeted by Ellagic acid in hepatocellular carcinoma cells. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 129911.	1.1	6

#	Article	IF	Citations
π 1787	Integrated global analysis reveals a vitamin E-vitamin K1 sub-network, downstream of COLD1,	2.9	22
1/0/	underlying rice chilling tolerance divergence. Cell Reports, 2021, 36, 109397.	2.9	
1788	Transcriptome analysis reveals the effect of high-grain pelleted and non-pelleted diets on ruminal epithelium of Hu-lamb. Animal, 2021, 15, 100278.	1.3	4
1789	LAMC1 upregulation via TGFβ induces inflammatory cancerâ€associated fibroblasts in esophageal squamous cell carcinoma via NFâ€₽B–CXCL1–STAT3. Molecular Oncology, 2021, 15, 3125-3146.	2.1	26
1790	Transcriptomic analyses of cacao flavonoids produced in photobioreactors. BMC Genomics, 2021, 22, 551.	1.2	3
1791	KRT18 Modulates Alternative Splicing of Genes Involved in Proliferation and Apoptosis Processes in Both Gastric Cancer Cells and Clinical Samples. Frontiers in Genetics, 2021, 12, 635429.	1.1	12
1792	Sex biased expression of hormone related genes at early stage of sex differentiation in papaya flowers. Horticulture Research, 2021, 8, 147.	2.9	12
1793	Comparative study on fruit development and oil synthesis in two cultivars of Camellia oleifera. BMC Plant Biology, 2021, 21, 348.	1.6	24
1794	Investigations of solid culture–induced acquisition of desiccation tolerance in liquid suspension culture of Nostoc flagelliforme. Journal of Applied Phycology, 2021, 33, 3657-3669.	1.5	5
1795	N-Acetylcysteine Reduces the Pro-Oxidant and Inflammatory Responses during Pancreatitis and Pancreas Tumorigenesis. Antioxidants, 2021, 10, 1107.	2.2	3
1796	Construction of Adipogenic ceRNA Network Based on IncRNA Expression Profile of Adipogenic Differentiation of Human MSC Cells. Biochemical Genetics, 2021, , 1.	0.8	1
1797	A Chromosome-level Genome Assembly of Wild Castor Provides New Insights into its Adaptive Evolution in Tropical Desert. Genomics, Proteomics and Bioinformatics, 2022, 20, 42-59.	3.0	18
1798	Co-expression network and comparative transcriptome analysis for fiber initiation and elongation reveal genetic differences in two lines from upland cotton CCRI70 RIL population. PeerJ, 2021, 9, e11812.	0.9	9
1799	<i>Serendipita</i> Fungi Modulate the Switchgrass Root Transcriptome to Circumvent Host Defenses and Establish a Symbiotic Relationship. Molecular Plant-Microbe Interactions, 2021, 34, 1128-1142.	1.4	6
1800	Transcriptome and metabolome profiling in naturally infested Casuarina equisetifolia clones by Ralstonia solanacearum. Genomics, 2021, 113, 1906-1918.	1.3	12
1801	Whole-Genome Resequencing to Study Brucellosis Susceptibility in Sheep. Frontiers in Genetics, 2021, 12, 653927.	1.1	5
1802	Transcriptomic analysis and molecular docking reveal genes involved in the response of Aedes aegypti larvae to an essential oil extracted from Eucalyptus. PLoS Neglected Tropical Diseases, 2021, 15, e0009587.	1.3	11
1803	Transcriptome and proteome of the corm, leaf and flower of Hypoxis hemerocallidea (African potato). PLoS ONE, 2021, 16, e0253741.	1.1	0
1804	Transcriptome analysis of the spleen provides insight into the immunoregulation of Cyprinus carpio koi under Aeromonas veronii infection. Aquaculture, 2021, 540, 736650.	1.7	7

#	Article	IF	CITATIONS
1805	Important innate differences in determining symbiotic responsiveness in host and non-hosts of arbuscular mycorrhiza. Scientific Reports, 2021, 11, 14444.	1.6	4
1806	Proteomic Analysis Demonstrates a Molecular Dialog Between Trichoderma guizhouense NJAU 4742 and Cucumber (Cucumis sativus L) Roots: Role in Promoting Plant Growth. Molecular Plant-Microbe Interactions, 2021, 34, MPMI-08-20-0240.	1.4	9
1807	Physiological and transcriptome analysis accentuates microtubules and calcium signaling in Ziziphus jujuba Mill â€~Dongzao' autotetraploids with sensitive cold tolerance. Scientia Horticulturae, 2021, 285, 110183.	1.7	8
1808	Abscisic Acid Mediates Drought-Enhanced Rhizosheath Formation in Tomato. Frontiers in Plant Science, 2021, 12, 658787.	1.7	13
1809	Motor Stereotypic Behavior Was Associated With Immune Response in Macaques: Insight From Transcriptome and Gut Microbiota Analysis. Frontiers in Microbiology, 2021, 12, 644540.	1.5	3
1810	Comparing the whole genome methylation landscape of dairy calf blood cells revealed intergenerational inheritance of the maternal metabolism. Epigenetics, 2021, , 1-10.	1.3	5
1812	The USDA-ARS Ag100Pest Initiative: High-Quality Genome Assemblies for Agricultural Pest Arthropod Research. Insects, 2021, 12, 626.	1.0	31
1813	Alterations of mRNA and IncRNA profiles associated with the extracellular matrix and spermatogenesis in goats. Animal Bioscience, 2022, 35, 544-555.	0.8	4
1814	Pathogen and drought stress affect cell wall and phytohormone signaling to shape host responses in a sorghum COMT bmr12 mutant. BMC Plant Biology, 2021, 21, 391.	1.6	13
1815	Integrated ionomic and transcriptomic dissection reveals the core transporter genes responsive to varying cadmium abundances in allotetraploid rapeseed. BMC Plant Biology, 2021, 21, 372.	1.6	3
1816	Effects of nonylphenol exposure on histological changes, apoptosis and time-course transcriptome in gills of white shrimp Litopenaeus vannamei. Science of the Total Environment, 2021, 781, 146731.	3.9	18
1817	Bidirectional deep neural networks to integrate RNA and DNA data for predicting outcome forÂpatients withÂhepatocellular carcinoma. Future Oncology, 2021, 17, 4481-4495.	1.1	9
1818	A Co-Expression Network Reveals the Potential Regulatory Mechanism of IncRNAs in Relapsed Hepatocellular Carcinoma. Frontiers in Oncology, 2021, 11, 745166.	1.3	7
1819	Transcriptome analysis reveals the promotive effect of potassium by hormones and sugar signaling pathways during adventitious roots formation in the apple rootstock. Plant Physiology and Biochemistry, 2021, 165, 123-136.	2.8	20
1820	Diverse energy metabolism patterns in females in Neodon fuscus, Lasiopodomys brandtii, and Mus musculus revealed by comparative transcriptomics under hypoxic conditions. Science of the Total Environment, 2021, 783, 147130.	3.9	9
1821	Expression of cyanobacterial genes enhanced CO <sub>2</sub> assimilation and biomass production in transgenic <i>Arabidopsis thaliana</i> . PeerJ, 2021, 9, e11860.	0.9	7
1822	FCER1G and PTGS2 Serve as Potential Diagnostic Biomarkers of Acute Myocardial Infarction Based on Integrated Bioinformatics Analyses. DNA and Cell Biology, 2021, 40, 1064-1075.	0.9	14
1823	Phylogenomics Based on Transcriptome Data Provides Evidence for the Internal Phylogenetic Relationships and Potential Terrestrial Evolutionary Genes of Lungfish. Frontiers in Marine Science, 2021, 8, .	1.2	5

#	Article	IF	CITATIONS
1824	Identification of Long Non-Coding RNAs Involved in Porcine Fat Deposition Using Two High-Throughput Sequencing Methods. Genes, 2021, 12, 1374.	1.0	6
1825	Comparative transcriptomic analysis of the brain in Takifugu rubripes shows its tolerance to acute hypoxia. Fish Physiology and Biochemistry, 2021, 47, 1669-1685.	0.9	10
1826	Chlorine disinfectants promote microbial resistance in Pseudomonas sp Environmental Research, 2021, 199, 111296.	3.7	29
1827	Seed dressing with mefenpyr-diethyl as a safener for mesosulfuron-methyl application in wheat: The evaluation and mechanisms. PLoS ONE, 2021, 16, e0256884.	1.1	9
1828	Enhanced SA and Ca2+ signaling results in PCD-mediated spontaneous leaf necrosis in wheat mutant wsl. Molecular Genetics and Genomics, 2021, 296, 1249-1262.	1.0	3
1829	Rice hybrid mimics have stable yields equivalent to those of the F1 hybrid and suggest a basis for hybrid vigour. Planta, 2021, 254, 51.	1.6	3
1830	Metabolome and transcriptome profiling of Theobroma cacao provides insights into the molecular basis of pod color variation. Journal of Plant Research, 2021, 134, 1323-1334.	1.2	10
1831	Analysis of Bulk RNA Sequencing Data Reveals Novel Transcription Factors Associated With Immune Infiltration Among Multiple Cancers. Frontiers in Immunology, 2021, 12, 644350.	2.2	6
1832	Characterization of Dynamic Regulatory Gene and Protein Networks in Wheat Roots Upon Perceiving Water Deficit Through Comparative Transcriptomics Survey. Frontiers in Plant Science, 2021, 12, 710867.	1.7	5
1833	Comparative transcriptome provides insights into the selection adaptation between wild and farmed foxes. Ecology and Evolution, 2021, 11, 13475-13486.	0.8	2
1834	Exploring the genes involved in biosynthesis of dihydroquercetin and dihydromyricetin in Ampelopsis grossedentata. Scientific Reports, 2021, 11, 15596.	1.6	10
1835	Niche differentiation of belowground microorganisms and their functional signatures in Assam type tea (Camellia sinensis var. assamica). Archives of Microbiology, 2021, 203, 5661-5674.	1.0	2
1836	Arginine Methyltransferase PRMT1 Regulates p53 Activity in Breast Cancer. Life, 2021, 11, 789.	1.1	10
1837	High BTBD7 expression positive is correlated with SLUG-predicted poor prognosis in hormone receptor-negative breast cancer. Annals of Translational Medicine, 2021, 9, 1252-1252.	0.7	2
1838	Brain transcriptome analysis reveals genes involved in parental care behaviour in discus fish (Symphysodon haraldi). General and Comparative Endocrinology, 2021, 309, 113793.	0.8	4
1839	Targeting P2RX1 alleviates renal ischemia/reperfusion injury by preserving mitochondrial dynamics. Pharmacological Research, 2021, 170, 105712.	3.1	16
1840	Expression Profiling of microRNA From Peripheral Blood of Dairy Cows in Response to Staphylococcus aureus-Infected Mastitis. Frontiers in Veterinary Science, 2021, 8, 691196.	0.9	14
1841	Tianma Formula Alleviates Dementia via ACER2-Mediated Sphingolipid Signaling Pathway Involving Aβ. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-20.	0.5	5

#	Article	IF	CITATIONS
1842	Dissecting the critical pathway crosstalk mechanisms of thyroid cancer based on drug-target genes and disease genes. Biologia (Poland), 2021, 76, 3489-3499.	0.8	1
1843	Metagenomic Analysis of Antibiotic Resistance Genes in Untreated Wastewater From Three Different Hospitals. Frontiers in Microbiology, 2021, 12, 709051.	1.5	19
1844	Dysregulated IncRNAs are Involved in the Progress of Sepsis by Constructing Regulatory Networks in Whole Blood Cells. Frontiers in Pharmacology, 2021, 12, 678256.	1.6	5
1845	Predicting bladder cancer prognosis by integrating multi-omics data through a transfer learning-based Cox proportional hazards network. CCF Transactions on High Performance Computing, 2021, 3, 311-319.	1.1	6
1846	New insights of low-temperature plasma effects on seeds germination of Platycodon grandiflorum. Israel Journal of Plant Sciences, 2021, 68, 1-13.	0.3	2
1847	Characterization on the P-associated and agronomic traits as well as associated molecular processes in wheat under Pi deprivation condition. Plant Cell, Tissue and Organ Culture, 2021, 147, 545-559.	1.2	3
1848	A comparative analysis of differential N6-methyladenosine (m6A) modification between non-transgenic and LBD15 overexpressing Poplar 84ÂK plants. Tree Genetics and Genomes, 2021, 17, 1.	0.6	3
1849	Comparison of Gene Expression Patterns in Articular Cartilage and Xiphoid Cartilage. Biochemical Genetics, 2022, 60, 676-706.	0.8	3
1850	De Novo Transcriptomic Characterization Enables Novel Microsatellite Identification and Marker Development in Betta splendens. Life, 2021, 11, 803.	1.1	3
1851	A bacterial effector protein uncovers a plant metabolic pathway involved in tolerance to bacterial wilt disease. Molecular Plant, 2021, 14, 1281-1296.	3.9	34
1852	SNPs in Mammary Gland Epithelial Cells Unraveling Potential Difference in Milk Production Between Jersey and Kashmiri Cattle Using RNA Sequencing. Frontiers in Genetics, 2021, 12, 666015.	1.1	5
1853	Transcriptome Analysis Provides New Insights into Host Response to Hepatopancreatic Necrosis Disease in the Black Tiger Shrimp Penaeus monodon. Journal of Ocean University of China, 2021, 20, 1183-1194.	0.6	2
1854	Identification of a New Giant Emrbryo Allele, and Integrated Transcriptomics and Metabolomics Analysis of Giant Embryo Development in Rice. Frontiers in Plant Science, 2021, 12, 697889.	1.7	7
1856	Transcriptome analysis reveals the hepatoprotective mechanism of soybean meal peptides against alcohol-induced acute liver injury mice. Food and Chemical Toxicology, 2021, 154, 112353.	1.8	14
1858	Transcriptomic Analysis Reveals Key Genes Involved in Oil and Linoleic Acid Biosynthesis during Artemisia sphaerocephala Seed Development. International Journal of Molecular Sciences, 2021, 22, 8369.	1.8	6
1859	Proteomics analysis of the secondary hair follicle cycle in Liaoning cashmere goat. Small Ruminant Research, 2021, 201, 106408.	0.6	4
1860	OsGF14b modulates defense signaling pathways in rice panicle blast response. Crop Journal, 2021, 9, 725-738.	2.3	16
1861	Comprehensive characterization of pathological stageâ€related genes of papillary thyroid cancer along with survival prediction. Journal of Cellular and Molecular Medicine, 2021, 25, 8390-8404.	1.6	2

#	Article	IF	CITATIONS
1862	High nitrate inhibited adventitious roots formation in apple rootstock by altering hormonal contents and miRNAs expression profiles. Scientia Horticulturae, 2021, 286, 110230.	1.7	14
1863	Development of a prognostic prediction model based on microRNA-1269a in esophageal cancer. World Journal of Gastrointestinal Oncology, 2021, 13, 943-958.	0.8	1
1864	Development of a prognostic prediction model based on microRNA-1269a in esophageal cancer. World Journal of Gastrointestinal Oncology, 2021, 13, 941-956.	0.8	0
1865	Comparative transcriptome analysis of <i>R3a</i> and <i> Avr3a</i> -mediated defense responses in transgenic tomato. PeerJ, 2021, 9, e11965.	0.9	2
1866	Transcriptome Analysis Revealed Plant Hormone Biosynthesis and Response Pathway Modification by EpichloA«gansuensis in Achnatheruminebrians under Different Soil Moisture Availability. Journal of Fungi (Basel, Switzerland), 2021, 7, 640.	1.5	17
1867	Morphological, Physiological, and Molecular Responses of Sweetly Fragrant Luculia gratissima During the Floral Transition Stage Induced by Short-Day Photoperiod. Frontiers in Plant Science, 2021, 12, 715683.	1.7	0
1868	Interspecies Evolution and Networks Investigation of the Auxin Response Protein (AUX/IAA) Family Reveals the Adaptation Mechanisms of Halophytes Crops in Nitrogen Starvation Agroecological Environments. Agriculture (Switzerland), 2021, 11, 780.	1.4	5
1869	Multi-Locus Genome-Wide Association Study of Four Yield-Related Traits in Chinese Wheat Landraces. Frontiers in Plant Science, 2021, 12, 665122.	1.7	5
1870	Comparative Transcriptomic Analysis Reveals the Effects of Drought on the Biosynthesis of Methyleugenol in Asarum sieboldii Miq Biomolecules, 2021, 11, 1233.	1.8	8
1871	Workflows for Rapid Functional Annotation of Diverse Arthropod Genomes. Insects, 2021, 12, 748.	1.0	9
1872	Pan-genome of Raphanus highlights genetic variation and introgression among domesticated, wild, and weedy radishes. Molecular Plant, 2021, 14, 2032-2055.	3.9	56
1873	The genome of <i>Cymbidium sinense</i> revealed the evolution of orchid traits. Plant Biotechnology Journal, 2021, 19, 2501-2516.	4.1	46
1874	Ribosomal RNA‑depleted RNA sequencing reveals the pathogenesis of refractory <i>Mycoplasma pneumoniae</i> pneumonia in children. Molecular Medicine Reports, 2021, 24, .	1.1	5
1875	Single-cell transcriptomics reveal DHX9 in mature B cell as a dynamic network biomarker before lymph node metastasis in CRC. Molecular Therapy - Oncolytics, 2021, 22, 495-506.	2.0	7
1876	Antimicrobial mechanisms of g-C3N4 nanosheets against the oomycetes Phytophthora capsici: Disrupting metabolism and membrane structures and inhibiting vegetative and reproductive growth. Journal of Hazardous Materials, 2021, 417, 126121.	6.5	18
1877	Identification of Potential Gene Regulatory Pathways Affecting the Ratio of Four-Seed Pod in Soybean. Frontiers in Genetics, 2021, 12, 717770.	1.1	4
1878	Disease-Associated Gut Microbiota Reduces the Profile of Secondary Bile Acids in Pediatric Nonalcoholic Fatty Liver Disease. Frontiers in Cellular and Infection Microbiology, 2021, 11, 698852.	1.8	16
1879	Up-regulation expression and prognostic significance of Syntaxin4 in kidney renal clear cell carcinoma. BMC Cancer, 2021, 21, 992.	1.1	2

#	Article	IF	CITATIONS
1880	Quantitative analysis of differentially expressed milk fat globule membrane proteins between donkey and bovine colostrum based on high-performance liquid chromatography with tandem mass spectrometry proteomics. Journal of Dairy Science, 2021, 104, 12207-12215.	1.4	10
1881	Activation of Cryptic Antibiotic Biosynthetic Gene Clusters Guided by RNA-seq Data from Both Streptomyces ansochromogenes and ΔwblA. Antibiotics, 2021, 10, 1097.	1.5	4
1882	MiR-552-3p promotes malignant progression of gallbladder carcinoma by reactivating the Akt/β-catenin signaling pathway due to inhibition of the tumor suppressor gene RGMA. Annals of Translational Medicine, 2021, 9, 1374-1374.	0.7	3
1883	Deep Investigating the Changes of Gut Microbiome and Its Correlation With the Shifts of Host Serum Metabolome Around Parturition in Sows. Frontiers in Microbiology, 2021, 12, 729039.	1.5	7
1884	CBF transcription factors involved in the cold response of <i>Camellia japonica</i> (Naidong). PeerJ, 2021, 9, e12155.	0.9	4
1885	Genome-Wide Transcriptional Changes of Rhodosporidium kratochvilovae at Low Temperature. Frontiers in Microbiology, 2021, 12, 727105.	1.5	5
1886	Comparative transcriptome analysis revealed omnivorous adaptation of the small intestine of Melinae. Scientific Reports, 2021, 11, 19162.	1.6	1
1887	Systematic analysis of the mechanism of Xiaochaihu decoction in hepatitis B treatment via network pharmacology and molecular docking. Computers in Biology and Medicine, 2021, 138, 104894.	3.9	10
1888	Dynamic Transcriptomic and Metabolomic Analyses of Madhuca pasquieri (Dubard) H. J. Lam During the Post-germination Stages. Frontiers in Plant Science, 2021, 12, 731203.	1.7	2
1889	Transcriptome analysis provides strategies for postharvest lotus seeds preservation. Postharvest Biology and Technology, 2021, 179, 111583.	2.9	11
1890	RNA-seq analysis of gene expression changes in cuticles during the larval-pupal metamorphosis of Plutella xylostella. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 39, 100869.	0.4	5
1891	Transcriptome profiling of Malus sieversii under freezing stress after being cold-acclimated. BMC Genomics, 2021, 22, 681.	1.2	18
1892	Epigenetic Regulation by <i>Suv4-20h1</i> in Cardiopulmonary Progenitor Cells Is Required to Prevent Pulmonary Hypertension and Chronic Obstructive Pulmonary Disease. Circulation, 2021, 144, 1042-1058.	1.6	9
1893	The <i>Euscaphis japonica</i> genome and the evolution of malvids. Plant Journal, 2021, 108, 1382-1399.	2.8	6
1894	RNA–RNA interactions between SARS-CoV-2 and host benefit viral development and evolution during COVID-19 infection. Briefings in Bioinformatics, 2022, 23, .	3.2	41
1895	A comparative study of libido in drakes: from phenotypes to molecules. Poultry Science, 2021, 100, 101503.	1.5	4
1896	Physio-ultrastructural footprints and iTRAQ-based proteomic approach unravel the role of Piriformospora indica-colonization in counteracting cadmium toxicity in rice. Ecotoxicology and Environmental Safety, 2021, 220, 112390.	2.9	24
1897	Comparative transcriptomic proï¬ling reveals the regulation of terpenoid biosynthesis in Sinocalycanthus chinensis. Plant Physiology and Biochemistry, 2021, 166, 477-484.	2.8	1

ARTICLE IF CITATIONS Metabolomic and Transcriptomic Changes Induced by Potassium Deficiency During Sarocladium oryzae 1898 1.7 10 Infection Reveal Insights into Rice Sheath Rot Disease Resistance. Rice, 2021, 14, 81. Antiatherosclerotic effect of dehydrocorydaline on ApoEâ<sup>^</sup>/â<sup>^</sup> mice: inhibition of macrophage 1899 2.8 inflammation. Acta Pharmacologíca Sinića, 2022, 43, 1408-1418. Extensive transcriptome changes underlying the fruit skin colour intensity variation in purple 1901 0.5 3 eggplant. Notulae Botanicae Horti Agrobotanici Cluj-Napoca, 2021, 49, 12434. Transcriptome analysis to elucidate the toxicity mechanisms of fenvalerate, sulfide gatifloxacin, and ridomil on the hepatopancreas of Procambarus clarkii. Fish and Shellfish Immunology, 2021, 116, 140-149. Screening of key genes during early embryonic development of Nile tilapia (Oreochromis niloticus). 1903 0.4 0 Gene Reports, 2021, 24, 101262. Transcriptomics analysis of the infected tissue of gibel carp (Carassius auratus gibelio) with liver myxobolosis infers the underlying defense mechanisms from the perspective of immune-metabolic interactions. Aquaculture, 2021, 542, 736867. 1.7 Circular RNAs Repertoire and Expression Profile during Brassica rapa Pollen Development. 1905 1.8 13 International Journal of Molecular Sciences, 2021, 22, 10297. CXCL8, CXCL9, and CXCL10 serum levels increase in syphilitic patients with seroresistance. Journal of 1906 Clinical Laboratory Analysis, 2021, 35, e24016. Potassium Alginate Oligosaccharides Alter Gut Microbiota, and Have Potential to Prevent the 1907 Development of Hypertension and Heart Failure in Spontaneously Hypertensive Rats. International 1.8 17 Journal of Molecular Sciences, 2021, 22, 9823. SUN-Family Protein UvSUN1 Regulates the Development and Virulence of Ustilaginoidea virens. 1.5 Frontiers in Microbiology, 2021, 12, 739453. Genome-wide association study reveals a quantitative trait locus and two candidate genes on Sus 1909 1.3 14 scrofa chromosome 5 affecting intramuscular fat content in Suhuai pigs. Animal, 2021, 15, 100341. Comparative analysis of spleen transcriptome of immune response in <i>Sebastes schlegeli</i> <i>Photobacterium damselae</i> subsp. <i>damselae</i> infection. Aquaculture Research, 2022, 53, 0.9 232-242. The effects of corticosterone and background colour on tadpole physiological plasticity. 1911 0.4 4 Comparative Biochemistry and Physiology Part D: Genomics and Próteomics, 2021, 39, 100872. Integrated Analysis of IncRNA-Associated ceRNA Network Identifies Two IncRNA Signatures as a Prognostic Biomarker in Gastric Cancer. Disease Markers, 2021, 2021, 1-16. QKI-Regulated Alternative Splicing Events in Cervical Cancer: Pivotal Mechanism and Potential 1913 0.9 3 Therapeutic Strategy. DNA and Cell Biology, 2021, 40, 1261-1277. An atherosclerotic plaque-targeted single-chain antibody for MR/NIR-II imaging of atherosclerosis and 1914 anti-atherosclerosis therapy. Journal of Nanobiotechnology, 2021, 19, 296. Parallel subgenome structure and divergent expression evolution of allo-tetraploid common carp 1915 9.4 52 and goldfish. Nature Genetics, 2021, 53, 1493-1503. Response process and adaptation mechanism of estuarine benthic microbiota to polyvinyl chloride 1916 microplastics with and without phthalates. Science of the Total Environment, 2022, 806, 150693.

~	_	
CITATI	12 E D O	DT
CILAD	ILL FU	

#	Article	IF	CITATIONS
1918	Comparative transcriptomics analysis reveals differential Cd response processes in roots of two turnip landraces with different Cd accumulation capacities. Ecotoxicology and Environmental Safety, 2021, 220, 112392.	2.9	11
1919	Female developmental environment delays development of male honeybee (Apis mellifera). BMC Genomics, 2021, 22, 699.	1.2	1
1920	An Adaptive Transfer-Learning-Based Deep Cox Neural Network for Hepatocellular Carcinoma Prognosis Prediction. Frontiers in Oncology, 2021, 11, 692774.	1.3	7
1921	Serial Transcriptome Analysis Reveals Genes Associated with Late Blight Resistance in Potato Cultivar Qingshu 9. Agronomy, 2021, 11, 1919.	1.3	3
1922	Serum exosome-derived biomarkers for the early detection of oral squamous cell carcinoma. Molecular and Cellular Biochemistry, 2021, 476, 4435-4447.	1.4	7
1923	Domestication and Feed Restriction Programming Organ Index, Dopamine, and Hippocampal Transcriptome Profile in Chickens. Frontiers in Veterinary Science, 2021, 8, 701850.	0.9	4
1924	Protein homeostasis, regulation of energy production and activation of <scp>DNA</scp> damageâ€repair pathways are involved in the heat stress response of <i>Pseudogymnoascus</i> spp Environmental Microbiology, 2022, 24, 1849-1864.	1.8	2
1925	Global gene expression analysis of pigeonpea with male sterility conditioned by A 2 cytoplasm. Plant Genome, 2021, 14, e20132.	1.6	7
1926	Comparative physiological, biochemical and transcriptomic analysis of hexaploid wheat (T. aestivum) Tj ETQq0 0 ( and Zn starvation. Genomics, 2021, 113, 3357-3372.	0 rgBT /Ov 1.3	erlock 10 T 8
1927	Dissection of the genetic basis of genotype-by-environment interactions for grain yield and main agronomic traits in Iranian bread wheat landraces and cultivars. Scientific Reports, 2021, 11, 17742.	1.6	13
1927 1928		1.6 0.6	13 2
	agronomic traits in Iranian bread wheat landraces and cultivars. Scientific Reports, 2021, 11, 17742. Relationship between HSPA1A-regulated gene expression and alternative splicing in mouse		
1928	agronomic traits in Iranian bread wheat landraces and cultivars. Scientific Reports, 2021, 11, 17742. Relationship between HSPA1A-regulated gene expression and alternative splicing in mouse cardiomyocytes and cardiac hypertrophy. Journal of Thoracic Disease, 2021, 13, 5517-5533. RNA sequencing and functional analysis of adult gonadal tissue to identify candidate key genes in	0.6	2
1928 1929	agronomic traits in Iranian bread wheat landraces and cultivars. Scientific Reports, 2021, 11, 17742. Relationship between HSPA1A-regulated gene expression and alternative splicing in mouse cardiomyocytes and cardiac hypertrophy. Journal of Thoracic Disease, 2021, 13, 5517-5533. RNA sequencing and functional analysis of adult gonadal tissue to identify candidate key genes in Macrobrachium rosenbergii sex development. Aquaculture International, 2021, 29, 2805-2821. Comparative transcriptome analysis reveals differential gene expression in sterile and fertile rubber	0.6	2
1928 1929 1930	agronomic traits in Iranian bread wheat landraces and cultivars. Scientific Reports, 2021, 11, 17742. Relationship between HSPA1A-regulated gene expression and alternative splicing in mouse cardiomyocytes and cardiac hypertrophy. Journal of Thoracic Disease, 2021, 13, 5517-5533. RNA sequencing and functional analysis of adult gonadal tissue to identify candidate key genes in Macrobrachium rosenbergii sex development. Aquaculture International, 2021, 29, 2805-2821. Comparative transcriptome analysis reveals differential gene expression in sterile and fertile rubber tree varieties during flower bud differentiation. Journal of Plant Physiology, 2021, 265, 153506.	0.6 1.1 1.6	2 0 2
1928 1929 1930 1931	agronomic traits in Iranian bread wheat landraces and cultivars. Scientific Reports, 2021, 11, 17742. Relationship between HSPA1A-regulated gene expression and alternative splicing in mouse cardiomyocytes and cardiac hypertrophy. Journal of Thoracic Disease, 2021, 13, 5517-5533. RNA sequencing and functional analysis of adult gonadal tissue to identify candidate key genes in Macrobrachium rosenbergii sex development. Aquaculture International, 2021, 29, 2805-2821. Comparative transcriptome analysis reveals differential gene expression in sterile and fertile rubber tree varieties during flower bud differentiation. Journal of Plant Physiology, 2021, 265, 153506. Comprehensive transcriptome-based characterization of differentially expressed genes involved in carotenoid biosynthesis of different ripening stages of Capsicum. Scientia Horticulturae, 2021, 288, 110311.	0.6 1.1 1.6 1.7	2 0 2 11
1928 1929 1930 1931 1932	agronomic traits in Iranian bread wheat landraces and cultivars. Scientific Reports, 2021, 11, 17742. Relationship between HSPA1A-regulated gene expression and alternative splicing in mouse cardiomyocytes and cardiac hypertrophy. Journal of Thoracic Disease, 2021, 13, 5517-5533. RNA sequencing and functional analysis of adult gonadal tissue to identify candidate key genes in Macrobrachium rosenbergii sex development. Aquaculture International, 2021, 29, 2805-2821. Comparative transcriptome analysis reveals differential gene expression in sterile and fertile rubber tree varieties during flower bud differentiation. Journal of Plant Physiology, 2021, 265, 153506. Comprehensive transcriptome-based characterization of differentially expressed genes involved in carotenoid biosynthesis of different ripening stages of Capsicum. Scientia Horticulturae, 2021, 288, 110311. Concentration-dependent transcriptome of zebrafish larvae for environmental bisphenol S assessment. Ecotoxicology and Environmental Safety, 2021, 223, 112574. Molecular and metabolic insights into anthocyanin biosynthesis during leaf coloration in autumn.	0.6 1.1 1.6 1.7 2.9	2 0 2 11 3

#	Article	IF	CITATIONS
1936	Interferon-inducible protein, IFIX, has tumor-suppressive effects in oral squamous cell carcinoma. Scientific Reports, 2021, 11, 19593.	1.6	4
1937	Identification of differentially expressed long noncoding RNAs and pathways in liver tissues from rats with hepatic fibrosis. PLoS ONE, 2021, 16, e0258194.	1.1	0
1938	Application and mechanism of benzyl-isothiocyanate, a natural antimicrobial agent from cruciferous vegetables, in controlling postharvest decay of strawberry. Postharvest Biology and Technology, 2021, 180, 111604.	2.9	22
1939	Genome-wide association studies reveals polygenic genetic architecture of litter traits in Duroc pigs. Theriogenology, 2021, 173, 269-278.	0.9	12
1940	Analysis of transcriptome profiles of two Pyrus pyrifolia cultivars reveals genes associated with stone cell development. Scientia Horticulturae, 2021, 288, 110380.	1.7	1
1941	Isoforskolin, an adenylyl cyclase activator, attenuates cigarette smoke-induced COPD in rats. Phytomedicine, 2021, 91, 153701.	2.3	6
1942	iTRAQ-based quantitative proteomic analysis reveals the toxic mechanism of diclofenac sodium on the kidney of broiler chicken. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2021, 249, 109129.	1.3	7
1943	Dynamic interaction mechanism of environment, microorganisms, and functions in anaerobic digestion of food waste with magnetic powder supplement. Bioresource Technology, 2021, 340, 125656.	4.8	13
1944	Identification of microRNA transcriptome in apple response to Alternaria alternata infection and evidence that miR390 is negative regulator of defense response. Scientia Horticulturae, 2021, 289, 110435.	1.7	6
1945	Global transcriptome analysis reveals dynamic gene expression profiling and provides insights into biosynthesis of resveratrol and anthraquinones in a medicinal plant Polygonum cuspidatum. Industrial Crops and Products, 2021, 171, 113919.	2.5	9
1946	Acute acidification stress weakens the head kidney immune function of juvenile Lates calcarifer. Ecotoxicology and Environmental Safety, 2021, 225, 112712.	2.9	3
1947	Silver birch pollen-derived microRNAs promote NF-κB-mediated inflammation in human lung cells. Science of the Total Environment, 2021, 800, 149531.	3.9	2
1948	Transcriptome analysis of growth variation in early juvenile stage sandfish Holothuria scabra. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 40, 100904.	0.4	2
1949	Identifying the mechanism underlying antidepressant-like effects of loganin by network pharmacology in combination with experimental validation. Journal of Ethnopharmacology, 2021, 281, 114526.	2.0	11
1950	Transcriptome profiles reveal the protective role of seed coating with zinc against boron toxicity in maize (Zea mays L.). Journal of Hazardous Materials, 2022, 423, 127105.	6.5	4
1951	Multi-omic approach to evaluate the response of gilt-head sea bream (Sparus aurata) exposed to the UV filter sulisobenzone. Science of the Total Environment, 2022, 803, 150080.	3.9	16
1952	Comparative transcriptome analysis of thiamethoxam susceptible and resistant Asian citrus psyllid, <i>Diaphorina citri</i> (Hemiptera: Liviidae), using RNAâ€sequencing. Insect Science, 2021, 28, 1708-1720.	1.5	9
1953	Comparative Proteomics of Ostreid Herpesvirus 1 and Pacific Oyster Interactions With Two Families Exhibiting Contrasted Susceptibility to Viral Infection. Frontiers in Immunology, 2020, 11, 621994.	2.2	10

#	Article	IF	Citations
1954	Transcriptome analysis reveals <scp>TOR</scp> signallingâ€mediated plant flush shoots governing <scp><i>Diaphorina citri</i> Kuwayama</scp> oviposition. Insect Molecular Biology, 2021, 30, 264-276.	1.0	4
1955	The effect of heat stress on proliferation, synthesis of steroids, and gene expression of duck granulosa cells. Animal Science Journal, 2021, 92, e13617.	0.6	4
1957	Gonadotropin inhibitory hormone downregulates steroid hormone secretion and genes expressions in duck granulosa cells. Animal Reproduction, 2021, 18, e20210036.	0.4	7
1958	Immune Responses to Gram-Negative Bacteria in Hemolymph of the Chinese Horseshoe Crab, Tachypleus tridentatus. Frontiers in Immunology, 2020, 11, 584808.	2.2	11
1959	Transcriptome Analysis Reveals Candidate Genes Involved in Anthocyanin Biosynthesis in Flowers of the Pagoda Tree (Sophora japonica L.). Journal of Plant Growth Regulation, 2022, 41, 1-14.	2.8	11
1960	ITRAQ-based quantitative proteomic analysis of Fusarium moniliforme (Fusarium verticillioides) in response to Phloridzin inducers. Proteome Science, 2021, 19, 2.	0.7	4
1961	Transcriptome based high-throughput SSRs and SNPs discovery in the medicinal plant Lagenaria siceraria. Biocell, 2021, 45, 371-386.	0.4	3
1962	Integrated Analysis of circRNA-miRNA-mRNA Regulatory Networks in the Intestine of Sebastes schlegelii Following Edwardsiella tarda Challenge. Frontiers in Immunology, 2020, 11, 618687.	2.2	19
1963	MicroRNA-193a-5p Regulates the Synthesis of Polyunsaturated Fatty Acids by Targeting Fatty Acid Desaturase 1 (FADS1) in Bovine Mammary Epithelial Cells. Biomolecules, 2021, 11, 157.	1.8	10
1964	YjbH mediates the oxidative stress response and infection by regulating SpxA1 and the phosphoenolpyruvate-carbohydrate phosphotransferase system (PTS) in <i>Listeria monocytogenes</i> . Gut Microbes, 2021, 13, 1-19.	4.3	6
1965	Comparative transcriptomic analysis between â€~Summer Black' and its bud sport â€~Nantaihutezao' duri developmental stages. Planta, 2021, 253, 23.	ng 1.6	6
1966	Integrated Analysis of the Transcriptome and Metabolome Revealed the Molecular Mechanisms Underlying the Enhanced Salt Tolerance of Rice Due to the Application of Exogenous Melatonin. Frontiers in Plant Science, 2020, 11, 618680.	1.7	48
1967	RNA-Seq Highlights Molecular Events Associated With Impaired Pollen-Pistil Interactions Following Short-Term Heat Stress in Brassica napus. Frontiers in Plant Science, 2020, 11, 622748.	1.7	18
1968	An integrated approach in gene-expression landscape profiling to identify housekeeping and tissue-specific genes in cattle. Animal Production Science, 2021, , .	0.6	1
1969	Genomeâ€wide identification of long nonâ€coding <scp>RNAs</scp> ( <scp>lncRNAs</scp> ) associated with malathion resistance in <scp><i>Bactrocera dorsalis</i></scp> . Pest Management Science, 2021, 77, 2292-2301.	1.7	19
1970	Application of Hi-C and other omics data analysis in human cancer and cell differentiation research. Computational and Structural Biotechnology Journal, 2021, 19, 2070-2083.	1.9	10
1971	Transcriptome analysis of Botrytis cinerea in response to tea tree oil and its two characteristic components. Applied Microbiology and Biotechnology, 2020, 104, 2163-2178.	1.7	33
1972	Screening of Biomarkers Related to Ovarian Maturation and Spawning in Blunt Snout Bream (Megalobrama amblycephala) Based on Metabolomics and Transcriptomics. Marine Biotechnology, 2020, 22, 180-193.	1.1	8

#	Article	IF	CITATIONS
1973	Functional analysis of miRNAs combined with TGF-β1/Smad3 inhibitor in an intrauterine rat adhesion cell model. Molecular and Cellular Biochemistry, 2020, 470, 15-28.	1.4	11
1974	CHO cell productivity improvement by genome-scale modeling and pathway analysis: Application to feed supplements. Biochemical Engineering Journal, 2020, 160, 107638.	1.8	30
1975	De novo transcriptome analysis of the mussel Perna viridis after exposure to the toxic dinoflagellate Prorocentrum lima. Ecotoxicology and Environmental Safety, 2020, 192, 110265.	2.9	25
1976	WheatGmap: a comprehensive platform for wheat gene mapping and genomic studies. Molecular Plant, 2021, 14, 187-190.	3.9	34
1977	Developmental toxicity and transcriptome analysis of 4-epianhydrotetracycline to zebrafish (Danio) Tj ETQq0 0 0	rgBT /Ove	rlock 10 Tf 50

1978	Proteome and transcriptome profile analysis reveals regulatory and stress-responsive networks in the russet fruit skin of sand pear. Horticulture Research, 2020, 7, 16.	2.9	31
1979	MicroRNA and mRNA interactions coordinate the immune response in non-lethal heat stressed Litopenaeus vannamei against AHPND-causing Vibrio parahaemolyticus. Scientific Reports, 2020, 10, 787.	1.6	19
1980	An integrative bioinformatics analysis of microarray data for identifying hub genes as diagnostic biomarkers of preeclampsia. Bioscience Reports, 2019, 39, .	1.1	28
1981	Circular RNA expression profile of lung squamous cell carcinoma: identification of potential biomarkers and therapeutic targets. Bioscience Reports, 2020, 40, .	1.1	21
1982	Chromosomal genome of <i>Triplophysa bleekeri</i> provides insights into its evolution and environmental adaptation. GigaScience, 2020, 9, .	3.3	19
1983	Prevention of Severe Intestinal Barrier Dysfunction Through a Single-Species Probiotics is Associated With the Activation of Microbiome-Mediated Glutamate–Glutamine Biosynthesis. Shock, 2021, 55, 128-137.	1.0	7
1984	Raineya orbicola gen. nov., sp. nov. a slightly thermophilic bacterium of the phylum Bacteroidetes and the description of Raineyaceae fam. nov International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 982-989.	0.8	19
1985	Solimicrobium silvestre gen. nov., sp. nov., isolated from alpine forest soil. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2491-2498.	0.8	11
1994	Chromosomeâ€level genome assembly for the largemouth bass <i>Micropterus salmoides</i> provides insights into adaptation to fresh and brackish water. Molecular Ecology Resources, 2021, 21, 301-315.	2.2	42
1995	Transcriptomic characterization of candidate genes responsive to salt tolerance of <i>Miscanthus</i> energy crops. GCB Bioenergy, 2017, 9, 1222-1237.	2.5	13
1996	Identification of the Regulon of AphB and Its Essential Roles in LuxR and Exotoxin Asp Expression in the Pathogen Vibrio alginolyticus. Journal of Bacteriology, 2017, 199, .	1.0	14
1998	Transcriptome analysis and differential gene expression profiling of two contrasting quinoa genotypes in response to salt stress. BMC Plant Biology, 2020, 20, 568.	1.6	27
1999	Comprehensive transcriptomic and proteomic analyses of antroquinonol biosynthetic genes and enzymes in Antrodia camphorata. AMB Express, 2020, 10, 136.	1.4	5

#	Article	IF	CITATIONS
2000	Identification of Critical Genes and Five Prognostic Biomarkers Associated with Colorectal Cancer. Medical Science Monitor, 2018, 24, 4625-4633.	0.5	32
2001	Combined Use of Three Machine Learning Modeling Methods to Develop a Ten-Gene Signature for the Diagnosis of Ventilator-Associated Pneumonia. Medical Science Monitor, 2020, 26, e919035.	0.5	4
2002	Bioinformatics Analysis Identifies the Estrogen Receptor 1 (ESR1) Gene and hsa-miR-26a-5p as Potential Prognostic Biomarkers in Patients with Intrahepatic Cholangiocarcinoma. Medical Science Monitor, 2020, 26, e921815.	0.5	6
2003	Integrated Analysis of Hub Genes and Pathways In Esophageal Carcinoma Based on NCBl's Gene Expression Omnibus (GEO) Database: A Bioinformatics Analysis. Medical Science Monitor, 2020, 26, e923934.	0.5	11
2004	CFLAP1 and CFLAP2 Are Two bHLH Transcription Factors Participating in Synergistic Regulation of AtCFL1-Mediated Cuticle Development in Arabidopsis. PLoS Genetics, 2016, 12, e1005744.	1.5	22
2005	The Effect of In Vitro Cultivation on the Transcriptome of Adult Brugia malayi. PLoS Neglected Tropical Diseases, 2016, 10, e0004311.	1.3	22
2006	Proteomic Analysis of Oesophagostomum dentatum (Nematoda) during Larval Transition, and the Effects of Hydrolase Inhibitors on Development. PLoS ONE, 2013, 8, e63955.	1.1	16
2007	Human Transporter Database: Comprehensive Knowledge and Discovery Tools in the Human Transporter Genes. PLoS ONE, 2014, 9, e88883.	1.1	24
2008	Blood Feeding and Plasmodium Infection Alters the miRNome of Anopheles stephensi. PLoS ONE, 2014, 9, e98402.	1.1	38
2009	A Comparative Transcriptome Analysis between Wild and Albino Yellow Catfish (Pelteobagrus) Tj ETQq1 1 0.784	314 rgBT / 1.1	Oygrlock 10
2010	De Novo Transcriptome Assembly of the Chinese Swamp Buffalo by RNA Sequencing and SSR Marker Discovery. PLoS ONE, 2016, 11, e0147132.	1.1	43
2011	Identification of Multiple Stress Responsive Genes by Sequencing a Normalized cDNA Library from Sea-Land Cotton (Gossypium barbadense L.). PLoS ONE, 2016, 11, e0152927.	1.1	33
2012	Genome-Wide Identification of the Transcription Factors Involved in Citrus Fruit Ripening from the Transcriptomes of a Late-Ripening Sweet Orange Mutant and Its Wild Type. PLoS ONE, 2016, 11, e0154330.	1.1	25
2013	Sugarcane transcriptome analysis in response to infection caused by Acidovorax avenae subsp. avenae. PLoS ONE, 2016, 11, e0166473.	1.1	41
2014	Perigone Lobe Transcriptome Analysis Provides Insights into Rafflesia cantleyi Flower Development. PLoS ONE, 2016, 11, e0167958.	1.1	13
2015	Whole-Genome Resequencing of Holstein Bulls for Indel Discovery and Identification of Genes Associated with Milk Composition Traits in Dairy Cattle. PLoS ONE, 2016, 11, e0168946.	1.1	26
2016	Analysis of long noncoding RNA and mRNA using RNA sequencing during the differentiation of intramuscular preadipocytes in chicken. PLoS ONE, 2017, 12, e0172389.	1.1	39
2017	Comparative transcriptome analysis of the different tissues between the cultivated and wild tomato. PLoS ONE, 2017, 12, e0172411.	1.1	22

#	Article	IF	CITATIONS
2018	Integrated network analysis reveals potentially novel molecular mechanisms and therapeutic targets of refractory epilepsies. PLoS ONE, 2017, 12, e0174964.	1.1	13
2019	De novo RNA sequencing transcriptome of Rhododendron obtusum identified the early heat response genes involved in the transcriptional regulation of photosynthesis. PLoS ONE, 2017, 12, e0186376.	1.1	24
2020	Transcriptome analysis of Phelipanche aegyptiaca seed germination mechanisms stimulated by fluridone, TIS108, and GR24. PLoS ONE, 2017, 12, e0187539.	1.1	24
2021	Transcriptome profiling of claw muscle of the mud crab (Scylla paramamosain) at different fattening stages. PLoS ONE, 2017, 12, e0188067.	1.1	9
2022	Evaluation of changes arising in the pig mesenchymal stromal cells transcriptome following cryopreservation and Trichostatin A treatment. PLoS ONE, 2018, 13, e0192147.	1.1	5
2023	De novo transcriptomic analysis of leaf and fruit tissue of Cornus officinalis using Illumina platform. PLoS ONE, 2018, 13, e0192610.	1.1	19
2024	Physiological and transcriptomic analyses of yellow horn (Xanthoceras sorbifolia) provide important insights into salt and saline-alkali stress tolerance. PLoS ONE, 2020, 15, e0244365.	1.1	39
2025	Data- and knowledge-based modeling of gene regulatory networks: an update. EXCLI Journal, 2015, 14, 346-78.	0.5	35
2026	LncRNA mediated regulation of aging pathways in Drosophila melanogaster during dietary restriction. Aging, 2016, 8, 2182-2203.	1.4	36
2027	Involvement of SPATA31 copy number variable genes in human lifespan. Aging, 2018, 10, 674-688.	1.4	7
2028	Identification of functional tRNA-derived fragments in senescence-accelerated mouse prone 8 brain. Aging, 2019, 11, 10485-10498.	1.4	35
2029	Age-related changes in microbial composition and function in cynomolgus macaques. Aging, 2019, 11, 12080-12096.	1.4	25
2030	RNA-seq analysis of the key long noncoding RNAs and mRNAs related to cognitive impairment after cardiac arrest and cardiopulmonary resuscitation. Aging, 2020, 12, 14490-14505.	1.4	5
2031	Identification of a competing endogenous RNA axis related to gastric cancer. Aging, 2020, 12, 20540-20560.	1.4	9
2032	Integrative miRNA and mRNA analysis in penile carcinomas reveals markers and pathways with potential clinical impact. Oncotarget, 2017, 8, 15294-15306.	0.8	39
2033	<i>HABP2</i> p.G534E variant in patients with family history of thyroid and breast cancer. Oncotarget, 2017, 8, 40896-40905.	0.8	7
2034	Identification of aberrantly expressed long non-coding RNAs in stomach adenocarcinoma. Oncotarget, 2017, 8, 49201-49216.	0.8	55
2035	Genome-wide comparison of the protein-coding repertoire reveals fast evolution of immune-related genes in cephalochordates and Osteichthyes superclass. Oncotarget, 2018, 9, 83-95.	0.8	14

#	Article	IF	CITATIONS
2036	Overexpression of HSD17B4 exerts tumor suppressive function in adrenocortical carcinoma and is not associated with hormone excess. Oncotarget, 2017, 8, 114736-114745.	0.8	7
2037	NF-Y activates genes of metabolic pathways altered in cancer cells. Oncotarget, 2016, 7, 1633-1650.	0.8	50
2038	dbCPG: A web resource for cancer predisposition genes. Oncotarget, 2016, 7, 37803-37811.	0.8	15
2039	Transcriptomic analysis of <i>Bursaphelenchus xylophilus</i> treated by a potential phytonematicide, punicalagin. Journal of Nematology, 2020, 52, 1-14.	0.4	4
2040	Use of Chou's 5-Steps Rule to Reveal Active Compound and Mechanism of Shuangshen Pingfei San on Idiopathic Pulmonary Fibrosis. Current Molecular Medicine, 2020, 20, 220-230.	0.6	26
2041	Dual RNA-seq provides novel insight into the roles of <i>dksA</i> from <i>Pseudomonas plecoglossicida</i> in pathogen-host interactions with large yellow croakers ( <i>Larimichthys crocea</i> ). Zoological Research, 2020, 41, 410-422.	0.9	21
2042	Effects of aging on gene expression in blood of captive Tibetan macaques ( <i>Macaca) Tj ETQq0 0 0 rgBT /C</i>	verlock 10 0.9	D Ţf 50 502 T
2043	Transcriptome analysis deciphers the mechanisms of exogenous nitric oxide action on the response of melon leaves to chilling stress. Biologia Plantarum, 0, 64, 465-472.	1.9	10
2044	Transcriptional Profiles of Long Non-coding RNA and mRNA in Sheep Mammary Gland During Lactation Period. Frontiers in Genetics, 2020, 11, 946.	1.1	8
2045	Metabolomic and Proteomic Profiles Associated With Ketosis in Dairy Cows. Frontiers in Genetics, 2020, 11, 551587.	1.1	15
2046	Transcriptome Analysis of Juvenile Tilapia (Oreochromis niloticus) Blood, Fed With Different Concentrations of Resveratrol. Frontiers in Physiology, 2020, 11, 600730.	1.3	10
2047	Differential Gene Expression between Leaf and Rhizome in Atractylodes lancea: A Comparative Transcriptome Analysis. Frontiers in Plant Science, 2016, 7, 348.	1.7	34
2048	Transcriptome Profiling of the Elongating Internode of Cotton (Gossypium hirsutum L.) Seedlings in Response to Mepiquat Chloride. Frontiers in Plant Science, 2019, 10, 1751.	1.7	19
2049	Tillage Practice Impacts on the Carbon Sequestration Potential of Topsoil Microbial Communities in an Agricultural Field. Agronomy, 2021, 11, 60.	1.3	9
2050	Transcriptomic and Metabolomic Changes Triggered by Fusarium solani in Common Bean (Phaseolus) Tj ETQq0 0	0 <sub>1</sub> .9BT /O	verlock 10 Th
2051	MiR-205 mediated APC regulation contributes to pancreatic cancer cell proliferation. World Journal of Gastroenterology, 2019, 25, 3775-3786.	1.4	20
2052	Elevated CELSR3 expression is associated with hepatocarcinogenesis and poor prognosis. Oncology Letters, 2020, 20, 1083-1092.	0.8	6
2053	Integrated bioinformatics analysis for the identification of potential key genes affecting the pathogenesis of clear cell renal cell carcinoma. Oncology Letters, 2020, 20, 1573-1584.	0.8	6

#	Article	IF	CITATIONS
2054	Identification of diagnostic and prognostic biomarkers, and candidate targeted agents for hepatitis B virusâ€ʿassociated early stage hepatocellular carcinoma based on RNAâ€ʿsequencing data. Oncology Letters, 2020, 20, 1-1.	0.8	4
2055	Effect of let‑7c on the PI3K/Akt/FoxO signaling pathway in hepatocellular carcinoma. Oncology Letters, 2020, 21, 96.	0.8	24
2056	Filamin B extensively regulates transcription and alternative splicing, and is associated with apoptosis in HeLa cells. Oncology Reports, 2020, 43, 1536-1546.	1.2	10
2057	SRSF6 regulates alternative splicing of genes involved in DNA damage response and DNA repair in HeLa cells. Oncology Reports, 2020, 44, 1851-1862.	1.2	13
2058	Differential gene and protein expression between rat tibial nerve and common peroneal nerve during Wallerian degeneration. Neural Regeneration Research, 2019, 14, 2183.	1.6	11
2059	Altered microRNA profiles of testicular biopsies from patients with nonobstructive azoospermia. Asian Journal of Andrology, 2020, 22, 100.	0.8	25
2060	Genome-wide identification and analysis of long noncoding RNAs in longissimus muscle tissue from Kazakh cattle and Xinjiang brown cattle. Asian-Australasian Journal of Animal Sciences, 2021, 34, 1739-1748.	2.4	9
2061	Transcriptome and gene expression analysis of Rhynchophorus ferrugineus (Coleoptera:) Tj ETQq1 1 0.784314	rgBT. <u>/</u> Overl	oc <u>k</u> 10 Tf 50
2062	Transcriptome analysis of <i>Polygonum minus</i> reveals candidate genes involved in important secondary metabolic pathways of phenylpropanoids and flavonoids. PeerJ, 2017, 5, e2938.	0.9	37
2063	Comparative transcriptome analysis of isonuclear-alloplasmic lines unmask key transcription factor genes and metabolic pathways involved in sterility of maize CMS-C. PeerJ, 2017, 5, e3408.	0.9	22
2064	Gene expression profiling and functional analysis reveals that p53 pathway-related gene expression is highly activated in cancer cells treated by cold atmospheric plasma-activated medium. PeerJ, 2017, 5, e3751.	0.9	31
2065	Gonadal transcriptome sequencing of the critically endangered <i>Acipenser dabryanus</i> to discover candidate sex-related genes. PeerJ, 2018, 6, e5389.	0.9	20
2066	<i>De novo</i> transcriptome sequencing and analysis of genes related to salt stress response in <i>Glehnia littoralis</i> . PeerJ, 2018, 6, e5681.	0.9	21
2067	Screening of prognostic biomarkers for endometrial carcinoma based on a ceRNA network. PeerJ, 2018, 6, e6091.	0.9	10
2068	Aberrantly hydroxymethylated differentially expressed genes and the associated protein pathways in osteoarthritis. PeerJ, 2019, 7, e6425.	0.9	27
2069	Integrated bioinformatics analysis of As, Au, Cd, Pb and Cu heavy metal responsive marker genes through <i>Arabidopsis thaliana</i> GEO datasets. PeerJ, 2019, 7, e6495.	0.9	14
2070	Synthesis of light-inducible and light-independent anthocyanins regulated by specific genes in grape â€~Marselan' ( <i>V. vinifera</i> L.). PeerJ, 2019, 7, e6521.	0.9	31
2071	Comparative analysis of the liver transcriptome in the red-eared slider <i>Trachemys scripta elegans</i> under chronic salinity stress. PeerJ, 2019, 7, e6538.	0.9	7

#	Article	IF	CITATIONS
2072	Integrated analysis reveals five potential ceRNA biomarkers in human lung adenocarcinoma. PeerJ, 2019, 7, e6694.	0.9	15
2073	Transcriptome analysis of <i>Chelidonium majus</i> elaiosomes and seeds provide insights into fatty acid biosynthesis. PeerJ, 2019, 7, e6871.	0.9	4
2074	Characterization of aminopeptidase encoding gene anp-1 and its association with development in Caenorhabditis elegans. PeerJ, 2019, 7, e7944.	0.9	1
2075	Genome-wide analysis of transcription factors related to anthocyanin biosynthesis in carmine radish ( <i>Raphanus sativus</i> L.) fleshy roots. PeerJ, 2019, 7, e8041.	0.9	15
2076	Comparative transcriptomic analyses of powdery mildew resistant and susceptible cultivated cucumber ( <i>Cucumis sativus</i> L.) varieties to identify the genes involved in the resistance to <i>Sphaerotheca fuliginea</i> infection. PeerJ, 2020, 8, e8250.	0.9	7
2077	RNA-sequencing analysis of the effect of luteolin on methamphetamine-induced hepatotoxicity in rats: a preliminary study. PeerJ, 2020, 8, e8529.	0.9	16
2078	Genome-wide identification and analysis of circular RNAs differentially expressed in the longissimus dorsi between Kazakh cattle and Xinjiang brown cattle. PeerJ, 2020, 8, e8646.	0.9	13
2079	Multi-omics analysis to examine microbiota, host gene expression and metabolites in the intestine of black tiger shrimp ( <i>Penaeus monodon</i> ) with different growth performance. PeerJ, 2020, 8, e9646.	0.9	22
2081	Integrated Proteotranscriptomics of Human Myometrium in Labor Landscape Reveals the Increased Molecular Associated With Inflammation Under Hypoxia Stress. Frontiers in Immunology, 2021, 12, 722816.	2.2	14
2082	Identification of SNPs and Candidate Genes for Milk Production Ability in Yorkshire Pigs. Frontiers in Genetics, 2021, 12, 724533.	1.1	1
2083	Methyl jasmonate treatment, aphid resistance assay, and transcriptomic analysis revealed different herbivore defensive roles between tobacco glandular and non-glandular trichomes. Plant Cell Reports, 2022, 41, 195-208.	2.8	6
2084	The transcription factor NF-Y participates to stem cell fate decision and regeneration in adult skeletal muscle. Nature Communications, 2021, 12, 6013.	5.8	12
2085	The Genomic and Transcriptomic Analyses of Floccularia luteovirens, a Rare Edible Fungus in the Qinghai–Tibet Plateau, Provide Insights into the Taxonomy Placement and Fruiting Body Formation. Journal of Fungi (Basel, Switzerland), 2021, 7, 887.	1.5	4
2086	Improvement of Nonâ€Alcoholic Fatty Liver Disease in Mice by Intermittent Use of a Fastingâ€Mimicking Diet. Molecular Nutrition and Food Research, 2021, 65, e2100381.	1.5	9
2087	Transcriptome Profiling of Maize (Zea mays L.) Leaves Reveals Key Cold-Responsive Genes, Transcription Factors, and Metabolic Pathways Regulating Cold Stress Tolerance at the Seedling Stage. Genes, 2021, 12, 1638.	1.0	20
2088	Genome-wide analysis of deletions in maize population reveals abundant genetic diversity and functional impact. Theoretical and Applied Genetics, 2021, 135, 273.	1.8	4
2089	Heat-stress-induced sprouting and differential gene expression in growing potato tubers: Comparative transcriptomics with that induced by postharvest sprouting. Horticulture Research, 2021, 8, 226.	2.9	9
2090	Comparative physiological and transcriptomic analysis reveals salinity tolerance mechanisms in Sorghum bicolor (L.) Moench. Planta, 2021, 254, 98.	1.6	7

#	Article	IF	Citations
2091	Integrated Transcriptomic and Bioinformatics Analyses Reveal the Molecular Mechanisms for the Differences in Seed Oil and Starch Content Between Glycine max and Cicer arietinum. Frontiers in Plant Science, 2021, 12, 743680.	1.7	4
2092	Distribution, expression and methylation analysis of positively selected genes provides insights into the evolution in Brassica rapa. PLoS ONE, 2021, 16, e0256120.	1.1	0
2093	Transcriptome Analysis Reveals the Complex Molecular Mechanisms of Brassica napus–Sclerotinia sclerotiorum Interactions. Frontiers in Plant Science, 2021, 12, 716935.	1.7	8
2094	Comparison of the Nutritional Properties and Transcriptome Profiling Between the Two Different Harvesting Periods of Auricularia polytricha. Frontiers in Nutrition, 2021, 8, 771757.	1.6	0
2095	The Divergent Roles of the Rice bcl-2 Associated Athanogene (BAG) Genes in Plant Development and Environmental Responses. Plants, 2021, 10, 2169.	1.6	6
2096	Comparative genomics reveals molecular mechanisms underlying health and reproduction in cryptorchid mammals. BMC Genomics, 2021, 22, 763.	1.2	2
2097	Transcriptional changes involved in kumquat (Fortunella spp) defense response to Xanthomonas citri subsp. citri in early stages of infection. Physiological and Molecular Plant Pathology, 2021, 116, 101729.	1.3	4
2098	Comparative genomics suggests local adaptations in the invasive small hive beetle. Ecology and Evolution, 2021, 11, 15780-15791.	0.8	8
2099	Cytokinin Inhibits Fungal Development and Virulence by Targeting the Cytoskeleton and Cellular Trafficking. MBio, 2021, 12, e0306820.	1.8	10
2100	Identification of Novel Quantitative Trait Nucleotides and Candidate Genes for Bacterial Wilt Resistance in Tobacco (Nicotiana tabacum L.) Using Genotyping-by-Sequencing and Multi-Locus Genome-Wide Association Studies. Frontiers in Plant Science, 2021, 12, 744175.	1.7	10
2101	Transcriptome analysis of the influence of high plant protein based diet on Trachinotus ovatus liver. Fish and Shellfish Immunology, 2021, 119, 339-346.	1.6	3
2102	Integrated transcriptome profiling in THP-1 macrophages infected with bunyavirus SFTSV. Virus Research, 2021, 306, 198594.	1.1	4
2103	The contributions of fliG gene to the pathogenicity of Pseudomonas plecoglossicida and pathogen-host interactions with Epinephelus coioides. Fish and Shellfish Immunology, 2021, 119, 238-248.	1.6	12
2104	Genome-wide analysis of long non-coding RNAs and their association with wing development in Aphis citricidus (Hemiptera: Aphididae). Insect Biochemistry and Molecular Biology, 2021, 139, 103666.	1.2	5
2105	Insights into the evolution and hypoglycemic metabolite biosynthesis of autotetraploid Cyclocarya paliurus by combining genomic, transcriptomic and metabolomic analyses. Industrial Crops and Products, 2021, 173, 114154.	2.5	13
2106	Interplay between ferric uptake regulator Fur and horizontally acquired virulence regulator EsrB coordinates virulence gene expression in Edwardsiella piscicida. Microbiological Research, 2021, 253, 126892.	2.5	21
2107	Transcriptomic analysis reveals innate immune mechanisms of an underlying parasite-resistant grouper hybrid (Epinephelus fuscogutatus × Epinephelus lanceolatus). Fish and Shellfish Immunology, 2021, 119, 67-75.	1.6	9
2108	Selection of breed-specific SNPs in three Indian sheep breeds using ovine 50†K array. Small Ruminant Research, 2021, 205, 106545.	0.6	9

#	Article	IF	CITATIONS
2109	Effect of L-arginine on the oxygen balance of the liver and its bile secretion function. , 2013, 59, 31-38.		1
2117	Specific Gene Expression and Small-Molecule Drug Investigation in Ankylosing Spondylitis under Interferon-Î <sup>3</sup> Stimulation. International Journal of Pharmacology, 2018, 14, 1020-1028.	0.1	Ο
2118	Evaluación de la erosión de riberas de rÃos en regiones semiáridas mediante datos de teledetección y SIG: caso del rÃo Rdat (Marrakech, Marruecos). Estudios Geologicos, 2018, 74, 081.	0.7	4
2132	Identification and Analysis of Differentially Expressed Genes in Human Saphenous Vein Endothelial Cells Overexpressing Domain-Containing mTOR-Interacting Protein (DEPTOR) by RNA-Seq. Medical Science Monitor, 2019, 25, 6965-6971.	0.5	1
2134	Bioinformatics analysis of competing endogenous RNA and screening of biomarkers in childhood wilms tumor. , 2019, , .		1
2135	Molecular basis of degenerative spinal disorders from a proteomic perspective (Review). Molecular Medicine Reports, 2020, 21, 9-19.	1.1	9
2142	Bioinformatics analysis of the network of histone H3 lysine 9 trimethylation in acute myeloid leukaemia. Oncology Reports, 2020, 44, 543-554.	1.2	4
2144	Integrative analysis of miRNAs-mRNAs reveals that miR-182 up-regulation contributes to proliferation and invasion of nasopharyngeal carcinoma by targeting PTEN. Aging, 2020, 12, 11568-11578.	1.4	6
2147	STAU1 selectively regulates the expression of inflammatory and immune response genes and alternative splicing of the nerve growth factor receptor signaling pathway. Oncology Reports, 2020, 44, 1863-1874.	1.2	9
2148	Molecular and Chemical Screening for Inherent Disease Resistance Factors of Norway Spruce ( <i>Picea abies</i> ) Clones Against Conifer Stem Rot Pathogen <i>Heterobasidion parviporum</i> . Phytopathology, 2022, 112, 872-880.	1.1	3
2149	Hypoxia causes mitochondrial dysfunction and brain memory disorder in a manner mediated by the reduction of Cirbp. Science of the Total Environment, 2022, 806, 151228.	3.9	8
2150	Identifying long non-coding RNAs and characterizing their functional roles in swine mammary gland from colostrogenesis to lactogenesis. Animal Bioscience, 2022, 35, 814-825.	0.8	2
2151	The Aphelenchus avenae genome highlights evolutionary adaptation to desiccation. Communications Biology, 2021, 4, 1232.	2.0	19
2152	Transcriptional Changes in Pearl Millet Leaves under Heat Stress. Genes, 2021, 12, 1716.	1.0	11
2153	Hypothalamic Transcriptome Analysis Reveals the Crucial MicroRNAs and mRNAs Affecting Litter Size in Goats. Frontiers in Veterinary Science, 2021, 8, 747100.	0.9	10
2154	Transcriptome in Combination Proteome Unveils the Phenylpropane Pathway Involved in Garlic (Allium sativum) Greening. Frontiers in Nutrition, 2021, 8, 764133.	1.6	4
2155	Integrating full-length transcriptomics and metabolomics reveals the regulatory mechanisms underlying yellow pigmentation in tree peony (Paeonia suffruticosa Andr.) flowers. Horticulture Research, 2021, 8, 235.	2.9	26
2156	Cancer survival prognosis with Deep Bayesian Perturbation Cox Network. Computers in Biology and Medicine, 2022, 141, 105012.	3.9	9

#	Article	IF	CITATIONS
2157	Oxidative stress response and programmed cell death guided by NAC013 modulate pithiness in radish taproots. Plant Journal, 2021, , .	2.8	2
2161	Up-regulated miR-155 is associated with poor prognosis in childhood acute lymphoblastic leukemia and promotes cell proliferation targeting ZNF238. Hematology, 2021, 26, 16-25.	0.7	10
2163	Effect of EZH2 on pulmonary artery smooth muscle cell migration in pulmonary hypertension. Molecular Medicine Reports, 2020, 23, .	1.1	6
2164	Identifying an Eight-Gene Signature to Optimize Overall Survival Prediction of Esophageal Adenocarcinoma Using Bioinformatics Analysis of ceRNA Network. OncoTargets and Therapy, 2020, Volume 13, 13041-13054.	1.0	7
2166	Integrated transcriptomic and metabolomic analyses reveal regulation of terpene biosynthesis in the stems of Sindora glabra. Tree Physiology, 2021, 41, 1087-1102.	1.4	14
2167	Identification of key genes and pathways associated with duck (Anas platyrhynchos) embryonic skin development using weighted gene co-expression network analysis. Genome, 2020, 63, 615-628.	0.9	2
2168	On the NF-Y regulome as in ENCODE (2019). PLoS Computational Biology, 2020, 16, e1008488.	1.5	6
2170	Genome-wide association study identifies quantitative trait loci affecting cattle temperament. Zoological Research, 2022, 43, 14-25.	0.9	8
2171	Rhizosphere effect alters the soil microbiome composition and C, N transformation in an arid ecosystem. Applied Soil Ecology, 2022, 170, 104296.	2.1	25
2172	Mining Similar Aspects for Gene Similarity Explanation Based on Gene Information Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	1.9	2
2175	Clinical and prognostic association of oncogene cadherin 11 in gastric cancer. Oncology Letters, 2020, 19, 4011-4023.	0.8	4
2176	Comparative transcriptomics characterized the distinct biosynthetic abilities of terpenoid and paeoniflorin biosynthesis in herbaceous peony strains. PeerJ, 2020, 8, e8895.	0.9	4
2177	Putative MicroRNA-mRNA Networks Upon Mdfi Overexpression in C2C12 Cell Differentiation and Muscle Fiber Type Transformation. Frontiers in Molecular Biosciences, 2021, 8, 675993.	1.6	5
2178	Integrative analysis of Iso-Seq and RNA-seq data reveals transcriptome complexity and differentially expressed transcripts in sheep tail fat. PeerJ, 2021, 9, e12454.	0.9	16
2179	Fibronectin 1B Gene Plays an Important Role in Loach Barbel Air-Breathing. International Journal of Molecular Sciences, 2021, 22, 11928.	1.8	3
2180	BAP1 loss augments sensitivity to BET inhibitors in cancer cells. Acta Pharmacologica Sinica, 2022, 43, 1803-1815.	2.8	7
2181	Reproductive Regulation of PrRPs in Teleost: The Link Between Feeding and Reproduction. Frontiers in Endocrinology, 2021, 12, 762826.	1.5	3
2182	MicroRNA-222 Transferred From Semen Extracellular Vesicles Inhibits Sperm Apoptosis by Targeting BCL2L11. Frontiers in Cell and Developmental Biology, 2021, 9, 736864.	1.8	11

	C	CITATION REPORT		
#	Article	I	F	Citations
2184	The Elite Alleles of OsSPL4 Regulate Grain Size and Increase Grain Yield in Rice. Rice, 2021, 14, 90.	1	L.7	23
2185	Gastrointestinal Goblet Cell Adenocarcinomas Harbor Distinctive Clinicopathological, Immune, and Genomic Landscape. Frontiers in Oncology, 2021, 11, 758643.		L.3	6
2187	A Cyclophilin OsCYP20–2 Interacts with OsSYF2 to Regulate Grain Length by Pre-mRNA Splicing. R 2020, 13, 64.	ice, 1	L <b>.</b> 7	3
2188	Analysis of transcriptomic differences between NK603 maize and near-isogenic varieties using RNA sequencing and RT-qPCR. Environmental Sciences Europe, 2020, 32, .	2	2.6	2
2192	Genome-Wide Analyses Provide Insights into the Scavenging Lifestyle of the Striped Hyena ( <i>Hyae</i>	1a) Tj ETQq0 0 <sub>(</sub>	0_rgBT /0 ).9	Dyerlock 10
2193	Genome-wide analysis of PRR gene family uncovers their roles in circadian rhythmic changes and response to drought stress in <i>Gossypium hirsutum</i> L PeerJ, 2020, 8, e9936.	C	0.9	7
2194	NEDD4 single nucleotide polymorphism rs2271289 is associated with keloids in Chinese Han population. American Journal of Translational Research (discontinued), 2016, 8, 544-55.	(	0.0	13
2195	Phylogenetic analysis of basic helix-loop-helix transcription factors in the genome of a typical human-disease vector. American Journal of Translational Research (discontinued), 2016, 8, 4844-485	6.	0.0	0
2196	Comprehensive circular RNA profiling reveals the regulatory role of circRNA_0007694 in papillary thyroid carcinoma. American Journal of Translational Research (discontinued), 2020, 12, 1362-1378.	(	0.0	8
2197	Integrative genomics analysis identifies promising SNPs and genes implicated in tuberculosis risk bas on multiple omics datasets. Aging, 2020, 12, 19173-19220.	ed 1	l.4	2
2198	Inflammation is involved in response of gastric mucosal epithelial cells under simulated microgravity by integrated transcriptomic analysis. American Journal of Translational Research (discontinued), 2021, 13, 9195-9207.	(	0.0	0
2199	RNA-seq for revealing the function of the transcriptome. , 2022, , 105-129.			3
2200	Combined analysis of mRNA and miRNA transcriptomes reveals the regulatory mechanism of PVY resistance in tobacco. Industrial Crops and Products, 2022, 176, 114322.	2	2.5	3
2201	Whole genome analysis and specific PCR primer development for Vibrio coralliilyticus, combined with transcription and metabolome analysis of red spotting disease in the sea urchin, Strongylocentrotus intermedius. Aquaculture Reports, 2022, 22, 100957.		).7	3
2202	Comparative transcriptome analysis of Tamarixia radiata (Hymenoptera: Eulophidae) reveals differentially expressed genes upon heat shock. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2022, 41, 100940.	(	).4	3
2203	Transcriptome-based insights into the calcium transport mechanism of chick chorioallantoic membrane. Food Science and Human Wellness, 2022, 11, 383-392.		2.2	4

2204	Transcriptomic survey reveals multiple adaptation mechanisms in response to nitrogen deprivation in marine Porphyridium cruentum. PLoS ONE, 2021, 16, e0259833.	1.1	1

2205	Insulin-like growth factor 2 mRNA binding protein 2 regulates proliferation, migration, and angiogenesis of keratinocytes by modulating heparanase stability. Bioengineered, 2021, 12, 11267-11276.	1.4	11	
------	---	-----	----	--

#	Article	IF	Citations
2206	Nanopore-Based Comparative Transcriptome Analysis Reveals the Potential Mechanism of High-Temperature Tolerance in Cotton (Gossypium hirsutum L.). Plants, 2021, 10, 2517.	1.6	2
2207	Genome-Wide Identification and Functional Characterization of CCHC-Type Zinc Finger Genes in Ustilaginoidea virens. Journal of Fungi (Basel, Switzerland), 2021, 7, 947.	1.5	7
2208	Comparative Transcriptomic Analysis Provides Novel Insights into the Blanched Stem of Oenanthe javanica. Plants, 2021, 10, 2484.	1.6	5
2209	Treatment with mixed probiotics induced, enhanced and diversified modulation of the gut microbiome of healthy rats. FEMS Microbiology Ecology, 2021, 97, .	1.3	4
2210	Olfactory dysfunction and potential mechanisms caused by volatile organophosphate dichlorvos in the silkworm as a model animal. Journal of Hazardous Materials, 2022, 425, 127940.	6.5	9
2211	Oregano Essential Oils Promote Rumen Digestive Ability by Modulating Epithelial Development and Microbiota Composition in Beef Cattle. Frontiers in Nutrition, 2021, 8, 722557.	1.6	20
2212	PPR proteins in the tea plant (Camellia sinensis) and their potential roles in the leaf color changes. Scientia Horticulturae, 2022, 293, 110745.	1.7	6
2213	Transcriptome profiling based on Illumina- and SMRT-based RNA-seq reveals circadian regulation of key pathways in flower bud development in walnut. PLoS ONE, 2021, 16, e0260017.	1.1	1
2214	In silico Methods for Identification of Potential Therapeutic Targets. Interdisciplinary Sciences, Computational Life Sciences, 2022, 14, 285-310.	2.2	17
2215	Integrated transcriptomics and metabolomics uncover the molecular basis of flavonoid accumulation in the rhizomes of two Cymbidium tortisepalum var. longibracteatum cultivars. Scientia Horticulturae, 2022, 293, 110738.	1.7	2
2216	Transcriptome Profiling of Duodenum Reveals the Importance of Boron Supplementation in Modulating Immune Activities in Rats. Biological Trace Element Research, 2022, 200, 3762-3773.	1.9	6
2217	Data-Independent Acquisition-Based Proteome and Phosphoproteome Profiling Reveals Early Protein Phosphorylation and Dephosphorylation Events in Arabidopsis Seedlings upon Cold Exposure. International Journal of Molecular Sciences, 2021, 22, 12856.	1.8	10
2219	Downregulation of the Coiled-Coil Domain Containing 80 and Its Perspective Mechanisms in Ovarian Carcinoma: A Comprehensive Study. International Journal of Genomics, 2021, 2021, 1-20.	0.8	7
2220	Characterization of Host IncRNAs in Response to Vibrio splendidus Infection and Function as Efficient miRNA Sponges in Sea Cucumber. Frontiers in Immunology, 2021, 12, 792040.	2.2	1
2221	Arbuscular Mycorrhizal Fungus Alters Root System Architecture in Camellia sinensis L. as Revealed by RNA-Seq Analysis. Frontiers in Plant Science, 2021, 12, 777357.	1.7	10
2222	Anaerobic oxidation of methane (AOM) driven by multiple electron acceptors in constructed wetland and the related mechanisms of carbon, nitrogen, sulfur cycles. Chemical Engineering Journal, 2022, 433, 133663.	6.6	8
2223	Single-molecule real-time transcript sequencing of developing cotton anthers facilitates genome annotation and fertility restoration candidate gene discovery. Genomics, 2021, 113, 4245-4253.	1.3	5
2224	Plasma extracellular vesicle microRNA profiling and the identification of a diagnostic signature for stage I lung adenocarcinoma. Cancer Science, 2022, 113, 648-659.	1.7	16

#	Article	IF	CITATIONS
2225	The dark septate endophyte <i>Phialocephala sphaeroides</i> confers growth fitness benefits and mitigates pathogenic effects of <i>Heterobasidion</i> on Norway spruce. Tree Physiology, 2022, 42, 891-906.	1.4	8
2226	Transcriptomic responses to drought stress in Polygonatum kingianum tuber. BMC Plant Biology, 2021, 21, 537.	1.6	7
2227	Bacillus sp. WR12 alleviates iron deficiency in wheat via enhancing siderophore- and phenol-mediated iron acquisition in roots. Plant and Soil, 2022, 471, 247-260.	1.8	7
2228	Transcriptomic Analysis Reveals the Positive Role of Abscisic Acid in Endodormancy Maintenance of Leaf Buds of Magnolia wufengensis. Frontiers in Plant Science, 2021, 12, 742504.	1.7	3
2229	Genetic divergence and local adaptation of <i>Liriodendron</i> driven by heterogeneous environments. Molecular Ecology, 2022, 31, 916-933.	2.0	13
2230	Change in Cav3.2 T-Type Calcium Channel Induced by Varicella-Zoster Virus Participates in the Maintenance of Herpetic Neuralgia. Frontiers in Neurology, 2021, 12, 741054.	1.1	8
2231	Chromosome Genome Sequencing and Comparative Transcriptome-Based Analyses of Kloeckera apiculata 34-9 Unveil the Potential Biocontrol Mechanisms Against Citrus Green Mold. Frontiers in Microbiology, 2021, 12, 752529.	1.5	3
2233	The Effect of Oxidized Fish Oil on the Spleen Index, Antioxidant Activity, Histology and Transcriptome in Juvenile Hybrid Grouper (♀ Epinephelus fuscoguttatus × â™, Epinephelus lanceolatus). Frontiers in Marine Science, 2021, 8, .	1.2	2
2234	Pan-Cancer Analysis Reveals Alternative Splicing Characteristics Associated With Immune-Related Adverse Events Elicited by Checkpoint Immunotherapy. Frontiers in Pharmacology, 2021, 12, 797852.	1.6	8
2235	Transcriptomic Characterization of the Effects of Selenium on Maize Seedling Growth. Frontiers in Plant Science, 2021, 12, 737029.	1.7	8
2236	Endogenic upregulations of HIF/VEGF signaling pathway genes promote air breathing organ angiogenesis in bimodal respiration fish. Functional and Integrative Genomics, 2022, 22, 65-76.	1.4	2
2237	Combined transcriptome and metabolome integrated analysis of Acer mandshuricum to reveal candidate genes involved in anthocyanin accumulation. Scientific Reports, 2021, 11, 23148.	1.6	10
2238	Global genome and comparative transcriptomic analysis reveal the inulin consumption strategy of Lactiplantibacillus plantarum QS7T. Food Research International, 2022, 151, 110846.	2.9	3
2239	Comprehensive Transcriptome and Metabolic Profiling of Petal Color Development in Lycoris sprengeri. Frontiers in Plant Science, 2021, 12, 747131.	1.7	7
2240	Identification of genes related to tipburn resistance in Chinese cabbage and preliminary exploration of its molecular mechanism. BMC Plant Biology, 2021, 21, 567.	1.6	4
2241	Regulatory circuits involving bud dormancy factor PpeDAM6. Horticulture Research, 2021, 8, 261.	2.9	13
2242	Organic waste conversion through anaerobic digestion: A critical insight into the metabolic pathways and microbial interactions. Metabolic Engineering, 2022, 69, 323-337.	3.6	27
2243	PCBP1 regulates the transcription and alternative splicing of metastasis‑related genes and pathways in hepatocellular carcinoma. Scientific Reports, 2021, 11, 23356.	1.6	18

#	Article	IF	CITATIONS
2244	Metagenomic analysis of microflora structure and functional capacity in probiotic Tibetan kefir grains. Food Research International, 2022, 151, 110849.	2.9	24
2245	Screening of bioactivity-oriented extraction approach and quality control standards of lotus leaf extracts with dual functions. Food Bioscience, 2021, 44, 101462.	2.0	6
2246	Kinaseâ€dead mutation: A novel strategy for improving soybean resistance to soybean cyst nematode <i>Heterodera glycines</i> . Molecular Plant Pathology, 2022, 23, 417-430.	2.0	9
2247	The <scp>miR</scp> â€282â€5p regulates larval moulting process by targeting chitinase 5 in <i>Bombyx mori</i> . Insect Molecular Biology, 2022, 31, 190-201.	1.0	9
2248	Protective mechanism of mung bean coat against hyperlipidemia in mice fed with a high-fat diet: insight from hepatic transcriptome analysis. Food and Function, 2021, 12, 12434-12447.	2.1	9
2249	Omicron N501Y mutation among SARS-CoV-2 lineages: In silico analysis of potent binding to tyrosine kinase and hypothetical repurposed medicine. Travel Medicine and Infectious Disease, 2022, 45, 102242.	1.5	25
2250	Influence of Light Supplement on Duck Sternal Calcification from Integrated Analysis of Metabolome and Transcriptome. Poultry Science, 2022, 101, 101697.	1.5	2
2251	Discovery of Therapeutic Candidates for Diabetic Retinopathy Based on Molecular Switch Analysis: Application of a Systematic Process. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-20.	1.9	6
2252	Integrative omics analysis identifies biomarkers of idiopathic pulmonary fibrosis. Cellular and Molecular Life Sciences, 2022, 79, 66.	2.4	8
2253	Physiological and Transcriptomic Analysis Reveals the Responses and Difference to High Temperature and Humidity Stress in Two Melon Genotypes. International Journal of Molecular Sciences, 2022, 23, 734.	1.8	12
2254	Construction and analysis of mRNA, IncRNA, and transcription factor regulatory networks after retinal ganglion cell injury. Experimental Eye Research, 2022, 215, 108915.	1.2	4
2255	Changes in precipitation regime lead to acceleration of the N cycle and dramatic N2O emission. Science of the Total Environment, 2022, 808, 152140.	3.9	20
2256	Effect of dietary oxidized fish oil on liver function in hybrid grouper (♀ Epinephelus fuscoguttatus × â™,) Tj E		rgBT /Overlo
2257	Response signatures of intestinal microbiota and gene transcription of the tiger grouper Epinephelus fuscoguttatus to nervous necrosis virus infection. Aquaculture, 2022, 550, 737848.	1.7	6
2259	Integrative genomics analysis identifies promising SNPs and genes implicated in tuberculosis risk based on multiple omics datasets. Aging, 2020, 12, 19173-19220.	1.4	6
2260	Antineoplastic action of sulforaphane on HeLa cells by modulation of signaling pathways and epigenetic pathways. Minerva Medica, 2022, 112, .	0.3	3
2262	Physiological, Biochemical and Transcriptomic Analysis of the Aerial Parts (Leaf-Blade and Petiole) of Asarum sieboldii Responding to Drought Stress. International Journal of Molecular Sciences, 2021, 22, 13402.	1.8	1
2263	Identification and Fine Mapping of the Recessive Gene BK-5, Which Affects Cell Wall Biosynthesis and Plant Brittleness in Maize. International Journal of Molecular Sciences, 2022, 23, 814.	1.8	3

#	ARTICLE In Vivo and In Vitro Matured Oocytes From Mice of Advanced Reproductive Age Exhibit Alternative	IF	CITATIONS
2264	Splicing Processes for Mitochondrial Oxidative Phosphorylation. Frontiers in Endocrinology, 2022, 13, 816606.	1.5	4
2265	Primingâ€induced alterations in histone modifications modulate transcriptional responses in soybean under salt stress. Plant Journal, 2022, 109, 1575-1590.	2.8	22
2266	Skin and heart allograft rejection solely by long-lived alloreactive T <sub>RM</sub> cells in skin of severe combined immunodeficient mice. Science Advances, 2022, 8, eabk0270.	4.7	14
2267	Genome-Wide Association Analysis Reveals Genetic Loci and Candidate Genes for Chest, Abdominal, and Waist Circumferences in Two Duroc Pig Populations. Frontiers in Veterinary Science, 2021, 8, 807003.	0.9	7
2268	Characterization of RNA Editome in the Mammary Gland of Yaks during the Lactation and Dry Periods. Animals, 2022, 12, 207.	1.0	1
2269	An association study on imputed wholeâ€genome resequencing from highâ€ŧhroughput sequencing data for body traits in crossbred pigs. Animal Genetics, 2022, 53, 212-219.	0.6	10
2270	Integrative Genomic Analyses of 1,145 Patient Samples Reveal New Biomarkers in Esophageal Squamous Cell Carcinoma. Frontiers in Molecular Biosciences, 2021, 8, 792779.	1.6	4
2271	Comparative transcriptome analyses reveal genes related to pigmentation in the petals of a flower color variation cultivar of Rhododendron obtusum. Molecular Biology Reports, 2022, 49, 2641-2653.	1.0	10
2272	Expression level of B- and C-class MADS-box genes is associated with the petaloidy of stamens in cultivated amaryllis ( <i>Hippeastrum hybridum</i> ). Journal of Horticultural Science and Biotechnology, 2022, 97, 211-223.	0.9	3
2273	Transcriptomic and Physiological Analyses of Pigment Accumulation in Eucommia ulmoides â€~Hongye'. Phyton, 2022, 91, 1027-1044.	0.4	3
2274	Deletion of all three MAP kinase genes results in severe defects in stress responses and pathogenesis in Fusarium graminearum. Stress Biology, 2022, 2, 1.	1.5	14
2276	The Candida albicans Cdk8-dependent phosphoproteome reveals repression of hyphal growth through a Flo8-dependent pathway. PLoS Genetics, 2022, 18, e1009622.	1.5	10
2277	Comparative transcriptome analysis reveals variations of bioactive constituents in Lonicera japonica flowers under salt stress. Plant Physiology and Biochemistry, 2022, 173, 87-96.	2.8	8
2278	Identification of mRNA-miRNA-IncRNA regulatory network associated with the immune response to Aeromonas salmonicides infection in the black rockfish (Sebastes schlegelii). Developmental and Comparative Immunology, 2022, 130, 104357.	1.0	13
2279	CD169-positive macrophages enhance abscopal effect of radiofrequency ablation therapy in liver cancer. Translational Oncology, 2022, 15, 101306.	1.7	8
2280	Transcriptome analysis of Auricularia fibrillifera fruit-body responses to drought stress and rehydration. BMC Genomics, 2022, 23, 58.	1.2	9
2281	Transcriptome Profile of a Long-Juvenile Soybean Genotype Huaxia-3 Under Short and Long Photoperiod. Plant Molecular Biology Reporter, 2022, 40, 433-445.	1.0	2
2282	Identify known and novel candidate genes associated with backfat thickness in Duroc pigs by large-scale genome-wide association analysis. Journal of Animal Science, 2022, 100, .	0.2	16

#	Article	IF	CITATIONS
2283	Deoxyshikonin-Induced Gene Expression Profile in Porcine Epithelial Cells. Frontiers in Veterinary Science, 2021, 8, 711721.	0.9	1
2284	Seasonal shift of the gut microbiome synchronizes host peripheral circadian rhythm for physiological adaptation to a low-fat diet in the giant panda. Cell Reports, 2022, 38, 110203.	2.9	49
2285	Transcriptome and HPLC Analysis Reveal the Regulatory Mechanisms of Aurantio-Obtusin in Space Environment-Induced Senna obtusifolia Lines. International Journal of Environmental Research and Public Health, 2022, 19, 898.	1.2	0
2286	Neoadjuvant PD-1 Blockade Combined With Chemotherapy Followed by Concurrent Immunoradiotherapy in Locally Advanced Anal Canal Squamous Cell Carcinoma Patients: Antitumor Efficacy, Safety and Biomarker Analysis. Frontiers in Immunology, 2021, 12, 798451.	2.2	3
2287	Effects of alternative splicing events and transcriptome changes on kidney stone formation. Urolithiasis, 2022, , 1.	1.2	3
2288	Network analysis of host-pathogen protein interactions in microbe induced cardiovascular diseases. In Silico Biology, 2022, 14, 115-133.	0.4	1
2289	CYP4G8 is responsible for the synthesis of methyl-branched hydrocarbons in the polyphagous caterpillar of Helicoverpa armigera. Insect Biochemistry and Molecular Biology, 2022, 140, 103701.	1.2	2
2290	DNA topoisomerase inhibition with the HIF inhibitor acriflavine promotes transcription of IncRNAs in endothelial cells. Molecular Therapy - Nucleic Acids, 2022, 27, 1023-1035.	2.3	7
2291	Cantaloupe melon genome reveals 3D chromatin features and structural relationship with the ancestral cucurbitaceae karyotype. IScience, 2022, 25, 103696.	1.9	12
2292	Identifying individualized risk subpathways reveals pan-cancer molecular classification based on multi-omics data. Computational and Structural Biotechnology Journal, 2022, 20, 838-849.	1.9	2
2293	A chromosome-level genome assembly of an alpine plant <i>Crucihimalaya lasiocarpa</i> provides insights into high-altitude adaptation. DNA Research, 2022, 29, .	1.5	13
2294	Transcriptome Analysis Revealed the Key Genes and Pathways Involved in Seed Germination of Maize Tolerant to Deep-Sowing. Plants, 2022, 11, 359.	1.6	1
2295	<i>&gt;Vibrio gazogenes</i> Inhibits Aflatoxin Production Through Downregulation of Aflatoxin Biosynthetic Genes in <i>Aspergillus flavus</i> . PhytoFrontiers, 2022, 2, 218-229.	0.8	1
2296	Bacterial diversity evolution process based on physicochemical characteristics of sludge treating hydroquinone during acclimation. Environmental Science and Pollution Research, 2022, 29, 31686-31699.	2.7	1
2297	RNA sequencing-based exploration of the effects of blue laser irradiation on mRNAs involved in functional metabolites of <i>D. officinales</i> . PeerJ, 2022, 9, e12684.	0.9	3
2298	Global interpretation of novel alternative splicing events in human congenital pulmonary airway malformations: A pilot study. Journal of Cellular Biochemistry, 2022, , .	1.2	1
2299	Mogroside-rich extract from <i>Siraitia grosvenorii</i> fruits protects against the depletion of ovarian reserves in aging mice by ameliorating inflammatory stress. Food and Function, 2022, 13, 121-130.	2.1	5
2300	Expression Profile Analysis to Identify Circular RNA Expression Signatures in the Prolificacy Trait of Yunshang Black Goat Pituitary in the Estrus Cycle. Frontiers in Genetics, 2021, 12, 801357.	1.1	4

#	Article	IF	CITATIONS
2301	Transcriptomic Analysis and Comparison of the Gene Expression Profiles in Fast- and Slow-Growing Pearl Oysters Pinctada fucata martensii. Journal of Ocean University of China, 2022, 21, 186-194.	0.6	0
2302	RNA-Seq with a novel glabrous-ZM24fl reveals some key lncRNAs and the associated targets in fiber initiation of cotton. BMC Plant Biology, 2022, 22, 61.	1.6	5
2303	Transcriptome landscape of early inflorescence developmental stages identifies key flowering time regulators in chickpea. Plant Molecular Biology, 2022, 108, 565-583.	2.0	5
2304	Distinct molecular phenotypes involving several human diseases are induced by IFN-λ3 and IFN-λ4 in monocyte-derived macrophages. Genes and Immunity, 2022, 23, 73-84.	2.2	2
2305	Unravelling the role of GntR on the regulation of alkane hydroxylase AlkB2 in <i>Pseudomonas aeruginosa</i> DN1 based on transcriptome analysis. Journal of Applied Microbiology, 2022, 132, 2812-2822.	1.4	1
2306	Combined RNA-seq and Phenotype Analysis Reveals a Potential Molecular Mechanism of the Difference in Grain Size of Naked Barley From the Qinghai–Tibetan Plateau. Frontiers in Plant Science, 2022, 13, 822607.	1.7	0
2307	Transcriptome analysis reveals the potential biological function of FSCN1 in HeLa cervical cancer cells. PeerJ, 2022, 10, e12909.	0.9	3
2308	Ubiquitin-proteasome pathway plays an essential regulatory role during spermatangium formation in Neopyropia yezoensis. Algal Research, 2022, 62, 102623.	2.4	1
2309	Liver transcriptome of rabbits supplemented with oral Moringa oleifera leaf powder under heat stress is associated with modulation of lipid metabolism and up-regulation of genes for thermo-tolerance, antioxidation, and immunity. Nutrition Research, 2022, 99, 25-39.	1.3	6
2310	Pharmacotranscriptomic profiling of resistant triple-negative breast cancer cells treated with lapatinib and berberine shows upregulation of PI3K/Akt signaling under cytotoxic stress. Gene, 2022, 816, 146171.	1.0	3
2311	Triplication is the main evolutionary driving force of NLP transcription factor family in Chinese cabbage and related species. International Journal of Biological Macromolecules, 2022, 201, 492-506.	3.6	4
2312	Long-term fasting leads to preferential catabolism of His, Arg, and branched-chain amino acids in the dorsal muscle of gibel carp (Carassius auratus gibelio): Potential preferential use of amino acids as energy substrates. Aquaculture, 2022, 552, 737967.	1.7	8
2313	Comparative transcriptome analysis reveals distinct responsive biological processes in radish genotypes contrasting for Plasmodiophora brassicae interaction. Gene, 2022, 817, 146170.	1.0	4
2314	Identification of inflammatory response and alternative splicing in acute kidney injury and experimental verification of the involvement of RNAâ€ʿbinding protein RBFOX1 in this disease. International Journal of Molecular Medicine, 2022, 49, .	1.8	10
2315	Developmental Transcriptome Profiling of the Tibial Reveals the Underlying Molecular Basis for Why Newly Hatched Quails Can Walk While Newly Hatched Pigeons Cannot. Frontiers in Cell and Developmental Biology, 2022, 10, 745129.	1.8	1
2316	Leaf color formation mechanisms in Alternanthera bettzickiana elucidated by metabolite and transcriptome analyses. Planta, 2022, 255, 59.	1.6	5
2317	Genetic Perturbation of the Starch Biosynthesis in Maize Endosperm Reveals Sugar-Responsive Gene Networks. Frontiers in Plant Science, 2021, 12, 800326.	1.7	8
2318	Time-course analysis and transcriptomic identification of key response strategies of <i>Nelumbo nucifera</i> to complete submergence. Horticulture Research, 2022, 9, .	2.9	9

#	Article	IF	CITATIONS
2319	Upâ€regulation of <scp>miR</scp> â€335 and <scp>miR</scp> â€674â€3p in the rostral ventrolateral medulla contributes to stressâ€induced hypertension. Journal of Neurochemistry, 2022, 161, 387-404.	2.1	6
2320	Identification of genes involved in drought tolerance in seedlings of the desert grass, Psammochloa villosa (Poaceae), based on full-length isoform sequencing and de novo assembly from short reads. Journal of Plant Physiology, 2022, 271, 153630.	1.6	2
2321	Physio-Morphological, Biochemical and Transcriptomic Analyses Provide Insights Into Drought Stress Responses in Mesona chinensis Benth. Frontiers in Plant Science, 2022, 13, 809723.	1.7	6
2322	Transcriptomic Analysis of Gill and Hepatopancreas in Razor Clam (Sinonovacula constricta) Exposed to Acute Ammonia. Frontiers in Marine Science, 2022, 9, .	1.2	9
2323	HPRT1 Promotes Chemoresistance in Oral Squamous Cell Carcinoma via Activating MMP1/PI3K/Akt Signaling Pathway. Cancers, 2022, 14, 855.	1.7	17
2324	Multi-Omics Analysis Reveals the Dynamic Changes of RNA N6-Methyladenosine in Pear (Pyrus) Tj ETQq1 1 0.784 Microbiology, 2021, 12, 803512.	1314 rgBT 1.5	/Overlock 10 3
2325	Dynamic Gene Expression and Alternative Splicing Events Demonstrate Co-Regulation of Testicular Differentiation and Maturation by the Brain and Gonad in Common Carp. Frontiers in Endocrinology, 2021, 12, 820463.	1.5	1
2326	Identification of Candidate Genes for Meat Color of Chicken by Combing Selection Signature Analyses and Differentially Expressed Genes. Genes, 2022, 13, 307.	1.0	5
2327	Biomedical application community based on China high-performance computing environment. CCF Transactions on High Performance Computing, 0, , .	1.1	0
2329	Perturbation of Wnt/βâ€catenin signaling and sexual dimorphism in nonâ€alcoholic fatty liver disease. Hepatology Research, 2022, 52, 433-448.	1.8	2
2330	Reprint of Organic waste conversion through anaerobic digestion: A critical insight into the metabolic pathways and microbial interactions. Metabolic Engineering, 2022, 71, 62-76.	3.6	24
2331	Genome-Wide Identification of Direct Targets of ZjVND7 Reveals the Putative Roles of Whole-Genome Duplication in Sour Jujube in Regulating Xylem Vessel Differentiation and Drought Tolerance. Frontiers in Plant Science, 2022, 13, 829765.	1.7	1
2332	Transcriptome Profiling Revealed Basis for Growth Heterosis in Hybrid Tilapia (Oreochromis niloticus) Tj ETQq0 0	0 rgBT /O 0.7	verlock 10 Tf
2333	Multi-Omics Landscape of DNA Methylation Regulates Browning in "Fuji―Apple. Frontiers in Nutrition, 2021, 8, 800489.	1.6	7
2334	Regulation of phenylpropanoid metabolism during moderate freezing and post-freezing recovery in <i>Dendrobium ofi¢inale</i> . Journal of Plant Interactions, 2022, 17, 290-300.	1.0	3
2335	Whole-genome resequencing reveals genetic indels of feathered-leg traits in domestic chickens. Journal of Genetics, 2019, 98, .	0.4	3
2336	Variation and Influential Factors Underlying P Cycling in Rhizosphere Microbial Communities Along Water Gradients in an Arid Desert Region. SSRN Electronic Journal, 0, , .	0.4	0

A high-quality assembly reveals genomic characteristics, phylogenetic status, and causal genes for leucism plumage of Indian peafowl. GigaScience, 2022, 11, .

#	Article	IF	CITATIONS
2338	Bioinformatics Analysis of Differential Gene and MicroRNA Expression in Lung Adenocarcinoma: Genetic Effects on Patient Prognosis, as Indicated by the TCGA Database. Cancer Informatics, 2022, 21, 117693512210820.	0.9	1
2339	Proxied Therapeutic Inhibition on Wnt Signaling Antagonists and Risk of Cardiovascular Diseases: Multi-Omics Analyses. SSRN Electronic Journal, 0, , .	0.4	0
2340	Comparison of the root, leaf and internode transcriptomes in sugarcane (Saccharum spp. hybrids). Current Research in Biotechnology, 2022, 4, 167-178.	1.9	2
2341	Fatty acid synthase (Fasn) inhibits the expression levels of immune response genes via alteration of alternative splicing in islet cells. Journal of Diabetes and Its Complications, 2022, 36, 108159.	1.2	5
2342	Genome-Wide Identification of Immune-Related Alternative Splicing and Splicing Regulators Involved in Abdominal Aortic Aneurysm. Frontiers in Genetics, 2022, 13, 816035.	1.1	9
2343	Integrated Analysis of Metabolomics and Transcriptomics for Assessing Effects of Fish Meal and Fish Oil Replacement on the Metabolism of Rainbow Trout (Oncorhynchus mykiss). Frontiers in Marine Science, 2022, 9, .	1.2	3
2344	Transcriptome and Metabolome Analyses Provide Insights Into the Composition and Biosynthesis of Grassy Aroma Volatiles in White-Fleshed Pitaya. ACS Omega, 2022, 7, 6518-6530.	1.6	8
2345	Static Magnetic Field Inhibits Growth of Escherichia coli Colonies via Restriction of Carbon Source Utilization. Cells, 2022, 11, 827.	1.8	6
2346	MicroRNA editing patterns in Huntington's disease. Scientific Reports, 2022, 12, 3173.	1.6	11
2347	Soil Properties Interacting With Microbial Metagenome in Decreasing CH4 Emission From Seasonally Flooded Marshland Following Different Stages of Afforestation. Frontiers in Microbiology, 2022, 13, 830019.	1.5	1
2348	Microbial Community and Metabolite Dynamics During Soy Sauce Koji Making. Frontiers in Microbiology, 2022, 13, 841529.	1.5	14
2349	Transcriptomics-Based Identification of Genes Related to Tapetum Degradation and Microspore Development in Lily. Genes, 2022, 13, 366.	1.0	0
2350	Non-Coding Transcriptome Provides Novel Insights into the Escherichia coli F17 Susceptibility of Sheep Lamb. Biology, 2022, 11, 348.	1.3	6
2351	Transcriptome changes in the developing sugarcane culm associated with high yield and early-season high sugar content. Theoretical and Applied Genetics, 2022, 135, 1619-1636.	1.8	1
2352	Study of Dimorphism Transition Mechanism of Tremella fuciformis Based on Comparative Proteomics. Journal of Fungi (Basel, Switzerland), 2022, 8, 242.	1.5	1
2353	Identification and Functional Analysis of IncRNA by CRISPR/Cas9 During the Cotton Response to Sap-Sucking Insect Infestation. Frontiers in Plant Science, 2022, 13, 784511.	1.7	12
2354	MiR-24-3p Conservatively Regulates Muscle Cell Proliferation and Apoptosis by Targeting Common Gene CAMK2B in Rat and Cattle. Animals, 2022, 12, 505.	1.0	4
2355	Transcriptome analysis of genes associated with autolysis of Coprinus comatus. Scientific Reports, 2022, 12, 2476.	1.6	0

#	Article	IF	CITATIONS
2356	Small RNA sequencing reveals placenta-derived exosomal microRNAs associated with preeclampsia. Journal of Hypertension, 2022, 40, 1030-1041.	0.3	5
2357	Transcriptome analysis and differential gene expression profiling of wucai (Brassica campestris L.) in response to cold stress. BMC Genomics, 2022, 23, 137.	1.2	11
2358	Metabolome and Whole-Transcriptome Analyses Reveal the Molecular Mechanisms Underlying Hypoglycemic Nutrient Metabolites Biosynthesis in Cyclocarya paliurus Leaves During Different Harvest Stages. Frontiers in Nutrition, 2022, 9, 851569.	1.6	6
2359	A productive immunocompetent mouse model of cryptosporidiosis with long oocyst shedding duration for immunological studies. Journal of Infection, 2022, 84, 710-721.	1.7	7
2360	Cultivating Lentinula edodes on Substrate Containing Composted Sawdust Affects the Expression of Carbohydrate and Aromatic Amino Acid Metabolism-Related Genes. MSystems, 2022, 7, e0082721.	1.7	5
2361	A Genome Wide Association Study Revealed Key Single Nucleotide Polymorphisms/Genes Associated With Seed Germination in Gossypium hirsutum L. Frontiers in Plant Science, 2022, 13, 844946.	1.7	3
2362	Expression characteristics and interaction networks of microRNAs in spleen tissues of grass carp (Ctenopharyngodon idella). PLoS ONE, 2022, 17, e0266189.	1.1	5
2363	Baculoviruses hijack the visual perception of their caterpillar hosts to induce climbing behaviour thus promoting virus dispersal. Molecular Ecology, 2022, 31, 2752-2765.	2.0	6
2364	CELF1 promotes matrix metalloproteinases gene expression at transcriptional level in lens epithelial cells. BMC Ophthalmology, 2022, 22, 122.	0.6	3
2365	Insights into the Impact of Rosmarinic Acid on CHO Cell Culture Improvement through Transcriptomics Analysis. Processes, 2022, 10, 533.	1.3	1
2366	Zinc-binding proteins in stallion seminal plasma as potential sperm function regulators. Annals of Animal Science, 2022, 22, 961-976.	0.6	1
2367	A Feature Selection Approach Guided an Early Prediction of Anthocyanin Accumulation Using Massive Untargeted Metabolomics Data in Mulberry. Plant and Cell Physiology, 2022, , .	1.5	1
2368	LncCCAT1 interaction protein PKM2 upregulates SREBP2 phosphorylation to promote osteosarcoma tumorigenesis by enhancing the Warburg effect and lipogenesis. International Journal of Oncology, 2022, 60, .	1.4	11
2369	Genome-Wide Detection of Copy Number Variants in Chinese Indigenous Horse Breeds and Verification of CNV-Overlapped Genes Related to Heat Adaptation of the Jinjiang Horse. Genes, 2022, 13, 603.	1.0	5
2370	Transcriptome Analysis Revealed a Cold Stress-Responsive Transcription Factor, PaDREB1A, in Plumbago auriculata That Can Confer Cold Tolerance in Transgenic Arabidopsis thaliana. Frontiers in Plant Science, 2022, 13, 760460.	1.7	3
2371	Transcriptional atlas analysis from multiple tissues reveals the expression specificity patterns in beef cattle. BMC Biology, 2022, 20, 79.	1.7	12
2372	Root endophyte differentially regulates plant response to NO <sub>3</sub> <sup>â^`</sup> and NH <sub>4</sub> <sup>+</sup> nutrition by modulating N fluxes at the plant–fungal interface. Plant, Cell and Environment, 2022, 45, 1813-1828.	2.8	9
2373	De Novo Assembly of 20 Chicken Genomes Reveals the Undetectable Phenomenon for Thousands of Core Genes on Microchromosomes and Subtelomeric Regions. Molecular Biology and Evolution, 2022, 39, .	3.5	40

#	Article	IF	CITATIONS
2374	Transcriptome Analysis of Bovine Rumen Tissue in Three Developmental Stages. Frontiers in Genetics, 2022, 13, 821406.	1.1	4
2375	Transcriptomic Profiling of Circular RNAs in the Goat Rumen During Fetal and Prepubertal Period. Frontiers in Physiology, 2022, 13, 858991.	1.3	2
2376	Profiling and functional analysis of differentially expressedÂcircularÂRNAs identified in foot-and-mouth disease virus infected PK-15 cells. Veterinary Research, 2022, 53, 24.	1.1	2
2377	Dormant Nfatc1 reporter-marked basal stem/progenitor cells contribute to mammary lobuloalveoli formation. IScience, 2022, 25, 103982.	1.9	2
2378	Full-length transcriptome reconstruction reveals genetic differences in hybrids of Oryza sativa and Oryza punctata with different ploidy and genome compositions. BMC Plant Biology, 2022, 22, 131.	1.6	4
2379	SIAH ubiquitin E3 ligases as modulators of inflammatory gene expression. Heliyon, 2022, 8, e09029.	1.4	2
2380	Cold stress after swimming fatigue decreases immunity-related gene expression in the spleen of the Chinese sucker. Fish and Shellfish Immunology, 2022, 122, 455-464.	1.6	1
2381	The Crosstalk of the Salicylic Acid and Jasmonic Acid Signaling Pathways Contributed to Different Resistance to Phytoplasma Infection Between the Two Genotypes in Chinese Jujube. Frontiers in Microbiology, 2022, 13, 800762.	1.5	6
2383	Dynamic mRNA and miRNA expression of the head during early development in bighead carp (Hypophthalmichthys nobilis). BMC Genomics, 2022, 23, 168.	1.2	4
2384	Magnetic biochar affects the metabolic pathway in methanogenesis of anaerobic digestion of food waste. GCB Bioenergy, 2022, 14, 572-584.	2.5	9
2385	Integration of mRNA and miRNA Profiling Reveals Heterosis in Oreochromis niloticus × O. aureus Hybrid Tilapia. Animals, 2022, 12, 640.	1.0	6
2386	Xenogeneic nucleoid-associated EnrR thwarts H-NS silencing of bacterial virulence with unique DNA binding. Nucleic Acids Research, 2022, 50, 3777-3798.	6.5	6
2387	Population Genetic Structure and Selection Signature Analysis of Beijing Black Pig. Frontiers in Genetics, 2022, 13, 860669.	1.1	9
2388	An analysis of skin thickness in the Dezhou donkey population and identification of candidate genes by RNAâ€seq. Animal Genetics, 2022, 53, 368-379.	0.6	5
2389	Exploiting the antibacterial mechanism of phenazine substances from Lysobacter antibioticus 13-6 against Xanthomonas oryzae pv. oryzicola. Journal of Microbiology, 2022, 60, 496-510.	1.3	5
2390	Transcriptome profiling of cashew apples (Anacardium occidentale) genotypes reveals specific genes linked to firmness and color during pseudofruit development. Plant Molecular Biology, 2022, , .	2.0	2
2392	Hybrid RNA Sequencing Strategy for the Dynamic Transcriptomes of Winter Dormancy in an Evergreen Herbaceous Perennial, Iris japonica. Frontiers in Genetics, 2022, 13, 841957.	1.1	5
2393	Transcriptomic analysis of Vigna radiata in response to chilling stress and uniconazole application. BMC Genomics, 2022, 23, 205.	1.2	9

#	Article	IF	CITATIONS
2394	Mammary epithelial cell transcriptome reveals potential roles of lncRNAs in regulating milk synthesis pathways in Jersey and Kashmiri cattle. BMC Genomics, 2022, 23, 176.	1.2	4
2395	Assessment the effect of genomic selection and detection of selective signature in broilers. Poultry Science, 2022, 101, 101856.	1.5	9
2396	Next-Generation Sequencing of Circular RNAs Reveals the Molecular Mechanisms of Chondrogenic Differentiation in Human Adipose-derived Stem Cells. Cell Biochemistry and Biophysics, 2022, , 1.	0.9	0
2397	UV <i>-</i> B and UV <i>-</i> C radiation trigger both common and distinctive signal perceptions and transmissions in <i>Pinus tabuliformis</i> Carr Tree Physiology, 2022, 42, 1587-1600.	1.4	4
2398	RNA-Seq analysis discovers the critical role of Rel in ppGpp synthesis, pathogenicity, and the VBNC state of <i>Clavibacter michiganensis</i> . Phytopathology, 2022, , .	1.1	1
2399	Assessing Genomic Diversity and Selective Pressures in Bohai Black Cattle Using Whole-Genome Sequencing Data. Animals, 2022, 12, 665.	1.0	4
2400	Terpinen-4-ol inhibits the proliferation and mobility of pancreatic cancer cells by downregulating Rho-associated coiled-coil containing protein kinase 2. Bioengineered, 2022, 13, 8643-8656.	1.4	7
2401	The long non-coding RNA LNC_000397 negatively regulates PRRSV replication through induction of interferon-stimulated genes. Virology Journal, 2022, 19, 40.	1.4	7
2402	Regulatory mechanism of downregulation of SOD1 expression on cardiomyocyte function. Sleep and Breathing, 2023, 27, 399-410.	0.9	1
2403	In Silico Characterisation of the Late Embryogenesis Abundant (LEA) Protein Families and Their Role in Desiccation Tolerance in Ramonda serbica Panc. International Journal of Molecular Sciences, 2022, 23, 3547.	1.8	11
2404	Chromosome-scale Echinococcus granulosus (genotype G1) genome reveals the Eg95 gene family and conservation of the EG95-vaccine molecule. Communications Biology, 2022, 5, 199.	2.0	7
2405	Autophagy-Related Genes Predict the Progression of Periodontitis Through the ceRNA Network. Journal of Inflammation Research, 2022, Volume 15, 1811-1824.	1.6	16
2406	High-content analysis of microRNAs involved in the phenotype regulation of vascular smooth muscle cells. Scientific Reports, 2022, 12, 3498.	1.6	2
2407	Revealing key IncRNAs in cytogenetically normal acute myeloid leukemia by reconstruction of the IncRNA–mRNA–mRNA network. Scientific Reports, 2022, 12, 4973.	1.6	3
2408	Identification of Genes Involved in Resistance to High Exogenous 20-Hydroxyecdysone in Spodoptera litura. Insects, 2022, 13, 297.	1.0	1
2409	Fine Mapping and Characterization of a Major Gene Responsible for Chlorophyll Biosynthesis in Brassica napus L. Biomolecules, 2022, 12, 402.	1.8	3
2410	Heat Shock Procedure Affects Cell Division-Associated Genes in Gynogenetic Manipulation. Marine Biotechnology, 2022, 24, 354.	1.1	2
2412	Genome-Wide Expression and Physiological Profiling of Pearl Millet Genotype Reveal the Biological Pathways and Various Gene Clusters Underlying Salt Resistance. Frontiers in Plant Science, 2022, 13, 849618.	1.7	15

#	Article	IF	CITATIONS
2413	Transcriptome Analysis Reveals the Alternative Splicing Changes in the Immune-Related Genes of the Giant Panda (Ailuropoda melanoleuca), in Response to the Canine Distemper Vaccine. Zoological Science, 2022, 39, .	0.3	3
2414	Preliminary Results about Lamb Meat Tenderness Based on the Study of Novel Isoforms and Alternative Splicing Regulation Pathways Using Iso-seq, RNA-seq and CTCF ChIP-seq Data. Foods, 2022, 11, 1068.	1.9	7
2415	Accumulation of functional metabolites and transcriptomics in postharvest fumeâ€drying and airâ€drying process in rhubarb. Journal of the Science of Food and Agriculture, 2022, , .	1.7	0
2416	Comparative analyses of American and Asian lotus genomes reveal insights into petal color, carpel thermogenesis and domestication. Plant Journal, 2022, 110, 1498-1515.	2.8	21
2417	MicroRNAs Influence the Migratory Ability of Human Umbilical Vein Endothelial Cells. Genes, 2022, 13, 640.	1.0	1
2418	Dynamic transcriptome profiling reveals essential roles of the Receptor Tyrosine Kinases (RTK) family in feather development of duck. British Poultry Science, 2022, , .	0.8	0
2419	Transcriptomic profiling and novel insights into the effect of AG ablation on gonad development in Macrobrachium rosenbergii. Aquaculture, 2022, 556, 738224.	1.7	4
2420	Genome-wide identification of PEBP gene family members in potato, their phylogenetic relationships, and expression patterns under heat stress. Molecular Biology Reports, 2022, 49, 4683-4697.	1.0	5
2421	Transcriptomic and Proteomic Analysis of Marine Nematode Litoditis marina Acclimated to Different Salinities. Genes, 2022, 13, 651.	1.0	5
2422	Metatranscriptomic Analyses Reveal the Functional Role of Botrytis cinerea in Biochemical and Textural Changes during Noble Rot of Grapevines. Journal of Fungi (Basel, Switzerland), 2022, 8, 378.	1.5	3
2423	Knockdown of CDR1as Decreases Differentiation of Goat Skeletal Muscle Satellite Cells via Upregulating miR-27a-3p to Inhibit ANGPT1. Genes, 2022, 13, 663.	1.0	6
2424	Differentially Expressed Circular RNA Profile Signatures Identified in Prolificacy Trait of Yunshang Black Goat Ovary at Estrus Cycle. Frontiers in Physiology, 2022, 13, 820459.	1.3	7
2425	Chromosomeâ€scale genome assembly provides insights into speciation of allotetraploid and massive biomass accumulation of elephant grass ( <i>Pennisetum purpureum</i> Schum.). Molecular Ecology Resources, 2022, 22, 2363-2378.	2.2	11
2426	Integrative Analysis of Long- and Short-Read Transcriptomes Identify the Regulation of Terpenoids Biosynthesis Under Shading Cultivation in Oenanthe javanica. Frontiers in Genetics, 2022, 13, 813216.	1.1	6
2428	Comparative transcriptome analysis of the Eureka lemon in response to Citrus yellow vein virus infection at different temperatures. Physiological and Molecular Plant Pathology, 2022, 119, 101832.	1.3	3
2429	Transcriptome analysis of the reproduction of silkworm (Bombyx mori) under dimethoate stress. Pesticide Biochemistry and Physiology, 2022, 183, 105081.	1.6	9
2430	Bioinformatics role of the WGCNA analysis and co-expression network identifies of prognostic marker in lung cancer. Saudi Journal of Biological Sciences, 2022, 29, 3519-3527.	1.8	9
2431	Transcriptomic and proteomic analysis of Chinese rare minnow (Gobiocypris rarus) larvae in response to acute waterborne cadmium or mercury stress. Aquatic Toxicology, 2022, 246, 106134.	1.9	8

#	Article	IF	CITATIONS
2432	Integrating Genome-wide association and whole transcriptome analysis to reveal genetic control of leaf traits in Gossypium arboreum L Genomics, 2022, 114, 110331.	1.3	2
2433	Transcriptome and DNA methylome provide insights into the molecular regulation of drought stress in sea buckthorn. Genomics, 2022, 114, 110345.	1.3	5
2434	A transcriptomics and molecular biology based investigation reveals the protective effect and mechanism of carnosol on t-BHP induced HRMECs via Nrf2 signaling pathway. European Journal of Pharmacology, 2022, 923, 174933.	1.7	3
2435	The CDK1 inhibitor, Ro-3306, is a potential antiviral candidate against influenza virus infection. Antiviral Research, 2022, 201, 105296.	1.9	4
2436	Acute septicemia and immune response of spotted sea bass (Lateolabrax maculatus) to Aeromonas veronii infection. Fish and Shellfish Immunology, 2022, 124, 47-55.	1.6	11
2437	Identification and functional analysis of miRNAs in skeletal muscle of juvenile and adult largemouth bass, Micropterus salmoides. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2022, 42, 100985.	0.4	1
2438	Three root hair defective genes, GhRHD3-1, GhRHD4-1, and GhRSL4-1, regulate fiber cell elongation in cotton. Industrial Crops and Products, 2022, 180, 114751.	2.5	1
2439	Effects of a soil collembolan on the growth and metal uptake of a hyperaccumulator: Modification of root morphology and the expression of plant defense genes. Environmental Pollution, 2022, 303, 119169.	3.7	3
2440	Integrated transcriptome, small RNA and degradome analysis provide insights into the transcriptional regulatory networks underlying cold acclimation in jojoba. Scientia Horticulturae, 2022, 299, 111050.	1.7	3
2441	Time-course transcriptome analysis identifies rewiring patterns of transcriptional regulatory networks in rice under Rhizoctonia solani infection. Gene, 2022, 828, 146468.	1.0	5
2442	Comparative analysis of anatomical structure, assimilate accumulation and gene expression in lignin and carbohydrate metabolism pathway during taproot thickening of taicai and pak choi. Scientia Horticulturae, 2022, 301, 111046.	1.7	1
2443	Transcriptome sequencing reveals mechanism of improved antioxidant capacity and maintained postharvest quality of winter jujube during cold storage after salicylic acid treatment. Postharvest Biology and Technology, 2022, 189, 111929.	2.9	20
2444	Intraspecific hybridization as a mitigation strategy of ocean acidification in marine bivalve noble scallop Chlamys nobilis. Science of the Total Environment, 2022, 832, 154736.	3.9	3
2445	Long-term pruning modulates microbial community structure and their functional potential in Tea (Camellia sinensis L.) soils. Applied Soil Ecology, 2022, 176, 104483.	2.1	9
2446	Comparative transcriptome profiling of <i>Termitomyces</i> sp. between monocultures inÂvitro and linkâ€stipe of fungusâ€combs inÂsitu. Letters in Applied Microbiology, 2022, 74, 429-443.	1.0	0
2447	Full-Length Transcriptome Sequencing: An Insight Into the Dog Model of Heart Failure. Frontiers in Cardiovascular Medicine, 2021, 8, 712797.	1.1	4
2448	Comparative de novo transcriptome analysis identifies salinity stress responsive genes and metabolic pathways in sugarcane and its wild relative Erianthus arundinaceus [Retzius] Jeswiet. Scientific Reports, 2021, 11, 24514.	1.6	5
2449	Potential biomarkers of acute myocardial infarction based on co‑expression network analysis. Experimental and Therapeutic Medicine, 2021, 23, 162.	0.8	6

#	Article	IF	CITATIONS
2452	Comparative Transcriptome Analysis of Female and Male Fine-Patterned Puffer: Identification of Candidate Genes Associated with Growth and Sex Differentiation. Fishes, 2021, 6, 79.	0.7	4
2453	Transcriptome-wide association study identifies multiple genes and pathways associated with thyroid function. Human Molecular Genetics, 2021, , .	1.4	2
2454	Carnosine concentration and expression profiles of carnosine related genes in Mytilus after beta-alanine injection. Journal of Oceanology and Limnology, 0, , 1.	0.6	1
2455	CREM Is Correlated With Immune-Suppressive Microenvironment and Predicts Poor Prognosis in Gastric Adenocarcinoma. Frontiers in Cell and Developmental Biology, 2021, 9, 697748.	1.8	9
2456	Chromosome-Level Genome Assembly and HazelOmics Database Construction Provides Insights Into Unsaturated Fatty Acid Synthesis and Cold Resistance in Hazelnut (Corylus heterophylla). Frontiers in Plant Science, 2021, 12, 766548.	1.7	7
2457	Chemical Characterization, Antitumor, and Immune-Enhancing Activities of Polysaccharide from Sargassum pallidum. Molecules, 2021, 26, 7559.	1.7	10
2458	Transcriptomic analysis provides insights into the immune responses and nutrition in <i>Ostrinia furnacalis</i> larvae parasitized by <i>Macrocentrus cingulum</i> . Archives of Insect Biochemistry and Physiology, 2022, 109, e21863.	0.6	6
2459	Genetic Basis of Follicle Development in Dazu Black Goat by Whole-Transcriptome Sequencing. Animals, 2021, 11, 3536.	1.0	4
2460	Genome-wide association and selective sweep analyses reveal genetic loci for FCR of egg production traits in ducks. Genetics Selection Evolution, 2021, 53, 98.	1.2	7
2461	Screening and Identification of Muscle-Specific Candidate Genes via Mouse Microarray Data Analysis. Frontiers in Veterinary Science, 2021, 8, 794628.	0.9	3
2462	Survival stratification for colorectal cancer via multi-omics integration using an autoencoder-based model. Experimental Biology and Medicine, 2022, 247, 898-909.	1.1	12
2463	Repression of the expression of proinflammatory genes by mitochondrial transcription factor A is linked to its alternative splicing regulation in human lung epithelial cells. BMC Immunology, 2021, 22, 74.	0.9	4
2464	Identification of Unique Key miRNAs, TFs, and mRNAs in Virulent MTB Infection Macrophages by Network Analysis. International Journal of Molecular Sciences, 2022, 23, 382.	1.8	6
2465	Decabromodiphenyl Ethane Mainly Affected the Muscle Contraction and Reproductive Endocrine System in Female Adult Zebrafish. Environmental Science & Technology, 2022, 56, 470-479.	4.6	27
2466	Transcriptome analysis and potential mechanisms of bovine oocytes under seasonal heat stress. Animal Biotechnology, 2023, 34, 1179-1195.	0.7	1
2467	Identification of Co-Expressed Genes Related to Theacrine Synthesis in Tea Flowers at Different Developmental Stages. International Journal of Molecular Sciences, 2021, 22, 13394.	1.8	6
2468	Evaluation of the effect of high temperature on the full-length transcriptome and biochemical parameters of chili pepper fruit (Capsicum annuum L.) at different developmental stages. European Journal of Horticultural Science, 2021, 86, 651-662.	0.3	0
2469	Identification of key gene networks controlling vernalization development characteristics of Isatis indigotica by full-length transcriptomes and gene expression profiles. Physiology and Molecular Biology of Plants, 2021, 27, 2679-2693.	1.4	1

#	Article	IF	CITATIONS
2470	Transcriptomic analysis reveals that non-forage or forage fiber source promotes rumen development through different metabolic processes in lambs. Animal Biotechnology, 2023, 34, 1058-1071.	0.7	2
2471	Quantitative Trait Loci and Transcriptome Analysis Reveal Genetic Basis of Fiber Quality Traits in CCRI70 RIL Population of Gossypium hirsutum. Frontiers in Plant Science, 2021, 12, 753755.	1.7	5
2472	RNA-Binding Profiles of CKAP4 as an RNA-Binding Protein in Myocardial Tissues. Frontiers in Cardiovascular Medicine, 2021, 8, 773573.	1.1	2
2473	Cytological, Biochemical, and Transcriptomic Analyses of a Novel Yellow Leaf Variation in a Paphiopedilum (Orchidaceae) SCBG COP15. Genes, 2022, 13, 71.	1.0	4
2474	Comparative transcriptome analysis of two sugarcane varieties in response to diazotrophic plant growth promoting endophyte <i>Enterobacter roggenkampii</i> ED5. Journal of Plant Interactions, 2022, 17, 75-84.	1.0	10
2475	Effects of Neck-Arm Restraint Suspension of Beef Carcasses on Meat Quality and Proteome of Different Muscles During Post-mortem Aging. Frontiers in Nutrition, 2021, 8, 774529.	1.6	2
2476	Molecular diagnosis of Kallmann syndrome with diabetes by whole exome sequencing and bioinformatic approaches. World Journal of Diabetes, 2021, 12, 2058-2072.	1.3	2
2477	Integrated Study of Transcriptome-wide m6A Methylome Reveals Novel Insights Into the Character and Function of m6A Methylation During Yak Adipocyte Differentiation. Frontiers in Cell and Developmental Biology, 2021, 9, 689067.	1.8	7
2478	The mechanism of bud dehyperhydricity by the method of â€~̃starvation drying combined with AgNO3' in <i>Lycium ruthenicum</i> . Tree Physiology, 2022, 42, 1841-1857.	1.4	2
2479	Linkage and association analyses reveal that hub genes in energy-flow and lipid biosynthesis pathways form a cluster in upland cotton. Computational and Structural Biotechnology Journal, 2022, 20, 1841-1859.	1.9	6
2480	Deciphering the Molecular Mechanisms of Insecticide Resistance From the Transcriptome Data of Field Evolved Spinosad Resistant and Susceptible Populations of <i>Plutella xylostella</i> (Lepidoptera:) Tj ETQqO 0 0	rg <b>₿</b> T8∕Ove	rloæk 10 Tf 50
2481	Integrated Analysis of the ceRNA Network and M-7474 Function in Testosterone-Mediated Fat Deposition in Pigs. Genes, 2022, 13, 668.	1.0	2
2482	Whole blood transcriptome profiling identifies candidate genes associated with alopecia in male giant pandas (Ailuropoda melanoleuca). BMC Genomics, 2022, 23, 297.	1.2	1
2483	Long noncoding RNA SH3PXD2A-AS1 promotes NSCLC proliferation and accelerates cell cycle progression by interacting with DHX9. Cell Death Discovery, 2022, 8, 192.	2.0	4
2484	Temporal Transcriptional Responses of a Vibrio alginolyticus Strain to <i>Podoviridae</i> Phage HH109 Revealed by RNA-Seq. MSystems, 2022, 7, e0010622.	1.7	4
2485	Mapping of Quantitative Trait Loci Underlying Nodule Traits in Soybean (Glycine max (L.) Merr.) and Identification of Genes Whose Expression Is Affected by the Sinorhizobium fredii HH103 Effector Proteins NopL and NopT. Agronomy, 2022, 12, 946.	1.3	7
2486	Network Pharmacology with Experimental Investigation of the Mechanisms of <i>Rhizoma Polygonati</i> against Prostate Cancer with Additional Herbzymatic Activity. ACS Omega, 2022, 7, 14465-14477.	1.6	9
2487	High-quality chromosome-scale de novo assembly of the Paspalum notatum â€~Flugge' genome. BMC Genomics, 2022, 23, 293.	1.2	1

#	Article	IF	CITATIONS
2488	Interactome and Ubiquitinome Analyses Identify Functional Targets of Herpes Simplex Virus 1 Infected Cell Protein 0. Frontiers in Microbiology, 2022, 13, 856471.	1.5	3
2489	Gene expression profiles provide insights into the survival strategies in deep-sea mussel (Bathymodiolus platifrons) of different developmental stages. BMC Genomics, 2022, 23, 311.	1.2	2
2490	DEK modulates both expression and alternative splicing of cancer‑related genes. Oncology Reports, 2022, 47, .	1.2	2
2491	Effect of Monoacylglycerol Lipase Inhibition on Intestinal Permeability of Rats With Severe Acute Pancreatitis. Frontiers in Pharmacology, 2022, 13, 869482.	1.6	3
2492	Transcriptome analysis of skin color variation during and after overwintering of Malaysian red tilapia. Fish Physiology and Biochemistry, 2022, 48, 669-682.	0.9	4
2493	Serum mitochondrial tsRNA serves as a novel biomarker for hepatocarcinoma diagnosis. Frontiers of Medicine, 2022, 16, 216-226.	1.5	15
2494	Analysis of Transcriptome Difference between Blood-Fed and Starved Tropical Bed Bug, Cimex hemipterus (F.) (Hemiptera: Cimicidae). Insects, 2022, 13, 387.	1.0	0
2495	Transcriptomic and Metabolomic Analysis Provides Insights into the Fruit Quality and Yield Improvement in Tomato under Soilless Substrate-Based Cultivation. Agronomy, 2022, 12, 923.	1.3	5
2496	Rice sl-MH-1 mutant induces cell death and confers blast resistance via the synergistic roles of signaling systems. Crop Journal, 2022, , .	2.3	0
2497	Insights Into Long Non-Coding RNA and mRNA Expression in the Jejunum of Lambs Challenged With Escherichia coli F17. Frontiers in Veterinary Science, 2022, 9, 819917.	0.9	4
2498	Depletion of LOXL2 improves respiratory capacity: From air-breathing fish to mammal under hypoxia. International Journal of Biological Macromolecules, 2022, 209, 563-575.	3.6	6
2860	Valproic Acid Initiates Transdifferentiation of the Human Ductal Adenocarcinoma Cell-line Panc-1 Into α-Like Cells. Experimental and Clinical Endocrinology and Diabetes, 2022, , .	0.6	0
2861	Divergence in the Regulation of the Salt Tolerant Response Between Arabidopsis thaliana and Its Halophytic Relative Eutrema salsugineum by mRNA Alternative Polyadenylation. Frontiers in Plant Science, 2022, 13, 866054.	1.7	9
2862	A High-Quality Haplotype-Resolved Genome of Common Bermudagrass (Cynodon dactylon L.) Provides Insights Into Polyploid Genome Stability and Prostrate Growth. Frontiers in Plant Science, 2022, 13, 890980.	1.7	4
2863	Mutational Pattern Induced by 5-Fluorouracil and Oxaliplatin in the Gut Microbiome. Frontiers in Microbiology, 2022, 13, 841458.	1.5	3
2864	Protective Effects of Nuciferine in Middle Cerebral Artery Occlusion Rats Based on Transcriptomics. Brain Sciences, 2022, 12, 572.	1.1	7
2865	Transcriptome Analysis of the Nematodes Caenorhabditis elegans and Litoditis marina in Different Food Environments. Journal of Marine Science and Engineering, 2022, 10, 580.	1.2	1
2866	CsbZIP2-miR9748-CsNPF4.4 Module Mediates High Temperature Tolerance of Cucumber Through Jasmonic Acid Pathway. Frontiers in Plant Science, 2022, 13, 883876.	1.7	4

#	Article	IF	CITATIONS
2867	Genetic Dissection of Tobacco (Nicotiana tabacum L.) Plant Height Using Single-Locus and Multi-Locus Genome-Wide Association Studies. Agronomy, 2022, 12, 1047.	1.3	5
2868	Traditional Chinese Medicine Tanreqing Targets Both Cell Division and Virulence in Staphylococcus aureus. Frontiers in Cellular and Infection Microbiology, 2022, 12, 884045.	1.8	5
2869	piRNA-guided intron removal from pre-mRNAs regulates density-dependent reproductive strategy. Cell Reports, 2022, 39, 110593.	2.9	4
2870	Biocontrol and Action Mechanism of Bacillus subtilis Lipopeptides' Fengycins Against Alternaria solani in Potato as Assessed by a Transcriptome Analysis. Frontiers in Microbiology, 2022, 13, .	1.5	13
2871	Effect of an inorganic nitrogen source (NH4)2SO4 on the production of welan gum from Sphingomonas sp. mutant obtained through UV-ARTP compound mutagenesis. International Journal of Biological Macromolecules, 2022, 210, 630-638.	3.6	10
2872	Evaluation of miR-141-3p over-expression in ovarian cancer. Electronic Journal of Biotechnology, 2022,	1.2	1
2873	Whole Genome Sequencing Provides New Insights Into the Genetic Diversity and Coat Color of Asiatic Wild Ass and Its Hybrids. Frontiers in Genetics, 2022, 13, .	1.1	0
2874	Sex-relevant genes in the embryo stage of Chinese soft-shelled turtles as revealed by RNA-Seq analysis. Animal Biology, 2022, -1, 1-19.	0.6	0
2875	Transcriptome sequencing of black and white hair follicles in the giant panda. Integrative Zoology, 2023, 18, 552-568.	1.3	3
2876	The genome sequencing and comparative analysis of a wild kiwifruit Actinidia eriantha. Molecular Horticulture, 2022, 2, .	2.3	13
2877	Long non-coding RNA transcriptome landscape of anthers at different developmental stages in response to drought stress in tomato. Genomics, 2022, 114, 110383.	1.3	17
2878	Comparative RNA-Seq analysis to understand anthocyanin biosynthesis and regulations in <i>Curcuma alismatifolia</i> . Folia Horticulturae, 2022, 34, 65-83.	0.6	1
2879	Peroxisomal Proteome Mining of Sweet Pepper (Capsicum annuum L.) Fruit Ripening Through Whole Isobaric Tags for Relative and Absolute Quantitation Analysis. Frontiers in Plant Science, 2022, 13, .	1.7	5
2880	Extent and complexity of RNA processing in honey bee queen and worker caste development. IScience, 2022, 25, 104301.	1.9	9
2881	Comparative Transcriptome Analysis Reveals Candidate Genes and Pathways for Potential Branch Growth in Elm (Ulmus pumila) Cultivars. Biology, 2022, 11, 711.	1.3	2
2882	Comparative Transcriptome Analysis of Agrobacterium tumefaciens Reveals the Molecular Basis for the Recalcitrant Genetic Transformation of Camellia sinensis L Biomolecules, 2022, 12, 688.	1.8	2
2883	Characterization of Phytohormones and Transcriptomic Profiling of the Female and Male Inflorescence Development in Manchurian Walnut (Juglans mandshurica Maxim.). International Journal of Molecular Sciences, 2022, 23, 5433.	1.8	2
2884	Leaf and rhizome transcriptome assembly and expression analysis of genes involved in terpene biosynthesis in Dioscorea opposita. Journal of Plant Biochemistry and Biotechnology, 0, , 1.	0.9	0

		CITATION RI	EPORT	
#	Article		IF	Citations
2885	Network Pharmacology-Based Prediction and Verification of Ginsenoside Rh2-Induced A A549 Cells via the PI3K/Akt Pathway. Frontiers in Pharmacology, 2022, 13, .	Apoptosis of	1.6	4
2886	Anthocyanin regulatory networks in Solanum tuberosum L. leaves elucidated via integr metabolomics, transcriptomics, and StAN1 overexpression. BMC Plant Biology, 2022, 2		1.6	12
2887	Probiotics mitigate Helicobacter pyloriâ€induced gastric inflammation and premalignar INSâ€GAS mice with the modulation of gastrointestinal microbiota. Helicobacter, 2022		1.6	16
2888	Physiological Effects and Transcriptomic Analysis of sbGnRH on the Liver in Pompano (	Trachinotus) Tj ETQq1 1 C	.784314 rg 1.5	gBŢ /Overloo
2889	Indigenous Microorganisms Offset Arbuscular Mycorrhizal Fungi-Induced Plant Growth Acquisition Through Negatively Modulating the Genes of Phosphorus Transport and Nit Assimilation. Frontiers in Plant Science, 2022, 13, .	and Nutrient trogen	1.7	9
2890	Phage resistance mutation triggered by OmpC deficiency in Klebsiella pneumoniae indufitness costs. Microbial Pathogenesis, 2022, 167, 105556.	uced limited	1.3	7
2891	Characterization, expression, and functional analysis of the pathogenesis-related gene transgenic poplar. International Journal of Biological Macromolecules, 2022, 210, 182-2		3.6	9
2892	Combined effects of S-metolachlor and benoxacor on embryo development in zebrafish Ecotoxicology and Environmental Safety, 2022, 238, 113565.	n (Danio rerio).	2.9	11
2893	Transcriptome analysis revealed that jasmonic acid biosynthesis/signaling is involved in response to Strontium stress. Ecotoxicology and Environmental Safety, 2022, 237, 113		2.9	10
2894	Multi-omics analysis reveals the influence of tetracycline on the growth of ryegrass roo Hazardous Materials, 2022, 435, 129019.	t. Journal of	6.5	10
2895	Transcriptome profiling of tiger pufferfish (Takifugu rubripes) gills in response to acute Aquaculture, 2022, 557, 738324.	hypoxia.	1.7	5
2896	Transcriptomic Evidence of the Immune Response Activation in Individuals With Limb C Dystrophy Dominant 2 (LGMDD2) Contributes to Resistance to HIV-1 Infection. Frontie Developmental Biology, 2022, 10, .		1.8	1
2897	Energy metabolism and genetic information processing mark major transitions in the li Scrippsiella acuminata (Dinophyceae). Harmful Algae, 2022, 116, 102248.	fe history of	2.2	4
2898	miR778 mediates gene expression, histone modification, and DNA methylation during o parasitism. Plant Physiology, 2022, 189, 2432-2453.	cyst nematode	2.3	4
2899	DNA sequence features underlying large-scale duplications and deletions in human. Jou Genetics, 2022, , .	rnal of Applied	1.0	0
2900	Transcriptome and metabolome reveal the accumulation of secondary metabolites in d varieties of Cinnamomum longepaniculatum. BMC Plant Biology, 2022, 22, 243.	ifferent	1.6	13
2901	Spheroid Formation Enhances the Regenerative Capacity of Nucleus Pulposus Cells via N-CDH and ITGβ1 Interaction. International Journal of Biological Sciences, 2022, 18, 36	Regulating 576-3696.	2.6	4
2903	Gene Co-expression Network and Regression Analysis Identify the Transcriptomic, Phys Biochemical Indicators of the Response of Alpine Woody Plant Rhododendron rex to Dr Frontiers in Plant Science, 2022, 13, .	iological, and rought Stress.	1.7	2

#	Article	IF	CITATIONS
2904	Expression Level Dominance and Homeolog Expression Bias Upon Cold Stress in the F1 Hybrid Between the Invasive Sphagneticola trilobata and the Native S. calendulacea in South China, and Implications for Its Invasiveness. Frontiers in Genetics, 2022, 13, .	1.1	1
2906	Single-molecule long-read sequencing analysis improves genome annotation and sheds new light on the transcripts and splice isoforms of Zoysia japonica. BMC Plant Biology, 2022, 22, .	1.6	7
2907	Transcriptomics Integrated with Metabolomics Unveil Carotenoids Accumulation and Correlated Gene Regulation in White and Yellow-Fleshed Turnip (Brassica rapa ssp. rapa). Genes, 2022, 13, 953.	1.0	0
2908	Serpin Family E Member 1 Enhances Myometrium Contractility By Increasing ATP Production During Labor. SSRN Electronic Journal, 0, , .	0.4	0
2909	Identification of novel regulatory pathways across normal human bronchial epithelial cell lines (NHBEs) and peripheral blood mononuclear cell lines (PBMCs) in COVID-19 patients using transcriptome analysis. Informatics in Medicine Unlocked, 2022, 31, 100979.	1.9	4
2910	DNA methylation plays an important role in iron-overloaded Tibetans. Genes and Genetic Systems, 2022, 97, 55-66.	0.2	6
2911	Integrative Metabolome and Transcriptome Analysis of Flavonoid Biosynthesis Genes in Broussonetia papyrifera Leaves From the Perspective of Sex Differentiation. Frontiers in Plant Science, 2022, 13, .	1.7	2
2912	Host-virus interactions in PK-15 cells infected with Pseudorabies virus Becker strain based on RNA-seq. Virus Research, 2022, 318, 198829.	1.1	3
2913	Dual transcriptome based reconstruction of Salmonella-human integrated metabolic network to screen potential drug targets. PLoS ONE, 2022, 17, e0268889.	1.1	7
2914	Circular RNAs Represent a Novel Class of Human Cytomegalovirus Transcripts. Microbiology Spectrum, 2022, 10, .	1.2	8
2915	Whole-Genome Sequencing of KMR3 and Oryza rufipogon-Derived Introgression Line IL50-13 (Chinsurah) Tj ETQq Plant Science, 2022, 13, .	0 0 0 rgB1 1.7	[ /Overlock ] 2
2916	Effect of berberine on global modulation of lncRNAs and mRNAs expression profiles in patients with stable coronary heart disease. BMC Genomics, 2022, 23, .	1.2	1
2917	Mucosa-Colonizing Microbiota Correlate With Host Autophagy Signaling in Patients With Inflammatory Bowel Disease. Frontiers in Microbiology, 2022, 13, .	1.5	5
2918	Comparative Transcriptomics of Gonads Reveals the Molecular Mechanisms Underlying Gonadal Development in Giant Freshwater Prawns (Macrobrachium rosenbergii). Journal of Marine Science and Engineering, 2022, 10, 737.	1.2	4
2919	Transcriptomic and Metabolomic Analysis Unravels the Molecular Regulatory Mechanism of Fatty Acid Biosynthesis in Styrax tonkinensis Seeds under Methyl Jasmonate Treatment. International Journal of Molecular Sciences, 2022, 23, 6190.	1.8	2
2920	Integrated Analysis of Glutathione Metabolic Pathway in Pancreatic Cancer. Frontiers in Cell and Developmental Biology, 2022, 10, .	1.8	1
2921	Transcriptome analysis reveals the spinal expression profiles of non-coding RNAs involved in anorectal malformations in rat fetuses. Journal of Pediatric Surgery, 2022, , .	0.8	0
2922	The Transcription Factor MdERF78 Is Involved in ALA-Induced Anthocyanin Accumulation in Apples. Frontiers in Plant Science, 2022, 13, .	1.7	10

#	Article	IF	Citations
 2923	High-quality chromosome-level genome assembly of Litsea coreana L. provides insights into Magnoliids evolution and flavonoid biosynthesis. Genomics, 2022, 114, 110394.	1.3	2
2924	Detecting Genetic Variation of Colonizing Streptococcus agalactiae Genomes in Humans: A Precision Protocol. Frontiers in Bioinformatics, 2022, 2, .	1.0	0
2925	Screening and Identification of Hub Genes in the Development of Early Diabetic Kidney Disease Based on Weighted Gene Co-Expression Network Analysis. Frontiers in Endocrinology, 2022, 13, .	1.5	8
2926	The Isolation and Full-Length Transcriptome Sequencing of a Novel Nidovirus and Response of Its Infection in Japanese Flounder (Paralichthys olivaceus). Viruses, 2022, 14, 1216.	1.5	2
2927	Genome-wide DNA methylation reveals potential epigenetic mechanism of age-dependent viral susceptibility in grass carp. Immunity and Ageing, 2022, 19, .	1.8	6
2928	WeCoNET: a host–pathogen interactome database for deciphering crucial molecular networks of wheat-common bunt cross-talk mechanisms. Plant Methods, 2022, 18, .	1.9	6
2929	Stocking density affects transcriptome changes in the hypothalamic-pituitary-gonadal axis and reproductive performance in ducks. Italian Journal of Animal Science, 2022, 21, 955-966.	0.8	0
2930	Pharmacological inhibition of sphingolipid synthesis reduces ferroptosis by stimulating the HIF-1 pathway. IScience, 2022, 25, 104533.	1.9	11
2931	Effects of low salinity on hemolymph osmolality and transcriptome of the Iwagaki oyster, Crassostrea nippona. Fish and Shellfish Immunology, 2022, 126, 211-216.	1.6	7
2932	Metagenomic insights into comparative study of nitrogen metabolic potential and microbial community between primitive and urban river sediments. Environmental Research, 2022, 212, 113592.	3.7	14
2933	Tobacco straw biochar improved the growth of Chinese cherry (Prunus pseudocerasus) via altering plant physiology and shifting the rhizosphere bacterial community. Scientia Horticulturae, 2022, 303, 111244.	1.7	7
2934	Comparative transcriptome analysis on candidate genes involved in lipid biosynthesis of developing kernels for three walnut cultivars in Xinjiang. Food Science and Human Wellness, 2022, 11, 1201-1214.	2.2	8
2935	FMR1 is identified as an immune-related novel prognostic biomarker for renal clear cell carcinoma: A bioinformatics analysis of TAZ/YAP. Mathematical Biosciences and Engineering, 2022, 19, 9295-9320.	1.0	3
2936	Transcriptome Analysis of Artificial Cultivated Mushrooms in Qinba Mountains. SSRN Electronic Journal, 0, , .	0.4	0
2937	Blocking ATM Attenuates SKOV3 Cell Proliferation and Migration by Disturbing OGT/OGA Expression via hsa-miR-542-5p. Frontiers in Oncology, 0, 12, .	1.3	3
2938	Combined transcriptome and metabolome analysis of Nerium indicum L. elaborates the key pathways that are activated in response to witches' broom disease. BMC Plant Biology, 2022, 22, .	1.6	5
2939	Activated Carbon Facilitates Anaerobic Digestion of Furfural Wastewater: Effect of Direct Interspecies Electron Transfer. ACS Sustainable Chemistry and Engineering, 2022, 10, 8206-8215.	3.2	14
2940	DNA Methylation Correlates with the Expression of Drought-Responsive Genes and Drought Resistance in Rice. Agronomy, 2022, 12, 1445.	1.3	7

ARTICLE IF CITATIONS Epigenetic reactivation of transcriptional programs orchestrating fetal lung development in human 2941 5.8 15 pulmonary hypertension. Science Translational Medicine, 2022, 14, . Chromosome-level and haplotype-resolved genome provides insight into the tetraploid hybrid origin 2942 5.8 of patchouli. Nature Communications, 2022, 13, . Chlorophyll decomposition is accelerated in banana leaves after the long-term magnesium deficiency 2943 1.1 3 according to transcriptome analysis. PLoS ONE, 2022, 17, e0270610. Hereditary Basis of Coat Color and Excellent Feed Conversion Rate of Red Angus Cattle by 2944 1.0 Next-Generation Sequencing Data. Animals, 2022, 12, 1509. Effects of 5-azaC on Iridoid Glycoside Accumulation and DNA Methylation in Rehmannia glutinosa. 2945 1.7 0 Frontiers in Plant Science, 0, 13, . Bacillus subtilis biofilm matrix components target seed oil bodies to promote growth and anti-fungal resistance in melon. Nature Microbiology, 2022, 7, 1001-1015. 2946 Acetylome and Succinylome Profiling of Edwardsiella tarda Reveals Key Roles of Both Lysine 2947 1.5 3 Acylations in Bacterial Antibiotic Resistance. Antibiotics, 2022, 11, 841. Functional regulations between genetic alteration-driven genes and drug target genes acting as 2948 1.6 prognostic biomarkers in breast cancer. Scientific Reports, 2022, 12, . Systematic analysis and identification of regulators for SRS genes in Capsicum annuum. Plant Growth 2949 1.8 2 Régulation, 2022, 98, 51-64. Identification and analysis of miRNAsâ€IncRNAsâ€mRNAs modules involved in stemâ€elongation of deepwater 2950 rice (<i>Oryza sativa</i> L.). Physiologia Plantarum, 2022, 174, . Transcript Complexity and New Insights of Restorer Line in CMS-D8 Cotton Through Full-Length 2951 1 1.7 Transcriptomic Analysis. Frontiers in Plant Science, 0, 13, . An Integrated Analysis of Transcriptome and Metabolism Reveals an Inhibitory Effect of Low Light on 1.2 Anthocyanin Biosynthesis in Purple cai-tai (Brassicarapa L. var. purpurea). Horticulturae, 2022, 8, 566. Transcriptomic Characterization of Miscanthus sacchariflorus × M. lutarioriparius and Its 2953 1.6 4 Implications for Energy Crop Development in the Semiarid Mine Area. Plants, 2022, 11, 1568. Infection by endophytic Epichloë sibirica was associated with activation of defense hormone signal transduction pathways and enhanced pathogen resistance in the grass Achnatherum sibiricum. 2954 1.1 Phytopathology, 0, , . PCBP-1 Regulates the Transcription and Alternative Splicing of Inflammation and 2955 8 1.7 Ubiquitination-Related Genes in PC12 Cell. Frontiers in Aging Neuroscience, 0, 14, . Multiâ€omics profiling reveals comprehensive microbe–plant–metabolite regulation patterns for medicinal plant <i>Glycyrrhiza uralensis</i> Fisch. Plant Biotechnology Journal, 2022, 20, 1874-1887. Transcriptome of Endophyte-Positive and Endophyte-Free Tall Fescue Under Field Stresses. Frontiers in 2957 1.7 2 Plant Science, 0, 13, . Dynamic Changes of Transcriptome and Metabolites During Ripening of Alpinia Oxyphylla Fruit (AOF). 2958 Journal of Plant Biology, 2022, 65, 445-457.

#	Article	IF	CITATIONS
2959	The association of the expression pattern and functions of long non-coding RNA with the progression of diabetic nephropathy. Asian Journal of Surgery, 2022, , .	0.2	0
2960	Changes in the Transcriptome and Chromatin Landscape in BRAFi-Resistant Melanoma Cells. Frontiers in Oncology, 0, 12, .	1.3	3
2961	The Role of Intestinal Microbial Metabolites in the Immunity of Equine Animals Infected With Horse Botflies. Frontiers in Veterinary Science, 0, 9, .	0.9	2
2962	Genome-Wide Association Study of Sheath Blight Resistance within a Core Collection of Rice (Oryza) Tj ETQq1 1	0.784314 1.8	rgBT /Over
2963	CircRNAs in Xiang pig ovaries among diestrus and estrus stages. Porcine Health Management, 2022, 8, .	0.9	4
2964	Comparative Transcriptome and Proteome Analysis Provides New Insights Into the Mechanism of Protein Synthesis in Kenaf (Hibiscus cannabinus L.) Leaves. Frontiers in Plant Science, 0, 13, .	1.7	2
2965	Identification of Abietane-Type Diterpenoids and Phenolic Acids Biosynthesis Genes in Salvia apiana Jepson Through Full-Length Transcriptomic and Metabolomic Profiling. Frontiers in Plant Science, 0, 13, .	1.7	3
2966	Effects of Habitat River Microbiome on the Symbiotic Microbiota and Multi-Organ Gene Expression of Captive-Bred Chinese Giant Salamander. Frontiers in Microbiology, 0, 13, .	1.5	5
2967	Bacillus velezensis YYC promotes tomato growth and induces resistance against bacterial wilt. Biological Control, 2022, 172, 104977.	1.4	14
2968	Deciphering key regulators of Inonotus hispidus petroleum ether extract involved in anti-tumor through whole transcriptome and proteome analysis in H22 tumor-bearing mice model. Journal of Ethnopharmacology, 2022, 296, 115468.	2.0	8
2969	Renewable nitrogen-containing products by Maillard reaction of sewage sludge and glucose. Part I. Analysis of nitrogen composition and protein model based on AlphaFold2. Fuel, 2022, 325, 124968.	3.4	4
2970	Bioinformatics Analyses of Regulatory Network of Biomarkers in Chondrocytes from Patients with Osteoarthritis. Brazilian Archives of Biology and Technology, 0, 65, .	0.5	1
2971	Toxicity of Chronic Waterborne Zinc Exposure in Pacific White Shrimp Litopenaeus Vannamei. SSRN Electronic Journal, 0, , .	0.4	0
2972	Integrated transcriptome and metabolome analyses revealed regulatory mechanisms of flavonoid biosynthesis in <i>Radix Ardisia</i> . PeerJ, 0, 10, e13670.	0.9	1
2973	Intermittent Caloric Restriction Promotes Erythroid Development and Ameliorates Phenylhydrazine-Induced Anemia in Mice. Frontiers in Nutrition, 0, 9, .	1.6	2
2974	C. elegans monitor energy status via the AMPK pathway to trigger innate immune responses against bacterial pathogens. Communications Biology, 2022, 5, .	2.0	1
2975	Genome-Wide Identification of RNA Editing Sites Affecting Muscle Development in Yak. Frontiers in Veterinary Science, 0, 9, .	0.9	2
2976	Genome-Wide Detection of Copy Number Variations and Evaluation of Candidate Copy Number Polymorphism Genes Associated With Complex Traits of Pigs. Frontiers in Veterinary Science, 0, 9, .	0.9	3

#	Article	IF	Citations
2977	Profiling the neurovascular unit unveils detrimental effects of osteopontin on the blood–brain barrier in acute ischemic stroke. Acta Neuropathologica, 2022, 144, 305-337.	3.9	37
2978	Activin B-activated Cdc42 signaling plays a key role in regulating adipose-derived mesenchymal stem cells-mediated skin wound healing. Stem Cell Research and Therapy, 2022, 13, .	2.4	2
2979	Comparative Transcriptome Analysis of Differentially Expressed Genes in the Testis and Ovary of Sea Urchin (Strongylocentrotus intermedius). Fishes, 2022, 7, 152.	0.7	4
2980	De novo transcriptome assembly and comprehensive assessment provide insight into fruiting body formation of Sparassis latifolia. Scientific Reports, 2022, 12, .	1.6	2
2981	Regulation of OsPIL15 on rice quality. Molecular Breeding, 2022, 42, .	1.0	2
2982	Isolation, Identification, and Investigation of Pathogenic Bacteria From Common Carp (Cyprinus) Tj ETQq1	0.784314 rgBT	/Overlock 1
2983	Resistance to Powdery Mildew in Qingke Involves the Accumulation of Aromatic Phenolamides Through Jasmonate-Mediated Activation of Defense-Related Genes. Frontiers in Plant Science, 0, 13, .	1.7	4
2984	Metabolome and Transcriptome Analyses Unravels Molecular Mechanisms of Leaf Color Variation by Anthocyanidin Biosynthesis in Acer triflorum. Horticulturae, 2022, 8, 635.	1.2	3
2985	Systematic analysis on expression quantitative trait loci identifies a novel regulatory variant in ring finger and WD repeat domain 3 associated with prognosis of pancreatic cancer. Chinese Medical Journal, 2022, 135, 1348-1357.	0.9	3
2986	Characterization of a Novel Insect-Induced Sesquiterpene Synthase GbTPS1 Based on the Transcriptome of Gossypium barbadense Feeding by Cotton Bollworm. Frontiers in Plant Science, 0, 13, .	1.7	4
2987	Comparing Transcriptomes Reveals Key Metabolic Mechanisms in Superior Growth Performance Nile Tilapia (Oreochromis niloticus). Frontiers in Genetics, 0, 13, .	1.1	1
2988	A de novo assembled high-quality chromosome-scale Trifolium pratense genome and fine-scale phylogenetic analysis. BMC Plant Biology, 2022, 22, .	1.6	6
2989	Whole-genome sequence analysis reveals selection signatures for important economic traits in Xiang pigs. Scientific Reports, 2022, 12, .	1.6	11
2990	Transcriptome Analysis of Soursop (Annona muricata L.) Fruit under Postharvest Storage Identifies Genes Families Involved in Ripening. Plants, 2022, 11, 1798.	1.6	3
2991	Physiological and Transcriptome Analysis on Diploid and Polyploid Populus ussuriensis Kom. under Salt Stress. International Journal of Molecular Sciences, 2022, 23, 7529.	1.8	10
2992	Transcriptomic Down-Regulation of Immune System Components in Barrier and Hematopoietic Tissues after Lipopolysaccharide Injection in Antarctic Notothenia coriiceps. Fishes, 2022, 7, 171.	0.7	3
2993	Comprehensive comparative analysis of histopathology and gene expression in subchondral bone between kashin-beck disease and primary osteoarthritis. Frontiers in Genetics, 0, 13, .	1.1	2
2994	Comparative analysis of the structure and function of rhizosphere microbiome of the Chinese medicinal herb Alisma in different regions. Archives of Microbiology, 2022, 204, .	1.0	4

#	Article	IF	CITATIONS
2995	Induced oxidative equilibrium damage and reduced toxin synthesis in <i>Fusarium oxysporum</i> f. sp <i>. niveum</i> by secondary metabolites from <i>Bacillus velezensis</i> WB. FEMS Microbiology Ecology, 2022, 98, .	1.3	4
2996	Toxicological and transcriptomic effects in <i>Mythimna separata</i> (Lepidoptera: Noctuidae) exposed to chlorantraniliprole and functional characterization of glutathione Sâ€ŧransferases. Pest Management Science, 2022, 78, 4517-4532.	1.7	9
2997	Transcriptome analysis and characterization of genes associated to leaf tannin content in foxtail millet [Setaria italica (L.) P. Beauv.]. BMC Genomics, 2022, 23, .	1.2	3
2998	Xylem Transcriptome Analysis in Contrasting Wood Phenotypes of Eucalyptus urophylla × tereticornis Hybrids. Forests, 2022, 13, 1102.	0.9	2
2999	Comparative Transcriptome Analysis Provides Novel Insights into the Effect of Lipid Metabolism on Laying of Geese. Animals, 2022, 12, 1775.	1.0	2
3000	Comparative Transcriptome and Pigment Analyses Reveal Changes in Gene Expression Associated with Flavonol Metabolism in Yellow Camellia. Forests, 2022, 13, 1094.	0.9	5
3001	The Qc5 Allele Increases Wheat Bread-Making Quality by Regulating SPA and SPR. International Journal of Molecular Sciences, 2022, 23, 7581.	1.8	2
3002	Mapping stripe rust resistance QTL in N2496, a synthetic hexaploid wheat derivative. Plant Disease, 0, , .	0.7	1
3003	Changes in the Species and Functional Composition of Activated Sludge Communities Revealed Mechanisms of Partial Nitrification Established by Ultrasonication. Frontiers in Microbiology, 0, 13, .	1.5	0
3004	Networkâ€based quantitative proteomics identified significant proteins associated with growth heterosis in triploid fish. Aquaculture Research, 0, , .	0.9	0
3005	RNA-sequencing of human aortic valves identifies that miR-629-3pÂand TAGLNÂmiRNA-mRNA pair involving inÂcalcified aortic valve disease. Journal of Physiology and Biochemistry, 2022, 78, 819-831.	1.3	7
3006	Genome-Wide Identification of Powdery Mildew Responsive Long Non-Coding RNAs in Cucurbita pepo. Frontiers in Genetics, 0, 13, .	1.1	6
3007	An Integrative Transcriptomic Analysis Reveals EGFR Exon-19 E746-A750 Fragment Deletion Regulated miRNA, circRNA, mRNA and IncRNA Networks in Lung Carcinoma. International Journal of General Medicine, 0, Volume 15, 6031-6042.	0.8	0
3008	Glia Maturation Factor $\hat{I}^2$ as a Novel Independent Prognostic Biomarker and Potential Therapeutic Target of Kidney Renal Clear Cell Carcinoma. Frontiers in Oncology, 0, 12, .	1.3	1
3009	The role and mechanisms of the two omponent system <scp>EnvZ</scp> / <scp>OmpR</scp> on the intracellular survival of <i>Aeromonas hydrophila</i> . Journal of Fish Diseases, 2022, 45, 1609-1621.	0.9	9
3010	Genome-Wide Analysis Identifies Candidate Genes Encoding Feather Color in Ducks. Genes, 2022, 13, 1249.	1.0	9
3011	WAL3 encoding a PLS-type PPR protein regulates chloroplast development in rice. Plant Science, 2022, 323, 111382.	1.7	6
3012	Chromosome 5P of Agropyron cristatum induces chromosomal translocation by disturbing homologous chromosome pairing in a common wheat background. Crop Journal, 2023, 11, 228-237.	2.3	2

#	Article	IF	CITATIONS
3013	A newlyÂcharacterized allele of ZmR1 increases anthocyanin content in whole maize plant and the regulation mechanism of different ZmR1 alleles. Theoretical and Applied Genetics, 2022, 135, 3039-3055.	1.8	5
3014	Dynamic Transcriptomic Profiling During Liver Development in Schizothorax Prenanti. Frontiers in Physiology, 0, 13, .	1.3	3
3015	The EGFR-STYK1-FGF1 axis sustains functional drug tolerance to EGFR inhibitors in EGFR-mutant non-small cell lung cancer. Cell Death and Disease, 2022, 13, .	2.7	3
3016	Cuticular Wax Modification by Epichloë Endophyte in Achnatherum inebrians under Different Soil Moisture Availability. Journal of Fungi (Basel, Switzerland), 2022, 8, 725.	1.5	2
3017	Genome sequencing reveals chromosome fusion and extensive expansion of genes related to secondary metabolism in <i>Artemisia argyi</i> . Plant Biotechnology Journal, 2022, 20, 1902-1915.	4.1	25
3018	Genome-Wide Analysis Identifies Candidate Genes Encoding Beak Color of Duck. Genes, 2022, 13, 1271.	1.0	7
3019	Transcriptome analysis of the spleen of heterophils to lymphocytes ratio-selected chickens revealed their mechanism of differential resistance to Salmonella. Journal of Integrative Agriculture, 2022, 21, 2372-2383.	1.7	3
3020	Comparative transcriptome analysis on the mangrove Acanthus ilicifolius and its two terrestrial relatives provides insights into adaptation to intertidal habitats. Gene, 2022, 839, 146730.	1.0	3
3021	A genome-wide association study of important reproduction traits in large white pigs. Gene, 2022, 838, 146702.	1.0	2
3022	Localized intensification of arsenic methylation within landfill leachate-saturated zone. Science of the Total Environment, 2022, 842, 156979.	3.9	0
3023	Effects of air exposure stress on crustaceans: Histopathological changes, antioxidant and immunity of the red swamp crayfish Procambarus clarkii. Developmental and Comparative Immunology, 2022, 135, 104480.	1.0	6
3024	Blue light increases anthocyanin content and delays fruit ripening in purple pepper fruit. Postharvest Biology and Technology, 2022, 192, 112024.	2.9	23
3025	Metabolic Profiling and Transcriptional Analysis of Carotenoid Accumulation in a Red-Fleshed Mutant of Pummelo (Citrus grandis). Molecules, 2022, 27, 4595.	1.7	5
3026	HnRNP K regulates inflammatory gene expression by mediating splicing pattern of transcriptional factors. Experimental Biology and Medicine, 2023, 248, 1479-1491.	1.1	2
3027	Transcriptome and Metabolome Analyses of Codonopsis convolvulacea Kurz Tuber, Stem, and Leaf Reveal the Presence of Important Metabolites and Key Pathways Controlling Their Biosynthesis. Frontiers in Genetics, 0, 13, .	1.1	2
3028	PD-L1 regulates cell proliferation and apoptosis in acute myeloid leukemia by activating PI3K-AKT signaling pathway. Scientific Reports, 2022, 12, .	1.6	18
3029	Comparative transcriptome analysis unveiling reactive oxygen species scavenging system of Sonneratia caseolaris under salinity stress. Frontiers in Plant Science, 0, 13, .	1.7	5
3030	Genome-Wide Identification and Characterization of RNA/DNA Differences Associated with Fusarium graminearum Infection in Wheat. International Journal of Molecular Sciences, 2022, 23, 7982.	1.8	2

#	Article	IF	CITATIONS
3031	Liver fat metabolism of broilers regulated by Bacillus amyloliquefaciens TL via stimulating IGF-1 secretion and regulating the IGF signaling pathway. Frontiers in Microbiology, 0, 13, .	1.5	1
3032	Proteomics data analysis using multiple statistical approaches identified proteins and metabolic networks associated with sucrose accumulation in sugarcane. BMC Genomics, 2022, 23, .	1.2	2
3033	Comparative physiological and transcriptome analysis reveals the potential mechanism of selenium accumulation and tolerance to selenate toxicity of <i>Broussonetia papyrifera</i> . Tree Physiology, 2022, 42, 2578-2595.	1.4	2
3034	Early feeding strategies in lambs affect rumen development and growth performance, with advantages persisting for two weeks after the transition to fattening diets. Frontiers in Veterinary Science, 0, 9, .	0.9	3
3035	Identification of Differential Expression Genes between Volume and Pressure Overloaded Hearts Based on Bioinformatics Analysis. Genes, 2022, 13, 1276.	1.0	0
3036	Cell damage repair mechanism in a desert green algae Chlorella sp. against UV-B radiation. Ecotoxicology and Environmental Safety, 2022, 242, 113916.	2.9	14
3037	miR-301b-5p and its target gene nfatc2ip regulate inflammatory responses in the liver of rainbow trout (Oncorhynchus mykiss) under high temperature stress. Ecotoxicology and Environmental Safety, 2022, 242, 113915.	2.9	5
3038	Characteristics and candidate genes associated with excellent stalk strength in maize (Zea mays L.). Frontiers in Plant Science, 0, 13, .	1.7	3
3039	RNA-binding protein CELF6 modulates transcription and splicing levels of genes associated with tumorigenesis in lung cancer A549 cells. PeerJ, 0, 10, e13800.	0.9	3
3040	Transcriptomic responses are sex-dependent in the skeletal muscle and liver in offspring of obese mice. American Journal of Physiology - Endocrinology and Metabolism, 2022, 323, E336-E353.	1.8	6
3041	An Age Effect of Rumen Microbiome in Dairy Buffaloes Revealed by Metagenomics. Microorganisms, 2022, 10, 1491.	1.6	2
3042	Analysis of transcriptome data and quantitative trait loci enables the identification of candidate genes responsible for fiber strength in <i>Gossypium barbadense</i> . G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	3
3043	Transcriptomic Analysis of Fusarium oxysporum Stress-Induced Pathosystem and Screening of Fom-2 Interaction Factors in Contrasted Melon Plants. Frontiers in Plant Science, 0, 13, .	1.7	3
3044	Belowground and aboveground herbivory differentially affect the transcriptome in roots and shoots of maize. Plant Direct, 2022, 6, .	0.8	8
3045	Alternative Splicing Isoforms of Porcine CREB Are Differentially Involved in Transcriptional Transactivation. Genes, 2022, 13, 1304.	1.0	1
3046	Role of ferroptosis-related genes in periodontitis based on integrated bioinformatics analysis. PLoS ONE, 2022, 17, e0271202.	1.1	8
3047	Insights into the complicated networks contribute to adventitious rooting in transgenic <i>MdWOX11</i> apple microshoots under nitrate treatments. Plant, Cell and Environment, 2022, 45, 3134-3156.	2.8	8
3048	The combination of genomic offset and niche modelling provides insights into climate change-driven vulnerability. Nature Communications, 2022, 13, .	5.8	10

#	Article	IF	CITATIONS
3049	24-Epibrassinolide Promotes Fatty Acid Accumulation and the Expression of Related Genes in Styrax tonkinensis Seeds. International Journal of Molecular Sciences, 2022, 23, 8897.	1.8	5
3050	The bHLH1-DTX35/DFR module regulates pollen fertility by promoting flavonoid biosynthesis in <i>Capsicum annuum</i> L. Horticulture Research, 2022, 9, .	2.9	5
3051	Andrographolide suppresses breast cancer progression by modulating tumorâ€associated macrophage polarization through the Wnt/ <i>β</i> â€catenin pathway. Phytotherapy Research, 2022, 36, 4587-4603.	2.8	7
3052	High bacterial diversity and siderophore-producing bacteria collectively suppress Fusarium oxysporum in maize/faba bean intercropping. Frontiers in Microbiology, 0, 13, .	1.5	6
3053	Deciphering the transcriptomic response of <i>llyonectria robusta</i> in relation to ginsenoside Rg1 treatment and the development of ginseng rusty root rot. FEMS Microbiology Letters, 2022, 369, .	0.7	3
3054	A Global Transcriptome and Co-expression Analysis Reveals Robust Host Defense Pathway Reprogramming and Identifies Key Regulators of Early Phases of <i>Cicer-Ascochyta</i> Interactions. Molecular Plant-Microbe Interactions, 2022, 35, 1034-1047.	1.4	5
3055	Comparative histology, transcriptome, and metabolite profiling unravel the browning mechanisms of calli derived from ginkgo (Ginkgo biloba L.). Journal of Forestry Research, 2023, 34, 677-691.	1.7	9
3056	Transcriptome analyses reveal photosynthesis-related genes involved in chloroplast development of the EMS-induced maize mutant. Plant Biotechnology Reports, 0, , .	0.9	1
3057	Identification of Alkaline Salt Tolerance Genes in Brassica napus L. by Transcriptome Analysis. Genes, 2022, 13, 1493.	1.0	2
3058	Transcriptome analysis reveals candidate genes of the synthesis of branched-chain fatty acids related to mutton flavor in the lamb liver using <i>Allium mongolicum</i> Regel extract. Journal of Animal Science, 2022, 100, .	0.2	4
3059	RALY regulate the proliferation and expression of immune/inflammatory response genes via alternative splicing of FOS. Genes and Immunity, 2022, 23, 246-254.	2.2	5
3060	Human CIDEC transgene improves lipid metabolism and protects against high-fat diet–induced glucose intolerance in mice. Journal of Biological Chemistry, 2022, 298, 102347.	1.6	5
3061	Age-Dependent Variations in Functional Quality and Proteomic Characteristics of Canine (Canis lupus) Tj ETQq0 (	0 0 rgBT /0 1.8	Dvgrlock 10 T
3062	Comparative evaluation of the microbial diversity and metabolite profiles of Japanese-style and Cantonese-style soy sauce fermentation. Frontiers in Microbiology, 0, 13, .	1.5	14
3063	Chromosome-level genome assembly and population genomic analyses provide insights into adaptive evolution of the red turpentine beetle, Dendroctonus valens. BMC Biology, 2022, 20, .	1.7	5
3064	Identification of long non-coding RNAs and microRNAs involved in anther development in the tropical Camellia oleifera. BMC Genomics, 2022, 23, .	1.2	2
3065	Biological Functions and Cross-Kingdom Host Gene Regulation of Small RNAs in Lactobacillus plantarum-Derived Extracellular Vesicles. Frontiers in Microbiology, 0, 13, .	1.5	2
3066	Behavioral innovation and genomic novelty are associated with the exploitation of a challenging dietary opportunity by an avivorous bat. IScience, 2022, 25, 104973.	1.9	7

#	Article	IF	CITATIONS
3067	Yak rumen microbiome elevates fiber degradation ability and alters rumen fermentation pattern to increase feed efficiency. Animal Nutrition, 2022, 11, 201-214.	2.1	16
3068	Phosphoproteome profiling of mouse liver during normal aging. Proteome Science, 2022, 20, .	0.7	4
3069	Honghua extract mediated potent inhibition of COVID-19 host cell pathways. Scientific Reports, 2022, 12, .	1.6	5
3070	The Comparison of Temporal Transcriptome Changes Between Morning-Opening and Afternoon-Opening Iris Flowers Reveals the Candidate Genes Regulating Flower Opening and Closing. Journal of Plant Biology, 0, , .	0.9	1
3071	A Transcriptomic Analysis of Phenotypic Plasticity in Crassostrea virginica Larvae under Experimental Acidification. Genes, 2022, 13, 1529.	1.0	10
3072	Combined de novo transcriptomic and physiological analyses reveal RyALS3-mediated aluminum tolerance in Rhododendron yunnanense Franch. Frontiers in Plant Science, 0, 13, .	1.7	2
3073	A composite strategy of genome-wide association study and copy number variation analysis for carcass traits in a Duroc pig population. BMC Genomics, 2022, 23, .	1.2	11
3074	De novo transcriptome revealed genes involved in anthocyanin biosynthesis, transport, and regulation in a mutant of Acer pseudosieboldianum. BMC Genomics, 2022, 23, .	1.2	2
3075	Integration of RNA-seq and ATAC-seq identifies muscle-regulated hub genes in cattle. Frontiers in Veterinary Science, 0, 9, .	0.9	2
3076	Moisture Controls the Suppression of <i>Panax notoginseng</i> Root Rot Disease by Indigenous Bacterial Communities. MSystems, 2022, 7, .	1.7	4
3077	Transcriptome and biochemical response to 60Co gamma radiation exposure on the grafted seedlings of Paeonia suffruticosa. Acta Physiologiae Plantarum, 2022, 44, .	1.0	1
3078	Comprehensive analysis of differentially expressed profiles of mRNA, IncRNA, and miRNA of Yili geese ovary at different egg-laying stages. BMC Genomics, 2022, 23, .	1.2	7
3079	Reduced Hypoxia Tolerance and Altered Gill Morphology at Elevated Temperatures May Limit the Survival of Tilapia (GIFT, Oreochromis niloticus) under Global Warming. Fishes, 2022, 7, 216.	0.7	6
3080	Comparative transcriptomic analysis of rabbit interscapular brown adipose tissue whitening under physiological conditions. Adipocyte, 2022, 11, 529-549.	1.3	3
3081	De novo transcriptome assembly reveals characteristics of flower sex determination of Excoecaria agallocha. Annals of Forest Science, 2022, 79, .	0.8	0
3083	Target RNA expression omics approach to reveal the liver detoxification effect induced by Chinese medicine prescription Niu Huang Jie Du against realgar overexposure to mice. Journal of Ethnopharmacology, 2022, 298, 115610.	2.0	0
3084	Transcriptional, chromatin, and metabolic landscapes of LDHA inhibitor–resistant pancreatic ductal adenocarcinoma. Frontiers in Oncology, 0, 12, .	1.3	1
3085	Overexpression of an NF-YC2 gene confers alkali tolerance to transgenic alfalfa (Medicago sativa L.). Frontiers in Plant Science, 0, 13, .	1.7	2

#	Article	IF	CITATIONS
3086	High-throughput circular RNA sequencing reveals the profiles of circular RNA in non-cirrhotic hepatocellular carcinoma. BMC Cancer, 2022, 22, .	1.1	0
3087	Genomic Insights into Genetic Diploidization in the Homosporous Fern <i>Adiantum nelumboides</i> . Genome Biology and Evolution, 2022, 14, .	1.1	7
3088	A different transcriptional landscape sheds light on Russian sturgeon (Acipenser gueldenstaedtii) mechanisms to cope with bacterial infection and chronic heat stress. Fish and Shellfish Immunology, 2022, 128, 505-522.	1.6	5
3089	The potential toxicity of polystyrene nanoplastics to human trophoblasts in vitro. Environmental Pollution, 2022, 311, 119924.	3.7	15
3090	Active compound analysis of Ziziphus jujuba cv. Jinsixiaozao in different developmental stages using metabolomic and transcriptomic approaches. Plant Physiology and Biochemistry, 2022, 189, 14-23.	2.8	5
3091	Characterization of a new Bacillus velezensis as a powerful biocontrol agent against tomato gray mold. Pesticide Biochemistry and Physiology, 2022, 187, 105199.	1.6	9
3092	Neuroblastoma SH-SY5Y Cell Differentiation to Mature Neuron by AM580 Treatment. Neurochemical Research, 2022, 47, 3723-3732.	1.6	2
3093	Candidate chemosensory receptors in the antennae and maxillae of Spodoptera frugiperda (J. E. Smith) larvae. Frontiers in Physiology, 0, 13, .	1.3	3
3094	Patterns and Crucial Regulation of Alternative Splicing During Early Development in Zebrafish. Journal of Molecular Biology, 2022, 434, 167821.	2.0	0
3095	Genome-wide analysis reveals selection signatures for body size and drought adaptation in Liangzhou donkey. Genomics, 2022, 114, 110476.	1.3	5
3096	Comparative transcriptomic analysis identifies KcMYB1 as a R2R3-MYB anthocyanin activator in Kadsura coccinea. Plant Science, 2022, 324, 111458.	1.7	3
3097	Hainanolide inhibits the progression of colon cancer via inducing the cell cycle arrest, cell apoptosis and activation of the MAPK signaling pathway. Toxicology and Applied Pharmacology, 2022, 454, 116249.	1.3	5
3098	Biocontrol of antifungal volatiles produced by Ceriporia lacerate HG2011 against citrus fruit rot incited by Penicillium spp Postharvest Biology and Technology, 2022, 194, 112094.	2.9	6
3099	Coordinated regulation of symbiotic adaptation by NodD proteins and NolA in the type I peanut bradyrhizobial strain Bradyrhizobium zhanjiangense CCBAU51778. Microbiological Research, 2022, 265, 127188.	2.5	3
3100	Dietary threonine deficiency affects expression of genes involved in lipid metabolism in adipose tissues of Pekin ducks in a genotype-dependent manner. Journal of Integrative Agriculture, 2022, 21, 2691-2699.	1.7	2
3101	Discovery of exercise-related genes and pathway analysis based on comparative genomes of Mongolian originated Abaga and Wushen horse. Open Life Sciences, 2022, 17, 1269-1281.	0.6	2
3102	Reduce Bioaccumulation of Cd Pollutants Through the Antagonism of Se:Bioaccumulation of Cd and Comparative Transcriptome Analysis in the Hepatopancreas of Estuary Mud Crab (Scylla) Tj ETQq0 0 0 rgBT /Ove	rlæki 10 T	f 500 97 Td (P

8103 RNA Analysis of Diet-Induced Sarcopenic Obesity in Rat. SSRN Electronic Journal, 0, , .

#	Article	IF	CITATIONS
3104	Transcriptome analysis of tea (Camellia sinensis) leaves in response to ammonium starvation and recovery. Frontiers in Plant Science, 0, 13, .	1.7	2
3105	Effect of Water Activity on Conidia Germination in Aspergillus flavus. Microorganisms, 2022, 10, 1744.	1.6	0
3106	The vital role of covS in the establishment of Streptococcus equi subsp. zooepidemicus virulence. Journal of Integrative Agriculture, 2023, 22, 568-584.	1.7	0
3107	Comparative transcriptome analysis of compatible and incompatible Brassica napus—Xanthomonas campestris interactions. Frontiers in Plant Science, 0, 13, .	1.7	0
3108	Evidence that Transcriptional Alterations in Sarcoptes scabiei Are under Tight Post-Transcriptional (microRNA) Control. International Journal of Molecular Sciences, 2022, 23, 9719.	1.8	1
3109	Integrated Analysis of Transcriptome and Metabolome Reveals the Regulation of Chitooligosaccharide on Drought Tolerance in Sugarcane (Saccharum spp. Hybrid) under Drought Stress. International Journal of Molecular Sciences, 2022, 23, 9737.	1.8	8
3110	Population transcriptomic analysis identifies the comprehensive IncRNAs landscape of spike in wheat (Triticum aestivum L.). BMC Plant Biology, 2022, 22, .	1.6	6
3111	Comparative RNA-seq analysis reveals a critical role for ethylene in rose (Rosa hybrida) susceptible response to Podosphera pannosa. Frontiers in Plant Science, 0, 13, .	1.7	5
3113	Biochemical, transcriptome and metabolome analysis of the pulp of Citrus sinensis (L.) Osbeck †Hong Jiang' and its two variants reveal pathways regulating pulp taste, mastication, and color. Electronic Journal of Biotechnology, 2022, , .	1.2	0
3114	Orai2 deficiency attenutates experimental colitis by facilitating the colonization of Akkermansia muciniphila. Genomics, 2022, 114, 110479.	1.3	4
3115	Evaluation of <i>Hamiltonella</i> on <i>Aphis gossypii</i> fitness based on life table parameters and <scp>RNA</scp> sequencing. Pest Management Science, 0, , .	1.7	1
3116	Revealing phosphorylation regulatory networks during embryogenesis of honey bee worker and drone (Apis mellifera). Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	2
3117	Genetic Diversity and Selective Signature in Dabieshan Cattle Revealed by Whole-Genome Resequencing. Biology, 2022, 11, 1327.	1.3	4
3118	Multifaceted analyses reveal carbohydrate metabolism mainly affecting the quality of postharvest bamboo shoots. Frontiers in Plant Science, 0, 13, .	1.7	1
3119	Comparative transcriptome meta-analysis reveals a set of genes involved in the responses to multiple pathogens in maize. Frontiers in Plant Science, 0, 13, .	1.7	5
3120	Comparative RNA-Seq analysis reveals insights in Salmonella disease resistance of chicken; and database development as resource for gene expression in poultry. Genomics, 2022, 114, 110475.	1.3	8
3121	Comparative analysis of Neptunea cumingii growth, related digestive and immune enzyme indicators, and liver transcriptome under different feeding conditions. Frontiers in Marine Science, 0, 9, .	1.2	2
3122	Transcriptome analysis reveals the mechanism of chronic heat stress on meat quality of broilers. Journal of Animal Science and Biotechnology, 2022, 13, .	2.1	11

ARTICLE IF CITATIONS Elucidating the Molecular Responses to Waterlogging Stress in Cucumis melo by Comparative 3123 1.2 6 Transcriptome Profiling. Horticulturae, 2022, 8, 891. Transcriptomic Analysis Reveals <i>Lactobacillus reuteri</i> Alleviating Alcohol-Induced Liver Injury in Mice by Enhancing the Farnesoid X Receptor Signaling Pathway. Journal of Agricultural and Food 2.4 Chemistry, 2022, 70, 12550-12564. Comparative study of the function and structure of the gut microbiota in Siberian musk deer and 3126 3 1.7 Forest musk deer. Applied Microbiology and Biotechnology, 2022, 106, 6799-6817. Anti-proliferative and pro-apoptotic effects of curcumin on skin cutaneous melanoma: Bioinformatics 3127 1.1 analysis and in vitro experimental studies. Frontiers in Genetics, 0, 13, . RNA sequencing reveals IncRNA-mediated non-mendelian inheritance of feather growth change in 3128 0.5 3 chickens. Genes and Genomics, 2022, 44, 1323-1331. Combined transcriptome and metabolome reveal glutathione metabolism plays a critical role in resistance to salinity in rice landraces HD961. Frontiers in Plant Science, 0, 13, . 3129 1.7 Genome-wide identification of alternative splicing associated with histone deacetylase inhibitor in 3130 1.1 0 cutaneous T-cell lymphomas. Frontiers in Genetics, 0, 13, . Multi-omics data integration for hepatocellular carcinoma subtyping with multi-kernel learning. 1.1 Frontiers in Genetics, 0, 13, . Comparative Transcriptome Analysis and Genetic Methods Revealed the Biocontrol Mechanism of 3132 Paenibacilluspolymyxa NSY50 against Tomato Fusarium Wilt. International Journal of Molecular 1.8 5 Sciences, 2022, 23, 10907. Discovery of a Novel C-Quadruplex and Histone Deacetylase (HDAC) Dual-Targeting Agent for the Treatment of Triple-Negative Breast Cancer. Journal of Medicinal Chemistry, 2022, 65, 12346-12366. Systemic proteomics and miRNA profile analysis of exosomes derived from human pluripotent stem 3134 22 2.4 cells. Stem Cell Research and Therapy, 2022, 13, . Comparative transcriptome profiling and molecular marker development for oil palm fruit color. 1.6 Scientific Reports, 2022, 12, . Dynamic transcriptome and network-based analysis of yellow leaf mutant Ginkgo biloba. BMC Plant 3136 1.6 3 Biology, 2022, 22, . Different responses to glucose overload between two strains of largemouth bass (Micropterus) Tj ETQq1 1 0.784314, rgBT /Qverlock Full-length transcriptional analysis reveals the complex relationship of leaves and roots in responses 3138 5 1.7 to cold-drought combined stress in common vetch. Frontiers in Plant Science, 0, 13, . De novo transcriptome analysis of high-salinity stress-induced antioxidant activity and plant phytohormone alterations in Sesuvium portulacastrum. Frontiers in Plant Science, 0, 13, . Network pharmacology and computer-aided drug design to explored potential targets of Lianhua 3140 1.6 3 Qingwen and Qingfei Paidu decoction for COVID-19. Frontiers in Pharmacology, 0, 13, . Toxicity Effects and Mechanisms of MgO Nanoparticles on the Oomycete Pathogen Phytophthora 3141 1.6 infestans and Its Host Solanum tuberosum. Toxics, 2022, 10, 553.

		CITATION REPORT		
#	Article		IF	CITATIONS
3142	Polyadenylate-binding protein cytoplasmic 1 mediates alternative splicing events of immune-relate genes in gastric cancer cells. Experimental Biology and Medicine, 2022, 247, 1907-1916.	ď	1.1	3
3143	Genome resequencing and transcriptome profiling reveal molecular evidence of tolerance to water deficit in barley. Journal of Advanced Research, 2023, 49, 31-45.		4.4	3
3144	Adaptation and evolution of the sea anemone <i>Alvinactis</i> sp. to deepâ€sea hydrothermal ver comparison using transcriptomes. Ecology and Evolution, 2022, 12, .	ıts: A	0.8	2
3145	DDX17 modulates the expression and alternative splicing of genes involved in apoptosis and proliferation in lung adenocarcinoma cells. PeerJ, 0, 10, e13895.		0.9	2
3146	Determination of Zn Responsive Genes Involved in Zn Fertilization in Peanuts Based on Transcripto Analysis. Journal of Plant Growth Regulation, 0, , .	ome	2.8	0
3147	Comparative physiological, transcriptomic, and WGCNA analyses reveal the key genes and regulat pathways associated with drought tolerance in Tartary buckwheat. Frontiers in Plant Science, 0, 1		1.7	9
3148	SERBP1 affects the apoptotic level by regulating the expression and alternative splicing of cellular and metabolic process genes in HeLa cells. Peerl, 0, 10, e14084.		0.9	1
3149	Physiological and transcriptomic analysis uncovers salinity stress mechanisms in a facultative crassulacean acid metabolism plant Dendrobium officinale. Frontiers in Plant Science, 0, 13, .		1.7	2
3150	Transcriptome analysis and mining of genes related to shade tolerance in foxtail millet ( <i>Setaria</i>	) Tj ETQq0 0 0 rş	gBT /Over	lock 10 Tf 5
3151	Genome-wide meta-QTL analyses provide novel insight into disease resistance repertoires in comm bean. BMC Genomics, 2022, 23, .	ion	1.2	8
3152	LncRNA TP53TG1 plays an anti-oncogenic role in cervical cancer by synthetically regulating transcriptome profile in HeLa cells. Frontiers in Genetics, 0, 13, .		1,1	2

3153	Transcriptomic and genomic profiling revealed the unique cellular response mechanism involved in arsenite stress in Thermus tengchongensis. International Biodeterioration and Biodegradation, 2022, 175, 105504.	1.9	1
3154	Systematic identification and characterization of IncRNAs and IncRNA-miRNA-mRNA networks in the liver of turbot (Scophthalmus maximus L.) induced with Vibrio anguillarum. Fish and Shellfish Immunology, 2022, 131, 21-29.	1.6	4
3155	Microbial mediated arsenate reducing behavior in landfill leachate-saturated zone. Environmental Pollution, 2022, 314, 120281.	3.7	1
3156	Toxicity of chronic waterborne zinc exposure in the hepatopancreas of white shrimp Litopenaeus vannamei. Chemosphere, 2022, 309, 136553.	4.2	8
3157	GlycAP, a glycoproteomic analysis platform for site-specific N-glycosylation research. International Journal of Mass Spectrometry, 2022, 482, 116947.	0.7	1
3158	FGF21 at physiological concentrations regulates vascular endothelial cell function through multiple pathways. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2022, 1868, 166558.	1.8	7
3159	Genome-wide association studies uncover genes associated with litter traits in the pig. Animal, 2022, 16, 100672.	1.3	6

#	Article	IF	CITATIONS
3160	Transcriptome analysis reveals immune and metabolic regulation effects of Poria cocos polysaccharides on Bombyx mori larvae. Frontiers in Immunology, 0, 13, .	2.2	1
3161	Construction and Transcriptomic Study of Chicken IFNAR1-Knockout Cell Line Reveals the Essential Roles of Cell Growth- and Apoptosis-Related Pathways in Duck Tembusu Virus Infection. Viruses, 2022, 14, 2225.	1.5	4
3162	Zearalenone damages the male reproductive system of rats by destroying testicular focal adhesion. Environmental Toxicology, 2023, 38, 278-288.	2.1	3
3163	Leaf-transcriptome profiles of phoebe bournei provide insights into temporal drought stress responses. Frontiers in Plant Science, 0, 13, .	1.7	6
3164	Integrative Analysis of miRNA-mRNA in Ovarian Granulosa Cells Treated with Kisspeptin in Tan Sheep. Animals, 2022, 12, 2989.	1.0	2
3165	Whole-Genome Sequencing and Transcriptome Analysis of Ganoderma lucidum Strain Yw-1-5 Provides New Insights into the Enhanced Effect of Tween80 on Exopolysaccharide Production. Journal of Fungi (Basel, Switzerland), 2022, 8, 1081.	1.5	4
3166	Effects of Glutamine Starvation on SHVV Replication by Quantitative Proteomics Analysis. Fishes, 2022, 7, 315.	0.7	0
3167	Transcriptome analysis of floral bud development and function analysis of a novel CO gene in Paeonia × lemoinei â€~High Noon'. Scientific Reports, 2022, 12, .	1.6	0
3168	Citric Acid in Rice Root Exudates Enhanced the Colonization and Plant Growth-Promoting Ability of Bacillus altitudinis LZP02. Microbiology Spectrum, 2022, 10, .	1.2	8
3169	Molecular and physiologic mechanisms of advanced ripening by trunk girdling at early veraison of â€~Summer Black' grape. Frontiers in Plant Science, 0, 13, .	1.7	2
3170	Novel insights on genes and pathways involved in <i>Pinus elliottii</i> response to resinosis. Tree Physiology, 0, , .	1.4	1
3171	Comparative Physiological and Transcriptomic Analysis Provide New Insights of Crucial Pathways and Genes Regulating Kenaf Salt Tolerance. Journal of Plant Growth Regulation, 2023, 42, 3582-3605.	2.8	2
3172	Central gene transcriptional regulatory networks shaping monocyte development in bone marrow. Frontiers in Immunology, 0, 13, .	2.2	1
3174	Analyzing the interactions of mRNAs, miRNAs and lncRNAs to predict ceRNA networks in bovine cystic follicular granulosa cells. Frontiers in Veterinary Science, 0, 9, .	0.9	1
3175	Data-independent acquisition-based quantitative proteomic analysis of m.3243A>G MELAS reveals novel potential pathogenesis and therapeutic targets. Medicine (United States), 2022, 101, e30938.	0.4	0
3176	Genome-centric investigation of bile acid metabolizing microbiota of dairy cows and associated diet-induced functional implications. ISME Journal, 2023, 17, 172-184.	4.4	16
3177	Investigating on the influence mechanism of sausage of sea bass on calcium absorption and transport based on Caco-2 cell monolayer model. Frontiers in Nutrition, 0, 9, .	1.6	1
3178	Novel pituitary actions of GnRH in teleost: The link between reproduction and feeding regulation. Frontiers in Endocrinology, 0, 13, .	1.5	1

#	Article	IF	CITATIONS
3179	BmAbl1 Regulates Silk Protein Synthesis via Glutathione Metabolism in Bombyx mori. Insects, 2022, 13, 967.	1.0	1
3180	Transcriptome Analysis of Early Senescence in the Post-Anthesis Flag Leaf of Wheat (Triticum aestivum) Tj ETQq1	1_0,7843	I4₁rgBT /Ov
3181	Tissue-specific transcriptome responses to Fusarium head blight and Fusarium root rot. Frontiers in Plant Science, 0, 13, .	1.7	1
3182	Different adaptive patterns of wheat with different drought tolerance under drought stresses and rehydration revealed by integrated metabolomic and transcriptomic analysis. Frontiers in Plant Science, 0, 13, .	1.7	7
3183	Transcriptomic, cytological, and physiological analyses reveal the potential regulatory mechanism in Tartary buckwheat under cadmium stress. Frontiers in Plant Science, 0, 13, .	1.7	3
3184	Identifying Key Lysosome-Related Genes Associated with Drug-Resistant Breast Cancer Using Computational and Systems Biology Approach. Iranian Journal of Pharmaceutical Research, 2022, 21, .	0.3	2
3185	Comparative Transcriptome Analysis Reveals the Key Genes Involved in Lipid Deposition in Pekin Ducks (Anas platyrhynchos domesticus). Agriculture (Switzerland), 2022, 12, 1775.	1.4	0
3186	HIF-3α-Induced miR-630 Expression Promotes Cancer Hallmarks in Cervical Cancer Cells by Forming a Positive Feedback Loop. Journal of Immunology Research, 2022, 2022, 1-19.	0.9	4
3188	Integrated Analysis of Transcriptome and microRNA Profile Reveals the Toxicity of Euphorbia Factors toward Human Colon Adenocarcinoma Cell Line Caco-2. Molecules, 2022, 27, 6931.	1.7	2
3189	Dynamic analysis of physiological indices and transcriptome profiling revealing the mechanisms of the allelopathic effects of phenolic acids on Pinellia ternata. Frontiers in Plant Science, 0, 13, .	1.7	7
3190	ESRP1-regulated isoform switching of LRRFIP2 determines metastasis of gastric cancer. Nature Communications, 2022, 13, .	5.8	13
3191	Multi-omics reveals the key and specific miRNA-mRNA modules underlying salt tolerance in wild emmer wheat (Triticum dicoccoides L.). BMC Genomics, 2022, 23, .	1.2	2
3192	De Novo Assembly of a Sarcocarp Transcriptome Set Identifies AaMYB1 as a Regulator of Anthocyanin Biosynthesis in Actinidia arguta var. purpurea. International Journal of Molecular Sciences, 2022, 23, 12120.	1.8	0
3194	Integrated analysis of the whole transcriptome of skeletal muscle reveals the ceRNA regulatory network related to the formation of muscle fibers in Tan sheep. Frontiers in Genetics, 0, 13, .	1.1	4
3195	Whole-genome sequencing unravels novel genetic determinants and regulatory pathways associated with triamcinolone acetonide-induced ocular hypertension. Molecular Genetics and Genomics, 0, , .	1.0	0
3196	RNA-Seq and Iso-Seq Reveal the Important Role of COMT and CCoAOMT Genes in Accumulation of Scopoletin in Noni (Morinda citrifolia). Genes, 2022, 13, 1993.	1.0	4
3198	Identification of two QTLs, BPH41 and BPH42, and their respective gene candidates for brown planthopper resistance in rice. Scientific Reports, 2022, 12, .	1.6	2
3199	Castration alters the cecal microbiota and inhibits growth in Holstein cattle. Journal of Animal Science, 2022, 100, .	0.2	2

#	Article	IF	CITATIONS
3200	Behavioral and transcriptomic changes in butenolide treated larvae of the cosmopolitan fouling bryozoan Bugulina (Bugula) neritina. Frontiers in Marine Science, 0, 9, .	1.2	0
3201	Hepatic transcriptome analysis reveals the metabolic strategies of largemouth bass (Micropterus) Tj ETQq1 1 0.7 Part D: Genomics and Proteomics, 2023, 45, 101032.	84314 rgE 0.4	3T /Overlock 3
3202	The impact of Piscirickettsia salmonis infection on genome-wide DNA methylation profile in Atlantic Salmon. Genomics, 2022, 114, 110503.	1.3	5
3203	The expression of apoptosis related genes in HK-2 cells overexpressing PPM1K was determined by RNA-seq analysis. Frontiers in Genetics, 0, 13, .	1.1	2
3204	Study on microbes and antibiotic resistance genes in karst primitive mountain marshes – A case study of Niangniang Mountain in Guizhou, China. Ecotoxicology and Environmental Safety, 2022, 247, 114210.	2.9	0
3205	Immune function modulation during artificial ovarian maturation in Japanese eel (Anguilla japonica): A transcriptome profiling approach. Fish and Shellfish Immunology, 2022, 131, 662-671.	1.6	3
3206	Toxic effects and transcriptional responses in zebrafish liver cells following perfluorooctanoic acid exposure. Aquatic Toxicology, 2022, 253, 106328.	1.9	4
3207	The chromosome-level Melaleuca alternifolia genome provides insights into the molecular mechanisms underlying terpenoids biosynthesis. Industrial Crops and Products, 2022, 189, 115819.	2.5	4
3208	Identification of superior haplotypes and candidate genes for yield-related traits in tobacco (Nicotiana tabacum L.) using association mapping. Industrial Crops and Products, 2022, 189, 115886.	2.5	2
3209	An integrative analysis of IncRNAs and mRNAs highlights the potential roles of IncRNAs in the process of follicle selection in Taihang chickens. Theriogenology, 2023, 195, 122-130.	0.9	1
3210	Mechanisms underlying the succession of plant rhizosphere microbial community structure and function in an alpine open-pit coal mining disturbance zone. Journal of Environmental Management, 2023, 325, 116571.	3.8	7
3211	Transcriptome analysis of <i>Clematis lanuginosa</i> : Novel features of the molecular events occurring under heat-shock stress. Ornamental Plant Research, 2022, 2, 1-9.	0.2	0
3212	Microplastics reduce nitrogen uptake in peanut plants by damaging root cells and impairing soil nitrogen cycling. Journal of Hazardous Materials, 2023, 443, 130384.	6.5	35
3213	Multi-omics analysis the differences of VOCs terpenoid synthesis pathway in maintaining obligate mutualism between Ficus hirta Vahl and its pollinators. Frontiers in Plant Science, 0, 13, .	1.7	0
3214	Comparative transcriptomic analysis of the larval and adult stages of Dibothriocephalus dendriticus (Cestoda: Diphyllobothriidea). Parasitology Research, 2023, 122, 145-156.	0.6	2
3215	Time Course RNA-seq Reveals Soybean Responses against Root-Lesion Nematode and Resistance Players. Plants, 2022, 11, 2983.	1.6	1
3216	Integrated Transcriptome and Metabolome Analysis to Identify Sugarcane Gene Defense against Fall Armyworm (Spodoptera frugiperda) Herbivory. International Journal of Molecular Sciences, 2022, 23, 13712.	1.8	5
3217	Comparative transcriptome sequencing analysis of female and male <i>Decapterus macrosoma</i> . Peerl, 0, 10, e14342.	0.9	0

#	Article	IF	CITATIONS
3218	Proteomic analysis of zebrafish (Danio rerio) embryos exposed to benzyl benzoate. Environmental Science and Pollution Research, 2023, 30, 26375-26386.	2.7	4
3219	Revealing the mechanisms of the bioactive ingredients accumulation in Polygonatum cyrtonema by multiomics analyses. Frontiers in Plant Science, 0, 13, .	1.7	2
3220	Comparison of the signaling pathways of wing dimorphism regulated by biotic and abiotic stress in the brown planthopper. Insect Science, 2023, 30, 1046-1062.	1.5	2
3221	The molecular basis of socially induced egg-size plasticity in honey bees. ELife, 0, 11, .	2.8	3
3222	Identification of microRNA editing sites in three subtypes of leukemia. Frontiers in Molecular Biosciences, 0, 9, .	1.6	2
3223	Comparative Transcriptome Analysis Identifies Key Defense Genes and Mechanisms in Mulberry (Morus) Tj ETQq1 13519.	1 0.78431 1.8	14 rgBT /C 2
3224	Integrated Metabolome and Transcriptome Analysis Reveals a Regulatory Network of Fruit Peel Pigmentation in Eggplant (Solanum melongena L.). International Journal of Molecular Sciences, 2022, 23, 13475.	1.8	8
3225	Integrated physiological, biochemical, and transcriptomic analysis of thallium toxicity in zebrafish (Danio rerio) larvae. Science of the Total Environment, 2023, 859, 160265.	3.9	7
3226	Integrated analysis identified prognostic microRNAs in breast cancer. BMC Cancer, 2022, 22, .	1.1	3
3227	Non-coding transcriptomic profiles in the sheep mammary gland during different lactation periods. Frontiers in Veterinary Science, 0, 9, .	0.9	2
3228	FABP5 controls macrophage alternative activation and allergic asthma by selectively programming long-chain unsaturated fatty acid metabolism. Cell Reports, 2022, 41, 111668.	2.9	19
3229	Identification of spermatogenesis-related IncRNA in Holstein bull testis after sexual maturity based on transcriptome analysis. Animal Reproduction Science, 2022, 247, 107146.	0.5	3
3230	Comparative Analysis of Alternative Splicing in Two Contrasting Apple Cultivars Defense against Alternaria alternata Apple Pathotype Infection. International Journal of Molecular Sciences, 2022, 23, 14202.	1.8	4
3231	Chenodeoxycholic Acid (CDCA) Promoted Intestinal Epithelial Cell Proliferation by Regulating Cell Cycle Progression and Mitochondrial Biogenesis in IPEC-J2 Cells. Antioxidants, 2022, 11, 2285.	2.2	4
3232	A facultative ectomycorrhizal association is triggered by organic nitrogen. Current Biology, 2022, 32, 5235-5249.e7.	1.8	5
3233	Revealing the Regulatory Mechanism of IncRNA-LMEP on Melanin Deposition Based on High-Throughput Sequencing in Xichuan Chicken Skin. Genes, 2022, 13, 2143.	1.0	4
3234	Study on the role of calcium channel protein TRPV4 in the inflammatory pathway of type 2 diabetic adipose tissue based on gene databases. Biochemical and Biophysical Research Communications, 2023, 639, 161-168.	1.0	1
3235	Coexistence of microplastics alters the inhibitory effect of antibiotics on sludge anaerobic digestion. Chemical Engineering Journal, 2023, 455, 140754.	6.6	25

#	Article	IF	CITATIONS
3236	Alternative transcribed 3' isoform of long non-coding RNA Malat1 inhibits mouse retinal oxidative stress. IScience, 2023, 26, 105740.	1.9	1
3237	AREG upregulates secreted protein acidic and rich in cysteine expression in human granulosa cells. Molecular and Cellular Endocrinology, 2023, 561, 111826.	1.6	1
3238	Unravelling microbial drivers of the sulfate-reduction process inside landfill using metagenomics. Chemosphere, 2023, 313, 137537.	4.2	3
3239	Rhizosphere effect and water constraint jointly determined the roles of microorganism in soil phosphorus cycling in arid desert regions. Catena, 2023, 222, 106809.	2.2	6
3240	Effects of short-term exposure to volatile pesticide dichlorvos on the olfactory systems in Spodoptera litura: Calcium homeostasis, synaptic plasticity and apoptosis. Science of the Total Environment, 2023, 864, 161050.	3.9	2
3241	Comparative transcriptome profiling reveals the defense pathways and mechanisms in the leaves and roots of blueberry to drought stress. Fruit Research, 2022, 2, 1-15.	0.9	Ο
3242	Quantitative phosphoproteomic analysis of chitin-triggered immune responses in the plasma membrane of Arabidopsis. Functional Plant Biology, 2022, , .	1.1	0
3243	Optimized Method for the Identification of Candidate Genes and Molecular Maker Development Related to Drought Tolerance in Oil Palm (Elaeis guineensis Jacq.). Plants, 2022, 11, 2317.	1.6	1
3244	Transcriptome-wide modulation by <i>Sargassum vulgare</i> and <i>Acanthophora spicifera</i> extracts results in a prime-triggered plant signalling cascade in tomato and sweet pepper. AoB PLANTS, 2022, 14, .	1.2	4
3245	Transcriptomic Sequencing Analysis on Key Genes and Pathways Regulating Cadmium (Cd) in Ryegrass (LoliumAperenne L.) under Different Cadmium Concentrations. Toxics, 2022, 10, 734.	1.6	2
3246	Albinism in the largest extant amphibian: A metabolic, endocrine, or immune problem?. Frontiers in Endocrinology, 0, 13, .	1.5	1
3247	Blocking IncRNA-SNHG16 sensitizes gastric cancer cells to 5-Fu through targeting the miR-506-3p-PTBP1-mediated glucose metabolism. Cancer & Metabolism, 2022, 10, .	2.4	4
3248	SYNTAXIN OF PLANTS81 regulates root meristem activity and stem cell niche maintenance via ROS signaling. Plant Physiology, 2023, 191, 1365-1382.	2.3	9
3249	Transcriptome Analysis Reveals Potential Mechanism in Storage Protein Trafficking within Developing Grains of Common Wheat. International Journal of Molecular Sciences, 2022, 23, 14851.	1.8	1
3250	Regulation of salt tolerance in the roots of Zea mays by L-histidine through transcriptome analysis. Frontiers in Plant Science, 0, 13, .	1.7	5
3251	Comparative transcriptome analysis of the effects of friction and exogenous gibberellin on germination in <i>Abrus cantoniensis</i> . Plant Signaling and Behavior, 2022, 17, .	1.2	0
3253	Morusin Protected Ruminal Epithelial Cells against Lipopolysaccharide-Induced Inflammation through Inhibiting EGFR-AKT/NF-ήB Signaling and Improving Barrier Functions. International Journal of Molecular Sciences, 2022, 23, 14428.	1.8	1
3254	KIAA1429 regulates alternative splicing events of cancer-related genes in hepatocellular carcinoma. Frontiers in Oncology, 0, 12, .	1.3	2

#	Article	IF	CITATIONS
3255	Global DNA and protein interactomes of FLT1P1 (Fms-related tyrosine kinase 1 pseudogene 1) revealed its molecular regulatory functions associated with preeclampsia. Molecular Biology Reports, 0, , .	1.0	0
3256	Identification and Characterization of Sex-Biased miRNAs in the Golden Pompano (Trachinotus) Tj ETQq1 1 0.784	1314 rgBT	/Qverlock 10
3257	Rumen microbiota-host transcriptome interaction mediates the protective effects of trans-10, cis-12 CLA on facilitating weaning transition of lambs. Animal Nutrition, 2023, 12, 345-359.	2.1	4
3258	Transcriptome analysis reveals the regulatory mode by which NAA promotes the growth of Armillaria gallica. PLoS ONE, 2022, 17, e0277701.	1.1	2
3259	The Combined Analysis of Transcriptome and Antioxidant Enzymes Revealed the Mechanism of EBL and ZnO NPs Enhancing Styrax tonkinensis Seed Abiotic Stress Resistance. Genes, 2022, 13, 2170.	1.0	4
3260	The nuclear factor of activated T cells 5 (NFAT5) contributes to the renal corticomedullary differences in gene expression. Scientific Reports, 2022, 12, .	1.6	2
3261	Global transcriptomic analysis reveals candidate genes associated with different phosphorus acquisition strategies among soybean varieties. Frontiers in Plant Science, 0, 13, .	1.7	3
3262	Integrated Transcriptome Analysis Reveals the Crucial mRNAs and miRNAs Related to Fecundity in the Hypothalamus of Yunshang Black Goats during the Luteal Phase. Animals, 2022, 12, 3397.	1.0	Ο
3263	Proteomic analysis of Sarcoptes scabiei reveals that proteins differentially expressed between eggs and female adult stages are involved predominantly in genetic information processing, metabolism and/or host-parasite interactions. PLoS Neglected Tropical Diseases, 2022, 16, e0010946.	1.3	0
3264	Differential miRNA expression profiles in the bone marrow of Beagle dogs at different stages of Toxocara canis infection. BMC Genomics, 2022, 23, .	1.2	0
3265	dSCOPE: a software to detect sequences critical for liquid–liquid phase separation. Briefings in Bioinformatics, 2023, 24, .	3.2	8
3266	A strategy can be used to analyze intracellular interaction proteomics of cell-surface receptors. Amino Acids, 2023, 55, 263-273.	1.2	2
3267	Transcriptomics Analysis Reveals a Putative Role for Hormone Signaling and MADS-Box Genes in Mature Chestnut Shoots Rooting Recalcitrance. Plants, 2022, 11, 3486.	1.6	5
3268	Hypoxia aggravates the burden of yellowstripe goby (Mugilogobius chulae) under atorvastatin exposure. Aquatic Toxicology, 2023, 255, 106381.	1.9	2
3269	Transcriptome profiling provides insights into leaf color changes in two Acer palmatum genotypes. BMC Plant Biology, 2022, 22, .	1.6	5
3270	AgNPs-Triggered Seed Metabolic and Transcriptional Reprogramming Enhanced Rice Salt Tolerance and Blast Resistance. ACS Nano, 2023, 17, 492-504.	7.3	23
3271	Transcriptomes of Testes at Different Developmental Stages in the Opsariichthys bidens Predict Key Genes for Testis Development and Spermatogenesis. Marine Biotechnology, 2023, 25, 123-139.	1.1	2
3272	Transcriptomic analysis reveals the molecular mechanisms underlying osteoclast differentiation in the estrogen-deficient pullets. Poultry Science, 2023, 102, 102453.	1.5	1

#	Article	IF	Citations
3273	Comparative effects of different bacterial lipopolysaccharides on modulation of immune levels to improve survival of the black tiger shrimp. Journal of Invertebrate Pathology, 2023, 197, 107872.	1.5	1
3274	Comparative Transcriptome Analysis of Eriocheir sinensis from Wild Habitats in Han River, Korea. Life, 2022, 12, 2027.	1.1	0
3275	Seed Myco-priming improves crop yield and herbivory induced defenses in maize by coordinating antioxidants and Jasmonic acid pathway. BMC Plant Biology, 2022, 22, .	1.6	8
3276	Role of exogenous abscisic acid in freezing tolerance of mangrove Kandelia obovata under natural frost condition at near 32°N. BMC Plant Biology, 2022, 22, .	1.6	4
3277	Integrated multi-omics of the gastrointestinal microbiome and ruminant host reveals metabolic adaptation underlying early life development. Microbiome, 2022, 10, .	4.9	4
3278	PHD-finger family genes in wheat (Triticum aestivum L.): Evolutionary conservatism, functional diversification, and active expression in abiotic stress. Frontiers in Plant Science, 0, 13, .	1.7	2
3279	Wholeâ€genome identification of transposable elements reveals the equine repetitive element insertion polymorphism in Chinese horses. Animal Genetics, 0, , .	0.6	0
3280	Computational analysis to define efficacy & molecular mechanisms of 7, 4'- Dihydroxyflavone on eosinophilic esophagitis: Ex-vivo validation in human esophagus biopsies. Frontiers in Immunology, 0, 13, .	2.2	1
3281	Three-Dimensional Organization of Chicken Genome Provides Insights into Genetic Adaptation to Extreme Environments. Genes, 2022, 13, 2317.	1.0	2
3282	De novo transcriptome sequencing of Impatiens uliginosa and the analysis of candidate genes related to spur development. BMC Plant Biology, 2022, 22, .	1.6	0
3283	ANRIL overexpression globally induces expression and alternative splicing of genes involved in inflammation in HUVECs. Molecular Medicine Reports, 2022, 27, .	1.1	5
3284	Comprehensive investigation and regulatory function of lncRNAs engaged in western honey bee larval immune response to Ascosphaera apis invasion. Frontiers in Physiology, 0, 13, .	1.3	5
3285	Genome-wide association study to identify genomic loci associated with early vigor in bread wheat under simulated water deficit complemented with quantitative trait loci meta-analysis. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	4
3286	The draft genome of the Tibetan partridge ( <i>Perdix hodgsoniae</i> ) provides insights into its phylogenetic position and high-altitude adaptation. Journal of Heredity, 0, , .	1.0	2
3287	Transcriptomics reveals the molecular mechanisms of flesh colour differences in eggplant (Solanum) Tj ETQq0 0 (	D rgBT /Ov	erlock 10 Tf
3288	Single-cell transcriptome in silico analysis reveals conserved regulatory programs in macrophages/monocytes of abdominal aortic aneurysm from multiple mouse models and human. Frontiers in Cardiovascular Medicine, 0, 9, .	1.1	1
3289	Differences in leaf cuticular wax induced by whole-genome duplication in autotetraploid sour jujube. Horticultural Plant Journal, 2024, 10, 66-76.	2.3	1
3290	Competing endogenous <scp>RNA</scp> network construction based on long nonâ€coding <scp>RNAs</scp> , <scp>microRNAs</scp> , and <scp>mRNAs</scp> related to fat deposition in Songliao black swine. Animal Genetics, 0, , .	0.6	0

#	Article	IF	CITATIONS
3291	Effect of static magnetic field on marine mollusc Elysia leucolegnote. Frontiers in Molecular Biosciences, 0, 9, .	1.6	0
3292	Integrated bioinformatical and in vitro study on drug targets for liver cirrhosis based on unsupervised consensus clustering and immune cell infiltration. Frontiers in Pharmacology, 0, 13, .	1.6	0
3293	Integrated Transcriptome and Untargeted Metabolomic Analyses Revealed the Role of Methyltransferase Lae1 in the Regulation of Phospholipid Metabolism in Trichoderma atroviride. Journal of Fungi (Basel, Switzerland), 2023, 9, 120.	1.5	1
3294	Metatranscriptomic Analyses Reveal Important Roles of the Gut Microbiome in Primate Dietary Adaptation. Genes, 2023, 14, 228.	1.0	5
3295	New insights into effects of Kaixin Powder on depression via lipid metabolism related adiponectin signaling pathway. Chinese Herbal Medicines, 2023, 15, 240-250.	1.2	1
3296	High-density genetic linkage mapping reveals low stability of QTLs across environments for economic traits in Eucalyptus. Frontiers in Plant Science, 0, 13, .	1.7	2
3297	Transcriptomic analysis reveals biosynthesis genes and transcription factors related to leaf anthocyanin biosynthesis in Aglaonema commutatum. BMC Genomics, 2023, 24, .	1.2	4
3298	Arbuscular mycorrhizal fungus alleviates anthracnose disease in tea seedlings. Frontiers in Plant Science, 0, 13, .	1.7	6
3299	Baicalin suppresses interleukin-1β-induced apoptosis, inflammatory response, oxidative stress, and extracellular matrix degradation in human nucleus pulposus cells. Immunopharmacology and Immunotoxicology, 2023, 45, 433-442.	1.1	1
3300	Comprehensive bulk and single-cell transcriptome profiling give useful insights into the characteristics of osteoarthritis associated synovial macrophages. Frontiers in Immunology, 0, 13, .	2.2	5
3301	Gonad transcriptome analysis reveals the differences in gene expression related to sex-biased and reproduction of clam Cyclina sinensis. Frontiers in Marine Science, 0, 9, .	1.2	2
3302	Integrating Analysis to Identify Differential circRNAs Involved in Goat Endometrial Receptivity. International Journal of Molecular Sciences, 2023, 24, 1531.	1.8	0
3303	Iris lactea var. chinensis plant drought tolerance depends on the response of proline metabolism, transcription factors, transporters and the ROS-scavenging system. BMC Plant Biology, 2023, 23, .	1.6	2
3304	Mechanisms of sex differentiation and sex reversal in hermaphrodite fish as revealed by the <i>Epinephelus coioides</i> genome. Molecular Ecology Resources, 2023, 23, 920-932.	2.2	4
3305	Comparative toxicogenomics of benzotriazole ultraviolet stabilizers at environmental concentrations in Asian clam (Corbicula fluminea): Insight into molecular networks and behavior. Journal of Hazardous Materials, 2023, 447, 130811.	6.5	5
3306	A natural allele of proteasome maturation factor improves rice resistance to multiple pathogens. Nature Plants, 2023, 9, 228-237.	4.7	5
3307	Effects of Different-Syllable Aggressive Calls on Food Intake and Gene Expression in Vespertilio sinensis. Animals, 2023, 13, 306.	1.0	0
3308	Cloning and Function study of PsMYB2 transcription factor of Potentilla sericea under Cadmium Stress. Canadian Journal of Plant Science, 0, , .	0.3	0

#	Article	IF	CITATIONS
3309	Deep-learning based approach to identify substrates of human E3 ubiquitin ligases and deubiquitinases. Computational and Structural Biotechnology Journal, 2023, 21, 1014-1021.	1.9	2
3310	Transcriptome analysis of hepatopancreas of Chinese grass shrimp, Palaemonetes sinensis, infected by Enterocytospora artemiae. Fish and Shellfish Immunology, 2023, 133, 108557.	1.6	3
3311	Metabolite profiling and transcriptome analyses provide insight into the regulatory network of graft incompatibility in litchi. Frontiers in Genetics, 0, 13, .	1.1	1
3312	Gut bacterial species in late trimester of pregnant sows influence the occurrence of stillborn piglet through pro-inflammation response. Frontiers in Immunology, 0, 13, .	2.2	2
3313	Histological, transcriptomic, and gene functional analyses reveal the regulatory events underlying gibberellin-induced parthenocarpy in tomato. Horticultural Plant Journal, 2024, 10, 156-170.	2.3	1
3314	Whole-Exome Sequencing Revealed the Mutational Profiles of Primary Central Nervous System Lymphoma. Clinical Lymphoma, Myeloma and Leukemia, 2023, 23, 291-302.	0.2	1
3315	Comprehensive Analysis of Whole-Transcriptome Profiles in Response to Acute Hypersaline Challenge in Chinese Razor Clam Sinonovacula constricta. Biology, 2023, 12, 106.	1.3	5
3316	Transcriptomic Analysis of Resistant and Wild-Type Botrytis cinerea Isolates Revealed Fludioxonil-Resistance Mechanisms. International Journal of Molecular Sciences, 2023, 24, 988.	1.8	1
3317	RNA sequencing and transcriptome analyses reveal differentially expressed genes in the defensive glands of the medicinal beetle <i>Blaps rhynchopetera</i> . Entomological Research, 2023, 53, 12-28.	0.6	1
3318	Relative quantification of phenolic compounds in exocarp-mesocarp and endocarp of sumac (Toxicodendron vernicifluum) combined with transcriptome analysis provides insights into glycosylation of flavonoids and biflavonoid biosynthesis. Plant Physiology and Biochemistry, 2023, 195, 275-287.	2.8	3
3319	Comparative transcriptional analysis of metabolic pathways and mechanisms regulating essential oil biosynthesis in four elite Cymbopogon spp International Journal of Biological Macromolecules, 2023, 229, 943-951.	3.6	2
3320	Starch granules of the sugar-pathway were eliminated under the stress of PEG-drought compared with Soil-drought. Industrial Crops and Products, 2023, 193, 116158.	2.5	6
3321	Identification of hub genes associated with human cystic fibrosis: A Meta-analysis approach. , 2023, 35, 201139.		3
3322	Single-cell transcriptome uncovers heterogeneity and immune responses of leukocytes after vaccination with inactivated Edwardsiella tarda in flounder (Paralichthys olivaceus). Aquaculture, 2023, 566, 739238.	1.7	7
3323	The wheat leaf delayed virescence of mutant dv4 is associated with the abnormal photosynthetic and antioxidant systems. Gene, 2023, 856, 147134.	1.0	2
3324	RNA analysis of diet-induced sarcopenic obesity in rats. Archives of Gerontology and Geriatrics, 2023, 108, 104920.	1.4	1
3325	TikTok for developing learning motivation and oral proficiency in MICE learners. Journal of Hospitality, Leisure, Sport and Tourism Education, 2023, 32, 100415.	1.9	2
3326	Responsive Transcriptome Analysis of Senecio vulgaris L. Under Different Drought Stresses. Journal of Plant Growth Regulation, 0, , .	2.8	0

#	Article	IF	CITATIONS
3327	Integrative analysis of transcriptome and metabolism reveals potential roles of carbon fixation and photorespiratory metabolism in response to drought in Shanlan upland rice. BMC Genomics, 2022, 23, .	1.2	5
3328	CELF1 Selectively Regulates Alternative Splicing of DNA Repair Genes Associated With Cataract in Human Lens Cell Line. Biochemical Genetics, 2023, 61, 1319-1333.	0.8	3
3329	OsPPR11 encoding P-type PPR protein that affects group II intron splicing and chloroplast development. Plant Cell Reports, 0, , .	2.8	0
3330	β-Hydroxy-β-Methylbutyric Acid Promotes Repair of Sheep Myoblast Injury by Inhibiting IL-17/NF-κB Signaling. International Journal of Molecular Sciences, 2023, 24, 444.	1.8	3
3331	High-throughput analysis of CircRNA in cows with naturally infected Staphylococcus aureus mammary gland. Animal Biotechnology, 2023, 34, 4236-4246.	0.7	2
3332	Integrative Multi-OMICs Identifies Therapeutic Response Biomarkers and Confirms Fidelity of Clinically Annotated, Serially Passaged Patient-Derived Xenografts Established from Primary and Metastatic Pediatric and AYA Solid Tumors. Cancers, 2023, 15, 259.	1.7	2
3333	Characterizing Relevant MicroRNA Editing Sites in Parkinson's Disease. Cells, 2023, 12, 75.	1.8	3
3334	Characterization and acceleration of genome shuffling and ploidy reduction in synthetic allopolyploids by genome sequencing and editing. Nucleic Acids Research, 2023, 51, 198-217.	6.5	5
3335	FABP5 Deficiency Impaired Macrophage Inflammation by Regulating AMPK/NF-ήB Signaling Pathway. Journal of Immunology, 2022, 209, 2181-2191.	0.4	14
3336	Identification and Mapping of QTLs for Sulfur-Containing Amino Acids in Soybean ( <i>Clycine max</i> ) Tj ETQq1	1 0.78431 2.4	4 rgBT /Over
3337	Common scab disease-induced changes in geocaulosphere microbiome assemblages and functional processes in landrace potato (Solanum tuberosum var. Rongpuria) of Assam, India. Archives of Microbiology, 2023, 205, .	1.0	1
3338	Genetic responses to adding nitrates to improve hydrophilic yellow pigment in Monascus fermentation. Applied Microbiology and Biotechnology, 2023, 107, 1341-1359.	1.7	4
3339	Two Strains of Lentinula edodes Differ in Their Transcriptional and Metabolic Patterns and Respond Differently to Thermostress. Journal of Fungi (Basel, Switzerland), 2023, 9, 179.	1.5	1
3340	Metabolomic and Transcriptome Analysis of the Inhibitory Effects of <i>Bacillus subtilis</i> Strain Z-14 against <i>Fusarium oxysporum</i> Causing Vascular Wilt Diseases in Cucumber. Journal of Agricultural and Food Chemistry, 2023, 71, 2644-2657.	2.4	4
3341	Transcriptional profiling of Pseudomonas aeruginosa mature single- and dual-species biofilms in response to meropenem. Microbiology (United Kingdom), 2023, 169, .	0.7	2
3342	Effector protein Hcp2a of avian pathogenic Escherichia coli interacts with the endoplasmatic reticulum associated RPL23 protein of chicken DF-1 fibroblasts. Veterinary Research, 2023, 54, .	1.1	1
3344	Feeding Asian honeybee queens with European honeybee royal jelly alters body color and expression of related coding and non-coding RNAs. Frontiers in Physiology, 0, 14, .	1.3	1
3345	Phosphorus availability and planting patterns regulate soil microbial effects on plant performance in a semiarid steppe. Annals of Botany, 2023, 131, 1081-1095.	1.4	1

#	Article	IF	CITATIONS
3346	Comparative Analyses Reveal the Genetic Mechanism of Ambergris Production in the Sperm Whale Based on the Chromosome-Level Genome. Animals, 2023, 13, 361.	1.0	1
3347	A comparative study on the tolerance of tilapia (Oreochromis niloticus) to high carbohydrate and high lipid diets. Animal Nutrition, 2023, 13, 160-172.	2.1	3
3348	Comparative analysis of the chrysanthemum transcriptome with DNA methylation inhibitors treatment and silencing MET1 lines. BMC Plant Biology, 2023, 23, .	1.6	0
3349	Transcriptome analysis and identification of genes associated with leaf crude protein content in foxtail millet [Setaria italica (L.) P. Beauv.]. Frontiers in Genetics, 0, 14, .	1.1	0
3350	Differential transcriptome analysis of Sporocytophaga sp. CX11 and identification of candidate genes involved in lignocellulose degradation. Bioresources and Bioprocessing, 2023, 10, .	2.0	0
3351	Stage-Specific Transcriptomes of the Mussel Mytilus coruscus Reveals the Developmental Program for the Planktonic to Benthic Transition. Genes, 2023, 14, 287.	1.0	2
3352	Transcriptome analysis reveals the key pathways and candidate genes involved in salt stress responses in Cymbidium ensifolium leaves. BMC Plant Biology, 2023, 23, .	1.6	1
3353	Dysregulated IncRNAs are involved in the progress of myocardial infarction by constructing regulatory networks. Open Medicine (Poland), 2023, 18, .	0.6	0
3354	Combined analysis of chromatin accessibility and gene expression profiles provide insight into Fucoxanthin biosynthesis in Isochrysis galbana under green light. Frontiers in Microbiology, 0, 14, .	1.5	0
3355	BnaSD.C3 is a novel major quantitative trait locus affecting semi-dwarf architecture in Brassica napus. Journal of Integrative Agriculture, 2023, 22, 2981-2992.	1.7	0
3356	Farnesyl diphosphate synthase promotes cell proliferation by regulating gene expression and alternative splicing profiles in HeLa cells. Oncology Letters, 2023, 25, .	0.8	1
3357	Integrative Transcriptome and Chlorophyll Fluorescence Test Analysis Shed New Light on the Leaf Senescence Mechanism of Zoysia japonica. Agronomy, 2023, 13, 623.	1.3	1
3358	NQO1 regulates expression and alternative splicing of apoptotic genes associated with Alzheimer's disease in PC12 cells. Brain and Behavior, 2023, 13, .	1.0	2
3359	Genomeâ€wide association study reveals candidate genes for pollution excreta traits in pigs. Animal Genetics, 0, , .	0.6	1
3360	Differential Gene Expression Analysis of Non-Small Cell Lung Cancer Samples to Classify Candidate Genes. Engineering, Technology & Applied Science Research, 2023, 13, 10571-10577.	0.8	1
3361	Effect of interfering TOR signaling pathway on the biosynthesis of terpenoids in <i>Salvia miltiorrhiza Bge</i> . Plant Signaling and Behavior, 2023, 18, .	1.2	1
3362	The genome sequence and demographic history of <i>Przewalskia tangutica</i> (Solanaceae), an endangered alpine plant on the Qinghai–Tibet Plateau. DNA Research, 2023, 30, .	1.5	1
3363	Co-incorporation of Chinese milk vetch (Astragalus sinicus L.) and chemical fertilizer alters microbial functional genes supporting short-time scale positive nitrogen priming effects in paddy soils. Pedosphere, 2023, , .	2.1	2

#	Article	IF	CITATIONS
3364	Mechanisms of Phaeocystis globosa blooms in the Beibu Gulf revealed by metatranscriptome analysis. Harmful Algae, 2023, 124, 102407.	2.2	3
3365	Analysis of volatile emission of tea (Camellia sinensis) shoots in response to temperature-dependent postharvest treatments. European Journal of Agronomy, 2023, 146, 126821.	1.9	1
3366	Triacylglycerol lipase a10 (SITGLa10) gene negatively regulates cold tolerance, vegetative and reproductive growth in tomato. Environmental and Experimental Botany, 2023, 209, 105289.	2.0	0
3367	STAU1 promotes adipogenesis by regulating the alternative splicing of PparÎ <sup>3</sup> 2 mRNA. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2023, 1868, 159293.	1.2	0
3368	Transcriptomic analysis of Mythimna separata ovaries and identification of genes involved in reproduction. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2023, 46, 101075.	0.4	0
3369	Tryptophan pretreatment adjusts transcriptome and metabolome profiles to alleviate cadmium toxicity in Arabidopsis. Journal of Hazardous Materials, 2023, 452, 131226.	6.5	1
3370	Identification of key genes and small molecule drugs in osteoarthritis by integrated bioinformatics analysis. Biochemistry and Biophysics Reports, 2023, 34, 101450.	0.7	0
3371	Transcriptome and weighted gene co-expression network analysis of jujube (Ziziphus jujuba Mill.) fruit reveal putative genes involved in proanthocyanin biosynthesis and regulation. Food Science and Human Wellness, 2023, 12, 1557-1570.	2.2	3
3372	Integrated physiological, transcriptomic, and metabolomic analyses reveal that low-nitrogen conditions improve the accumulation of flavonoids in snow chrysanthemum. Industrial Crops and Products, 2023, 197, 116574.	2.5	5
3380	Role of SNPs located in the exon 9 of ATAPA1 gene on goose egg production. Poultry Science, 2023, 102, 102488.	1.5	0
3382	Enhanced MFC sensor performances and extracellular electron transport efficiency mediated by biochar and underlying biochemical mechanisms. Journal of Environmental Management, 2023, 332, 117282.	3.8	7
3383	Genome-wide analysis of dysregulated RNA-binding proteins and alternative splicing genes in keloid. Frontiers in Genetics, 0, 14, .	1.1	1
3384	Characterization of the soybean KRP gene family reveals a key role for GmKRP2a in root development. Frontiers in Plant Science, 0, 14, .	1.7	1
3385	GhMYB102 promotes drought resistance by regulating drought-responsive genes and ABA biosynthesis in cotton (Gossypium hirsutum L.). Plant Science, 2023, 329, 111608.	1.7	2
3386	The neonicotinoid insecticide imidacloprid has unexpected effects on the growth and development of soil amoebae. Science of the Total Environment, 2023, 869, 161884.	3.9	5
3387	Transcriptome-wide analysis reveals the coregulation of RNA-binding proteins and alternative splicing genes in the development of atherosclerosis. Scientific Reports, 2023, 13, .	1.6	4
3388	Integrative analyses of biomarkers and pathways for metformin reversing cisplatin resistance in head and neck squamous cell carcinoma cells. Archives of Oral Biology, 2023, 147, 105637.	0.8	2
3389	Transcriptome and methylome dynamics in the gills of large yellow croaker (Larimichthys crocea) during low-salinity adaption. Frontiers in Marine Science, 0, 10, .	1.2	1

#	Article	IF	CITATIONS
3390	Transcriptomics-based investigation of molecular mechanisms underlying synergistic antimicrobial effects of AgNPs and Domiphen on the human fungal pathogen Aspergillus fumigatus. Frontiers in Microbiology, 0, 14, .	1.5	2
3391	Whole-genome sequencing identifies potential candidate genes for egg production traits in laying ducks (Anas platyrhynchos). Scientific Reports, 2023, 13, .	1.6	0
3392	VPS35 promotes cell proliferation via EGFR recycling and enhances EGFR inhibitors response in gastric cancer. EBioMedicine, 2023, 89, 104451.	2.7	4
3393	Analysis of bulk RNA-seq data from sepsis patients reveals sepsis-associated lncRNAs and targeted cell death-related genes contributing to immune microenvironment regulation. Frontiers in Immunology, 0, 14, .	2.2	1
3394	Human Muscle–Derived Cells Are Capable of Tenogenic Differentiation and Contribution to Tendon Repair. American Journal of Sports Medicine, 2023, 51, 786-797.	1.9	1
3395	Identification of MKNK1 and TOP3A as ovarian endometriosis risk-associated genes using integrative genomic analyses and functional experiments. Computational and Structural Biotechnology Journal, 2023, 21, 1510-1522.	1.9	6
3396	The MAX2â€KAI2 module promotes salicylic acidâ€mediated immune responses in <i>Arabidopsis</i> . Journal of Integrative Plant Biology, 2023, 65, 1566-1584.	4.1	1
3397	Constitutive expression of AtSINA2 from Arabidopsis improves grain yield, seed oil and drought tolerance in transgenic soybean. Plant Physiology and Biochemistry, 2023, 196, 444-453.	2.8	3
3398	Chemical constituents and mechanisms from Hemerocallis citrina Baroni with anti-neuroinflammatory activity. Journal of Functional Foods, 2023, 102, 105427.	1.6	4
3399	Integrative transcriptomic profiling reveals the key pathways in the regulation mechanism of fish intestine-spleen immunity during the bacterial challenges. Aquaculture, 2023, 568, 739320.	1.7	2
3400	Arbuscular mycorrhizal fungus changes alfalfa response to pathogen infection activated by pea aphid infestation. Frontiers in Microbiology, 0, 13, .	1.5	1
3401	Comparative transcriptome analysis identified crucial genes and pathways affecting sperm motility in the reproductive tract of drakes with different libido. Poultry Science, 2023, 102, 102560.	1.5	1
3402	High temperature inhibited the accumulation of anthocyanin by promoting ABA catabolism in sweet cherry fruits. Frontiers in Plant Science, 0, 14, .	1.7	6
3403	Exosome-derived Small RNAs in mouse Sertoli cells inhibit spermatogonial apoptosis. Theriogenology, 2023, 200, 155-167.	0.9	4
3404	Differential alternative polyadenylation of homoeologous genes of allohexaploid wheat <scp>ABD</scp> subgenomes during drought stress response. Plant Journal, 2023, 114, 499-518.	2.8	6
3405	Melatonin Alleviates Chromium Toxicity in Maize by Modulation of Cell Wall Polysaccharides Biosynthesis, Glutathione Metabolism, and Antioxidant Capacity. International Journal of Molecular Sciences, 2023, 24, 3816.	1.8	12
3406	Transcriptional dynamics of maize leaves, pollens and ovules to gain insights into heat stress-related responses. Frontiers in Plant Science, 0, 14, .	1.7	4
3407	Global Responses of Autopolyploid Sugarcane Badila (Saccharum officinarum L.) to Drought Stress Based on Comparative Transcriptome and Metabolome Profiling. International Journal of Molecular Sciences, 2023, 24, 3856.	1.8	4

	Сітатіо	n Report	
#	Article	IF	CITATIONS
3408	Cytidine diphosphate diacylglycerol synthase is essential for mitochondrial structure and energy production in <i>Arabidopsis thaliana</i> . Plant Journal, 2023, 114, 338-354.	2.8	1
3409	Comparative transcriptome analysis of non-germinated and germinated spores of Enterocytozoon hepatopenaei (EHP) in vitro. Journal of Invertebrate Pathology, 2023, 197, 107900.	1.5	3
3410	Identification of IncRNAs and Their Regulatory Network Involved in Oil Biosynthesis in Developing Seeds of Yellowhorn (Xanthoceras sorbifolium). Forests, 2023, 14, 407.	0.9	3
3411	The super-enhancer repertoire in porcine liver. Journal of Animal Science, 2023, 101, .	0.2	2
3412	Transcriptomic profiling reveals candidate allelopathic genes in rice responsible for interactions with barnyardgrass. Frontiers in Plant Science, 0, 14, .	1.7	1
3413	Inhibitory effect of carvacrol against Alternaria alternata causing goji fruit rot by disrupting the integrity and composition of cell wall. Frontiers in Microbiology, 0, 14, .	1.5	5
3414	Transcriptome-wide assessment of N6-methyladenosine modification identifies different gene expression and infection-associated pathways in Treponema pallidum-infected macrophage. Journal of Dermatological Science, 2023, 109, 108-116.	1.0	0
3415	The telomere-to-telomere genome of <i>Fragaria vesca</i> reveals the genomic evolution of <i>Fragaria</i> and the origin of cultivated octoploid strawberry. Horticulture Research, 2023, 10, .	2.9	23
3416	Chromosome-level genome assembly and population genomics of Mongolian racerunner (Eremias) Tj ETQq0	0 0 rgBT /Ove	rloçk 10 Tf 5
3417	Utilizing Variants Identified with Multiple Genome-Wide Association Study Methods Optimizes Genomic Selection for Growth Traits in Pigs. Animals, 2023, 13, 722.	1.0	2
3418	Long Non-Coding RNA BNIP3 Inhibited the Proliferation of Bovine Intramuscular Preadipocytes via Cell Cycle. International Journal of Molecular Sciences, 2023, 24, 4234.	1.8	1
3419	Enlarged fins of Tibetan catfish provide new evidence of adaptation to high plateau. Science China Life Sciences, 2023, 66, 1554-1568.	2.3	2
3421	Transcriptome and Proteome Analysis Identifies Salt Stress Response Genes in Bottle Gourd Rootstock-Grafted Watermelon Seedlings. Agronomy, 2023, 13, 618.	1.3	3
3422	GGC repeat expansion in <i>NOTCH2NLC</i> induces dysfunction in ribosome biogenesis and translation. Brain, 2023, 146, 3373-3391.	3.7	4
3423	Comparative analysis of two kinds of garlic seedings: qualities and transcriptional landscape. BMC Genomics, 2023, 24, .	1.2	0
3424	Systematic analysis of circRNA-related ceRNA networks of black rockfish (Sebastes schlegelii) in response to Aeromonas salmonicides infection. Fish and Shellfish Immunology, 2023, 135, 108648.	1.6	4
3425	Transcriptome sequencing leads to an improved understanding of the infection mechanism of Alternaria solani in potato. BMC Plant Biology, 2023, 23, .	1.6	2

3426	ldentification of a novel eighteen-gene signature of recurrent metastasis neuroblastoma. Journal of Molecular Medicine, 2023, 101, 403-417.		1.7	0
------	--	--	-----	---

#	Article	IF	CITATIONS
3427	Abiotic factors and endophytes co-regulate flavone and terpenoid glycoside metabolism in Glycyrrhiza uralensis. Applied Microbiology and Biotechnology, 2023, 107, 2671-2688.	1.7	2
3428	Analysis of genetic diversity and selection signals in Chaling cattle of <scp>southern China</scp> using <scp>wholeâ€genome</scp> scan. Animal Genetics, 2023, 54, 284-294.	0.6	1
3429	Silencing of Pepper CaFtsH1 or CaFtsH8 Genes Alters Normal Leaf Development. International Journal of Molecular Sciences, 2023, 24, 4927.	1.8	0
3430	Identification and Characterization of Long Non-Coding RNAs: Implicating Insights into Their Regulatory Role in Kiwifruit Ripening and Softening during Low-Temperature Storage. Plants, 2023, 12, 1070.	1.6	0
3432	Transcriptome analysis and exploration of genes involved in the biosynthesis of secoiridoids in <i>Gentiana rhodantha</i> . PeerJ, 0, 11, e14968.	0.9	0
3433	Transcriptional profiling of Xanthomonas campestris pv. campestris in viable but nonculturable state. BMC Genomics, 2023, 24, .	1.2	2
3434	Contrasting Metabolisms in Green and White Leaf Sectors of Variegated Pelargonium zonale—An Integrative Transcriptomic and Metabolomic Study. International Journal of Molecular Sciences, 2023, 24, 5288.	1.8	2
3435	LTA4H extensively associates with mRNAs and IncRNAs indicative of its novel regulatory targets. PeerJ, 0, 11, e14875.	0.9	1
3436	The diverging epigenomic landscapes of honeybee queens and workers revealed by multiomic sequencing. Insect Biochemistry and Molecular Biology, 2023, 155, 103929.	1.2	2
3437	Phenotypic dimorphism between honeybee queen and worker is regulated by complicated epigenetic modifications. IScience, 2023, 26, 106308.	1.9	0
3438	Genome-wide association study identifies a gene conferring high physiological phosphorus use efficiency in rice. Frontiers in Plant Science, 0, 14, .	1.7	0
3439	<scp>UV</scp> â€induced mutagenesis of <i>Beauveria bassiana</i> ( <scp>Hypocreales:) Tj ETQq1 1 0.784314 Management Science, 2023, 79, 2762-2779.</scp>	rgBT /Ove 1.7	rlock 10 Tf <mark>5</mark> ( 2
3440	Comprehensive transcriptomic profiling reveals complex molecular mechanisms in the regulation of style-length dimorphism in Guettarda speciosa (Rubiaceae), a species with "anomalous―distyly. Frontiers in Plant Science, 0, 14, .	1.7	2
3441	Diurnal transcriptome dynamics reveal the photoperiod response of <i>Pyrus</i> . Physiologia Plantarum, 2023, 175, .	2.6	0
3442	Transcriptome Analysis of Pecan (Carya illinoinensis) Differentially Expressed Genes in Response to Drought Stress. Forests, 2023, 14, 608.	0.9	1
3443	Conjoint Analysis of Genome-Wide IncRNA and mRNA Expression during the Salicylic Acid Response in Populus × euramericana. Plants, 2023, 12, 1377.	1.6	2
3444	Histological, microecological and transcriptomic physiological responses underlying hypoxia and reoxygenation adaptation in yellowtail kingfish (Seriola lalandi). Frontiers in Marine Science, 0, 10, .	1.2	0
3446	Studies on 1-deoxynojirimycin biosynthesis in mulberry ( <i>Morus alba</i> L.) seeds through comparative transcriptomics. Natural Product Research, 0, , 1-10.	1.0	2

#	Article	IF	CITATIONS
3447	Comparative transcriptomic and metabolite profiling reveals genotypeâ€specific responses to Fe starvation in chickpea. Physiologia Plantarum, 2023, 175, .	2.6	2
3448	Correlation between Parental Transcriptome and Field Data for the Characterization of Heterosis in Chinese Cabbage. Genes, 2023, 14, 776.	1.0	0
3449	Study on molecular mechanism of volatiles variation during Bupleurum scorzonerifolium root development based on metabolome and transcriptome analysis. Frontiers in Plant Science, 0, 14, .	1.7	0
3450	Integrative Analysis of the Transcriptome and Metabolome Reveals the Mechanism of Chinese Fir Seed Germination. Forests, 2023, 14, 676.	0.9	2
3451	Genetic diversity and signatures of selection in BoHuai goat revealed by whole-genome sequencing. BMC Genomics, 2023, 24, .	1.2	4
3452	QTL mapping and transcriptome analysis identify novel QTLs and candidate genes in Brassica villosa for quantitative resistance against Sclerotinia sclerotiorum. Theoretical and Applied Genetics, 2023, 136, .	1.8	2
3453	Construction and analysis of circular RNA-associated competing endogenous RNA network in the hippocampus of aged mice for the occurrence of postoperative cognitive dysfunction. Frontiers in Aging Neuroscience, 0, 15, .	1.7	1
3454	Highâ€ŧhroughput miRNA sequencing and identification of a novel ICE1â€ŧargeting miRNA in response to low temperature stress in <i>Eucalyptus camaldulensis</i> . Plant Biology, 2023, 25, 541-550.	1.8	0
3455	Integrative epigenome profiling of 47XXY provides insights into whole genomic DNA hypermethylation and active chromatin accessibility. Frontiers in Molecular Biosciences, 0, 10, .	1.6	0
3456	Proteins in pregnant swine serum promote the African swine fever virus replication: an iTRAQ-based quantitative proteomic analysis. Virology Journal, 2023, 20, .	1.4	0
3457	The Commensal Anaerobe Veillonella dispar Reprograms Its Lactate Metabolism and Short-Chain Fatty Acid Production during the Stationary Phase. Microbiology Spectrum, 2023, 11, .	1.2	5
3458	Mic60 is essential to maintain mitochondrial integrity and to prevent encephalomyopathy. Brain Pathology, 2023, 33, .	2.1	1
3459	BIND&MODIFY: a long-range method for single-molecule mapping of chromatin modifications in eukaryotes. Genome Biology, 2023, 24, .	3.8	5
3460	Understanding host response to infectious salmon anaemia virus in an Atlantic salmon cell line using single-cell RNA sequencing. BMC Genomics, 2023, 24, .	1.2	3
3461	Combined IncRNA and mRNA Expression Profiles Identified the IncRNA–miRNA–mRNA Modules Regulating the Cold Stress Response in Ammopiptanthus nanus. International Journal of Molecular Sciences, 2023, 24, 6502.	1.8	4
3462	Sucrose promotes branch-thorn occurrence of <i>Lycium ruthenicum</i> through dual effects of energy and signal. Tree Physiology, 2023, 43, 1187-1200.	1.4	3
3463	Whole transcriptome analysis reveals that immune infiltration- lncRNAs are related to cellular apoptosis in liver transplantation. Frontiers in Immunology, 0, 14, .	2.2	0
3464	TB insights, bioinformatics as a tool a search for biomarkers for point of care diagnostics. Indian Journal of Tuberculosis, 2023, , .	0.3	1

#	Article	IF	CITATIONS
3465	Transcriptomic responses of the liver of mandarin fish ( <i>Siniperca chuatsi</i> ) under hypoxic stress. Journal of Fish Biology, 2023, 103, 44-58.	0.7	5
3466	Melatonin promotes the development of the secondary hair follicles by regulating circMPP5. Journal of Animal Science and Biotechnology, 2023, 14, .	2.1	2
3467	Transcriptomics reveals the effects of NTRK1 on endoplasmic reticulum stress response-associated genes in human neuronal cell lines. PeerJ, 0, 11, e15219.	0.9	1
3468	Targeting Wnt-ß-Catenin-FOSL Signaling Ameliorates Right Ventricular Remodeling. Circulation Research, 2023, 132, 1468-1485.	2.0	6
3469	P4-ATPase subunit Cdc50 plays a role in yeast budding and cell wall integrity in Candida glabrata. BMC Microbiology, 2023, 23, .	1.3	1
3470	Hepatotoxic Components Effect of Chebulae Fructus and Associated Molecular Mechanism by Integrated Transcriptome and Molecular Docking. Molecules, 2023, 28, 3427.	1.7	1
3471	HSVâ€l infectionâ€induced herpetic neuralgia involves a CCL5/CCR5â€mediated inflammation mechanism. Journal of Medical Virology, 2023, 95, .	2.5	4
3472	SOX2 downregulation of PML increases HCMV gene expression and growth of glioma cells. PLoS Pathogens, 2023, 19, e1011316.	2.1	4
3473	Comparative Transcriptome and Targeted Metabolome Profiling Unravel the Key Role of Phenylpropanoid and Glucosinolate Pathways in Defense against <i>Alternaria brassicicola</i> in Broccoli. Journal of Agricultural and Food Chemistry, 2023, 71, 6499-6510.	2.4	4
3474	Genome-wide identification of alternative splicing and splicing regulated in immune infiltration in osteosarcoma patients. Frontiers in Genetics, 0, 14, .	1.1	0
3475	Acupuncture Ameliorated Behavioral Abnormalities in the Autism Rat Model via Pathways for Hippocampal Serotonin. Neuropsychiatric Disease and Treatment, 0, Volume 19, 951-972.	1.0	0
3476	Reproductive toxicity of polystyrene nanoplastics in Drosophila melanogaster under multi-generational exposure. Chemosphere, 2023, 330, 138724.	4.2	6
3477	Host-plant adaptation in xylophagous insect-microbiome systems: Contributionsof longicorns and gut symbionts revealed by parallel metatranscriptome. IScience, 2023, 26, 106680.	1.9	2
3478	Integrated metabolome and transcriptome analysis provides insights on the floral scent formation in <i>Hydrangea arborescens</i> . Physiologia Plantarum, 2023, 175, .	2.6	4
3479	RNA-binding protein ENO1 promotes the tumor progression of gastric cancer by binding to and regulating gastric cancer-related genes. Journal of Gastrointestinal Oncology, 2023, 14, 585-598.	0.6	1
3480	PAIP1 regulates expression of immune and inflammatory response associated genes at transcript level in liver cancer cell. PeerJ, 0, 11, e15070.	0.9	1
3481	Exogenous Brassinosteroid Enhances Zinc tolerance by activating the Phenylpropanoid Biosynthesis pathway in Citrullus lanatus L. Plant Signaling and Behavior, 2023, 18, .	1.2	4
3482	Comprehensive analysis of circular RNAs in porcine small intestine epithelial cells associated with susceptibility to Escherichia coli F4ac diarrhea. BMC Genomics, 2023, 24, .	1.2	0

#	Article	IF	CITATIONS
3483	Regulatory network mediated by CmMKK5–CmMPK13 cascade response to phosphorus starvation in chrysanthemum. Industrial Crops and Products, 2023, 199, 116730.	2.5	0