

Automated genome annotation and pathway identification as a controlled vocabulary

Bioinformatics

21, 3787-3793

DOI: [10.1093/bioinformatics/bti430](https://doi.org/10.1093/bioinformatics/bti430)

Citation Report

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1	Gene alterations in tumor-associated endothelial cells from endometrial cancer. <i>International Journal of Molecular Medicine</i> , 1998, 22, 619.	1.8	6
2	Constructing biological networks through combined literature mining and microarray analysis: a LMMA approach. <i>Bioinformatics</i> , 2006, 22, 2143-2150.	1.8	84
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4	Molecular analysis of early rice stamen development using organ-specific gene expression profiling. <i>Plant Molecular Biology</i> , 2006, 61, 845-861.	2.0	30
5	Genome comparison using Gene Ontology (GO) with statistical testing. <i>BMC Bioinformatics</i> , 2006, 7, 374.	1.2	15
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8	Transcriptome Profiling, Molecular Biological, and Physiological Studies Reveal a Major Role for Ethylene in Cotton Fiber Cell Elongation. <i>Plant Cell</i> , 2006, 18, 651-664.	3.1	518
9	Genome-wide in silico identification and analysis of cis natural antisense transcripts (cis-NATs) in ten species. <i>Nucleic Acids Research</i> , 2006, 34, 3465-3475.	6.5	155
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828	Genome-Wide Analysis of MicroRNAs in Relation to Pupariation in Oriental Fruit Fly. <i>Frontiers in Physiology</i> , 2019, 10, 301.	1.3	22
829	lnc TINCR induced by NOD1 mediates inflammatory response in 3T3-L1 adipocytes. <i>Gene</i> , 2019, 698, 150-156.	1.0	6
830	RNA-Seq Analysis Reveals Differential Responses of Potato (<i>Solanum tuberosum</i> L.) Plantlets Cultured in vitro to Red, Blue, Green, and White Light-emitting Diodes (LEDs). <i>Journal of Plant Growth Regulation</i> , 2019, 38, 1412-1427.	2.8	19
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832	Transcriptome analysis and discovery of genes involved in immune pathways in <i>Solen strictus</i> (Gould.) Tj ETQq1 1 0,784314 rgBT /Over	1.6	8
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847	Transcriptomic Diversification of Granulosa Cells during Follicular Development in Chicken. <i>Scientific Reports</i> , 2019, 9, 5462.	1.6	34
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905	Identification of Salt Stress Response Genes in <i>Rosa chinensis</i> Leaves by Comparative RNA-seq Analysis of Transcriptome Dynamics. <i>Russian Journal of Plant Physiology</i> , 2019, 66, 119-127.	0.5	3
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944	Transcriptome analysis of axillary bud differentiation in a new dual-axillary bud genotype of sugarcane. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 685-701.	0.8	3
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962	Exploration of key regulators driving primary feather follicle induction in goose skin. <i>Gene</i> , 2020, 731, 144338.	1.0	9
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969	Transcriptome analysis reveals gene expression changes of the fat body of silkworm (<i>Bombyx mori</i> L.) in response to selenium treatment. <i>Chemosphere</i> , 2020, 245, 125660.	4.2	24
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980	Systematic Characterization of Long Non-Coding RNAs and Their Responses to Drought Stress in Dongxiang Wild Rice. <i>Rice Science</i> , 2020, 27, 21-31.	1.7	25
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992	Melatonin enhances salt stress tolerance in rubber tree (<i>Hevea brasiliensis</i>) seedlings. <i>Industrial Crops and Products</i> , 2020, 145, 111990.	2.5	27
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1010	Genome-wide small RNA profiling reveals tiller development in tall fescue (<i>Festuca arundinacea</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.2	2
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1012	Exogenous $\hat{3}$ -aminobutyric acid promotes biomass and astaxanthin production in <i>Haematococcus pluvialis</i> . <i>Algal Research</i> , 2020, 52, 102089.	2.4	24
1013	Holistic insights into meningitic <i>Escherichia coli</i> infection of astrocytes based on whole transcriptome profiling. <i>Epigenomics</i> , 2020, 12, 1611-1632.	1.0	5
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1018	Exploring the mechanism of cisplatin resistance by transcriptome sequencing and reversing the chemoresistance by autophagy inhibition in small cell lung cancer. <i>Biochemical and Biophysical Research Communications</i> , 2020, 533, 474-480.	1.0	11
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1030	Transcriptome profiles of F1 hybrids (<i>Acanthopagrus schlegelii</i> TM × <i>Pagrus major</i> TM) and parents reveal hybrid effects on individual development. <i>Aquaculture Research</i> , 2020, 51, 4011-4021.	0.9	7
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1034	Investigation of genes associated with petal variations between diploid and autotetraploid in Chinese cabbage (<i>Brassica rapa</i> L. ssp. <i>pekinensis</i>) by RNA-seq and sRNA-seq. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1459-1476.	1.0	3
1035	Comparative analysis of the transcriptome, methylome, and metabolome during pollen abortion of a seedless citrus mutant. <i>Plant Molecular Biology</i> , 2020, 104, 151-171.	2.0	11
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1043	<i>Toxocara canis</i> Differentially Affects Hepatic MicroRNA Expression in Beagle Dogs at Different Stages of Infection. <i>Frontiers in Veterinary Science</i> , 2020, 7, 587273.	0.9	10
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1053	Effects of Trace Irrigation at Different Depths on Transcriptome Expression Pattern in Cotton (<i>G.</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	0.9	3
1054	Multi-omics analysis of cellular pathways involved in different rapid growth stages of moso bamboo. <i>Tree Physiology</i> , 2020, 40, 1487-1508.	1.4	39
1055	Integrated metabolomic and transcriptomic analysis of the anthocyanin regulatory networks in <i>Salvia miltiorrhiza</i> Bge. flowers. <i>BMC Plant Biology</i> , 2020, 20, 349.	1.6	70
1056	RNA-sequencing analysis revealed genes associated drought stress responses of different durations in hexaploid sweet potato. <i>Scientific Reports</i> , 2020, 10, 12573.	1.6	24
1057	Crosstalk of phenylpropanoid biosynthesis with hormone signaling in Chinese cabbage is key to counteracting salt stress. <i>Environmental and Experimental Botany</i> , 2020, 179, 104209.	2.0	26
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1061	Transcriptomic differences between male and female <i>Trachycarpus fortunei</i> . <i>Scientific Reports</i> , 2020, 10, 12338.	1.6	5
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1071	Mechanisms of Novel Host Use by <i>Bactrocera tau</i> (Tephritid: Diptera) Revealed by RNA Transcriptomes. <i>Journal of Insect Science</i> , 2020, 20, .	0.6	1
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1073	Transcriptome profiling of genes involved in nutrient uptake regulated by phosphate-solubilizing bacteria in pepper (<i>Capsicum annuum</i> L.). <i>Plant Physiology and Biochemistry</i> , 2020, 156, 611-626.	2.8	4
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1075	Transcriptomic analysis reveals the GRAS family genes respond to gibberellin in <i>Salvia miltiorrhiza</i> hairy roots. <i>BMC Genomics</i> , 2020, 21, 727.	1.2	5
1076	Comparative transcriptomic analysis provides insights into the coordinated mechanisms of leaves and roots response to cold stress in Common Vetch. <i>Industrial Crops and Products</i> , 2020, 158, 112949.	2.5	19
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1080	Early Molecular Events during Onset of Diapause in Silkworm Eggs Revealed by Transcriptome Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6180.	1.8	21
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1083	Global Transcriptome and Correlation Analysis Reveal Cultivar-Specific Molecular Signatures Associated with Fruit Development and Fatty Acid Determination in <i>Camellia oleifera</i> Abel. <i>International Journal of Genomics</i> , 2020, 2020, 1-16.	0.8	10
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1089	Transcriptome analysis provides new insights into the transcriptional regulation of methyl jasmonate-induced flavonoid biosynthesis in pear calli. <i>BMC Plant Biology</i> , 2020, 20, 388.	1.6	40
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1126	Transcriptome profiling of spike provides expression features of genes related to terpene biosynthesis in lavender. <i>Scientific Reports</i> , 2020, 10, 6933.	1.6	9
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1158	Characterization and Analysis of the Full-Length Transcriptomes of Multiple Organs in <i>Pseudotaxus chienii</i> (W.C.Cheng) W.C.Cheng. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4305.	1.8	4

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1165	Transcriptome Analysis Identifies Two Ethylene Response Factors That Regulate Proanthocyanidin Biosynthesis During <i>Malus Crabapple</i> Fruit Development. <i>Frontiers in Plant Science</i> , 2020, 11, 76.	1.7	14
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1171	Transcriptome profiling analysis of underlying regulation of growing follicle development in the chicken. <i>Poultry Science</i> , 2020, 99, 2861-2872.	1.5	25
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1173	Transcriptome Analysis of the Cytokinin Response in <i>Medicago truncatula</i> . <i>Journal of Plant Biology</i> , 2020, 63, 189-202.	0.9	2
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1211	Transcriptome analysis of <i>Lactobacillus paracasei</i> SMN-LBK under ethanol stress. <i>Journal of Dairy Science</i> , 2020, 103, 7813-7825.	1.4	9
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1213	Growth performance and transcriptomic response of <i>Calliptamus abbreviatus</i> Ikonn (Orthoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 605-612.	0.5	2
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1402	Transcriptome sequencing of wild soybean revealed gene expression dynamics under low nitrogen stress. <i>Journal of Applied Genetics</i> , 2021, 62, 389-404.	1.0	9
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1416	Identification and Characterization of Long Non-coding RNAs in the Intestine of Olive Flounder (<i>Paralichthys olivaceus</i>) During <i>Edwardsiella tarda</i> Infection. <i>Frontiers in Immunology</i> , 2021, 12, 623764.	2.2	21
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1426	Regulatory role of non-coding RNA in ginseng rusty root symptom tissue. <i>Scientific Reports</i> , 2021, 11, 9211.	1.6	7
1427	Antifungal Mechanism of Volatile Organic Compounds Produced by <i>Bacillus subtilis</i> CF-3 on <i>Colletotrichum gloeosporioides</i> Assessed Using Omics Technology. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 5267-5278.	2.4	19
1428	Epigenetic upregulation of ssc-miR-124a following treatment with <i>Clostridium perfringens</i> beta2-toxin attenuates both apoptosis and inflammation in intestinal porcine epithelial cells. <i>Archives of Biochemistry and Biophysics</i> , 2021, 701, 108806.	1.4	3
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1431	Comparative Genome-Wide Alternative Splicing Analysis of Longissimus Dorsi Muscles Between Japanese Black (Wagyu) and Chinese Red Steppes Cattle. <i>Frontiers in Veterinary Science</i> , 2021, 8, 634577.	0.9	10

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1444	MicroRNA expression profiles in the seminal plasma of nonobstructive azoospermia patients with different histopathologic patterns. <i>Fertility and Sterility</i> , 2021, 115, 1197-1211.	0.5	14
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1452	High-throughput sequencing reveals crucial miRNAs in skeletal muscle development of Bian chicken. <i>British Poultry Science</i> , 2021, 62, 658-665.	0.8	3
1453	Comparative transcriptome analysis of cells from different areas reveals ROS responsive mechanism at sclerotial initiation stage in <i>Morchella importuna</i> . <i>Scientific Reports</i> , 2021, 11, 9418.	1.6	7
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1466	Transcriptome analysis of immune-related genes in <i>Sesamops sinensis</i> hepatopancreas in reaction to peptidoglycan challenge. <i>Genomics</i> , 2021, 113, 946-954.	1.3	6
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1473	Comparative Transcriptome Analysis of <i>Sophora japonica</i> (L.) Roots Reveals Key Pathways and Genes in Response to PEG-Induced Drought Stress under Different Nitrogen Conditions. <i>Forests</i> , 2021, 12, 650.	0.9	4
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1476	Identification and Analysis of Long Non-coding RNAs in <i>Leuciscus waleckii</i> Adapted to Highly Alkaline Conditions. <i>Frontiers in Physiology</i> , 2021, 12, 665268.	1.3	11
1477	KOBAS-i: intelligent prioritization and exploratory visualization of biological functions for gene enrichment analysis. <i>Nucleic Acids Research</i> , 2021, 49, W317-W325.	6.5	727
1478	Identification of exosome miRNAs in bronchial epithelial cells after PM2.5 chronic exposure. <i>Ecotoxicology and Environmental Safety</i> , 2021, 215, 112127.	2.9	17
1479	Direct and heritable effects of natural tidal environments on DNA methylation in Pacific oysters (<i>Crassostrea gigas</i>). <i>Environmental Research</i> , 2021, 197, 111058.	3.7	15
1480	Acetic Acid-Producing Endophyte <i>Lysinibacillus fusiformis</i> Orchestrates Jasmonic Acid Signaling and Contributes to Repression of Cadmium Uptake in Tomato Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 670216.	1.7	6
1481	Full-length transcriptome analysis provides new insights into the early bolting occurrence in medicinal <i>Angelica sinensis</i> . <i>Scientific Reports</i> , 2021, 11, 13000.	1.6	10
1482	De novo Transcriptome Assembly and Comparative Analysis Highlight the Primary Mechanism Regulating the Response to Selenium Stimuli in Oats (<i>Avena sativa</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 625520.	1.7	2
1483	Transcriptomic responses to drought stress among natural populations provide insights into local adaptation of weeping forsythia. <i>BMC Plant Biology</i> , 2021, 21, 273.	1.6	8
1484	Analysis of lncRNA, miRNA, and mRNA Expression Profiling in Type I IFN and Type II IFN Overexpressed in Porcine Alveolar Macrophages. <i>International Journal of Genomics</i> , 2021, 2021, 1-28.	0.8	5
1485	Elucidation of the Regulatory Network of Flavonoid Biosynthesis by Profiling the Metabolome and Transcriptome in Tartary Buckwheat. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 7218-7229.	2.4	25
1486	Time-course transcriptome landscape of achene development in lettuce. <i>Horticultural Plant Journal</i> , 2022, 8, 99-109.	2.3	0
1487	Metabolic and transcriptomic analyses reveal different metabolite biosynthesis profiles between leaf buds and mature leaves in <i>Ziziphus jujuba</i> mill. <i>Food Chemistry</i> , 2021, 347, 129005.	4.2	51

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1488	Crucial Waterlogging-Responsive Genes and Pathways Revealed by Comparative Physiology and Transcriptome in Tropical and Temperate Maize (<i>Zea mays</i> L.) inbred Lines. <i>Journal of Plant Biology</i> , 2021, 64, 313-325.	0.9	10
1489	Transcriptome and metabolite analysis related to branch development in two genotypes of <i>Eucalyptus urophylla</i> . <i>Molecular Genetics and Genomics</i> , 2021, 296, 1071-1083.	1.0	4
1490	Scale Drop Disease Virus (SDDV) and Lates calcarifer Herpes Virus (LCHV) Coinfection Downregulate Immune-Relevant Pathways and Cause Splenic and Kidney Necrosis in Barramundi Under Commercial Farming Conditions. <i>Frontiers in Genetics</i> , 2021, 12, 666897.	1.1	18
1491	Genome-Wide Identification and Functional Analysis of Long Non-coding RNAs in Sesame Response to Salt Stress. <i>Journal of Plant Biology</i> , 2021, 64, 555-565.	0.9	6
1492	Identification and characterization of microRNAs in the immature stage of the beneficial predatory bug <i>Arma chinensis</i> Fallou (Hemiptera: Pentatomidae). <i>Archives of Insect Biochemistry and Physiology</i> , 2021, 107, e21796.	0.6	3
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1494	Integrated Analysis of mRNA and miRNA Changes in Two <i>Haliotis diversicolor</i> Genotypes and Their Hybrid. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
1495	The ERF VII transcription factor SmERF73 coordinately regulates tanshinone biosynthesis in response to stress elicitors in <i>Salvia miltiorrhiza</i> . <i>New Phytologist</i> , 2021, 231, 1940-1955.	3.5	25
1496	Transcriptome analysis provides insights into copper toxicology in piebald naked carp (<i>Gymnocypris</i>) Tj ETQq0 0 0 rBT /Overlock 10 Tf	1.2	3
1497	Melatonin Improves Cotton Salt Tolerance by Regulating ROS Scavenging System and Ca ²⁺ Signal Transduction. <i>Frontiers in Plant Science</i> , 2021, 12, 693690.	1.7	44
1498	Comparative Transcriptome Analysis of Two Contrasting Chinese Cabbage (<i>Brassica rapa</i> L.) Genotypes Reveals That Ion Homeostasis Is a Crucial Biological Pathway Involved in the Rapid Adaptive Response to Salt Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 683891.	1.7	10
1499	Transcriptional profiling of <i>Microtus fortis</i> responses to <i>S. japonicum</i> : New sight into MfHsp90 $\hat{\pm}$ resistance mechanism. <i>Parasite Immunology</i> , 2021, 43, e12842.	0.7	2
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1501	Analysis of long intergenic non-coding RNAs transcriptomic profiling in skeletal muscle growth during porcine embryonic development. <i>Scientific Reports</i> , 2021, 11, 15240.	1.6	2
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1503	Integrated miRNA-mRNA analysis provides potential biomarkers for selective breeding in bay scallop (<i>Argopecten irradians</i>). <i>Genomics</i> , 2021, 113, 2744-2755.	1.3	3
1504	LINC01614 promotes osteosarcoma progression via miR-520a-3p/SNX3 axis. <i>Cellular Signalling</i> , 2021, 83, 109985.	1.7	20
1505	Potential evidence for transgenerational epigenetic memory in <i>Arabidopsis thaliana</i> following spaceflight. <i>Communications Biology</i> , 2021, 4, 835.	2.0	17

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1507	Comprehensive analysis of genome-wide DNA methylation and transcriptomics between ovary and testis in <i>Monopterus albus</i> . <i>Aquaculture Research</i> , 2021, 52, 5829-5839.	0.9	5
1508	Transcriptome profiling of hepatic and renal mRNAs and lncRNAs under a nutritional restriction during pregnancy in a sheep model. <i>Genomics</i> , 2021, 113, 2769-2779.	1.3	0
1509	Integrated analysis of transcriptomics and proteomics provides insights into the molecular regulation of cold response in <i>Brassica napus</i> . <i>Environmental and Experimental Botany</i> , 2021, 187, 104480.	2.0	34
1510	Toxic effects of octocrylene on zebrafish larvae and liver cell line (ZFL). <i>Aquatic Toxicology</i> , 2021, 236, 105843.	1.9	11
1511	Physiological and interactomic analysis reveals versatile functions of <i>Arabidopsis</i> 14-3-3 quadruple mutants in response to Fe deficiency. <i>Scientific Reports</i> , 2021, 11, 15551.	1.6	4
1512	Genome-Wide Transcriptomic Analysis Reveals the Gene Regulatory Network Controlled by SRL1 in Regulating Rice Leaf Rolling. <i>Journal of Plant Growth Regulation</i> , 2022, 41, 2292-2304.	2.8	1
1513	Transcriptome and Small RNA Combined Sequencing Analysis of Cold Tolerance in Non-heading Chinese Cabbage. <i>Frontiers in Genetics</i> , 2021, 12, 605292.	1.1	0
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1516	Transcriptome analysis reveals the mechanism associated with dynamic changes in fatty acid and phytosterol content in foxtail millet (<i>Setaria italica</i>) during seed development. <i>Food Research International</i> , 2021, 145, 110429.	2.9	15
1517	Genetic and Functional Characterization of Novel Brown-Like Adipocytes Around the Lamprey Brain. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 674939.	1.8	2
1518	Integrated transcriptome and metabolite profiling highlights the role of benzoxazinoids in wheat resistance against <i>Fusarium</i> crown rot. <i>Crop Journal</i> , 2022, 10, 407-417.	2.3	13
1519	Comparative Transcriptome Analysis of Different <i>Actinidia arguta</i> Fruit Parts Reveals Difference of Light Response during Fruit Coloration. <i>Biology</i> , 2021, 10, 648.	1.3	4
1521	Transcriptional response of golden pompano <i>Trachinotus ovatus</i> larvae to cold and heat stress. <i>Aquaculture Reports</i> , 2021, 20, 100755.	0.7	3
1522	Exploring the genomic resources and analysing the genetic diversity and population structure of Chinese indigenous rabbit breeds by RAD-seq. <i>BMC Genomics</i> , 2021, 22, 573.	1.2	3
1523	Single-Molecule Real-Time and Illumina-Based RNA Sequencing Data Identified Vernalization-Responsive Candidate Genes in Faba Bean (<i>Vicia faba</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 656137.	1.1	4
1524	Identification, through transcriptome analysis, of transcription factors that regulate anthocyanin biosynthesis in different parts of red-fleshed apple "Maya"™ fruit. <i>Horticultural Plant Journal</i> , 2022, 8, 11-21.	2.3	6

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1526	Screening and Interaction Analysis Identify Genes Related to Anther Dehiscence in <i>Solanum melongena</i> L.. <i>Frontiers in Plant Science</i> , 2021, 12, 648193.	1.7	4
1527	Integrated Analysis of Long Non-Coding RNA and mRNA Expression Profiles in Testes of Calves and Sexually Mature Wandong Bulls (<i>Bos taurus</i>). <i>Animals</i> , 2021, 11, 2006.	1.0	6
1528	BrRNE cleaves RNA in chloroplasts, regulating retrograde signals in <i>Brassica rapa</i> L. ssp. <i>pekinensis</i> . <i>Theoretical and Applied Genetics</i> , 2021, , 1.	1.8	0
1529	Phosphate-solubilizing bacterium <i>Burkholderia</i> sp. strain N3 facilitates the regulation of gene expression and improves tomato seedling growth under cadmium stress. <i>Ecotoxicology and Environmental Safety</i> , 2021, 217, 112268.	2.9	11
1530	Folic acid supplementation during pregnancy modulates hepatic methyl metabolism and genes expression profile of neonatal lambs of different litter sizes. <i>British Journal of Nutrition</i> , 2022, 128, 1-12.	1.2	7
1531	Analysis of Transcripts of Uncertain Coding Potential Using RNA Sequencing During the Preattachment Phase in Goat Endometrium. <i>DNA and Cell Biology</i> , 2021, 40, 998-1008.	0.9	4
1532	The zinc finger protein StMR1 affects the pathogenicity and melanin synthesis of <i>Setosphaeria turcica</i> and directly regulates the expression of DHN melanin synthesis pathway genes. <i>Molecular Microbiology</i> , 2022, 117, 261-273.	1.2	7
1533	Whole transcriptome analysis resulted in the identification of Chinese sprangletop (<i>Leptochloa</i>) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 42	1.2	14
1534	Transcriptional landscape in rat intestines under hypobaric hypoxia. <i>PeerJ</i> , 2021, 9, e11823.	0.9	7
1535	DNA repair- and nucleotide metabolism-related genes exhibit differential CHG methylation patterns in natural and synthetic polyploids (<i>Brassica napus</i> L.). <i>Horticulture Research</i> , 2021, 8, 142.	2.9	12
1536	Dual species dynamic transcripts reveal the interaction mechanisms between <i>Chrysanthemum morifolium</i> and <i>Alternaria alternata</i> . <i>BMC Genomics</i> , 2021, 22, 523.	1.2	8
1537	The mechanism of antigen-presentation of avian bone marrowed dendritic cells suppressed by infectious bronchitis virus. <i>Genomics</i> , 2021, 113, 1719-1732.	1.3	7
1538	Investigation of Thermomorphogenesis-Related Genes for a Multi-Silique Trait in <i>Brassica napus</i> by Comparative Transcriptome Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 678804.	1.1	3
1539	Comprehensive analyses of potential key genes in active tuberculosis. <i>Medicine (United States)</i> , 2021, 100, e26582.	0.4	5
1540	Target of rapamycin controls hyphal growth and pathogenicity through FoTIP4 in <i>Fusarium oxysporum</i> . <i>Molecular Plant Pathology</i> , 2021, 22, 1239-1255.	2.0	8
1541	Transcriptomic Analysis of the Photosynthetic, Respiration, and Aerenchyma Adaptation Strategies in Bermudagrass (<i>Cynodon dactylon</i>) under Different Submergence Stress. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7905.	1.8	16
1542	RNA-seq between asexual archeospores and meiosis-related conchospores in <i>Neopyropia yezoensis</i> using Smart-seq2. <i>Journal of Phycology</i> , 2021, 57, 1648-1658.	1.0	6

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1543	Combination of Developmental Behaviors and Transcriptome Reveals Differential Response Mechanisms of <i>Phytophthora sojae</i> to Aspartic Acid and Glucose in Seed Exudates. <i>Phytopathology</i> , 2022, 112, 620-629.	1.1	3
1544	Proteomic and molecular evidences of Il1rl2, Ric8a, Krt18 and Hsp90b1 modulation during experimental hepatic fibrosis and pomegranate supplementation. <i>International Journal of Biological Macromolecules</i> , 2021, 185, 696-707.	3.6	7
1545	Comparative Transcriptome Profiling Reveals Changes of microRNAs Response to Exercise in Rats with Neuropathic Pain. <i>Neural Plasticity</i> , 2021, 2021, 1-23.	1.0	3
1546	Physiological and transcriptome analysis elucidates the metabolic mechanism of versatile <i>Porphyridium purpureum</i> under nitrogen deprivation for exopolysaccharides accumulation. <i>Bioresources and Bioprocessing</i> , 2021, 8, .	2.0	9
1547	Impact and mechanism of sulphur-deficiency on modern wheat farming nitrogen-related sustainability and gliadin content. <i>Communications Biology</i> , 2021, 4, 945.	2.0	29
1548	Unraveling the Genetic Basis of Fertility Restoration for Cytoplasmic Male Sterile Line WNJ01A Originated From <i>Brassica juncea</i> in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 721980.	1.7	4
1549	Comparative methylome reveals regulatory roles of DNA methylation in melon resistance to <i>Podosphaera xanthii</i> . <i>Plant Science</i> , 2021, 309, 110954.	1.7	11
1550	Seadragon genome analysis provides insights into its phenotype and sex determination locus. <i>Science Advances</i> , 2021, 7, .	4.7	32
1551	Microbial Composition and Genes for Key Metabolic Attributes in the Gut Digesta of Sea Urchins <i>Lytechinus variegatus</i> and <i>Strongylocentrotus purpuratus</i> Using Shotgun Metagenomics. <i>Current Issues in Molecular Biology</i> , 2021, 43, 978-995.	1.0	2
1552	Transcriptome Analysis Reveals Impaired Fertility and Immunity Under Salinity Exposure in Juvenile Grass Carp. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	1
1553	Effect of 4-chloro-2-methylphenoxy acetic acid on tomato gene expression and rhizosphere bacterial communities under inoculation with phosphate-solubilizing bacteria. <i>Journal of Hazardous Materials</i> , 2021, 416, 125767.	6.5	12
1554	Transcriptome profiling of differentially expressed genes of male and female inflorescences in spinach (<i>Spinacia oleracea</i> L.). <i>Genome</i> , 2021, 64, 777-788.	0.9	3
1555	A new insight to characterize immunomodulation based on hepatopancreatic transcriptome and humoral immune factor analysis of the <i>Cherax quadricarinatus</i> infected with <i>Aeromonas veronii</i> . <i>Ecotoxicology and Environmental Safety</i> , 2021, 219, 112347.	2.9	7
1556	Defining Color Change in Pitaya: A Close Look at Betacyanin Synthesis Genes in <i>Stenocereus queretaroensis</i> . <i>Frontiers in Sustainable Food Systems</i> , 2021, 5, .	1.8	1
1557	Profiling Analysis of Circular RNA and mRNA in Human Temporal Lobe Epilepsy with Hippocampal Sclerosis ILAE Type 1. <i>Cellular and Molecular Neurobiology</i> , 2022, 42, 2745-2755.	1.7	6
1558	Integrated Analysis of mRNA and Non-coding RNA Transcriptome in Pepper (<i>Capsicum chinense</i>) Hybrid at Seedling and Flowering Stages. <i>Frontiers in Genetics</i> , 2021, 12, 685788.	1.1	15
1559	Improve isobutanol tolerance and production by engineering of TATA-binding protein Spt15 in <i>Saccharomyces cerevisiae</i> . <i>Letters in Applied Microbiology</i> , 2021, 73, 694-707.	1.0	0
1560	Transcriptomic responses and physiological changes to cold stress among natural populations provide insights into local adaptation of weeping forsythia. <i>Plant Physiology and Biochemistry</i> , 2021, 165, 94-103.	2.8	8

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1562	Physiological and transcriptomic analyses to reveal underlying phenolic acid action in consecutive monoculture problem of <i>Polygonatum odoratum</i> . <i>BMC Plant Biology</i> , 2021, 21, 362.	1.6	6
1563	Population Genomics Reveals Gene Flow and Adaptive Signature in Invasive Weed <i>Mikania micrantha</i> . <i>Genes</i> , 2021, 12, 1279.	1.0	2
1564	Transcriptomic responses of haloalkalitolerant bacterium <i>Egicoccus halophilus</i> EGI 80432T to highly alkaline stress. <i>Extremophiles</i> , 2021, 25, 459-470.	0.9	0
1565	Transcriptome analysis of two <i>Pogostemon cablin</i> chemotypes reveals genes related to patchouli alcohol biosynthesis. <i>PeerJ</i> , 2021, 9, e12025.	0.9	11
1566	Production of purple Ma bamboo (<i>Dendrocalamus latiflorus</i> Munro) with enhanced drought and cold stress tolerance by engineering anthocyanin biosynthesis. <i>Planta</i> , 2021, 254, 50.	1.6	15
1567	Transcriptome Analysis Provides Insights into Hepatic Responses to Trichloroisocyanuric Acid Exposure in Goldfish (<i>Carassius auratus</i>). <i>Animals</i> , 2021, 11, 2775.	1.0	1
1568	Regulations of m6A methylation on tomato fruit chilling injury. <i>Horticultural Plant Journal</i> , 2021, 7, 434-442.	2.3	16
1569	Could co-substrate sodium acetate simultaneously promote <i>Chlorella</i> to degrade amoxicillin and produce bioresources?. <i>Journal of Hazardous Materials</i> , 2021, 417, 126147.	6.5	26
1570	Histopathological parameters, antioxidant enzyme levels, transcriptome, and hematology parameters of Amur minnow (<i>Phoxinus lagowskii</i>) infection with <i>Tetrahymena pyriformis</i> . <i>Aquaculture International</i> , 2021, 29, 2635-2659.	1.1	4
1571	Appetite Suppression and Interleukin 17 Receptor Signaling Activation of Colonic Mycobiota Dysbiosis Induced by High Temperature and High Humidity Conditions. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 657807.	1.8	3
1572	2-Arachidonoylglycerol as an Endogenous Cue Negatively Regulates Attachment of the Mussel <i>Perna viridis</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	2
1573	Genetic Mapping and Transcriptomic Analysis Revealed the Molecular Mechanism Underlying Leaf-Rolling and a Candidate Protein Phosphatase Gene for the Rolled Leaf-Dominant (RL-D) Mutant in Rice. <i>Plant Molecular Biology Reporter</i> , 2022, 40, 256-270.	1.0	2
1574	Membrane lipid metabolism, heat shock response and energy costs mediate the interaction between acclimatization and heat-hardening response in the razor clam <i>Sinonovacula constricta</i> . <i>Journal of Experimental Biology</i> , 2021, 224, .	0.8	8
1575	Transcriptional and Hormonal Responses in Ethephon-Induced Promotion of Femaleness in Pumpkin. <i>Frontiers in Plant Science</i> , 2021, 12, 715487.	1.7	5
1576	Transcriptomic analysis of salt tolerance-associated genes and diversity analysis using indel markers in yardlong bean (<i>Vigna unguiculata</i> ssp. <i>sesquipedialis</i>). <i>BMC Genomic Data</i> , 2021, 22, 34.	0.7	5
1577	LsAP2 regulates leaf morphology by inhibiting CIN-like TCP transcription factors and repressing LsKAN2 in lettuce. <i>Horticulture Research</i> , 2021, 8, 184.	2.9	12
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1580	Transcriptome analysis of differentially expressed genes in the red swamp crayfish <i>Procambarus clarkii</i> challenged with <i>Aeromonas hydrophila</i> . <i>Fish and Shellfish Immunology</i> , 2021, 119, 280-288.	1.6	12
1581	Comparative Transcriptomic Analyses of Antibiotic-Treated and Normally Reared <i>Bactrocera dorsalis</i> Reveals a Possible Gut Self-Immunity Mechanism. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 647604.	1.8	2
1582	Transcriptome analysis reveals the molecular mechanisms of response to an emergent yellow-flower disease in green Chinese prickly ash (<i>Zanthoxylum schinifolium</i>). <i>Scientific Reports</i> , 2021, 11, 18886.	1.6	2
1583	Genes related to circadian rhythm are involved in regulating tuberization time in potato. <i>Horticultural Plant Journal</i> , 2022, 8, 369-380.	2.3	12
1584	A Method for Assaying of Protein Kinase Activity In Vivo and Its Use in Studies of Signal Transduction in Strawberry Fruit Ripening. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10495.	1.8	0
1585	Hypoosmotic stress induced functional alternations of intestinal barrier integrity, inflammatory reactions, and neurotransmission along gut-brain axis in the yellowfin seabream (<i>Acanthopagrus</i>)	1.0	10
1586	Symbiont-regulated serotonin biosynthesis modulates tick feeding activity. <i>Cell Host and Microbe</i> , 2021, 29, 1545-1557.e4.	5.1	31
1587	Comparative transcriptome and microbial community sequencing provide insight into yellow-leaf phenotype of <i>Camellia japonica</i> . <i>BMC Plant Biology</i> , 2021, 21, 416.	1.6	4
1588	De novo analysis reveals transcriptomic responses to heat stress in loquat (<i>Eriobotrya japonica</i>)	1.4	2
1589	ERF9 of <i>Poncirus trifoliata</i> (L.) Raf. undergoes feedback regulation by ethylene and modulates cold tolerance via regulating a glutathione S-transferase U17 gene. <i>Plant Biotechnology Journal</i> , 2022, 20, 183-200.	4.1	57
1590	Identification and analysis of chemosensory genes encoding odorant-binding proteins, chemosensory proteins and sensory neuron membrane proteins in the antennae of <i>Lissorhoptrus oryzophilus</i> . <i>Bulletin of Entomological Research</i> , 2021, , 1-11.	0.5	2
1591	De novo transcriptome assembly, polymorphic SSR markers development and population genetics analyses for southern corn rust (<i>Puccinia polysora</i>). <i>Scientific Reports</i> , 2021, 11, 18029.	1.6	3
1592	Genome-wide high-resolution mapping of DNA methylation reveals epigenetic variation in the offspring of sexual and asexual propagation in <i>Robinia pseudoacacia</i> . <i>Plant Cell Reports</i> , 2021, 40, 2435-2447.	2.8	4
1593	Metabolomics integrated with transcriptomics reveals the distribution of iridoid and crocin metabolic flux in <i>Gardenia jasminoides</i> Ellis. <i>PLoS ONE</i> , 2021, 16, e0256802.	1.1	15
1594	Gut Microbiota Dysbiosis Influences Metabolic Homeostasis in <i>Spodoptera frugiperda</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 727434.	1.5	18
1595	Combining single-molecule sequencing and next-generation sequencing to provide insight into the complex response of <i>Iris halophila</i> Pall. to Pb exposure. <i>Industrial Crops and Products</i> , 2021, 168, 113623.	2.5	3
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1598	UV-C irradiation delays the physiological changes of bell pepper fruit during storage. <i>Postharvest Biology and Technology</i> , 2021, 180, 111506.	2.9	23
1599	Overexpression of <i>ATP-binding cassette transporter Mdr49-like</i> confers resistance to imidacloprid in the field populations of brown planthopper, <i>Nilaparvata lugens</i> . <i>Pest Management Science</i> , 2022, 78, 579-590.	1.7	11
1600	The transcriptome of saline-alkaline resistant industrial hemp (<i>Cannabis sativa</i> L.) exposed to NaHCO ₃ stress. <i>Industrial Crops and Products</i> , 2021, 170, 113766.	2.5	8
1601	Gradual effects of gradient concentrations of polystyrene nanoplastics on metabolic processes of the razor clams. <i>Environmental Pollution</i> , 2021, 287, 117631.	3.7	23
1602	Transcriptome analysis of genes in response to magnesium nitrate stress on cucumber leaf. <i>Scientia Horticulturae</i> , 2021, 288, 110391.	1.7	3
1603	Seasonal expressions of ER α , ER β , EGF, EGFR, PI3K and Akt in the scent glands of the muskrats (<i>Ondatra tiberica</i>). <i>Environmental Pollution</i> , 2021, 287, 117631.	1.2	8
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1767	Changes of Metabolites and Gene Expression under Different Feeding Systems Associated with Lipid Metabolism in Lamb Meat. <i>Foods</i> , 2021, 10, 2612.	1.9	9
1768	Comprehensive Analysis of Differentially Expressed mRNA, Non-coding RNA, and Their Competitive Endogenous RNA Network of Pacific Oyster <i>Crassostrea gigas</i> With Different Glycogen Content Between Different Environments. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	1
1769	A draft genome, resequencing, and metabolomes reveal the genetic background and molecular basis of the nutritional and medicinal properties of loquat (<i>Eriobotrya japonica</i> (Thunb.) Lindl). <i>Horticulture Research</i> , 2021, 8, 231.	2.9	14
1770	MicroRNA sequence analysis of plasma exosomes in early Leggã€“Calvã€“Perthes disease. <i>Cellular Signalling</i> , 2021, , 110184.	1.7	5
1771	An engineered IL-21 with half-life extension enhances anti-tumor immunity as a monotherapy or in combination with PD-1 or TIGIT blockade. <i>International Immunopharmacology</i> , 2021, 101, 108307.	1.7	7
1772	Whole-genome bisulfite sequencing of abdominal adipose reveals DNA methylation pattern variations in broiler lines divergently selected for fatness. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	1
1773	Whole-genome resequencing to investigate the determinants of the multi-lumbar vertebrae trait in sheep. <i>Gene</i> , 2022, 809, 146020.	1.0	4
1774	Transcriptome analysis provides insights into the molecular mechanism of hepatocyte apoptosis in response to feeding restriction in juvenile largemouth bass <i>Micropterus salmoides</i> . <i>Aquaculture</i> , 2022, 548, 737550.	1.7	7
1780	Comprehensive Genomic Characterization Analysis of lncRNAs in Cells With Porcine Delta Coronavirus Infection. <i>Frontiers in Microbiology</i> , 2019, 10, 3036.	1.5	7
1782	Pancreatic cancer differential methylation atlas in blood, peri-carcinomatous and diseased tissue. <i>Translational Cancer Research</i> , 2020, 9, 421-431.	0.4	1
1784	Transcriptome profiling of kenaf (<i>Hibiscus cannabinus</i> L.) under plumbic stress conditions implies the involvement of NAC transcription factors regulating reactive oxygen species-dependent programmed cell death. <i>PeerJ</i> , 2020, 8, e8733.	0.9	9
1788	RhWRKY33 Positively Regulates Onset of Floral Senescence by Responding to Wounding- and Ethylene-Signaling in Rose Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 726797.	1.7	9
1789	Salicylic acid fights against Fusarium wilt by inhibiting target of rapamycin signaling pathway in <i>Fusarium oxysporum</i> . <i>Journal of Advanced Research</i> , 2022, 39, 1-13.	4.4	21
1790	Transcriptomic analysis of gills in nitrite-tolerant and -sensitive families of <i>Litopenaeus vannamei</i> . <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2022, 253, 109212.	1.3	2
1791	Transcriptome analysis of <i>Tetranychus cinnabarinus</i> responses to an insecticide exposure. <i>Systematic and Applied Acarology</i> , 2020, 25, 1329-1342.	0.5	4
1792	Comprehensive transcriptome analyses of different <i>Crocus</i> flower tissues uncover genes involved in crocin biosynthesis. <i>Biologia Plantarum</i> , 0, 64, 504-511.	1.9	1
1793	Analysis of transcriptomic differences between NK603 maize and near-isogenic varieties using RNA sequencing and RT-qPCR. <i>Environmental Sciences Europe</i> , 2020, 32, .	2.6	2

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1794	Differentially expressed genes related to oxidoreductase activity and glutathione metabolism underlying the adaptation of <i>Phragmites australis</i> from the salt marsh in the Yellow River Delta, China. PeerJ, 2020, 8, e10024.	0.9	8
1795	Identification of candidate genes controlling chilling tolerance of rice in the cold region at the booting stage by BSA-Seq and RNA-Seq. Royal Society Open Science, 2020, 7, 201081.	1.1	15
1797	Transcription Analysis of Recombinant <i>Trichoderma reesei</i> HJ-48 to Compare the Molecular Basis for Fermentation of Glucose and Xylose. Journal of Microbiology and Biotechnology, 2020, 30, 1467-1479.	0.9	0
1798	Systematic analysis of lncRNAs, mRNAs, circRNAs and miRNAs in patients with postmenopausal osteoporosis. American Journal of Translational Research (discontinued), 2018, 10, 1498-1510.	0.0	43
1799	Forkhead box P3 promotes breast cancer cell apoptosis by regulating programmed cell death 4 expression. Oncology Letters, 2020, 20, 292.	0.8	0
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1801	Transcriptome and proteome analysis of pregnancy and postpartum anoestrus ovaries in yak. Journal of Veterinary Science, 0, 23, .	0.5	0
1802	Changes in metabolism modulate induced by viroid infection in the orchid <i>Dendrobium officinale</i> . Virus Research, 2022, 308, 198626.	1.1	13
1803	Transcriptome and proteome analysis of pregnancy and postpartum anoestrus ovaries in yak. Journal of Veterinary Science, 2022, 23, e3.	0.5	4
1804	Comparative full-length transcriptome analysis provides novel insights into the regulatory mechanism of natural rubber biosynthesis in <i>Taraxacum kok-saghyz</i> Rodin roots. Industrial Crops and Products, 2022, 175, 114278.	2.5	10
1805	BrWAX2 plays an essential role in cuticular wax biosynthesis in Chinese cabbage (<i>Brassica rapa</i> L. ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.8	6
1806	Leaf Size Development Differences and Comparative Transcriptome Analyses of Two Poplar Genotypes. Genes, 2021, 12, 1775.	1.0	15
1807	The Effect of Foliar Application of K ₂ SO ₄ or KH ₂ PO ₄ on Skin Color of the "Kyoho"™ Grape. Agronomy, 2021, 11, 2361.	1.3	6
1808	Genomic and GWAS analyses demonstrate phylogenomic relationships of <i>Gossypium barbadense</i> in China and selection for fibre length, lint percentage and <i>Fusarium wilt</i> resistance. Plant Biotechnology Journal, 2022, 20, 691-710.	4.1	33
1809	Comparatively analyzing the liver-specific transcriptomic profiles in Kunming mice afflicted with streptozotocin- and natural food-induced type 2 diabetes mellitus. Molecular Biology Reports, 2022, 49, 1369-1377.	1.0	1
1810	A comparative transcriptome and proteomics study of postpartum ovarian cycle arrest in yaks (<i>Bos</i>) Tj ETQq1_1_0.784314 rgBT 0	1.0	6
1811	Protoplast isolation and transcriptome analysis of developing xylem in <i>Pinus massoniana</i> (Pinaceae). Molecular Biology Reports, 2022, 49, 1857-1869.	1.0	1
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1814	Dynamic Changes of DNA Methylation During Wild Strawberry (<i>Fragaria nilgerrensis</i>) Tissue Culture. <i>Frontiers in Plant Science</i> , 2021, 12, 765383.	1.7	5
1815	Genome-wide identification and characterization of long noncoding RNAs in maize under rice black streaked dwarf virus infection. <i>Plant Pathology</i> , 0, , .	1.2	1
1816	Comparative Transcriptome Analysis Reveals the Molecular Immunopathogenesis of Chinese Soft-Shell Turtle (<i>Trionyx sinensis</i>) Infected with <i>Aeromonas hydrophila</i> . <i>Biology</i> , 2021, 10, 1218.	1.3	10
1817	Integrated Transcriptome Analysis and Single-Base Resolution Methylomes of Watermelon (<i>Citrullus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 2021, 12, 769712.	1.7	5
1818	Nutritional evaluation and transcriptome analyses of short-time germinated seeds in soybean (<i>Glycine</i>) Tj ETQq1 1 0.784314 rgBT /Over 2021, 12, 769712.	1.6	5
1819	Transcriptional Regulation of Different Rhizome Parts Reveal the Candidate Genes That Regulate Rhizome Development in <i>Poa pratensis</i> . <i>DNA and Cell Biology</i> , 2022, 41, 151-168.	0.9	3
1820	Integrated Lipidomic and Transcriptomic Analysis Reveals Lipid Metabolism in Foxtail Millet (<i>Setaria</i>) Tj ETQq1 1 0.784314 rgBT /Over 2021, 12, 769712.	1.1	1
1821	Transcriptome Profiles of Leaves and Roots of Goldenrain Tree (<i>Koeleria paniculata</i> Laxm.) in Response to Cadmium Stress. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 12046.	1.2	10
1822	ERK inhibition in glioblastoma is associated with autophagy activation and tumorigenesis suppression. <i>Journal of Neuro-Oncology</i> , 2022, 156, 123-137.	1.4	9
1823	A Competitive Endogenous RNA Network Based on Differentially Expressed lncRNA in Lipopolysaccharide-Induced Acute Lung Injury in Mice. <i>Frontiers in Genetics</i> , 2021, 12, 745715.	1.1	4
1824	MiRNA-mRNA Integration Analysis Reveals the Regulatory Roles of MiRNAs in Shell Pigmentation of the Manila clam (<i>Ruditapes philippinarum</i>). <i>Marine Biotechnology</i> , 2021, 23, 976-993.	1.1	6
1825	An Exploration of Non-Coding RNAs in Extracellular Vesicles Delivered by Swine Anterior Pituitary. <i>Frontiers in Genetics</i> , 2021, 12, 772753.	1.1	3
1827	Control of sucrose accumulation in sugarcane (<i>Saccharum</i> spp. hybrids) involves miRNA-mediated regulation of genes and transcription factors associated with sugar metabolism. <i>GCB Bioenergy</i> , 2022, 14, 173-191.	2.5	14
1828	Unravelling the distinctive growth mechanism of proso millet (<i>Panicum miliaceum</i> L.) under salt stress: From root-to-leaf adaptations to molecular response. <i>GCB Bioenergy</i> , 2022, 14, 192-214.	2.5	4
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1830	Integrated transcriptome and small RNA sequencing analyses reveal a drought stress response network in <i>Sophora tonkinensis</i> . <i>BMC Plant Biology</i> , 2021, 21, 566.	1.6	4
1831	Effects of Different Molecular Weight Polysaccharides From <i>Dendrobium officinale</i> Kimura & Migo on Human Colorectal Cancer and Transcriptome Analysis of Differentially Expressed Genes. <i>Frontiers in Pharmacology</i> , 2021, 12, 704486.	1.6	15

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1833	A New lncRNA, <i>lnc-LLMA</i> , Regulates Lipid Metabolism in Pig Hepatocytes. DNA and Cell Biology, 2022, 41, 202-214.	0.9	6
1834	Transcriptomics integrated with metabolomics reveals the effect of Lycium barbarum polysaccharide on apoptosis in Nile tilapia (<i>Oreochromis niloticus</i>). Genomics, 2022, 114, 229-240.	1.3	9
1835	Population Evolution, Genetic Diversity and Structure of the Medicinal Legume, <i>Glycyrrhiza uralensis</i> and the Effects of Geographical Distribution on Leaves Nutrient Elements and Photosynthesis. Frontiers in Plant Science, 2021, 12, 708709.	1.7	3
1836	Molecular toxicity and defense mechanisms induced by silver nanoparticles in <i>Drosophila melanogaster</i> . Journal of Environmental Sciences, 2023, 125, 616-629.	3.2	8
1837	Comparative Transcriptomic Analyses of Different Jujube Cultivars Reveal the Co-Regulation of Multiple Pathways during Fruit Cracking. Genes, 2022, 13, 105.	1.0	8
1838	Involvement of m6A regulatory factor IGF2BP1 in malignant transformation of human bronchial epithelial Beas-2B cells induced by tobacco carcinogen NNK. Toxicology and Applied Pharmacology, 2022, 436, 115849.	1.3	5
1839	Integrated analysis of small RNA, transcriptome and degradome sequencing reveals that micro-RNAs regulate anther development in CMS cotton. Industrial Crops and Products, 2022, 176, 114422.	2.5	3
1840	The immune response of fairy shrimp <i>Streptocephalus sirindhornae</i> against bacterial black disease by de novo transcriptome analysis. Fish and Shellfish Immunology, 2022, 121, 108-115.	1.6	6
1841	Cleaner production of proso millet (<i>Panicum miliaceum</i> L.) in salt-stressed environment using re-watering: From leaf structural alleviations to multi-omics responses. Journal of Cleaner Production, 2022, 334, 130205.	4.6	9
1842	C-type natriuretic peptide stimulates chicken myoblast differentiation through receptors and metabolism pathway. Journal of Integrative Agriculture, 2022, 21, 496-503.	1.7	0
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1844	Comparative proteomics and transcriptomics illustrate the allograft-induced stress response in the pearl oyster (<i>Pinctada fucata martensii</i>). Fish and Shellfish Immunology, 2022, 121, 74-85.	1.6	12
1845	Metabolomic and transcriptomic investigation of the mechanism involved in enantioselective toxicity of imazamox in <i>Lemna minor</i> . Journal of Hazardous Materials, 2022, 425, 127818.	6.5	21
1846	Identification of key gene networks controlling anthocyanin biosynthesis in peach flower. Plant Science, 2022, 316, 111151.	1.7	24
1847	Multi-omics analysis reveals specific modifications associated with reduced chilling injury in bell pepper fruit by methyl jamonate. Postharvest Biology and Technology, 2022, 185, 111799.	2.9	25
1848	Gene expression analysis revealed Hbr-miR396b as a key piece participating in reaction wood formation of <i>Hevea brasiliensis</i> (rubber tree). Industrial Crops and Products, 2022, 177, 114460.	2.5	4
1849	MicroRNA Transcriptomics Analysis Identifies Dysregulated Hedgehog Signaling Pathway in a Mouse Model of Acute Intracerebral Hemorrhage Exposed to Hyperglycemia. Journal of Stroke and Cerebrovascular Diseases, 2022, 31, 106281.	0.7	3

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1851	Comparative analysis of drought-responsive physiological and transcriptome in broomcorn millet (<i>Panicum miliaceum</i> L.) genotypes with contrasting drought tolerance. <i>Industrial Crops and Products</i> , 2022, 177, 114498.	2.5	20
1852	Temporal and tissue-specific transcriptome analyses reveal mechanistic insights into the <i>Solidago canadensis</i> response to cadmium contamination. <i>Chemosphere</i> , 2022, 292, 133501.	4.2	7
1853	Forkhead box P3 promotes breast cancer cell apoptosis by regulating programmed cell death 4 expression. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	3
1855	Circulating Exosomal circRNAs Contribute to Potential Diagnostic Value of Large Artery Atherosclerotic Stroke. <i>Frontiers in Immunology</i> , 2021, 12, 830018.	2.2	15
1856	The genome of low-chill Chinese plum “Sanyueli” (<i>Prunus salicina</i> Lindl.) provides insights into the regulation of the chilling requirement of flower buds. <i>Molecular Ecology Resources</i> , 2022, 22, 1919-1938.	2.2	11
1857	Comprehensive Transcriptome-Metabolome Analysis and Evaluation of the Dark_Pur Gene from <i>Brassica juncea</i> that Controls the Differential Regulation of Anthocyanins in <i>Brassica rapa</i> . <i>Genes</i> , 2022, 13, 283.	1.0	6
1858	Transcriptome analysis of the toxicity response of green macroalga <i>Caulerpa lentillifera</i> J. Agardh to high dissolved arsenite. <i>Environmental Science and Pollution Research</i> , 2022, 29, 38591-38605.	2.7	2
1859	Detrimental Impact of Î-cyhalothrin on the Biocontrol Efficacy of <i>Eocanthecona furcellata</i> by Affecting Global Transcriptome and Predatory Behavior. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 1037-1046.	2.4	7
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1861	Comparative transcriptome analysis of the cold resistance of the sterile rice line 33S. <i>PLoS ONE</i> , 2022, 17, e0261822.	1.1	3
1862	Transcriptomic analyses provide insight into adventitious root formation of <i>Eurydendron excelsum</i> H. T. Chang during ex vitro rooting. <i>Plant Cell, Tissue and Organ Culture</i> , 2022, 148, 649-666.	1.2	4
1863	A Lesion Microenvironment-Responsive Fungicide Nanoplatform for Crop Disease Prevention and Control. <i>Advanced Healthcare Materials</i> , 2022, 11, e2102617.	3.9	10
1864	Transcriptomic Analysis Reveals a Link Between Hippo Signaling Pathway and Macrophages in Lungs of Mice with OVA-Induced Allergic Asthma. <i>Journal of Inflammation Research</i> , 2022, Volume 15, 423-437.	1.6	4
1866	Methionine- and Choline-Deficient Diet Identifies an Essential Role for DNA Methylation in Plasmacytoid Dendritic Cell Biology. <i>Journal of Immunology</i> , 2022, 208, 881-897.	0.4	2
1867	Transcriptome and methylome changes in two contrasting mungbean genotypes in response to drought stress. <i>BMC Genomics</i> , 2022, 23, 80.	1.2	16
1868	miR-1 Regulates Differentiation and Proliferation of Goat Hair Follicle Stem Cells by Targeting IGF1R and LEF1 Genes. <i>DNA and Cell Biology</i> , 2022, 41, 190-201.	0.9	3
1869	Transcriptomic profiling suggests candidate molecular responses to waterlogging in cassava. <i>PLoS ONE</i> , 2022, 17, e0261086.	1.1	11

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1870	Transcriptome analysis of miRNAs during myoblasts adipogenic differentiation. <i>Animal Biotechnology</i> , 2022, , 1-7.	0.7	1
1871	Roles of miR-592-3p and Its Target Gene, <i>TMEFF1</i> , in the Nucleus Accumbens During Incubation of Morphine Craving. <i>International Journal of Neuropsychopharmacology</i> , 2022, 25, 412-424.	1.0	6
1872	Full-Length Transcriptome of Red Swamp Crayfish Hepatopancreas Reveals Candidate Genes in Hif-1 and Antioxidant Pathways in Response to Hypoxia-Reoxygenation. <i>Marine Biotechnology</i> , 2022, 24, 55-67.	1.1	4
1873	The Multistage Antimalarial Compound Calxinin Modulates Calcium Homeostasis Targeting a Unique Calcium Channel Involved in Subcellular Calcium Storage in <i>P. falciparum</i> . <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1874	Comparative physiological and transcriptomic profiles reveal regulatory mechanisms of soft rot disease resistance in <i>Amorphophallus</i> spp.. <i>Physiological and Molecular Plant Pathology</i> , 2022, 118, 101807.	1.3	7
1875	Chromosome-level genome assembly of <i>Zizania latifolia</i> provides insights into its seed shattering and phytocassane biosynthesis. <i>Communications Biology</i> , 2022, 5, 36.	2.0	11
1876	Genome-Wide Differential DNA Methylomes Provide Insights into the Infertility of Triploid Oysters. <i>Marine Biotechnology</i> , 2022, 24, 18-31.	1.1	4
1877	Transcriptomic analyses reveal the effect of nitric oxide on the lateral root development and growth of mangrove plant <i>Kandelia obovata</i> . <i>Plant and Soil</i> , 2022, 472, 543-564.	1.8	9
1878	Transcriptome analysis of genes potentially associated with white and black plumage formation in Chinese indigenous ducks (<i>Anas platyrhynchos</i>). <i>British Poultry Science</i> , 2022, 63, 466-474.	0.8	3
1879	RNA-seq and phytohormone analysis reveals the culm color variation of <i>Bambusa oldhamii</i> Munro. <i>PeerJ</i> , 2022, 10, e12796.	0.9	2
1880	Molecular Mechanisms of Epileptic Encephalopathy Caused by <i>KCNMA1</i> Loss-of-Function Mutations. <i>Frontiers in Pharmacology</i> , 2021, 12, 775328.	1.6	11
1881	Genome-Wide DNA Methylome and Transcriptome Analysis of Porcine Testicular Cells Infected With Transmissible Gastroenteritis Virus. <i>Frontiers in Veterinary Science</i> , 2021, 8, 779323.	0.9	1
1882	Promoting Effect of Choline-Phosphate Cytidyltransferase Gene (<i>pcyt-1</i>) on Departure of Pinewood Nematode from <i>Monochamus alternatus</i> . <i>Forests</i> , 2022, 13, 114.	0.9	0
1883	UCP1 and AOX1a contribute to regulation of carbon and nitrogen metabolism and yield in <i>Arabidopsis</i> under low nitrogen stress. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 1.	2.4	5
1884	Comparative Analysis of Proanthocyanidin Metabolism and Genes Regulatory Network in Fresh Leaves of Two Different Ecotypes of <i>Tetrastigma hemsleyanum</i> . <i>Plants</i> , 2022, 11, 211.	1.6	3
1885	Screening and functional validation of lipid metabolism-related lncRNA-46546 based on the transcriptome analysis of early embryonic muscle tissue in chicken. <i>Animal Bioscience</i> , 2023, 36, 175-190.	0.8	3
1886	PacBio Isoform Sequencing and Illumina RNA Sequencing Provide Novel Insights on Responses to Acute Heat Stress in <i>Apostichopus japonicus</i> Coelomocytes. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	1
1887	Synthesis of Abscisic Acid in <i>Neopyropia yezoensis</i> and Its Regulation of Antioxidase Genes Expressions Under Hypersaline Stress. <i>Frontiers in Microbiology</i> , 2021, 12, 775710.	1.5	3

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1888	Deciphering Molecular Mechanisms Involved in Salinity Tolerance in Guar (<i>Cyamopsis tetragonoloba</i>) Tj ETQq0 0 0 ggBT/Overlock 10 Tf 156	1.5	11
1889	Overexpression of <i>VqWRKY31</i> enhances powdery mildew resistance in grapevine by promoting salicylic acid signaling and specific metabolite synthesis. <i>Horticulture Research</i> , 2022, 9, .	2.9	44
1890	Molecular Responses to Thermal and Osmotic Stress in Arctic Intertidal Mussels (<i>Mytilus edulis</i>): The Limits of Resilience. <i>Genes</i> , 2022, 13, 155.	1.0	14
1891	Molecular Identification of <i>Nocardia seriolae</i> and Comparative Analysis of Spleen Transcriptomes of Hybrid Snakehead (<i>Channa maculata</i> Female × <i>Channa argus</i> Male) With Nocardiosis Disease. <i>Frontiers in Immunology</i> , 2022, 13, 778915.	2.2	0
1892	Cellular <i>Lnc_209997</i> suppresses <i>Bombyx mori</i> nucleopolyhedrovirus replication by targeting <i>miR-275-5p</i> in <i>B. mori</i> . <i>Insect Molecular Biology</i> , 2022, 31, 308-316.	1.0	8
1893	Comparative transcriptomic analysis reveals potential mechanisms for high tolerance to submergence in arbor willows. <i>PeerJ</i> , 2022, 10, e12881.	0.9	3
1894	Identification of Potential Blind-Side Hypermelanosis-Related lncRNA-miRNA-mRNA Regulatory Network in a Flatfish Species, Chinese Tongue Sole (<i>Cynoglossus semilaevis</i>). <i>Frontiers in Genetics</i> , 2021, 12, 817117.	1.1	6
1895	DNA methylation differences between male and female gonads of the oyster reveal the role of epigenetics in sex determination. <i>Gene</i> , 2022, 820, 146260.	1.0	16
1896	Lauric Acid Induces Apoptosis of Rice Sheath Blight Disease Caused by <i>Rhizoctonia solani</i> by Affecting Fungal Fatty Acid Metabolism and Destroying the Dynamic Equilibrium of Reactive Oxygen Species. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 153.	1.5	7
1897	Profiling the Bisecting N-acetylglucosamine Modification in Amniotic Membrane via Mass Spectrometry. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 648-656.	3.0	2
1898	A Calmodulin-Like Gene (<i>GbCML7</i>) for Fiber Strength and Yield Improvement Identified by Resequencing Core Accessions of a Pedigree in <i>Gossypium barbadense</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 815648.	1.7	4
1899	Transcriptome analysis of grass carp (<i>Ctenopharyngodon idella</i>) and Holland's spinibarbel (<i>Spinibarbus hollandi</i>) infected with <i>Ichthyophthirius multifiliis</i> . <i>Fish and Shellfish Immunology</i> , 2022, 121, 305-315.	1.6	7
1900	Integrative Genome-Wide DNA Methylome and Transcriptome Analysis of Ovaries from Hu Sheep with High and Low Prolific. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 820558.	1.8	4
1901	Transcriptional, secondary metabolic, and antioxidative investigations elucidate the rapid response mechanism of <i>Pontederia cordata</i> to cadmium. <i>Ecotoxicology and Environmental Safety</i> , 2022, 232, 113236.	2.9	10
1902	Estrogen signaling regulates seasonal changes of the prostate in wild ground squirrels (<i>Spermophilus dauricus</i>). <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2022, 218, 106058.	1.2	3
1903	Transcriptomic responses to air exposure stress in coelomocytes of the sea cucumber, <i>Apostichopus japonicus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 42, 100963.	0.4	3
1904	Comparative transcriptomics analysis of testicular miRNA from indicine and taurine cattle. <i>Animal Biotechnology</i> , 2022, , 1-11.	0.7	1
1905	Identification of sodium homeostasis genes in <i>Camelus bactrianus</i> by whole transcriptome sequencing. <i>FEBS Open Bio</i> , 2022, 12, 864-876.	1.0	0

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1907	Circulating MicroRNAs From Plasma Small Extracellular Vesicles as Potential Diagnostic Biomarkers in Pediatric Epilepsy and Drug-Resistant Epilepsy. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, 823802.	1.4	7
1909	Single-molecule long-read sequencing reveals the potential impact of posttranscriptional regulation on gene dosage effects on the avian Z chromosome. <i>BMC Genomics</i> , 2022, 23, 122.	1.2	2
1910	Comparative transcriptome study of the elongating internode in elephant grass (<i>Cenchrus purpureus</i>) seedlings in response to exogenous gibberellin applications. <i>Industrial Crops and Products</i> , 2022, 178, 114653.	2.5	10
1911	Novel Insights into Anthocyanin Metabolism and Molecular Characterization of Associated Genes in Sugarcane Rinds Using the Metabolome and Transcriptome. <i>International Journal of Molecular Sciences</i> , 2022, 23, 338.	1.8	12
1912	Screening of differentially expressed miRNAs during osteogenic/odontogenic differentiation of human dental pulp stem cells exposed to mechanical stress. <i>American Journal of Translational Research (discontinued)</i> , 2021, 13, 11126-11143.	0.0	0
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1915	Functional Verification of <i>Arthrinium Phaeospermum</i> Effectors Apce12 and Apce22 Based on Dual Rna-Seq Analysis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
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1958	Transcriptional multiomics reveals the mechanism of seed deterioration in <i>Nicotiana tabacum</i> L. and <i>Oryza sativa</i> L.. <i>Journal of Advanced Research</i> , 2022, 42, 163-176.	4.4	5
1959	Adaptive divergence and underlying mechanisms in response to salinity gradients between two <i>Crassostrea</i> oysters revealed by phenotypic and transcriptomic analyses. <i>Evolutionary Applications</i> , 2023, 16, 234-249.	1.5	9
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1963	De novo Transcriptome Analysis Revealed the Putative Pathway Genes Involved in Biosynthesis of Moracins in <i>Morus alba</i> L.. <i>ACS Omega</i> , 2022, 7, 11343-11352.	1.6	2
1964	Sex-Biased miRNAs in the Gonads of Adult Chinese Alligator (<i>Alligator sinensis</i>) and Their Potential Roles in Sex Maintenance. <i>Frontiers in Genetics</i> , 2022, 13, 843884.	1.1	0
1965	Transcriptome analysis of <i>Tamarix ramosissima</i> leaves in response to NaCl stress. <i>PLoS ONE</i> , 2022, 17, e0265653.	1.1	9
1966	Gene-coexpression network analysis identifies specific modules and hub genes related to cold stress in rice. <i>BMC Genomics</i> , 2022, 23, 251.	1.2	17
1967	Transcriptome analysis of Pacific white shrimp (<i>Litopenaeus vannamei</i>) hepatopancreas challenged by <i>Vibrio alginolyticus</i> reveals lipid metabolic disturbance. <i>Fish and Shellfish Immunology</i> , 2022, 123, 238-247.	1.6	21
1968	Integrated Analysis of Physiological, mRNA Sequencing, and miRNA Sequencing Data Reveals a Specific Mechanism for the Response to Continuous Cropping Obstacles in <i>Pogostemon cablin</i> Roots. <i>Frontiers in Plant Science</i> , 2022, 13, 853110.	1.7	8
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1970	The <i>Gastrodia menghaiensis</i> (Orchidaceae) genome provides new insights of orchid mycorrhizal interactions. <i>BMC Plant Biology</i> , 2022, 22, 179.	1.6	13
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1973	Comparative transcriptome analyses unravel the response to acute thermal stress in the razor clam, <i>Sinonovacula constricta</i> . <i>Aquaculture Reports</i> , 2022, 23, 101079.	0.7	6
1974	Antioxidant Regulation and DNA Methylation Dynamics During <i>Mikania micrantha</i> Seed Germination Under Cold Stress. <i>Frontiers in Plant Science</i> , 2022, 13, 856527.	1.7	4
1975	Total and Mitochondrial Transcriptomic and Proteomic Insights into Regulation of Bioenergetic Processes for Shoot Fast-Growth Initiation in Moso Bamboo. <i>Cells</i> , 2022, 11, 1240.	1.8	7
1976	Whole-transcriptome RNA sequencing revealed the roles of chitin-related genes in the eyestalk abnormality of a novel mud crab hybrid (<i>Scylla serrata</i> × <i>S. paramamosain</i>). <i>International Journal of Biological Macromolecules</i> , 2022, 208, 611-626.	3.6	14
1977	Comparative transcriptomic analysis of the liver and spleen in marbled rockfish (<i>Sebastes</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 554, 738144.	1.7	5
1978	Phenotypic plasticity couples with transcriptomic flexibility in <i>Leymus chinensis</i> under diverse edaphic conditions. <i>Environmental and Experimental Botany</i> , 2022, 197, 104838.	2.0	1

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1982	The effects of blunt snout bream (<i>Megalobrama amblycephala</i>) IL-6 trans-signaling on immunity and iron metabolism via JAK/STAT3 pathway. <i>Developmental and Comparative Immunology</i> , 2022, 131, 104372.	1.0	2
1983	Impact of microplastics from polyethylene and biodegradable mulch films on rice (<i>Oryza sativa</i> L.). <i>Science of the Total Environment</i> , 2022, 828, 154579.	3.9	69
1984	Neurotoxic effects of synthetic phenolic antioxidants on dopaminergic, serotonergic, and GABAergic signaling in larval zebrafish (<i>Danio rerio</i>). <i>Science of the Total Environment</i> , 2022, 830, 154688.	3.9	16
1985	Intraspecific hybridization as a mitigation strategy of ocean acidification in marine bivalve noble scallop <i>Chlamys nobilis</i> . <i>Science of the Total Environment</i> , 2022, 832, 154736.	3.9	3
1986	Transcriptomic and physiological analysis reveals interplay between salicylic acid and drought stress in citrus tree floral initiation. <i>Planta</i> , 2022, 255, 24.	1.6	20
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1988	Elucidating the Molecular Mechanisms by which Seed-Borne Endophytic Fungi, <i>Epichloa gansuensis</i> , Increases the Tolerance of <i>Achnatherum inebrians</i> to NaCl Stress. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13191.	1.8	7
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1990	Exploration of the Effect on Genome-Wide DNA Methylation by miR-143 Knock-Out in Mice Liver. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13075.	1.8	5
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1994	Transcriptome analysis of ovary culture-induced embryogenesis in cucumber (<i>Cucumis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.9	2
1995	Transcriptomics Integrated With Metabolomics Reveal the Effects of Ultraviolet-B Radiation on Flavonoid Biosynthesis in Antarctic Moss. <i>Frontiers in Plant Science</i> , 2021, 12, 788377.	1.7	16
1996	MicroRNA-6498-5p Inhibits <i>Nosema bombycis</i> Proliferation by Downregulating BmPLPP2 in <i>Bombyx mori</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1051.	1.5	4

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1999	Emerging roles of circRNAs in regulating thermal and hypoxic stresses in <i>Apostichopus japonicus</i> (Echinodermata: Holothuroidea). <i>Ecotoxicology and Environmental Safety</i> , 2021, 228, 112994.	2.9	5
2000	Transcriptome of miRNA during inhibition of <i>Bombyx mori</i> nuclear polyhedrosis virus by geldanamycin in BmN cells. <i>Archives of Insect Biochemistry and Physiology</i> , 2022, 110, e21880.	0.6	3
2001	Transcriptome provides insights into bovine mammary regulatory mechanisms during the lactation cycle. <i>Journal of Applied Animal Research</i> , 2022, 50, 275-288.	0.4	0
2002	Comparative Analysis of miRNA Expression Profiles in Skeletal Muscle of Bian Chickens at Different Embryonic Ages. <i>Animals</i> , 2022, 12, 1003.	1.0	2
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2394	<i>Chrysanthemum</i> <i>grandiflora</i> leaf and root transcript profiling in response to salinity stress. <i>BMC Plant Biology</i> , 2022, 22, 240.	1.6	3
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2409	Enhanced reactive oxygen detoxification occurs in salt-stressed soybean roots expressing <i>GmSALT3</i> . <i>Physiologia Plantarum</i> , 2022, 174, e13709.	2.6	13
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