

Gene ontology analysis for RNA-seq: accounting for selection

Genome Biology

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Use of homologous and heterologous gene expression profiling tools to characterize transcription dynamics during apple fruit maturation and ripening. <i>BMC Plant Biology</i> , 2010, 10, 229.	1.6	79
2	Gene set enrichment; a problem of pathways. <i>Briefings in Functional Genomics</i> , 2010, 9, 385-390.	1.3	9
3	Statistical Issues in the Analysis of ChIP-Seq and RNA-Seq Data. <i>Genes</i> , 2010, 1, 317-334.	1.0	17
4	From RNA-seq reads to differential expression results. <i>Genome Biology</i> , 2010, 11, 220.	13.9	603
5	Cell-type specific analysis of translating RNAs in developing flowers reveals new levels of control. <i>Molecular Systems Biology</i> , 2010, 6, 419.	3.2	155
6	Differential expression in RNA-seq: A matter of depth. <i>Genome Research</i> , 2011, 21, 2213-2223.	2.4	1,456
7	Bioaccumulation and Effects of CdTe/CdS Quantum Dots on <i>Chlamydomonas reinhardtii</i> " Nanoparticles or the Free Ions?. <i>Environmental Science & Technology</i> , 2011, 45, 7664-7669.	4.6	111
8	On Differential Gene expression Using RNA-Seq Data. <i>Cancer Informatics</i> , 2011, 10, CIN.S7473.	0.9	18
9	Control of Embryonic Stem Cell Lineage Commitment by Core Promoter Factor, TAF3. <i>Cell</i> , 2011, 146, 720-731.	13.5	155
10	GC-Content Normalization for RNA-Seq Data. <i>BMC Bioinformatics</i> , 2011, 12, 480.	1.2	712
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22	RNA-Seq of the xylose-fermenting yeast <i>Scheffersomyces stipitis</i> cultivated in glucose or xylose. <i>Applied Microbiology and Biotechnology</i> , 2011, 92, 1237-1249.	1.7	30
23	Statistical methods on detecting differentially expressed genes for RNA-seq data. <i>BMC Systems Biology</i> , 2011, 5, S1.	3.0	49
24	Functional annotation of the transcriptome of <i>Sorghum bicolor</i> in response to osmotic stress and abscisic acid. <i>BMC Genomics</i> , 2011, 12, 514.	1.2	197
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42	A bias-reducing pathway enrichment analysis of genome-wide association data confirmed association of the MHC region with schizophrenia. <i>Journal of Medical Genetics</i> , 2012, 49, 96-103.	1.5	68
43	Next-generation sequencing technologies for gene expression profiling in plants. <i>Briefings in Functional Genomics</i> , 2012, 11, 63-70.	1.3	135
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1001	Full-length transcriptome sequences of ephemeral plant <i>Arabidopsis pumila</i> provides insight into gene expression dynamics during continuous salt stress. <i>BMC Genomics</i> , 2018, 19, 717.	1.2	54
1002	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. <i>Nature Communications</i> , 2018, 9, 4079.	5.8	121
1003	Transcriptomic insights into the blue light-induced female floral sex expression in cucumber (<i>Cucumis sativus</i> L.). <i>Scientific Reports</i> , 2018, 8, 14261.	1.6	12
1004	Which Genes in a Typical Intertidal Seagrass (<i>Zostera japonica</i>) Indicate Copper-, Lead-, and Cadmium Pollution?. <i>Frontiers in Plant Science</i> , 2018, 9, 1545.	1.7	11
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1008	WRKY Transcription Factors Associated With NPR1-Mediated Acquired Resistance in Barley Are Potential Resources to Improve Wheat Resistance to <i>Puccinia triticina</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1486.	1.7	32
1009	Characterization of kinase gene expression and splicing profile in prostate cancer with RNA-Seq data. <i>BMC Genomics</i> , 2018, 19, 564.	1.2	6
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1012	Extremophiles as a Model of a Natural Ecosystem: Transcriptional Coordination of Genes Reveals Distinct Selective Responses of Plants Under Climate Change Scenarios. <i>Frontiers in Plant Science</i> , 2018, 9, 1376.	1.7	10

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1018	Non-target site-based resistance to tribenuron-methyl and essential involved genes in <i>Myosoton aquaticum</i> (L.). <i>BMC Plant Biology</i> , 2018, 18, 225.	1.6	37
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1023	Single cell RNA-seq reveals profound transcriptional similarity between Barrett's oesophagus and oesophageal submucosal glands. <i>Nature Communications</i> , 2018, 9, 4261.	5.8	65
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1028	Co-expression analysis aids in the identification of genes in the cuticular wax pathway in maize. <i>Plant Journal</i> , 2019, 97, 530-542.	2.8	34
1029	Transcriptome analysis of extended-spectrum β -lactamase-producing <i>Escherichia coli</i> and methicillin-resistant <i>Staphylococcus aureus</i> exposed to cefotaxime. <i>Scientific Reports</i> , 2018, 8, 16076.	1.6	12
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1042	Transcriptome analysis of <i>Nicotiana benthamiana</i> infected by Tobacco curly shoot virus. <i>Virology Journal</i> , 2018, 15, 138.	1.4	37
1043	Systematic transcriptomic analysis provides insights into lotus (<i>Nelumbo nucifera</i>) seed development. <i>Plant Growth Regulation</i> , 2018, 86, 339-350.	1.8	21
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1048	De novo assembly and comparative transcriptome characterization of <i>Poecilobdella javanica</i> provide insight into blood feeding of medicinal leeches. <i>Molecular Omics</i> , 2018, 14, 352-361.	1.4	7

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1061	Identification of the RNA polymerase I-RNA interactome. <i>Nucleic Acids Research</i> , 2018, 46, 11002-11013.	6.5	19
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1063	Molecular Mechanism of Modified Clay Controlling the Brown Tide Organism <i>Aureococcus anophagefferens</i> Revealed by Transcriptome Analysis. <i>Environmental Science & Technology</i> , 2018, 52, 7006-7014.	4.6	23
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1065	Activity-dependent neuroprotective protein recruits HP1 and CHD4 to control lineage-specifying genes. <i>Nature</i> , 2018, 557, 739-743.	13.7	169
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1078	Intraflagellar transport 46 (IFT46) is essential for trafficking IFT proteins between cilia and cytoplasm in <i>Paramecium</i> . <i>Scientific Reports</i> , 2018, 8, 9259.	1.6	11
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1080	RNA-seq Reveals the Overexpression of IGSF9 in Endometrial Cancer. <i>Journal of Oncology</i> , 2018, 2018, 1-13.	0.6	12
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1082	Deep Transcriptomic Analysis of Black Rockfish (<i>Sebastes schlegelii</i>) Provides New Insights on Responses to Acute Temperature Stress. <i>Scientific Reports</i> , 2018, 8, 9113.	1.6	53
1083	Differential aging-related changes in neurophysiology and gene expression in IB4-positive and IB4-negative nociceptive neurons. <i>Aging Cell</i> , 2018, 17, e12795.	3.0	6
1084	Whole genome comparison of <i>Aspergillus flavus</i> L-morphotype strain NRRL 3357 (type) and S-morphotype strain AF70. <i>PLoS ONE</i> , 2018, 13, e0199169.	1.1	27

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1088	Analysis of long non-coding RNA expression profiles using RNA sequencing in ovarian endometriosis. <i>Gene</i> , 2018, 673, 140-148.	1.0	30
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1091	Transcriptomic response to GABA-producing <i>Lactobacillus plantarum</i> CGMCC 1.2437T induced by L-MSG. <i>PLoS ONE</i> , 2018, 13, e0199021.	1.1	36
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1106	Establishing normal metabolism and differentiation in hepatocellular carcinoma cells by culturing in adult human serum. <i>Scientific Reports</i> , 2018, 8, 11685.	1.6	20
1107	Response gene to complement 32 suppresses adipose tissue thermogenic genes through inhibiting α -adrenergic receptor/mTORC1 signaling. <i>FASEB Journal</i> , 2018, 32, 4836-4847.	0.2	8
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1109	Genome-wide transcriptome analysis and identification of benzothiadiazole-induced genes and pathways potentially associated with defense response in banana. <i>BMC Genomics</i> , 2018, 19, 454.	1.2	16
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1122	Transcriptomic analysis identifies the key genes involved in stamen petaloid in lotus (<i>Nelumbo</i>) Tj ETQq1 1 0.784314rgBT /Oyerlock 10 1.2 24	1.2	24
1123	Transcriptome and metabolome analysis reveal candidate genes and biochemicals involved in tea geometrid defense in <i>Camellia sinensis</i> . <i>PLoS ONE</i> , 2018, 13, e0201670.	1.1	38
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1133	Trehalose Contributes to Gamma-Linolenic Acid Accumulation in <i>Cunninghamella echinulata</i> Based on de Novo Transcriptomic and Lipidomic Analyses. <i>Frontiers in Microbiology</i> , 2018, 9, 1296.	1.5	12
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1137	The interaction between DNA methylation and long non-coding RNA during the onset of puberty in goats. <i>Reproduction in Domestic Animals</i> , 2018, 53, 1287-1297.	0.6	5
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1140	Genome-Wide Analysis of Long Non-Coding RNAs in Potato and Their Potential Role in Tuber Sprouting Process. <i>International Journal of Molecular Sciences</i> , 2018, 19, 101.	1.8	22
1141	Transcriptome Analysis of Flounder (<i>Paralichthys olivaceus</i>) Gill in Response to Lymphocystis Disease Virus (LCDV) Infection: Novel Insights into Fish Defense Mechanisms. <i>International Journal of Molecular Sciences</i> , 2018, 19, 160.	1.8	43
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1153	Comparative transcriptome study of hairy and hairless tea plant (<i>Camellia sinensis</i>) shoots. <i>Journal of Plant Physiology</i> , 2018, 229, 41-52.	1.6	16
1154	Gene expression profiles of germ-free and conventional piglets from the same litter. <i>Scientific Reports</i> , 2018, 8, 10745.	1.6	26
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1163	Morphological Observation and Comparative Transcriptomic Analysis of <i>Clostridium perfringens</i> Biofilm and Planktonic Cells. <i>Current Microbiology</i> , 2018, 75, 1182-1189.	1.0	1
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1169	Developmental transcriptome analysis of floral transition in <i>Rosa odorata</i> var. <i>gigantea</i> . <i>Plant Molecular Biology</i> , 2018, 97, 113-130.	2.0	11
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1171	Exploration of the Regulatory Mechanism of Secondary Metabolism by Comparative Transcriptomics in <i>Aspergillus flavus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1568.	1.5	27
1172	Modulation of xenobiotic nuclear receptors in high-fat diet induced non-alcoholic fatty liver disease. <i>Toxicology</i> , 2018, 410, 199-213.	2.0	38
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1177	Transcriptome analysis in <i>Malus halliana</i> roots in response to iron deficiency reveals insight into sugar regulation. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1523-1534.	1.0	15
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1180	Heterologous Expression of a Novel <i>Zoysia japonica</i> C2H2 Zinc Finger Gene, ZJZFN1, Improved Salt Tolerance in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1159.	1.7	34
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1182	Common and differential transcriptional responses to different models of traumatic stress exposure in rats. <i>Translational Psychiatry</i> , 2018, 8, 165.	2.4	2
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1184	Life cycle adapted upstream open reading frames (uORFs) in <i>Trypanosoma congolense</i> : A post-transcriptional approach to accurate gene regulation. <i>PLoS ONE</i> , 2018, 13, e0201461.	1.1	7
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1187	Analysis of Transcriptional Responses of the Inflorescence Meristems in <i>Jatropha curcas</i> Following Gibberellin Treatment. <i>International Journal of Molecular Sciences</i> , 2018, 19, 432.	1.8	36
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1189	Developmental Dynamics of Long Noncoding RNA Expression during Sexual Fruiting Body Formation in <i>Fusarium graminearum</i> . <i>MBio</i> , 2018, 9, .	1.8	37
1190	Comparative transcriptome analysis of the interaction between <i>Actinidia chinensis</i> var. <i>chinensis</i> and <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> in absence and presence of acibenzolar-S-methyl. <i>BMC Genomics</i> , 2018, 19, 585.	1.2	33
1191	Algorithm for Physiological Interpretation of Transcriptome Profiling Data for Non-Model Organisms. <i>Molecular Biology</i> , 2018, 52, 497-509.	0.4	1
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1194	Transcriptome Analysis Identifies a Zinc Finger Protein Regulating Starch Degradation in Kiwifruit. <i>Plant Physiology</i> , 2018, 178, 850-863.	2.3	109
1195	Transcriptome profiling of short-term response to chilling stress in tolerant and sensitive <i>Oryza sativa</i> ssp. <i>Japonica</i> seedlings. <i>Functional and Integrative Genomics</i> , 2018, 18, 627-644.	1.4	34
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1197	Widespread antisense transcription of <i>Populus</i> genome under drought. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1017-1033.	1.0	2
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1199	RNA sequencing and differential expression reveals the effects of serial oestrus synchronisation on ovarian genes in dairy goats. <i>Reproduction, Fertility and Development</i> , 2018, 30, 1622.	0.1	4
1200	WSL5, a pentatricopeptide repeat protein, is essential for chloroplast biogenesis in rice under cold stress. <i>Journal of Experimental Botany</i> , 2018, 69, 3949-3961.	2.4	67
1201	Comparative analysis on liver transcriptome profiles of different methods to establish type 2 diabetes mellitus models in Guangxi Bama mini-pig. <i>Gene</i> , 2018, 673, 194-200.	1.0	20
1202	De novo transcriptome assembly and functional annotation of the southern rock lobster (<i>Jasus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.4	5
1203	Transcriptome profiling of pumpkin (<i>Cucurbita moschata</i> Duch.) leaves infected with powdery mildew. <i>PLoS ONE</i> , 2018, 13, e0190175.	1.1	51
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1206	Transcriptome analysis using RNA-Seq revealed the effects of nitrogen form on major secondary metabolite biosynthesis in tea (<i>Camellia sinensis</i>) plants. <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	29
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1208	Influence of isopropylmalate synthase <i>OsIPMS1</i> on seed vigour associated with amino acid and energy metabolism in rice. <i>Plant Biotechnology Journal</i> , 2019, 17, 322-337.	4.1	69
1209	Transcriptome Analysis. , 2019, , 792-805.		8
1210	Transcriptome analysis of <i>Lilium Oriental</i> – <i>Trumpet</i> hybrid roots reveals auxin-related genes and stress-related genes involved in picloram-induced somatic embryogenesis induction. <i>Journal of Horticultural Science and Biotechnology</i> , 2019, 94, 317-330.	0.9	8

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1212	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. <i>Molecular Psychiatry</i> , 2019, 24, 1685-1695.	4.1	40
1213	Transcriptome profiling of the low-salinity stress responses in the gills of the juvenile <i>Pseudopleuronectes yokohamae</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 32, 100612.	0.4	18
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1215	Expansion of Luminal Progenitor Cells in the Aging Mouse and Human Prostate. <i>Cell Reports</i> , 2019, 28, 1499-1510.e6.	2.9	56
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1217	Evaluation of dynamic developmental processes and the molecular basis of the high body fat percentage of different proglottid types of <i>Moniezia expansa</i> . <i>Parasites and Vectors</i> , 2019, 12, 390.	1.0	8
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1222	N4-Cytosine DNA Methylation Is Involved in the Maintenance of Genomic Stability in <i>Deinococcus radiodurans</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1905.	1.5	27
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1224	Gene Coexpression Networks Reveal Key Drivers of Flavonoid Variation in Eleven Tea Cultivars (<i>Camellia sinensis</i>). <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 9967-9978.	2.4	20
1225	RNASeq analysis of giant cane reveals the leaf transcriptome dynamics under long-term salt stress. <i>BMC Plant Biology</i> , 2019, 19, 355.	1.6	37
1226	Genome-Wide Identification and Characterization of Long Noncoding RNAs of Brown to White Adipose Tissue Transformation in Goats. <i>Cells</i> , 2019, 8, 904.	1.8	20
1227	Transcriptomic analysis of Pacific white shrimp (<i>Litopenaeus vannamei</i> , Boone 1931) in response to acute hepatopancreatic necrosis disease caused by <i>Vibrio parahaemolyticus</i> . <i>PLoS ONE</i> , 2019, 14, e0220993.	1.1	43
1228	Transcriptomic Analysis of the Influence of Methanol Assimilation on the Gene Expression in the Recombinant <i>Pichia pastoris</i> Producing Hirudin Variant 3. <i>Genes</i> , 2019, 10, 606.	1.0	14

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1230	S-Adenosylmethionine Affects Cell Cycle Pathways and Suppresses Proliferation in Liver Cells. <i>Journal of Cancer</i> , 2019, 10, 4368-4379.	1.2	9
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1234	Transcriptome sequencing of a toxic dinoflagellate, <i>Karenia mikimotoi</i> subjected to stress from solar ultraviolet radiation. <i>Harmful Algae</i> , 2019, 88, 101640.	2.2	15
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1241	Transcriptome analysis reveals corresponding genes and key pathways involved in heat stress in Hu sheep. <i>Cell Stress and Chaperones</i> , 2019, 24, 1045-1054.	1.2	13
1242	Sex-specific changes in gene expression in response to estrogen pollution around the onset of sex differentiation in grayling (<i>Salmonidae</i>). <i>BMC Genomics</i> , 2019, 20, 583.	1.2	11
1243	DUX4 Suppresses MHC Class I to Promote Cancer Immune Evasion and Resistance to Checkpoint Blockade. <i>Developmental Cell</i> , 2019, 50, 658-671.e7.	3.1	76
1244	Transcriptome profiling of <i>Puccinellia tenuiflora</i> during seed germination under a long-term saline-alkali stress. <i>BMC Genomics</i> , 2019, 20, 589.	1.2	34
1245	Transcriptome Analysis of Differentially Expressed Genes Related to the Growth and Development of the Jinghai Yellow Chicken. <i>Genes</i> , 2019, 10, 539.	1.0	19
1246	Transcriptomic analysis of differentially expressed genes in the oviduct of <i>Rhacophorus omeimontis</i> provides insights into foam nest construction. <i>BMC Genomics</i> , 2019, 20, 562.	1.2	4

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1248	Transcriptomic analysis reveals key factors in fruit ripening and rubbery texture caused by 1-MCP in papaya. <i>BMC Plant Biology</i> , 2019, 19, 309.	1.6	41
1249	Hypothalamic and pituitary transcriptome profiling using RNA-sequencing in high-yielding and low-yielding laying hens. <i>Scientific Reports</i> , 2019, 9, 10285.	1.6	30
1250	Transcriptome analysis of oriental river Prawn (<i>Macrobrachium nipponense</i>) Hepatopancreas in response to ammonia exposure. <i>Fish and Shellfish Immunology</i> , 2019, 93, 223-231.	1.6	36
1251	The roles of Nrf2 and autophagy in modulating inflammation mediated by TLR4 - NF κ B in A549 cell exposed to layer house particulate matter 2.5 (PM2.5). <i>Chemosphere</i> , 2019, 235, 1134-1145.	4.2	37
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1253	Exploration of long noncoding RNA in bovine milk exosomes and their stability during digestion in vitro. <i>Journal of Dairy Science</i> , 2019, 102, 6726-6737.	1.4	49
1254	A Gene Regulatory Network Controlled by BpERF2 and BpMYB102 in Birch under Drought Conditions. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3071.	1.8	18
1255	Artificial selection on GmOLEO1 contributes to the increase in seed oil during soybean domestication. <i>PLoS Genetics</i> , 2019, 15, e1008267.	1.5	75
1256	Transcriptional Analysis of the Early Ripening of "Kyoho" Grape in Response to the Treatment of Riboflavin. <i>Genes</i> , 2019, 10, 514.	1.0	11
1257	Early Response of Radish to Heat Stress by Strand-Specific Transcriptome and miRNA Analysis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3321.	1.8	28
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1261	MTOR involved in bacterial elimination against <i>Trueperella pyogenes</i> infection based on mice model by transcriptome and biochemical analysis. <i>Veterinary Microbiology</i> , 2019, 235, 199-208.	0.8	9
1262	<i>Trichoderma atroviride</i> P1 Colonization of Tomato Plants Enhances Both Direct and Indirect Defense Barriers Against Insects. <i>Frontiers in Physiology</i> , 2019, 10, 813.	1.3	51
1263	Identification of putative genes for polyphenol biosynthesis in olive fruits and leaves using full-length transcriptome sequencing. <i>Food Chemistry</i> , 2019, 300, 125246.	4.2	39
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1268	Evolution of Lineage-Specific Gene Networks Underlying the Considerable Fruit Shape Diversity in Persimmon. <i>Plant and Cell Physiology</i> , 2019, 60, 2464-2477.	1.5	16
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1270	Flavonoid Biosynthesis Is Likely More Susceptible to Elevation and Tree Age Than Other Branch Pathways Involved in Phenylpropanoid Biosynthesis in Ginkgo Leaves. <i>Frontiers in Plant Science</i> , 2019, 10, 983.	1.7	31
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1273	Transcriptome analysis reveals the influence of anaesthetic stress on the immune system of crucian carp (<i>Carassius auratus</i>) under the process of treatment and low concentration transport by MS&E222 and Eugenol. <i>Aquaculture Research</i> , 2019, 50, 3138-3153.	0.9	9
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1275	Integrated Genome-Scale Analysis Identifies Novel Genes and Networks Underlying Senescence in Maize. <i>Plant Cell</i> , 2019, 31, 1968-1989.	3.1	63
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1285	Morphological, Transcriptomic and Hormonal Characterization of Trimonoecious and Subandroecious Pumpkin (<i>Cucurbita maxima</i>) Suggests Important Roles of Ethylene in Sex Expression. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3185.	1.8	12
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1327	Transcriptome profiling reveals exposure to predicted end-of-century ocean acidification as a stealth stressor for Atlantic cod larvae. <i>Scientific Reports</i> , 2019, 9, 16908.	1.6	7
1328	Activation and Characterization of Cryptic Gene Cluster: Two Series of Aromatic Polyketides Biosynthesized by Divergent Pathways. <i>Angewandte Chemie</i> , 2019, 131, 18214-18222.	1.6	0
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1354	Transcriptome Analysis of Female and Male <i>Conopomorpha sinensis</i> (Lepidoptera: Gracilariidae) Adults With a Focus on Hormone and Reproduction. <i>Journal of Economic Entomology</i> , 2019, 112, 2966-2975.	0.8	3

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1356	Transcriptome Analysis of <i>Cordyceps militaris</i> Reveals Genes Associated With Carotenoid Synthesis and Identification of the Function of the <i>Cmtns</i> Gene. <i>Frontiers in Microbiology</i> , 2019, 10, 2105.	1.5	18
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1383	Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. <i>Nature Communications</i> , 2019, 10, 331.	5.8	146
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1537	The protein elicitor Hrip1 enhances resistance to insects and early bolting and flowering in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2019, 14, e0216082.	1.1	7
1538	Transcriptome Sequencing Reveals Potential Mechanisms of the Maternal Effect on Egg Diapause Induction of <i>Locusta migratoria</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 1974.	1.8	21
1539	Dual Transcriptomic Analysis Reveals a Delayed Antiviral Response of <i>Haliotis diversicolor supertexta</i> against Haliotid Herpesvirus-1. <i>Viruses</i> , 2019, 11, 383.	1.5	10
1540	<i>Pinus massoniana</i> Introgression Hybrids Display Differential Expression of Reproductive Genes. <i>Forests</i> , 2019, 10, 230.	0.9	5
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1542	Multiple microRNAs Regulate the Floral Development and Sex Differentiation in the Dioecious <i>Cucurbit Coccinia grandis</i> (L.) Voigt. <i>Plant Molecular Biology Reporter</i> , 2019, 37, 111-128.	1.0	11
1543	Differential gene expression associated with fungal trophic shifts along the senescence gradient of the moss <i>Dicranum scoparium</i> . <i>Environmental Microbiology</i> , 2019, 21, 2273-2289.	1.8	11
1544	Comparative Transcriptome Profile Analysis of Anther Development in Reproductive Stage of Rice in Cold Region Under Cold Stress. <i>Plant Molecular Biology Reporter</i> , 2019, 37, 129-145.	1.0	12
1545	High-level production of <i>Monascus</i> pigments in <i>Monascus ruber</i> CICC41233 through ATP-citrate lyase overexpression. <i>Biochemical Engineering Journal</i> , 2019, 146, 160-169.	1.8	18
1546	Transcriptome profiling of the meristem tissue of <i>Saccharina japonica</i> (Phaeophyceae, Laminariales) under severe stress of copper. <i>Marine Genomics</i> , 2019, 47, 100671.	0.4	18
1547	The transcriptome analysis of <i>Protaetia brevitarsis</i> Lewis larvae. <i>PLoS ONE</i> , 2019, 14, e0214001.	1.1	8
1548	Acting locally - affecting globally: RNA sequencing of gilthead sea bream with a mild <i>Sparicotyle chrysophrii</i> infection reveals effects on apoptosis, immune and hypoxia related genes. <i>BMC Genomics</i> , 2019, 20, 200.	1.2	53
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1551	Metabolome and Transcriptome Sequencing Analysis Reveals Anthocyanin Metabolism in Pink Flowers of Anthocyanin-Rich Tea (<i>Camellia sinensis</i>). <i>Molecules</i> , 2019, 24, 1064.	1.7	52
1552	Insights into the molecular basis of immunosuppression and increasing pathogen infection severity of ammonia toxicity by transcriptome analysis in pacific white shrimp <i>Litopenaeus vannamei</i> . <i>Fish and Shellfish Immunology</i> , 2019, 88, 528-539.	1.6	22
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1555	The Molecular Basis of Freshwater Adaptation in Prawns: Insights from Comparative Transcriptomics of Three <i>Macrobrachium</i> Species. <i>Genome Biology and Evolution</i> , 2019, 11, 1002-1018.	1.1	23
1556	Physiological and Transcriptome Analyses of Early Leaf Senescence for <i>ospls1</i> Mutant Rice (<i>Oryza</i>)	1.8	17
1557	Phenotypic and transcriptomic characterization of canine myeloid-derived suppressor cells. <i>Scientific Reports</i> , 2019, 9, 3574.	1.6	26
1558	BES/BZR Transcription Factor <i>TaBZR2</i> Positively Regulates Drought Responses by Activation of <i>TaGST1</i> .	2.3	151
1559	Transcriptome Profiling of the Whitefly <i>Bemisia tabaci</i> MED in Response to Single Infection of Tomato yellow leaf curl virus, Tomato chlorosis virus, and Their Co-infection. <i>Frontiers in Physiology</i> , 2019, 10, 302.	1.3	30
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1566	Rearing system causes changes of behavior, microbiome, and gene expression of chickens. <i>Poultry Science</i> , 2019, 98, 3365-3376.	1.5	35
1567	RNA-seq reveals the involvement of key genes for aerobic adaptation in rice. <i>Scientific Reports</i> , 2019, 9, 5235.	1.6	25
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1569	Transcriptome analysis and discovery of genes involved in immune pathways in <i>Solen strictus</i> (Gould.)	1.6	8
1570	Behavioural and transcriptional changes in post-mating females of an egg parasitoid wasp species. <i>Royal Society Open Science</i> , 2019, 6, 181453.	1.1	21
1571	De novo comparative transcriptome analysis of a rare cicada, with identification of candidate genes related to adaptation to a novel host plant and drier habitats. <i>BMC Genomics</i> , 2019, 20, 182.	1.2	19

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1573	Transcriptome analysis of the curry tree (<i>Berbera koenigii</i> L., Rutaceae) during leaf development. <i>Scientific Reports</i> , 2019, 9, 4230.	1.6	2
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1576	Gene Expression Pattern and Regulatory Network of $\hat{\pm}$ -Toxin Treatment in <i>Bombyx mori</i> . <i>International Journal of Genomics</i> , 2019, 2019, 1-11.	0.8	1
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1581	Transcriptomic analysis of fetal membranes reveals pathways involved in preterm birth. <i>BMC Medical Genomics</i> , 2019, 12, 53.	0.7	20
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1588	Integrative analysis of long noncoding RNA and mRNA reveals candidate lncRNAs responsible for meat quality at different physiological stages in Gushi chicken. <i>PLoS ONE</i> , 2019, 14, e0215006.	1.1	18
1589	Functional Characterization of Target of Rapamycin Signaling in <i>Verticillium dahliae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 501.	1.5	24

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1597	Physiological and Growth Response of Pepper (<i>Capsicum annum</i> L.) Seedlings to Supplementary Red/Blue Light Revealed through Transcriptomic Analysis. <i>Agronomy</i> , 2019, 9, 139.	1.3	15
1598	Differential microRNA expression profiles determined by next-generation sequencing in three fulvestrant-resistant human breast cancer cell lines. <i>Oncology Letters</i> , 2019, 17, 3765-3776.	0.8	7
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1605	Adaptive laboratory evolution of a genome-reduced <i>Escherichia coli</i> . <i>Nature Communications</i> , 2019, 10, 935.	5.8	114
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1610	Infection Strategies Deployed by <i>Botrytis cinerea</i> , <i>Fusarium acuminatum</i> , and <i>Rhizopus stolonifer</i> as a Function of Tomato Fruit Ripening Stage. <i>Frontiers in Plant Science</i> , 2019, 10, 223.	1.7	58
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1613	Molecular characterization of carbendazim resistance of <i>Fusarium</i> species complex that causes sugarcane pokkah boeng disease. <i>BMC Genomics</i> , 2019, 20, 115.	1.2	26
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1618	Transcriptomic and microbiota response on <i>Litopenaeus vannamei</i> intestine subjected to acute sulfide exposure. <i>Fish and Shellfish Immunology</i> , 2019, 88, 335-343.	1.6	33
1619	Exosomal transfer of obesity adipose tissue for decreased miR-141-3p mediate insulin resistance of hepatocytes. <i>International Journal of Biological Sciences</i> , 2019, 15, 351-368.	2.6	55
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1638	Molt-dependent transcriptome analysis of claw muscles in Chinese mitten crab <i>Eriocheir sinensis</i> . <i>Genes and Genomics</i> , 2019, 41, 515-528.	0.5	14
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1642	Combined Statistics for Differential Expression Analysis of RNA-Sequencing Data. , 2019, , .		0
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1656	HY5 Contributes to Light-Regulated Root System Architecture Under a Root-Covered Culture System. <i>Frontiers in Plant Science</i> , 2019, 10, 1490.	1.7	32
1657	Hydrogen cyanamide induces grape bud endodormancy release through carbohydrate metabolism and plant hormone signaling. <i>BMC Genomics</i> , 2019, 20, 1034.	1.2	28
1658	Comparative de novo transcriptomics and untargeted metabolomic analyses elucidate complicated mechanisms regulating celery (<i>Apium graveolens</i> L.) responses to selenium stimuli. <i>PLoS ONE</i> , 2019, 14, e0226752.	1.1	16
1659	Identification of Shoot Differentiation-Related Genes in <i>Populus euphratica</i> Oliv.. <i>Genes</i> , 2019, 10, 1034.	1.0	3
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1663	Transcriptome Analysis of the Cecal Tonsil of Jingxing Yellow Chickens Revealed the Mechanism of Differential Resistance to Salmonella. <i>Genes</i> , 2019, 10, 979.	1.0	12
1664	Transcriptional profiling reveals differentially expressed genes involved in lipid biosynthesis during cacao seed development. <i>Scientific Reports</i> , 2019, 9, 17263.	1.6	2
1665	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. <i>Genome Research</i> , 2019, 29, 1962-1973.	2.4	35
1666	Resistance of <i>Nicotiana tabacum</i> to <i>Phytophthora parasitica</i> var. <i>nicotianae</i> Race 0 Is Enhanced by the Addition of <i>N. plumbaginifolia</i> Chromosome 9 with a Slight Effect on Host Genomic Expression. <i>Crop Science</i> , 2019, 59, 2667-2678.	0.8	4
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1808	Transcriptome Analysis Reveals the Effects of Chinese Chive (<i>Allium tuberosum</i> R.) Extract on <i>Fusarium oxysporum</i> f. sp. <i>radicis-lycopersici</i> Spore Germination. <i>Current Microbiology</i> , 2020, 77, 855-864.	1.0	10
1809	Exploration of key regulators driving primary feather follicle induction in goose skin. <i>Gene</i> , 2020, 731, 144338.	1.0	9
1810	Impact of juvenile hormone analogue insecticides on the water flea <i>Moina macrocopa</i> : Growth, reproduction and transgenerational effect. <i>Aquatic Toxicology</i> , 2020, 220, 105402.	1.9	20
1811	Comparative transcriptome analysis of the genes involved in lipid biosynthesis pathway and regulation of oil body formation in <i>Torreya grandis</i> kernels. <i>Industrial Crops and Products</i> , 2020, 145, 112051.	2.5	24
1812	Molecular Insights into the Insensitivity of Lepidopteran Pests to Cycloxyaprid. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 982-988.	2.4	5
1813	Metabolome and Transcriptome Analysis Reveals Putative Genes Involved in Anthocyanin Accumulation and Coloration in White and Pink Tea (<i>Camellia sinensis</i>) Flower. <i>Molecules</i> , 2020, 25, 190.	1.7	56
1814	Transcriptome analysis of <i>Actinidia chinensis</i> in response to <i>Botryosphaeria dothidea</i> infection. <i>PLoS ONE</i> , 2020, 15, e0227303.	1.1	13
1815	Transcriptomic and metabolomic analysis reveals the role of CoA in the salt tolerance of <i>Zygophyllum</i> spp. <i>BMC Plant Biology</i> , 2020, 20, 9.	1.6	14
1816	Molecular and genetic analysis of resistance to MET-I acaricides in Iranian populations of the citrus red mite <i>Panonychus citri</i> . <i>Pesticide Biochemistry and Physiology</i> , 2020, 164, 73-84.	1.6	21
1817	Transcriptome and GWAS analyses reveal candidate gene for seminal root length of maize seedlings under drought stress. <i>Plant Science</i> , 2020, 292, 110380.	1.7	81
1818	Genome-wide analysis of ethylene-response factor family in adzuki bean and functional determination of VaERF3 under saline-alkaline stress. <i>Plant Physiology and Biochemistry</i> , 2020, 147, 215-222.	2.8	22
1819	Transcriptome profiling reveals the crucial biological pathways involved in cold response in Moso bamboo (<i>Phyllostachys edulis</i>). <i>Tree Physiology</i> , 2020, 40, 538-556.	1.4	27
1820	Genome-wide association study reveals new genes involved in leaf trichome formation in polyploid oilseed rape (<i>Brassica napus</i> L.). <i>Plant, Cell and Environment</i> , 2020, 43, 675-691.	2.8	28
1821	<i>Fusarium virguliforme</i> Transcriptional Plasticity Is Revealed by Host Colonization of Maize versus Soybean. <i>Plant Cell</i> , 2020, 32, 336-351.	3.1	28
1822	Transcriptomic and metabolomic analyses reveal several critical metabolic pathways and candidate genes involved in resin biosynthesis in <i>Pinus massoniana</i> . <i>Molecular Genetics and Genomics</i> , 2020, 295, 327-341.	1.0	15
1823	Transcriptomic Changes in Liver of Juvenile <i>Cynoglossus semilaevis</i> following Perfluorooctane Sulfonate Exposure. <i>Environmental Toxicology and Chemistry</i> , 2020, 39, 556-564.	2.2	10

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1824	Comparative transcriptomic analysis reveals novel insights into the response to Cr(VI) exposure in Cr(VI) tolerant ectomycorrhizal fungi <i>Pisolithus</i> sp. 1 LS-2017. <i>Ecotoxicology and Environmental Safety</i> , 2020, 188, 109935.	2.9	10
1825	Identification of functional lncRNAs in pseudorabies virus type II infected cells. <i>Veterinary Microbiology</i> , 2020, 242, 108564.	0.8	8
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1827	NK cell recruitment limits tissue damage during an enteric helminth infection. <i>Mucosal Immunology</i> , 2020, 13, 357-370.	2.7	20
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1829	Molecular responses to freshwater limitation in the mangrove tree <i>Avicennia germinans</i> (Acanthaceae). <i>Molecular Ecology</i> , 2020, 29, 344-362.	2.0	12
1830	Transcriptomic Analyses of Chilling Stress Responsiveness in Leaves of Tobacco (<i>Nicotiana tabacum</i>) Seedlings. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 1-13.	1.0	7
1831	Co-option of wing-patterning genes underlies the evolution of the treehopper helmet. <i>Nature Ecology and Evolution</i> , 2020, 4, 250-260.	3.4	38
1832	<i>WRKY</i> Transcription Factors Shared by BTH-Induced Resistance and <i>NPR1</i> -Mediated Acquired Resistance Improve Broad-Spectrum Disease Resistance in Wheat. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 433-443.	1.4	27
1833	RNA-seq reveals hormone-regulated synthesis of non-cellulose polysaccharides associated with fiber strength in a single-chromosomal-fragment-substituted upland cotton line. <i>Crop Journal</i> , 2020, 8, 273-286.	2.3	10
1834	Co-infection with <i>Wolbachia</i> and <i>Cardinium</i> may promote the synthesis of fat and free amino acids in a small spider, <i>Hylyphantes graminicola</i> . <i>Journal of Invertebrate Pathology</i> , 2020, 169, 107307.	1.5	16
1835	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
1836	Differential gene expression profiling of the goose pineal gland. <i>British Poultry Science</i> , 2020, 61, 200-208.	0.8	2
1837	Deciphering the high-quality genome sequence of coriander that causes controversial feelings. <i>Plant Biotechnology Journal</i> , 2020, 18, 1444-1456.	4.1	56
1838	RNA-Sequencing Highlights Inflammation and Impaired Integrity of the Vascular Wall in Brain Arteriovenous Malformations. <i>Stroke</i> , 2020, 51, 268-274.	1.0	22
1839	Transcriptome and physiology analysis identify key metabolic changes in the liver of the large yellow croaker (<i>Larimichthys crocea</i>) in response to acute hypoxia. <i>Ecotoxicology and Environmental Safety</i> , 2020, 189, 109957.	2.9	45
1840	Transcriptomics of <i>Cherax quadricarinatus</i> hepatopancreas during infection with Decapod iridescent virus 1 (DIV1). <i>Fish and Shellfish Immunology</i> , 2020, 98, 832-842.	1.6	30
1841	Transcriptional responses of soybean aphids to sublethal insecticide exposure. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 118, 103285.	1.2	11

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1843	Transcriptomic analysis of oligochaete immune responses to myxosporeans infection: <i>Branchiura sowerbyi</i> infected with <i>Myxobolus cultus</i> . <i>Journal of Invertebrate Pathology</i> , 2020, 169, 107283.	1.5	5
1844	Skin barrier damage after exposure to paraphenylenediamine. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 619-631.e2.	1.5	21
1845	Environmental hypoxia causes growth retardation, osteoclast differentiation and calcium dyshomeostasis in juvenile rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Science of the Total Environment</i> , 2020, 705, 135272.	3.9	32
1846	Identification of a genetic network for an ecologically relevant behavioural phenotype in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2020, 29, 502-518.	2.0	3
1847	Transcriptional and Functional Programming of Decidual Innate Lymphoid Cells. <i>Frontiers in Immunology</i> , 2019, 10, 3065.	2.2	21
1848	Global Gene Responses of Resistant and Susceptible Sugarcane Cultivars to <i>Acidovorax avenae</i> subsp. <i>avenae</i> Identified Using Comparative Transcriptome Analysis. <i>Microorganisms</i> , 2020, 8, 10.	1.6	20
1849	PCAT18, as a novel differentially regulated long noncoding RNA in adult acute myeloid leukemia patients revealed by next-generation sequencing. <i>International Journal of Laboratory Hematology</i> , 2020, 42, 858-865.	0.7	5
1850	A combination of genome-wide association study and transcriptome analysis in leaf epidermis identifies candidate genes involved in cuticular wax biosynthesis in <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2020, 20, 458.	1.6	7
1851	Mitochondrial DNA copy number can influence mortality and cardiovascular disease via methylation of nuclear DNA CpGs. <i>Genome Medicine</i> , 2020, 12, 84.	3.6	63
1852	Identification and Characterization of lncRNAs Related to the Muscle Growth and Development of Japanese Flounder (<i>Paralichthys olivaceus</i>). <i>Frontiers in Genetics</i> , 2020, 11, 1034.	1.1	11
1853	Genome-Wide Identification and Characterization of <i>Fusarium graminearum</i> -Responsive lncRNAs in <i>Triticum aestivum</i> . <i>Genes</i> , 2020, 11, 1135.	1.0	4
1854	Comparative Transcriptome Analysis Revealing the Different Germination Process in Aryloxyphenoxypropionate-Resistant and APP-Susceptible Asia Minor Bluegrass (<i>Polypogon fugax</i>). <i>Plants</i> , 2020, 9, 1191.	1.6	2
1855	Root-Secreted Coumarins and the Microbiota Interact to Improve Iron Nutrition in <i>Arabidopsis</i> . <i>Cell Host and Microbe</i> , 2020, 28, 825-837.e6.	5.1	199
1856	Analysis of lncRNA Expression Profile during the Formation of Male Germ Cells in Chickens. <i>Animals</i> , 2020, 10, 1850.	1.0	9
1857	Transgenerational accumulation of methylome changes discovered in commercially reared honey bee (<i>Apis mellifera</i>) queens. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 127, 103476.	1.2	4
1858	Alternative Splicing Enhances the Transcriptome Complexity of <i>Liriodendron chinense</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 578100.	1.7	14
1859	RNA-seq reveals the salt tolerance of <i>Ipomoea pes-caprae</i> , a wild relative of sweet potato. <i>Journal of Plant Physiology</i> , 2020, 255, 153276.	1.6	17

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1861	Comparative transcriptome analysis of <i>Tilletia horrida</i> infection in resistant and susceptible rice (<i>Oryza sativa</i> L.) male sterile lines reveals potential candidate genes and resistance mechanisms. <i>Genomics</i> , 2020, 112, 5214-5226.	1.3	5
1862	Integrative analysis of long non-coding RNA and mRNA in broilers with valgus-varus deformity. <i>PLoS ONE</i> , 2020, 15, e0239450.	1.1	10
1863	Bone Marrow Mesenchymal Stem Cells Support Acute Myeloid Leukemia Bioenergetics and Enhance Antioxidant Defense and Escape from Chemotherapy. <i>Cell Metabolism</i> , 2020, 32, 829-843.e9.	7.2	122
1864	tagHi-C Reveals 3D Chromatin Architecture Dynamics during Mouse Hematopoiesis. <i>Cell Reports</i> , 2020, 32, 108206.	2.9	43
1865	Comparative genome-wide DNA methylation analysis reveals epigenomic differences in response to heat-humidity stress in <i>Bombyx mori</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 164, 3771-3779.	3.6	9
1866	Transcriptomic Study for Identification of Major Nitrogen Stress Responsive Genes in Australian Bread Wheat Cultivars. <i>Frontiers in Genetics</i> , 2020, 11, 583785.	1.1	29
1867	Systematic Identification and Functional Analysis of Circular RNAs During Rice Black-Streaked Dwarf Virus Infection in the <i>Laodelphax striatellus</i> (FallÅ©n) Midgut. <i>Frontiers in Microbiology</i> , 2020, 11, 588009.	1.5	8
1868	Transcriptome analyses to reveal the dynamic change mechanism of pigeon magnum during one eggâ€œlaying cycle. <i>Molecular Reproduction and Development</i> , 2020, 87, 1141-1151.	1.0	6
1869	Transcriptome and metabolite profiling reveals the effects of <i>Funneliformis mosseae</i> on the roots of continuously cropped soybeans. <i>BMC Plant Biology</i> , 2020, 20, 479.	1.6	11
1870	Identification of Differentially Methylated Regions Associated with a Knockout of SUV39H1 in Prostate Cancer Cells. <i>Genes</i> , 2020, 11, 1188.	1.0	2
1871	Identification of Candidate Genes Involved in Fruit Ripening and Crispness Retention Through Transcriptome Analyses of a â€œHoneycrispâ€™ Population. <i>Plants</i> , 2020, 9, 1335.	1.6	11
1872	NOD-like receptors mediate inflammatory lung injury during plateau hypoxia exposure. <i>Journal of Physiological Anthropology</i> , 2020, 39, 32.	1.0	10
1873	Transcriptional profiling reveals molecular basis and the role of arginine in response to low-pH stress in <i>Pichia kudriavzevii</i> . <i>Journal of Bioscience and Bioengineering</i> , 2020, 130, 588-595.	1.1	6
1874	Transcriptomic profile analysis of the halophyte <i>Suaeda rigida</i> response and tolerance under NaCl stress. <i>Scientific Reports</i> , 2020, 10, 15148.	1.6	10
1875	JMJD3 acts in tandem with KLF4 to facilitate reprogramming to pluripotency. <i>Nature Communications</i> , 2020, 11, 5061.	5.8	24
1876	Transcriptome Analysis of <i>Psacothaea hilaris</i> : De Novo Assembly and Antimicrobial Peptide Prediction. <i>Insects</i> , 2020, 11, 676.	1.0	8
1877	Comprehensive analysis of lncRNA-mRNA regulatory network in BmNPV infected cells treated with Hsp90 inhibitor. <i>Molecular Immunology</i> , 2020, 127, 230-237.	1.0	8

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1879	GHRH-SST-GH-IGF axis regulates crosstalk between growth and immunity in rainbow trout (<i>Oncorhynchus mykiss</i>) infected with <i>Vibrio anguillarum</i> . <i>Fish and Shellfish Immunology</i> , 2020, 106, 887-897.	1.6	9
1880	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
1881	4EHP and GIGYF1/2 Mediate Translation-Coupled Messenger RNA Decay. <i>Cell Reports</i> , 2020, 33, 108262.	2.9	41
1882	Imbalanced cellular metabolism compromises cartilage homeostasis and joint function in a mouse model of mucopolidosis type III gamma. <i>DMM Disease Models and Mechanisms</i> , 2020, 13, .	1.2	4
1883	Transcriptional and physiological analyses of reduced density in apple provide insight into the regulation involved in photosynthesis. <i>PLoS ONE</i> , 2020, 15, e0239737.	1.1	4
1884	Integrative analysis of wood biomass and developing xylem transcriptome provide insights into mechanisms of lignin biosynthesis in wood formation of <i>Pinus massoniana</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 163, 1926-1937.	3.6	15
1885	Rare fungus, <i>Mortierella capitata</i> , promotes crop growth by stimulating primary metabolisms related genes and reshaping rhizosphere bacterial community. <i>Soil Biology and Biochemistry</i> , 2020, 151, 108017.	4.2	55
1886	Hair follicle regional specificity in different parts of bay Mongolian horse by histology and transcriptional profiling. <i>BMC Genomics</i> , 2020, 21, 651.	1.2	1
1887	Effects of Peptide C12-OOWW-NH2 on Transcriptome and Cell Wall of the Postharvest Fungal Pathogen <i>Penicillium digitatum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 574882.	1.5	6
1888	Transcriptome Profiling and Cytological Assessments for Identifying Regulatory Pathways Associated With Diorcinol N-Induced Autophagy in A3 Cells. <i>Frontiers in Pharmacology</i> , 2020, 11, 570450.	1.6	7
1889	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
1890	Comparative transcriptome analyses provide novel insights into etiolated shoot development of walnut (<i>Juglans regia</i> L.). <i>Planta</i> , 2020, 252, 74.	1.6	3
1891	Structural characteristics of a mannoglucan isolated from Chinese yam and its treatment effects against gut microbiota dysbiosis and DSS-induced colitis in mice. <i>Carbohydrate Polymers</i> , 2020, 250, 116958.	5.1	74
1892	The cleft palate candidate gene BAG6 supports FoxO1 acetylation to promote FasL-mediated apoptosis during palate fusion. <i>Experimental Cell Research</i> , 2020, 396, 112310.	1.2	8
1893	Giant Island Mice Exhibit Widespread Gene Expression Changes in Key Metabolic Organs. <i>Genome Biology and Evolution</i> , 2020, 12, 1277-1301.	1.1	1
1894	Global transcriptomic and proteomics analysis of <i>Lactobacillus plantarum</i> Y44 response to 2,2-azobis(2-methylpropionamide) dihydrochloride (AAPH) stress. <i>Journal of Proteomics</i> , 2020, 226, 103903.	1.2	8
1895	Sexual dimorphism and sex-biased gene expression in an egg parasitoid species, <i>Anastatus disparis</i> . <i>BMC Genomics</i> , 2020, 21, 492.	1.2	4

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1897	Analysis of Transcriptome and miRNAome in the Muscle of Bamei Pigs at Different Developmental Stages. <i>Animals</i> , 2020, 10, 1198.	1.0	11
1898	Transcriptomic exploration of genes related to the formation of archeospores in <i>Pyropia yezoensis</i> (Rhodophyta). <i>Journal of Applied Phycology</i> , 2020, 32, 3295-3304.	1.5	7
1899	Effect of diflubenzuron on the chitin biosynthesis pathway in <i>Conopomorpha sinensis</i> eggs. <i>Insect Science</i> , 2021, 28, 1061-1075.	1.5	8
1900	Shared up-regulation and contrasting down-regulation of gene expression distinguish desiccation-tolerant from intolerant green algae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17438-17445.	3.3	22
1901	Transcriptome analysis indicates dominant effects on ribosome and mitochondrial function of a premature termination codon mutation in the zebrafish gene <i>psen2</i> . <i>PLoS ONE</i> , 2020, 15, e0232559.	1.1	11
1902	Transcriptional Profiling of Normal, Stenotic, and Regurgitant Human Aortic Valves. <i>Genes</i> , 2020, 11, 789.	1.0	14
1903	Transcriptome analysis of grape leaves reveals insights into response to heat acclimation. <i>Scientia Horticulturae</i> , 2020, 272, 109554.	1.7	17
1904	The transcriptome analysis of the whole-body of the gastropod mollusk <i>Limax flavus</i> and screening of putative antimicrobial peptide and protein genes. <i>Genomics</i> , 2020, 112, 3991-3999.	1.3	5
1905	A synonymous <i>UPF3B</i> variant causing a speech disorder implicates NMD as a regulator of neurodevelopmental disorder gene networks. <i>Human Molecular Genetics</i> , 2020, 29, 2568-2578.	1.4	9
1906	Characterization of $\hat{1}^3$ -Radiation-Induced DNA Polymorphisms in the M1 Population of the Japonica Rice Variety Gaogengnuo by Whole-Genome Resequencing. <i>Russian Journal of Genetics</i> , 2020, 56, 693-705.	0.2	4
1907	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
1908	RNA-sequencing based gene expression landscape of guava cv. Allahabad Safeda and comparative analysis to colored cultivars. <i>BMC Genomics</i> , 2020, 21, 484.	1.2	18
1909	Transcriptome Profiling of Abscisic Acid-Related Pathways in SNAC4/9-Silenced Tomato Fruits. <i>Transactions of Tianjin University</i> , 2020, 27, 473.	3.3	3
1910	Long non-coding RNA366.2 controls endometrial epithelial cell proliferation and migration by upregulating WNT6 as a ceRNA of miR-1576 in sheep uterus. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194606.	0.9	11
1911	Comparative transcriptome analysis reveals metabolism transformation in <i>Coilia nasus</i> larvae during the mouth-open period. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 36, 100712.	0.4	6
1912	Transcriptomic and proteomic analyses of ovarian follicles reveal the role of VLDLR in chicken follicle selection. <i>BMC Genomics</i> , 2020, 21, 486.	1.2	29
1913	Genome-wide identification and characterization of long non-coding RNAs involved in grape berry ripening. <i>Journal of Berry Research</i> , 2020, 10, 475-496.	0.7	2

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1914	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
1915	Reciprocal H3.3 gene editing identifies K27M and G34R mechanisms in pediatric glioma including NOTCH signaling. <i>Communications Biology</i> , 2020, 3, 363.	2.0	32
1916	Interleukin-1 promotes autoimmune neuroinflammation by suppressing endothelial heme oxygenase-1 at the blood-brain barrier. <i>Acta Neuropathologica</i> , 2020, 140, 549-567.	3.9	47
1917	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
1918	Targeted Disruption of Mouse Dip2B Leads to Abnormal Lung Development and Prenatal Lethality. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8223.	1.8	11
1919	Multi-omics analysis reveals that natural hibernation is crucial for oocyte maturation in the female Chinese alligator. <i>BMC Genomics</i> , 2020, 21, 774.	1.2	5
1920	Analysis and Screening of Reproductive Long Non-coding RNAs Through Genome-Wide Analyses of Goat Endometrium During the Pre-attachment Phase. <i>Frontiers in Genetics</i> , 2020, 11, 568017.	1.1	13
1921	Comparative Transcript Profiling Suggests Distinct Flowering Response of Early- and Late-Flowering Phenotypes in Forage Grass <i>Dactylis glomerata</i> L. <i>Journal of Plant Growth Regulation</i> , 2020, 40, 2124.	2.8	2
1922	Transcriptomic investigation reveals toxic damage due to tilmicosin and potential resistance against tilmicosin in primary chicken myocardial cells. <i>Poultry Science</i> , 2020, 99, 6355-6370.	1.5	4
1923	Identification of candidate genes conferring tolerance to aluminum stress in <i>Pinus massoniana</i> inoculated with ectomycorrhizal fungus. <i>BMC Plant Biology</i> , 2020, 20, 521.	1.6	20
1924	Functional Implication of Exosomal miR-217 and miR-23b-3p in the Progression of Prostate Cancer. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 11595-11606.	1.0	36
1925	Temperature Differentially Affects Gene Expression in Antarctic Thraustochytrid <i>Oblongichytrium</i> sp. RT2316-13. <i>Marine Drugs</i> , 2020, 18, 563.	2.2	9
1926	Identification and Characterization of circRNAs in the Developing Stem Cambium of Poplar Seedlings. <i>Molecular Biology</i> , 2020, 54, 708-718.	0.4	2
1927	MADA: a web service for analysing DNA methylation array data. <i>BMC Bioinformatics</i> , 2020, 21, 403.	1.2	2
1928	Tissue-specific Transcriptome analysis reveals lignocellulose synthesis regulation in elephant grass (<i>Pennisetum purpureum</i> Schum). <i>BMC Plant Biology</i> , 2020, 20, 528.	1.6	5
1929	Contributions of Adaptive Plant Architecture to Transgressive Salinity Tolerance in Recombinant Inbred Lines of Rice: Molecular Mechanisms Based on Transcriptional Networks. <i>Frontiers in Genetics</i> , 2020, 11, 594569.	1.1	7
1930	Chemosensory-Related Gene Family Members of the Horn Fly, <i>Haematobia irritans irritans</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	5
1931	Comparative Transcriptome Analyses of <i>Longissimus thoracis</i> Between Pig Breeds Differing in Muscle Characteristics. <i>Frontiers in Genetics</i> , 2020, 11, 526309.	1.1	15

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1932	Transcriptome divergence between developmental senescence and premature senescence in <i>Nicotiana tabacum</i> L.. <i>Scientific Reports</i> , 2020, 10, 20556.	1.6	6
1933	Systemic paralogy and function of retinal determination network homologs in arachnids. <i>BMC Genomics</i> , 2020, 21, 811.	1.2	20
1934	RNA-Seq-Based Transcriptomic Analysis of <i>Saccharopolyspora spinosa</i> Revealed the Critical Function of PEP Phosphonmutase in the Replenishment Pathway. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 14660-14669.	2.4	5
1935	Transcriptome analysis of genes related to cadmium absorption and transportation in pepper. <i>Israel Journal of Ecology and Evolution</i> , 2020, 67, 29-38.	0.2	0
1936	Deciphering Novel Antimicrobial Peptides from the Transcriptome of <i>Papilio xuthus</i> . <i>Insects</i> , 2020, 11, 776.	1.0	6
1937	The Tetracentron genome provides insight into the early evolution of eudicots and the formation of vessel elements. <i>Genome Biology</i> , 2020, 21, 291.	3.8	23
1938	Comparative transcriptome analysis in three sorghum (<i>Sorghum bicolor</i>) cultivars reveal genomic basis of differential seed quality. <i>Plant Biosystems</i> , 2022, 156, 232-241.	0.8	3
1939	High-throughput profiling of diapause regulated genes from <i>Trichogramma dendrolimi</i> (Hymenoptera: Tj ETQq1 1 0.784314, 1.2, 25) <i>Over</i>	1.2	25
1940	Transcriptomic profiles of non-embryogenic and embryogenic callus cells in a highly regenerative upland cotton line (<i>Gossypium hirsutum</i> L.). <i>BMC Developmental Biology</i> , 2020, 20, 25.	2.1	19
1941	Endogenous Auxin Content Contributes to Larger Size of Apple Fruit. <i>Frontiers in Plant Science</i> , 2020, 11, 592540.	1.7	23
1942	Transcriptome analysis reveals mechanism of early ripening in Kyoho grape with hydrogen peroxide treatment. <i>BMC Genomics</i> , 2020, 21, 784.	1.2	29
1943	Osteoporosis Is Characterized by Altered Expression of Exosomal Long Non-coding RNAs. <i>Frontiers in Genetics</i> , 2020, 11, 566959.	1.1	11
1944	Characterization of microRNA-like RNAs associated with sclerotial development in <i>Sclerotinia sclerotiorum</i> . <i>Fungal Genetics and Biology</i> , 2020, 144, 103471.	0.9	16
1945	Synergistic Effect of <i>Beauveria bassiana</i> and <i>Trichoderma asperellum</i> to Induce Maize (<i>Zea mays</i> L.) Defense against the Asian Corn Borer, <i>Ostrinia furnacalis</i> (Lepidoptera, Crambidae) and Larval Immune Response. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8215.	1.8	27
1946	Genome-Wide Analysis Reveals Changes in Long Noncoding RNAs in the Differentiation of Canine BMSCs into Insulin-Producing Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5549.	1.8	5
1947	Uncovering candidate genes responsive to salt stress in <i>Salix matsudana</i> (Koidz) by transcriptomic analysis. <i>PLoS ONE</i> , 2020, 15, e0236129.	1.1	16
1948	Genome-Wide Differential DNA Methylation in Reproductive, Morphological, and Visual System Differences Between Queen Bee and Worker Bee (<i>Apis mellifera</i>). <i>Frontiers in Genetics</i> , 2020, 11, 770.	1.1	14
1949	Integrated physiological, transcriptomic and proteomic analyses revealed molecular mechanism for salt resistance in <i>Solidago canadensis</i> L.. <i>Environmental and Experimental Botany</i> , 2020, 179, 104211.	2.0	19

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1951	Parallel reaction monitoring revealed tolerance to drought proteins in weedy rice (<i>Oryza sativa</i> L.). <i>Transcriptomics</i> , 2020, 8, 100000.	1.6	4
1952	Effects of Trace Irrigation at Different Depths on Transcriptome Expression Pattern in Cotton (<i>G.</i>). <i>Transcriptomics</i> , 2020, 8, 100000.	0.9	3
1953	The Wheat GENIE3 Network Provides Biologically-Relevant Information in Polyploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3675-3686.	0.8	21
1954	Transcriptome analysis of pituitary gland revealed candidate genes and gene networks regulating the growth and development in goose. <i>Animal Biotechnology</i> , 2022, 33, 429-439.	0.7	7
1955	On-Site Treatment of Shale Gas Flowback and Produced Water in Sichuan Basin by Fertilizer Drawn Forward Osmosis for Irrigation. <i>Environmental Science & Technology</i> , 2020, 54, 10926-10935.	4.6	25
1956	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
1957	Transcription profiles reveal sugar and hormone signaling pathways mediating tree branch architecture in apple (<i>Malus domestica</i> Borkh.) grafted on different rootstocks. <i>PLoS ONE</i> , 2020, 15, e0236530.	1.1	8
1958	Transcriptome analysis of <i>Paris polyphylla</i> var. <i>yunnanensis</i> illuminates the biosynthesis and accumulation of steroidal saponins in rhizomes and leaves. <i>Phytochemistry</i> , 2020, 178, 112460.	1.4	16
1959	hsa-miR-106b-5p participates in the development of chronic thromboembolic pulmonary hypertension via targeting matrix metalloproteinase 2. <i>Pulmonary Circulation</i> , 2020, 10, 1-10.	0.8	8
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1961	Transcriptome Profiling Provides Molecular Insights into Auxin-Induced Adventitious Root Formation in Sugarcane (<i>Saccharum</i> spp. Interspecific Hybrids) Microshoots. <i>Plants</i> , 2020, 9, 931.	1.6	14
1962	Reduced Function of the Glutathione S-Transferase S1 Suppresses Behavioral Hyperexcitability in <i>Drosophila</i> Expressing Mutant Voltage-Gated Sodium Channels. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1327-1340.	0.8	1
1963	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
1964	Collagen Density Modulates the Immunosuppressive Functions of Macrophages. <i>Journal of Immunology</i> , 2020, 205, 1461-1472.	0.4	64
1965	Population variation in miRNAs and isomiRs and their impact on human immunity to infection. <i>Genome Biology</i> , 2020, 21, 187.	3.8	14
1966	Transcriptional mechanism of differential sugar accumulation in pulp of two contrasting mango (<i>Mangifera indica</i> L.) cultivars. <i>Genomics</i> , 2020, 112, 4505-4515.	1.3	18
1967	Transcriptomic and Metabolic Responses to a Live-Attenuated <i>Francisella tularensis</i> Vaccine. <i>Vaccines</i> , 2020, 8, 412.	2.1	17

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1969	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
1970	Full-length transcriptome sequences of ridgetail white prawn <i>Exopalaemon carinicauda</i> provide insight into gene expression dynamics during thermal stress. <i>Science of the Total Environment</i> , 2020, 747, 141238.	3.9	13
1971	Transcription factor CncC potentially regulates the expression of multiple detoxification genes that mediate indoxacarb resistance in <i>Spodoptera litura</i> . <i>Insect Science</i> , 2021, 28, 1426-1438.	1.5	28
1972	Transcriptome alterations of field-evolved resistance in <i>Pectinophora gossypiella</i> against Bt Bollgard II cotton in India. <i>Journal of Applied Entomology</i> , 2020, 144, 929-940.	0.8	2
1973	Comparative transcriptome analysis reveals ecological adaptation of cold tolerance in northward invasion of <i>Alternanthera philoxeroides</i> . <i>BMC Genomics</i> , 2020, 21, 532.	1.2	10
1974	Regulation of <i>Aegilops tauschii</i> Coss Tiller Bud Growth by Plant Density: Transcriptomic, Physiological and Phytohormonal Responses. <i>Frontiers in Plant Science</i> , 2020, 11, 1166.	1.7	8
1975	Host Transcriptional Response to Persistent Infection with a Live-Attenuated Porcine Reproductive and Respiratory Syndrome Virus Strain. <i>Viruses</i> , 2020, 12, 817.	1.5	6
1976	Exogenous abscisic acid induces the lipid and flavonoid metabolism of tea plants under drought stress. <i>Scientific Reports</i> , 2020, 10, 12275.	1.6	85
1977	Antimicrobial Peptide Cec4 Eradicates the Bacteria of Clinical Carbapenem-Resistant <i>Acinetobacter baumannii</i> Biofilm. <i>Frontiers in Microbiology</i> , 2020, 11, 1532.	1.5	32
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1979	Integration of QTL, Transcriptome and Polymorphism Studies Reveals Candidate Genes for Water Stress Response in Tomato. <i>Genes</i> , 2020, 11, 900.	1.0	18
1980	The neonicotinoid thiacloprid causes transcriptional alteration of genes associated with mitochondria at environmental concentrations in honey bees. <i>Environmental Pollution</i> , 2020, 266, 115297.	3.7	24
1981	De novo transcriptome assembly and functional annotation for Y-organs of the blue crab (<i>Callinectes</i>) Tj ETQq1 1 0.784314 rgBT /Overl... <i>Endocrinology</i> , 2020, 298, 113567.	0.8	7
1982	Expression profiling of microRNAs in the <i>Mycoplasma bovis</i> infected mammary gland tissue in Holstein Friesian cattle. <i>Microbial Pathogenesis</i> , 2020, 147, 104426.	1.3	2
1983	A transcriptomic analysis reveals the adaptability of the growth and physiology of immature tassel to long-term soil water deficit in <i>Zea mays</i> L. <i>Plant Physiology and Biochemistry</i> , 2020, 155, 756-768.	2.8	4
1984	Within-individual phenotypic plasticity in flowers fosters pollination niche shift. <i>Nature Communications</i> , 2020, 11, 4019.	5.8	29
1985	Distinct fibroblast subsets regulate lacteal integrity through YAP/TAZ-induced VEGF-C in intestinal villi. <i>Nature Communications</i> , 2020, 11, 4102.	5.8	36

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1986	Transcriptome and Flavonoids Metabolomic Analysis Identifies Regulatory Networks and Hub Genes in Black and White Fruits of <i>Lycium ruthenicum</i> Murray. <i>Frontiers in Plant Science</i> , 2020, 11, 1256.	1.7	18
1987	MAL62 overexpression enhances uridine diphosphoglucose-dependent trehalose synthesis and glycerol metabolism for cryoprotection of baker's yeast in lean dough. <i>Microbial Cell Factories</i> , 2020, 19, 196.	1.9	3
1988	Characterization of sediment toxicity in Shanghai Harbor using toxicity tests and digital gene expression analysis based on clams <i>Ruditapes philippinarum</i> . <i>Ecotoxicology and Environmental Safety</i> , 2020, 204, 111065.	2.9	2
1989	Early emergence of T central memory precursors programs clonal dominance during chronic viral infection. <i>Nature Immunology</i> , 2020, 21, 1563-1573.	7.0	38
1990	Metabolomic and transcriptomic analyses reveal the regulation of pigmentation in the purple variety of <i>Dendrobium officinale</i> . <i>Scientific Reports</i> , 2020, 10, 17700.	1.6	25
1991	Transcriptome sequencing and de novo assembly in red raspberry fruit development to elucidates the secondary metabolite pathways. <i>Journal of Berry Research</i> , 2020, 10, 497-511.	0.7	1
1992	Transcriptome analysis reveals temperature-dependent early immune response in flounder (<i>Paralichthys olivaceus</i>) after HIRRV infection. <i>Fish and Shellfish Immunology</i> , 2020, 107, 367-378.	1.6	17
1993	Transcriptome analysis reveals molecular mechanisms responsive to acute cold stress in the tropical stenothermal fish tiger barb (<i>Puntius tetrazona</i>). <i>BMC Genomics</i> , 2020, 21, 737.	1.2	39
1994	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
1995	Dual Oxidase Mutant Retards Mauthner-Cell Axon Regeneration at an Early Stage via Modulating Mitochondrial Dynamics in Zebrafish. <i>Neuroscience Bulletin</i> , 2020, 36, 1500-1512.	1.5	10
1996	ETV2 (Ets Variant Transcription Factor 2)- <i>Rhoj</i> Cascade Regulates Endothelial Progenitor Cell Migration During Embryogenesis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 40, 2875-2890.	1.1	13
1997	Transcriptomic and functional analyses reveal an antiviral role of autophagy during pepper mild mottle virus infection. <i>BMC Plant Biology</i> , 2020, 20, 495.	1.6	17
1998	Paper New Allele of HL6 Regulates Trichome Elongation in Rice. <i>Rice Science</i> , 2020, 27, 480-492.	1.7	5
1999	Graph-based exploitation of gene ontology using GOxploreR for scrutinizing biological significance. <i>Scientific Reports</i> , 2020, 10, 16672.	1.6	19
2000	Rewiring of gene expression in circulating white blood cells is associated with pregnancy outcome in heifers (<i>Bos taurus</i>). <i>Scientific Reports</i> , 2020, 10, 16786.	1.6	14
2001	Assessing alveolar rhabdomyosarcoma cell lines as tumor models by comparison of mRNA expression profiles. <i>Gene</i> , 2020, 760, 145025.	1.0	6
2002	Differential Gene Expression Between Polymorphic Zooids of the Marine Bryozoan <i>Bugulina stolonifera</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3843-3857.	0.8	8
2003	OsCRS2 encoding a peptidyl-tRNA hydrolase protein is essential for chloroplast development in rice. <i>Plant Growth Regulation</i> , 2020, 92, 535-545.	1.8	3

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2005	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
2006	The IAA- and ABA-responsive transcription factor CgMYB58 upregulates lignin biosynthesis and triggers juice sac granulation in pummelo. <i>Horticulture Research</i> , 2020, 7, 139.	2.9	43
2007	Expression profile analysis of circular RNAs in BmN cells (<i>Bombyx mori</i>) upon BmNPV infection. <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 105, e21735.	0.6	4
2008	Growth retardation-responsive analysis of mRNAs and long noncoding RNAs in the liver tissue of Leiqiong cattle. <i>Scientific Reports</i> , 2020, 10, 14254.	1.6	6
2009	Evolutionary Variation in MADS Box Dimerization Affects Floral Development and Protein Abundance in Maize. <i>Plant Cell</i> , 2020, 32, 3408-3424.	3.1	27
2010	Comparative transcriptome analysis uncovers different heat stress responses in heat-resistant and heat-sensitive jujube cultivars. <i>PLoS ONE</i> , 2020, 15, e0235763.	1.1	22
2011	Development of a novel prognostic score combining clinicopathologic variables, gene expression, and mutation profiles for lung adenocarcinoma. <i>World Journal of Surgical Oncology</i> , 2020, 18, 249.	0.8	4
2012	SmMYC2b Enhances Tanshinone Accumulation in <i>Salvia miltiorrhiza</i> by Activating Pathway Genes and Promoting Lateral Root Development. <i>Frontiers in Plant Science</i> , 2020, 11, 559438.	1.7	6
2013	Global Profiling of Dynamic Alternative Splicing Modulation in <i>Arabidopsis</i> Root upon <i>Ralstonia solanacearum</i> Infection. <i>Genes</i> , 2020, 11, 1078.	1.0	8
2014	Comparative Transcriptome and Proteome Analysis of Salt-Tolerant and Salt-Sensitive Sweet Potato and Overexpression of IbNAC7 Confers Salt Tolerance in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 572540.	1.7	42
2015	Whole-transcriptome sequencing (RNA-seq) study of the ZFL zebrafish liver cell line after acute exposure to Cd ²⁺ ions. <i>Aquatic Toxicology</i> , 2020, 228, 105628.	1.9	11
2016	Transcriptomic analysis of a <i>Clostridium thermocellum</i> strain engineered to utilize xylose: responses to xylose versus cellobiose feeding. <i>Scientific Reports</i> , 2020, 10, 14517.	1.6	6
2017	RNA-Seq profiling of microdissected glomeruli identifies potential biomarkers for human IgA nephropathy. <i>American Journal of Physiology - Renal Physiology</i> , 2020, 319, F809-F821.	1.3	15
2018	Identification of microRNAs Targeting the Transporter Associated with Antigen Processing TAP1 in Melanoma. <i>Journal of Clinical Medicine</i> , 2020, 9, 2690.	1.0	18
2019	Toxicological and molecular profiling of insecticide resistance in a Brazilian strain of fall armyworm resistant to Bt Cry1 proteins. <i>Pest Management Science</i> , 2021, 77, 3713-3726.	1.7	29
2020	Sacha inchi (<i>Plukenetia volubilis</i> L.) shell extract alleviates hypertension in association with the regulation of gut microbiota. <i>Food and Function</i> , 2020, 11, 8051-8067.	2.1	9
2021	Transcriptome analysis and comparison reveal divergence between the Mediterranean and the greenhouse whiteflies. <i>PLoS ONE</i> , 2020, 15, e0237744.	1.1	2

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2023	RNA-Seq analysis of differentially expressed genes of <i>Staphylococcus epidermidis</i> isolated from postoperative endophthalmitis and the healthy conjunctiva. <i>Scientific Reports</i> , 2020, 10, 14234.	1.6	4
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2027	Mating and blood-feeding induce transcriptome changes in the spermathecae of the yellow fever mosquito <i>Aedes aegypti</i> . <i>Scientific Reports</i> , 2020, 10, 14899.	1.6	21
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2030	Transcriptomic Analysis of <i>Streptococcus suis</i> in Response to Ferrous Iron and Cobalt Toxicity. <i>Genes</i> , 2020, 11, 1035.	1.0	2
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2038	Sharing a β -Glucan Meal: Transcriptomic Eavesdropping on a <i>Bacteroides ovatus</i> - <i>Subdoligranulum variabile</i> - <i>Hungatella hathewayi</i> Consortium. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	10
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2041	Wheat root transcriptional responses against <i>Gaeumannomyces graminis</i> var. <i>tritici</i> . <i>Phytopathology Research</i> , 2020, 2, .	0.9	6
2042	Heterologous expression of a glycosyl hydrolase and cellular reprogramming enable <i>Zymomonas mobilis</i> growth on cellobiose. <i>PLoS ONE</i> , 2020, 15, e0226235.	1.1	4
2043	Dual Host-Intracellular Parasite Transcriptome of Enucleated Cells Hosting <i>Leishmania amazonensis</i> : Control of Half-Life of Host Cell Transcripts by the Parasite. <i>Infection and Immunity</i> , 2020, 88, .	1.0	5
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2046	Comparative transcriptomics indicates endogenous differences in detoxification capacity after formic acid treatment between honey bees and varroa mites. <i>Scientific Reports</i> , 2020, 10, 21943.	1.6	9
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2049	Characterization of the TyrR Regulon in the Rhizobacterium <i>Enterobacter ludwigii</i> UW5 Reveals Overlap with the CpxR Envelope Stress Response. <i>Journal of Bacteriology</i> , 2020, 203, .	1.0	2
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2052	A Broad Response to Intracellular Long-Chain Polyphosphate in Human Cells. <i>Cell Reports</i> , 2020, 33, 108318.	2.9	33
2053	Physiological and Transcriptomic Changes During Autumn Coloration and Senescence in <i>Ginkgo biloba</i> Leaves. <i>Horticultural Plant Journal</i> , 2020, 6, 396-408.	2.3	14
2054	Long non-coding RNA expression profiles in peripheral blood mononuclear cells of patients with coronary artery disease. <i>Journal of Thoracic Disease</i> , 2020, 12, 6813-6825.	0.6	4
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2056	Transcriptomic and metabolomic profiling reveals the effect of LED light quality on morphological traits, and phenylpropanoid-derived compounds accumulation in <i>Sarcandra glabra</i> seedlings. <i>BMC Plant Biology</i> , 2020, 20, 476.	1.6	16
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2063	A Comparison of Transcriptional Diversity of Swine Macrophages Infected With TgHB1 Strain of <i>Toxoplasma gondii</i> Isolated in China. Frontiers in Cellular and Infection Microbiology, 2020, 10, 526876.	1.8	2
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2066	Challenges in detecting and quantifying intron retention from next generation sequencing data. Computational and Structural Biotechnology Journal, 2020, 18, 501-508.	1.9	28
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2069	Single-cell analysis of childhood leukemia reveals a link between developmental states and ribosomal protein expression as a source of intra-individual heterogeneity. Scientific Reports, 2020, 10, 8079.	1.6	37
2070	Retrograde Induction of phyB Orchestrates Ethylene-Auxin Hierarchy to Regulate Growth. Plant Physiology, 2020, 183, 1268-1280.	2.3	27
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2077	Transcriptome analysis reveals rapid defence responses in wheat induced by phytotoxic aphid <i>Schizaphis graminum</i> feeding. <i>BMC Genomics</i> , 2020, 21, 339.	1.2	23
2078	Performance and Transcriptional Response of the Green Peach Aphid <i>Myzus persicae</i> to the Restriction of Dietary Amino Acids. <i>Frontiers in Physiology</i> , 2020, 11, 487.	1.3	2
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2082	<p>Gene Expression Profiling of the Liver and Lung in Mice After Exposure to ZnO Quantum Dots</p>. <i>International Journal of Nanomedicine</i> , 2020, Volume 15, 2947-2955.	3.3	6
2083	Heat-evolved microalgal symbionts increase coral bleaching tolerance. <i>Science Advances</i> , 2020, 6, eaba2498.	4.7	129
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2085	Zebrafish brain RNA sequencing reveals that cell adhesion molecules are critical in brain aging. <i>Neurobiology of Aging</i> , 2020, 94, 164-175.	1.5	7
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2095	Genome-Wide Transcriptome and Metabolome Analyses Provide Novel Insights and Suggest a Sex-Specific Response to Heat Stress in Pigs. <i>Genes</i> , 2020, 11, 540.	1.0	11
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2100	Identification and functional prediction of soybean CircRNAs involved in low-temperature responses. <i>Journal of Plant Physiology</i> , 2020, 250, 153188.	1.6	21
2101	Compatibility of X-ray computed tomography with plant gene expression, rhizosphere bacterial communities and enzyme activities. <i>Journal of Experimental Botany</i> , 2020, 71, 5603-5614.	2.4	17
2102	Transcriptional analyses reveal the molecular mechanism governing shade tolerance in the invasive plant <i>Solidago canadensis</i> . <i>Ecology and Evolution</i> , 2020, 10, 4391-4406.	0.8	11
2103	Transcriptome analysis reveals improved root hair growth in trifoliolate orange seedlings by arbuscular mycorrhizal fungi. <i>Plant Growth Regulation</i> , 2020, 92, 195-203.	1.8	11
2104	Long non-coding RNAs in the alkaline stress response in sugar beet (<i>Beta vulgaris</i> L.). <i>BMC Plant Biology</i> , 2020, 20, 227.	1.6	13
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2108	A rice chloroplast-localized ABC transporter ARG1 modulates cobalt and nickel homeostasis and contributes to photosynthetic capacity. <i>New Phytologist</i> , 2020, 228, 163-178.	3.5	23
2109	Transcriptome profiling of porcine testis tissue reveals genes related to sperm hyperactive motility. <i>BMC Veterinary Research</i> , 2020, 16, 161.	0.7	5
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2117	An ontogenetic switch drives the positive and negative selection of B cells. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3718-3727.	3.3	22
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2119	Transcriptome Analysis of High-NUE (T29) and Low-NUE (T13) Genotypes Identified Different Responsive Patterns Involved in Nitrogen Stress in Ramie (<i>Boehmeria nivea</i> (L.) Gaudich). Plants, 2020, 9, 767.	1.6	3
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2121	Expression profile and bioinformatics analysis of circular RNAs in acute ischemic stroke in a South Chinese Han population. Scientific Reports, 2020, 10, 10138.	1.6	30
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2140	Intraspecific and interspecific investigations of skeletal DNA methylation and femur morphology in primates. <i>American Journal of Physical Anthropology</i> , 2020, 173, 34-49.	2.1	14
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2149	Trend analysis of the role of circular RNA in goat skeletal muscle development. <i>BMC Genomics</i> , 2020, 21, 220.	1.2	22
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2151	Transcriptome-based identification of small RNA in plants: The need for robust prediction algorithms. , 2020, , 65-97.		0
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2153	Gender differences in diet-induced steatotic disease in <i>Cyp2b</i> -null mice. <i>PLoS ONE</i> , 2020, 15, e0229896.	1.1	19
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2156	Identification of differentially expressed genes associated with egg production in black-boned chicken. <i>British Poultry Science</i> , 2020, 61, 350-356.	0.8	4
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2162	Combined transcriptomic and metabolomic analyses uncover rearranged gene expression and metabolite metabolism in tobacco during cold acclimation. <i>Scientific Reports</i> , 2020, 10, 5242.	1.6	29
2163	Transcriptome analysis uncovers the gene expression profile of salt-stressed potato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 662	1.6	32
2164	Genomeâ€™wide integrated analysis demonstrates widespread functions of lncRNAs in mammary gland development and lactation in dairy goats. <i>BMC Genomics</i> , 2020, 21, 254.	1.2	20
2165	Soybean aphids adapted to host-plant resistance by down regulating putative effectors and up regulating transposable elements. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 121, 103363.	1.2	10

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2167	Comparative time-course transcriptome analysis in contrasting <i>Carex rigescens</i> genotypes in response to high environmental salinity. <i>Ecotoxicology and Environmental Safety</i> , 2020, 194, 110435.	2.9	14
2168	Transcriptome profiling of lncRNA related to fat tissues of Qinchuan cattle. <i>Gene</i> , 2020, 742, 144587.	1.0	19
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2178	Screening of drought-resistance related genes and analysis of promising regulatory pathway in camel renal medulla. <i>Genomics</i> , 2020, 112, 2633-2639.	1.3	4
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2180	Uncloaking lncRNA-mediated gene expression as a potential regulator of CMS in cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	20
2181	Transcriptome analysis of genes related to gonad differentiation and development in Muscovy ducks. <i>BMC Genomics</i> , 2020, 21, 438.	1.2	15
2182	Comparative transcriptomic analysis of resistant and susceptible tea cultivars in response to <i>Empoasca onukii</i> (Matsuda) damage. <i>Planta</i> , 2020, 252, 10.	1.6	7
2183	RNA sequencing-based transcriptome analysis of kiwifruit infected by <i>Botrytis cinerea</i> . <i>Physiological and Molecular Plant Pathology</i> , 2020, 111, 101514.	1.3	18

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2200	<i>Candida auris</i> Phenotypic Heterogeneity Determines Pathogenicity <i>In Vitro</i> . <i>MSphere</i> , 2020, 5, .	1.3	46
2201	Transcription analysis of <i>Ganoderma lucidum</i> reveals candidate genes and pathways in response to excess exogenous indoleacetic acid (IAA). <i>Mycoscience</i> , 2020, 61, 226-234.	0.3	2

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2203	Integrative expression network analysis of microRNA and gene isoforms in sacred lotus. <i>BMC Genomics</i> , 2020, 21, 429.	1.2	8
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2207	Analysis of microRNA expression profiles dynamic in different life stages of <i>Haemaphysalis longicornis</i> ticks by deep sequencing of small RNA libraries. <i>Ticks and Tick-borne Diseases</i> , 2020, 11, 101427.	1.1	5
2208	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
2209	Integrated RNA-seq Analysis and Meta-QTLs Mapping Provide Insights into Cold Stress Response in Rice Seedling Roots. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4615.	1.8	25
2210	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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2218	Hydrotropism in the primary roots of maize. <i>New Phytologist</i> , 2020, 226, 1796-1808.	3.5	11
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2235	Integrative Transcriptomic and Metabolic Analyses Provide Insights into the Role of Trichomes in Tea Plant (<i>Camellia Sinensis</i>). <i>Biomolecules</i> , 2020, 10, 311.	1.8	16
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2254	Biotin proximity tagging favours unfolded proteins and enables the study of intrinsically disordered regions. <i>Communications Biology</i> , 2020, 3, 38.	2.0	26
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2270	Transcriptomic comparison of liver tissue between Anqing six-end-white pigs and Yorkshire pigs based on RNA sequencing. <i>Genome</i> , 2020, 63, 203-214.	0.9	23
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2502	SPTBN1 Prevents Primary Osteoporosis by Modulating Osteoblasts Proliferation and Differentiation and Blood Vessels Formation in Bone. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 653724.	1.8	8
2504	Comparative analyses of hypothalamus transcriptomes reveal fertility-, growth-, and immune-related genes and signal pathways in different ploidy cyprinid fish. <i>Genomics</i> , 2021, 113, 595-605.	1.3	13
2505	Comparative Transcriptome Analysis of Early- and Late-Bolting Traits in Chinese Cabbage (<i>Brassica</i>) Tj ETQq1 1 0.784314 rgBT ₁₁ /Overlock	1.1	11
2507	Transcriptome Analysis Unravels Key Factors Involved in Response to Potassium Deficiency and Feedback Regulation of K ⁺ Uptake in Cotton Roots. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3133.	1.8	15
2508	New insight into the rapid growth of the <i>Mikania micrantha</i> stem based on DIA proteomic and RNA-Seq analysis. <i>Journal of Proteomics</i> , 2021, 236, 104126.	1.2	9

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2510	MYB30 and ETHYLENE INSENSITIVE3 antagonistically modulate root hair growth in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2021, 106, 480-492.	2.8	18
2511	Association Mapping and Transcriptome Analysis Reveal the Genetic Architecture of Maize Kernel Size. <i>Frontiers in Plant Science</i> , 2021, 12, 632788.	1.7	3
2512	Impact of exogenous caffeine on regulatory networks of microRNAs in response to <i>Colletotrichum gloeosporioides</i> in tea plant. <i>Scientia Horticulturae</i> , 2021, 279, 109914.	1.7	11
2513	Transcriptome and metabolome analyses reveal the pivotal role of hydrogen sulfide in promoting submergence tolerance in <i>Arabidopsis</i> . <i>Environmental and Experimental Botany</i> , 2021, 183, 104365.	2.0	17
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2515	Acquisition of innate odor preference depends on spontaneous and experiential activities during critical period. <i>ELife</i> , 2021, 10, .	2.8	17
2516	Expression Level of Transcription Factor ART1 Is Responsible for Differential Aluminum Tolerance in <i>Indica Rice</i> . <i>Plants</i> , 2021, 10, 634.	1.6	6
2517	Comparative analysis of long noncoding RNAs in angiosperms and characterization of long noncoding RNAs in response to heat stress in Chinese cabbage. <i>Horticulture Research</i> , 2021, 8, 48.	2.9	38
2518	Molecular Characterization of <i>Donacia provosti</i> (Coleoptera: Chrysomelidae) Larval Transcriptome by De Novo Assembly to Discover Genes Associated with Underwater Environmental Adaptations. <i>Insects</i> , 2021, 12, 281.	1.0	1
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2523	Mitochondrial genotype alters the impact of rapamycin on the transcriptional response to nutrients in <i>Drosophila</i> . <i>BMC Genomics</i> , 2021, 22, 213.	1.2	9
2524	Identify of Fast-Growing Related Genes Especially in Height Growth by Combining QTL Analysis and Transcriptome in <i>Salix matsudana</i> (Koidz). <i>Frontiers in Genetics</i> , 2021, 12, 596749.	1.1	4
2525	Comparative Transcriptomic Analysis of <i>Riptortus pedestris</i> (Hemiptera: Alydidae) to Characterize Wing Formation across All Developmental Stages. <i>Insects</i> , 2021, 12, 226.	1.0	7
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2530	Comparative transcriptome analysis of the newly discovered insect vector of the pine wood nematode in China, revealing putative genes related to host plant adaptation. <i>BMC Genomics</i> , 2021, 22, 189.	1.2	14
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2532	Genome-wide analysis of changes in miRNA and target gene expression reveals key roles in heterosis for Chinese cabbage biomass. <i>Horticulture Research</i> , 2021, 8, 39.	2.9	28
2533	Transcriptome analyses of 7-day-old zebrafish larvae possessing a familial Alzheimer's disease-like mutation in <i>psen1</i> indicate effects on oxidative phosphorylation, ECM and MCM functions, and iron homeostasis. <i>BMC Genomics</i> , 2021, 22, 211.	1.2	8
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2536	Hormonal Regulation of Reproductive Diapause That Occurs in the Year-Round Mass Rearing of <i>Bombus terrestris</i> Queens. <i>Journal of Proteome Research</i> , 2021, 20, 2240-2250.	1.8	12
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2538	Transcriptome analysis reveals the effects of temperature on growth in tadpoles of spiny-bellied frog (<i>Quasipaa boulengeri</i>). <i>Aquaculture International</i> , 2021, 29, 925-939.	1.1	3
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2540	GmBTB/POZ promotes the ubiquitination and degradation of LHP1 to regulate the response of soybean to <i>Phytophthora sojae</i> . <i>Communications Biology</i> , 2021, 4, 372.	2.0	30
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2542	Full-Length Transcriptome Sequencing and Comparative Transcriptome Analysis to Evaluate Drought and Salt Stress in <i>Iris lactea</i> var. <i>chinensis</i> . <i>Genes</i> , 2021, 12, 434.	1.0	14
2543	IL-10 signaling reduces survival in mouse models of synucleinopathy. <i>Npj Parkinson's Disease</i> , 2021, 7, 30.	2.5	8
2544	Novel Transcriptome Study and Detection of Metabolic Variations in UV-B-Treated Date Palm (Phoenix) Tj ETQq1 1 0.784314.rgBT /Over	1.8	13
2547	Biosynthesis of the Sex Pheromone Component (E,Z)-7,9-Dodecadienyl Acetate in the European Grapevine Moth, <i>Lobesia botrana</i> , Involving Δ^{11} Desaturation and an Elusive Δ^7 Desaturase. <i>Journal of Chemical Ecology</i> , 2021, 47, 248-264.	0.9	8
2548	Transcriptional reprogramming caused by cold acclimation in <i>Meloidogyne incognita</i> eggs. <i>Genes and Genomics</i> , 2021, 43, 533-541.	0.5	2

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2561	Key metabolism pathways and regulatory mechanisms of high polysaccharide yielding in <i>Hericium erinaceus</i> . <i>BMC Genomics</i> , 2021, 22, 160.	1.2	9
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2564	Transcriptome analysis and candidate gene identification reveals insights into the molecular mechanisms of hypermelanosis in Chinese tongue sole (<i>Cynoglossus semilaevis</i>). <i>Aquaculture and Fisheries</i> , 2021, , .	1.2	4
2565	Comparative transcriptome analysis provides insight into the molecular mechanisms of anther dehiscence in eggplant (<i>Solanum melongena</i> L.). <i>Genomics</i> , 2021, 113, 497-506.	1.3	6
2566	Transcriptome and Comparative Chloroplast Genome Analysis of <i>Vincetoxicum versicolor</i> : Insights Into Molecular Evolution and Phylogenetic Implication. <i>Frontiers in Genetics</i> , 2021, 12, 602528.	1.1	10
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2569	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
2570	Comparative analysis of testis transcriptomes in laboratory cohorts of recently diverged allopatric <i>Drosophila nasuta nasuta</i> and <i>Drosophila nasuta albomicans</i> . <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 46-46.	0.4	0

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2572	Effects of the daily light/dark cycle on photosynthetic performance, oxidative stress and illumination-related genes in boring giant clam <i>Tridacna crocea</i> . <i>Marine Biology</i> , 2021, 168, 1.	0.7	7
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2576	Integrated analysis of miRNAome and transcriptome reveals miRNA-mRNA network regulation in <i>Vibrio alginolyticus</i> infected thick shell mussel <i>Mytilus coruscus</i> . <i>Molecular Immunology</i> , 2021, 132, 217-226.	1.0	6
2577	Cell-type-aware analysis of RNA-seq data. <i>Nature Computational Science</i> , 2021, 1, 253-261.	3.8	12
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2579	Transcriptome profiling of <i>Cysticercus Pisiformis</i> provides insight into responses to host bile acids. <i>Parasitology International</i> , 2021, 81, 102246.	0.6	2
2580	Characteristics and expression profiles of circRNAs during abdominal adipose tissue development in Chinese Gushi chickens. <i>PLoS ONE</i> , 2021, 16, e0249288.	1.1	11
2581	Comparative transcriptome analysis of lncRNAs of uncertain coding potential in septic myocardial depression. <i>BMC Cardiovascular Disorders</i> , 2021, 21, 166.	0.7	1
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2589	Regulatory role of non-coding RNA in ginseng rusty root symptom tissue. <i>Scientific Reports</i> , 2021, 11, 9211.	1.6	7
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2605	Transcriptomic Analysis of <i>Pseudomonas aeruginosa</i> Response to Pine Honey via RNA Sequencing Indicates Multiple Mechanisms of Antibacterial Activity. <i>Foods</i> , 2021, 10, 936.	1.9	18
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2607	<i>Fasciola gigantica</i> â€œDerived Excretory-Secretory Products Alter the Expression of mRNAs, miRNAs, lncRNAs, and circRNAs Involved in the Immune Response and Metabolism in Goat Peripheral Blood Mononuclear Cells. <i>Frontiers in Immunology</i> , 2021, 12, 653755.	2.2	4
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2614	Integration of Transcriptomic and Proteomic Data Reveals the Possible Action Mechanism of the Antimicrobial Zhongshengmycin Against <i>Didymella segeticola</i> , the Causal Agent of Tea Leaf Spot. <i>Phytopathology</i> , 2021, 111, 2238-2249.	1.1	7
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2616	In-Frame and Frameshift Mutations in Zebrafish Presenilin 2 Affect Different Cellular Functions in Young Adult Brains. <i>Journal of Alzheimer's Disease Reports</i> , 2021, 5, 395-404.	1.2	8
2617	Studies on the control effect of <i>Bacillus subtilis</i> on wheat powdery mildew. <i>Pest Management Science</i> , 2021, 77, 4375-4382.	1.7	20
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2625	Increased hippocampal excitability in miR-324-null mice. <i>Scientific Reports</i> , 2021, 11, 10452.	1.6	10
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2627	Root-secreted peptide OsPEP1 regulates primary root elongation in rice. <i>Plant Journal</i> , 2021, 107, 480-492.	2.8	7
2630	Multiple cellular compartments engagement in <i>Nicotiana benthamiana</i> -peanut stunt virus-satRNA interactions revealed by systems biology approach. <i>Plant Cell Reports</i> , 2021, 40, 1247-1267.	2.8	4
2631	Discordant regulation of eIF2 kinase GCN2 and mTORC1 during nutrient stress. <i>Nucleic Acids Research</i> , 2021, 49, 5726-5742.	6.5	26
2632	Argonaute-CLIP delineates versatile, functional RNAi networks in <i>Aedes aegypti</i> , a major vector of human viruses. <i>Cell Host and Microbe</i> , 2021, 29, 834-848.e13.	5.1	6

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2641	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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2647	Dual RNA-Sequencing Analysis of Resistant (<i>Pinus pinea</i>) and Susceptible (<i>Pinus radiata</i>) Hosts during <i>Fusarium circinatum</i> Challenge. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5231.	1.8	14
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3432	Dedicated transcriptomics combined with power analysis lead to functional understanding of genes with weak phenotypic changes in knockout lines. <i>PLoS Computational Biology</i> , 2020, 16, e1008354.	1.5	6
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3435	Screening of key genes responsible for <i>Pennisetum setaceum</i> "Rubrum" leaf color using transcriptome sequencing. <i>PLoS ONE</i> , 2020, 15, e0242618.	1.1	7
3436	Comparative transcriptome analysis of epithelial and fiber cells in newborn mouse lenses with RNA sequencing. <i>Molecular Vision</i> , 2014, 20, 1491-517.	1.1	58
3437	Transcriptomic profile analysis of brain microvascular pericytes in spontaneously hypertensive rats by RNA-Seq. <i>American Journal of Translational Research (discontinued)</i> , 2018, 10, 2372-2386.	0.0	13
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3441	Changes in metabolism modulate induced by viroid infection in the orchid <i>Dendrobium officinale</i> . <i>Virus Research</i> , 2022, 308, 198626.	1.1	13
3442	High fat diet induced gut dysbiosis alters corneal epithelial injury response in mice. <i>Ocular Surface</i> , 2022, 23, 49-59.	2.2	7
3443	Transcriptome and proteome analysis of pregnancy and postpartum anoestrus ovaries in yak. <i>Journal of Veterinary Science</i> , 2022, 23, e3.	0.5	4
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3446	BrWAX2 plays an essential role in cuticular wax biosynthesis in Chinese cabbage (<i>Brassica rapa</i> L. ssp.) Tj ETQq1 1 0.784314 ggBT /Over	1.8	1
3447	Nanopore-Based Comparative Transcriptome Analysis Reveals the Potential Mechanism of High-Temperature Tolerance in Cotton (<i>Gossypium hirsutum</i> L.). <i>Plants</i> , 2021, 10, 2517.	1.6	2
3448	Transcriptomic Analysis of the Effects of Chemokine Receptor CXCR3 Deficiency on Immune Responses in the Mouse Brain during <i>Toxoplasma gondii</i> Infection. <i>Microorganisms</i> , 2021, 9, 2340.	1.6	2
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3450	Biotinylated subunit of 3-methylcrotonyl-CoA carboxylase encoding gene (<i>AtMCCA</i>) participating in <i>Arabidopsis</i> resistance to carbonate Stress by transcriptome analysis. <i>Plant Science</i> , 2021, 315, 111130.	1.7	1
3451	Comparative Transcriptome Analysis Revealed the Key Genes Regulating Ascorbic Acid Synthesis in <i>Actinidia</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 12894.	1.8	6
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3454	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. <i>Plant Biotechnology Journal</i> , 2022, 20, 691-710.	4.1	33
3455	Transcriptomic analysis reveals that coxsackievirus B3 Woodruff and GD strains use similar key genes to induce FoxO signaling pathway activation in HeLa cells. <i>Archives of Virology</i> , 2022, 167, 131-140.	0.9	3
3456	Comparatively analyzing the liver-specific transcriptomic profiles in Kunming mice afflicted with streptozotocin- and natural food-induced type 2 diabetes mellitus. <i>Molecular Biology Reports</i> , 2022, 49, 1369-1377.	1.0	1
3457	Metabolome and transcriptome analysis predicts metabolism of violet-red color change in <i>Lilium</i> bulbs. <i>Journal of the Science of Food and Agriculture</i> , 2022, 102, 2903-2915.	1.7	7
3458	N6-Methyladenosine Methylation Analysis of Long Noncoding RNAs and mRNAs in IPEC-J2 Cells Treated With <i>Clostridium perfringens</i> beta2 Toxin. <i>Frontiers in Immunology</i> , 2021, 12, 769204.	2.2	3

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3460	Effects of <i>Laccaria bicolor</i> on Gene Expression of <i>Populus trichocarpa</i> Root under Poplar Canker Stress. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1024.	1.5	2
3461	A comparative transcriptome and proteomics study of postpartum ovarian cycle arrest in yaks (<i>Bos</i>) Tj ETQq0.0.0 rgBT /Overlock 10 T	0.6	6
3462	Single-Cell and Bulk RNA-Sequencing Reveal Differences in Monocyte Susceptibility to Influenza A Virus Infection Between Africans and Europeans. <i>Frontiers in Immunology</i> , 2021, 12, 768189.	2.2	14
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3468	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
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3471	Flavonoids Modulate the Accumulation of Toxins From <i>Aspergillus flavus</i> in Maize Kernels. <i>Frontiers in Plant Science</i> , 2021, 12, 761446.	1.7	5
3472	Temporal and spatial transcriptomic dynamics across brain development in <i>Xenopus laevis</i> tadpoles. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
3473	Transcriptome and metabolome analysis to reveal major genes of saikosaponin biosynthesis in <i>Bupleurum chinense</i> . <i>BMC Genomics</i> , 2021, 22, 839.	1.2	9
3474	Integrated Transcriptome Analysis and Single-Base Resolution Methylomes of Watermelon (<i>Citrullus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.7	5
3475	Nutritional evaluation and transcriptome analyses of short-time germinated seeds in soybean (<i>Glycine</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.6	5
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3478	Transcriptomics Analysis of Primordium Formation in <i>Pleurotus eryngii</i> . <i>Genes</i> , 2021, 12, 1863.	1.0	4

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3480	Symbiotic responses of <i>Lotus japonicus</i> to two isogenic lines of a mycorrhizal fungus differing in the presence/absence of an endobacterium. <i>Plant Journal</i> , 2021, 108, 1547-1564.	2.8	15
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3487	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
3488	Genetic divergence and local adaptation of <i>Liriodendron</i> driven by heterogeneous environments. <i>Molecular Ecology</i> , 2022, 31, 916-933.	2.0	13
3489	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
3490	Venoms for all occasions: The functional toxin profiles of different anatomical regions in sea anemones are related to their ecological function. <i>Molecular Ecology</i> , 2022, 31, 866-883.	2.0	21
3491	Di-(2-ethylhexyl) phthalate exposure leads to ferroptosis via the HIF-1 α /HO-1 signaling pathway in mouse testes. <i>Journal of Hazardous Materials</i> , 2022, 426, 127807.	6.5	63
3492	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
3494	Exosomes produced by melanoma cells significantly influence the biological properties of normal and cancer-associated fibroblasts. <i>Histochemistry and Cell Biology</i> , 2022, 157, 153-172.	0.8	17
3495	Brain transcriptomes of zebrafish and mouse Alzheimer's disease knock-in models imply early disrupted energy metabolism. <i>DMM Disease Models and Mechanisms</i> , 2022, 15, .	1.2	8
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3500	Transcriptomic and metabolomic analyses reveal the altitude adaptability and evolution of different-colored flowers in alpine <i>Rhododendron</i> species. <i>Tree Physiology</i> , 2022, 42, 1100-1113.	1.4	10
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3505	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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3509	OUP accepted manuscript. <i>Journal of Experimental Botany</i> , 2022, , .	2.4	4
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3512	Transcriptional analysis of <i>Bemisia tabaci</i> MEAM1 cryptic species under the selection pressure of neonicotinoids imidacloprid, acetamiprid and thiamethoxam. <i>BMC Genomics</i> , 2022, 23, 15.	1.2	5
3513	Molecular toxicity and defense mechanisms induced by silver nanoparticles in <i>Drosophila melanogaster</i> . <i>Journal of Environmental Sciences</i> , 2023, 125, 616-629.	3.2	8
3514	Comparative Transcriptomic Analyses of Different Jujube Cultivars Reveal the Co-Regulation of Multiple Pathways during Fruit Cracking. <i>Genes</i> , 2022, 13, 105.	1.0	8
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3516	CAG repeat-binding small molecule improves motor coordination impairment in a mouse model of Dentatorubral-pallidoluysian atrophy. <i>Neurobiology of Disease</i> , 2022, 163, 105604.	2.1	11
3517	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. <i>Journal of Cleaner Production</i> , 2022, 334, 130205.	4.6	9

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3519	Enhanced surface display efficiency of Î ² -glucosidase in <i>Saccharomyces cerevisiae</i> by disruption of cell wall protein-encoding genes YGP1 and CWP2. <i>Biochemical Engineering Journal</i> , 2022, 179, 108305.	1.8	14
3520	Potential differences in chitin synthesis ability cause different sensitivities to diflubenzuron among three strains of <i>Daphnia magna</i> . <i>Aquatic Toxicology</i> , 2022, 243, 106071.	1.9	3
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3524	Immunotoxicity and uterine transcriptome analysis of the effect of zearalenone (ZEA) in sows during the embryo attachment period. <i>Toxicology Letters</i> , 2022, 357, 33-42.	0.4	13
3525	Off-target lipid metabolism disruption by the mouse constitutive androstane receptor ligand TCPOBOP in humanized mice. <i>Biochemical Pharmacology</i> , 2022, 197, 114905.	2.0	7
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3528	MicroRNA Transcriptomics Analysis Identifies Dysregulated Hedgehog Signaling Pathway in a Mouse Model of Acute Intracerebral Hemorrhage Exposed to Hyperglycemia. <i>Journal of Stroke and Cerebrovascular Diseases</i> , 2022, 31, 106281.	0.7	3
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3530	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
3533	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
3534	Analysis of miRNAs Involved in Mouse Heart Injury Upon Coxsackievirus A2 Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 765445.	1.8	1
3536	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
3537	Identification of Drought-Resistant Genes in Shanlan Upland Rice. <i>Agriculture (Switzerland)</i> , 2022, 12, 150.	1.4	5
3538	Comparative transcriptome analyses reveal genes related to pigmentation in the petals of a flower color variation cultivar of <i>Rhododendron obtusum</i> . <i>Molecular Biology Reports</i> , 2022, 49, 2641-2653.	1.0	10

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3541	Morphological, physiological, biochemical, and transcriptome studies reveal the importance of transporters and stress signaling pathways during salinity stress in <i>Prunus</i> . <i>Scientific Reports</i> , 2022, 12, 1274.	1.6	15
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3544	Understanding nutritive need in <i>Harmonia axyridis</i> larvae: Insights from nutritional geometry. <i>Insect Science</i> , 2022, 29, 1433-1444.	1.5	4
3545	Androgen Receptor-Mediated Paracrine Signaling Induces Regression of Blood Vessels in the Dermal Papilla in Androgenetic Alopecia. <i>Journal of Investigative Dermatology</i> , 2022, 142, 2088-2099.e9.	0.3	17
3546	Transcriptomic analysis using dual RNA sequencing revealed a Pathogen-Host interaction after <i>Edwardsiella anguillarum</i> infection in European eel (<i>Anguilla anguilla</i>). <i>Fish and Shellfish Immunology</i> , 2022, 120, 745-757.	1.6	9
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3549	Gene expression alterations from reversible to irreversible stages during coral metamorphosis. <i>Zoological Letters</i> , 2022, 8, 4.	0.7	2
3550	Sporophyte Stage Genes Exhibit Stronger Selection Than Gametophyte Stage Genes in Haplodiplontic Giant Kelp. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	5
3551	Brain transcriptome analysis reveals gene expression differences associated with dispersal behaviour between range-front and range-core populations of invasive cane toads in Australia. <i>Molecular Ecology</i> , 2022, 31, 1700-1715.	2.0	9
3552	A Maize Necrotic Leaf Mutant Caused by Defect of Coproporphyrinogen III Oxidase in the Porphyrin Pathway. <i>Genes</i> , 2022, 13, 272.	1.0	10
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3555	Transcriptome and methylome changes in two contrasting mungbean genotypes in response to drought stress. <i>BMC Genomics</i> , 2022, 23, 80.	1.2	16
3556	Comparative analysis of the orange versus yellow petal of rapeseed (<i>Brassica</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 14	1.0	1
3557	Resistance to mesosulfuron-methyl in <i>Beckmannia syzigachne</i> may involve ROS burst and non-target-site resistance mechanisms. <i>Ecotoxicology and Environmental Safety</i> , 2022, 229, 113072.	2.9	10
3558	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

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3560	Grainyhead 1 acts as a drug-inducible conserved transcriptional regulator linked to insulin signaling and lifespan. <i>Nature Communications</i> , 2022, 13, 107.	5.8	5
3561	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
3562	Regulation of gene expression by the APP family in the adult cerebral cortex. <i>Scientific Reports</i> , 2022, 12, 66.	1.6	8
3563	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
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3565	Universal gene co-expression network reveals receptor-like protein genes involved in broad-spectrum resistance in pepper (<i>Capsicum annuum</i> L.). <i>Horticulture Research</i> , 2022, , .	2.9	10
3566	Identification and Pleiotropic Effect Analysis of GSE5 on Rice Chalkiness and Grain Shape. <i>Frontiers in Plant Science</i> , 2021, 12, 814928.	1.7	7
3567	BASiCS workflow: a step-by-step analysis of expression variability using single cell RNA sequencing data. <i>F1000Research</i> , 0, 11, 59.	0.8	0
3568	Genome-wide analysis of mRNAs, lncRNAs, and circRNAs during intramuscular adipogenesis in Chinese Guizhou Congjiang pigs. <i>PLoS ONE</i> , 2022, 17, e0261293.	1.1	4
3569	Peripheral nerve fibroblasts secrete neurotrophic factors to promote axon growth of motoneurons. <i>Neural Regeneration Research</i> , 2022, 17, 1833.	1.6	10
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3571	Potato tuber degradation is regulated by carbohydrate metabolism: Results of transcriptomic analysis. <i>Plant Direct</i> , 2022, 6, e379.	0.8	2
3572	Evolution of Gene Expression across Species and Specialized Zooids in Siphonophora. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	14
3573	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
3574	Crosstalk between sex-related genes and apoptosis signaling reveals molecular insights into sex change in a protogynous hermaphroditic teleost fish, ricefield eel <i>Monopterus albus</i> . <i>Aquaculture</i> , 2022, 552, 737918.	1.7	7
3575	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
3576	<i>Vibrio gazogenes</i> Inhibits Aflatoxin Production Through Downregulation of Aflatoxin Biosynthetic Genes in <i>Aspergillus flavus</i> . <i>PhytoFrontiers</i> , 2022, 2, 218-229.	0.8	1

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3583	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
3584	Deciphering Molecular Mechanisms Involved in Salinity Tolerance in Guar (<i>Cyamopsis tetragonoloba</i>) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	1.6	11
3585	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
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3595	A Calmodulin-Like Gene (GbCML7) 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

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3599	Ubiquitin-proteasome pathway plays an essential regulatory role during spermatangium formation in <i>Neopyropia yezoensis</i> . <i>Algal Research</i> , 2022, 62, 102623.	2.4	1
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3634	Modern Approaches for Transcriptome Analyses in Plants. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1346, 11-50.	0.8	0
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3663	The Fungal Endophyte <i>Penicillium olsonii</i> ML37 Reduces <i>Fusarium</i> Head Blight by Local Induced Resistance in Wheat Spikes. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 345.	1.5	8
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3665	Morphological, transcriptomic and metabolomic analyses of <i>Sophora davidii</i> mutants for plant height. <i>BMC Plant Biology</i> , 2022, 22, 144.	1.6	10
3666	Identification of Key Modules and Genes Associated with Major Depressive Disorder in Adolescents. <i>Genes</i> , 2022, 13, 464.	1.0	2
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3671	Critical roles of the activation of ethylene pathway genes mediated by DNA demethylation in <i>Arabidopsis</i> hyperhydricity. <i>Plant Genome</i> , 2022, 15, e20202.	1.6	1
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3691	Transcriptome Analysis Reveals miR-302a-3p Affects Granulosa Cell Proliferation by Targeting DRD1 in Chickens. <i>Frontiers in Genetics</i> , 2022, 13, 832762.	1.1	2
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3703	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
3704	Role of lncRNAs in cis- and trans-regulatory responses to salt in <i>Populus trichocarpa</i> . <i>Plant Journal</i> , 2022, 110, 978-993.	2.8	26
3705	Transcriptomic and proteomic analyses uncover the drought adaption landscape of <i>Phoebe zhennan</i> . <i>BMC Plant Biology</i> , 2022, 22, 95.	1.6	2
3706	Transcriptional Regulation of Reproductive Diapause in the Convergent Lady Beetle, <i>Hippodamia convergens</i> . <i>Insects</i> , 2022, 13, 343.	1.0	4
3707	Urbanization comprehensively impairs biological rhythms in coral holobionts. <i>Global Change Biology</i> , 2022, 28, 3349-3364.	4.2	14

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4795	Interaction of MdWRKY24 and MdRGL in Response to Tree Dwarfing in <i>Malus domestica</i> . <i>Agronomy</i> , 2022, 12, 2345.	1.3	1

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4919	Establishment of in vitro regeneration system and molecular analysis of early development of somatic callus in <i>Capsicum chinense</i> and <i>Capsicum baccatum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
4920	Reactive oxygen species-related genes participate in resistance to cucumber green mottle mosaic virus infection regulated by boron in <i>Nicotiana benthamiana</i> and watermelon. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
4921	Chromosome-scale assemblies of the male and female <i>Populus euphratica</i> genomes reveal the molecular basis of sex determination and sexual dimorphism. <i>Communications Biology</i> , 2022, 5, .	2.0	7
4922	Exosomal long noncoding RNAs MAGI2-AS3 and CCDC144NL-AS1 in oral squamous cell carcinoma development via the PI3K-AKT-mTOR signaling pathway. <i>Pathology Research and Practice</i> , 2022, 240, 154219.	1.0	4
4923	Comparative transcriptomics reveals unique pine wood decay strategies in the <i>Sparassis latifolia</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	0
4925	Revealing the Regulatory Mechanism of lncRNA-LMEP on Melanin Deposition Based on High-Throughput Sequencing in Xichuan Chicken Skin. <i>Genes</i> , 2022, 13, 2143.	1.0	4
4926	Pituitary-Gland-Based Genes Participates in Intrauterine Growth Restriction in Piglets. <i>Genes</i> , 2022, 13, 2141.	1.0	1
4927	Transcriptome analysis reveals the molecular mechanism of cinnamaldehyde against <i>Bacillus cereus</i> spores in ready-to-eat beef. <i>Food Research International</i> , 2023, 163, 112185.	2.9	4
4928	Integration of the transcriptome and metabolome reveals the mechanism of resistance to low phosphorus in wild soybean seedling leaves. <i>Plant Physiology and Biochemistry</i> , 2023, 194, 406-417.	2.8	3
4929	Exosomal long non-coding RNA TRAFD1-4:1 derived from fibroblast-like synoviocytes suppresses chondrocyte proliferation and migration by degrading cartilage extracellular matrix in rheumatoid arthritis. <i>Experimental Cell Research</i> , 2023, 422, 113441.	1.2	7
4930	A statistical perspective of gene set analysis with trait-specific QTL in molecular crop breeding. , 2023, , 17-43.		0
4931	Integrated biochemical, transcriptomic and metabolomic analyses provide insight into heat stress response in Yangtze sturgeon (<i>Acipenser dabryanus</i>). <i>Ecotoxicology and Environmental Safety</i> , 2023, 249, 114366.	2.9	12

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4932	Unraveling correlations between calcium deficiency and spongy tissue in mango fruit flesh. <i>Scientia Horticulturae</i> , 2023, 309, 111694.	1.7	3
4933	Comparative transcriptomic analysis of <i>Glycine soja</i> and <i>G. max</i> and functional identification of GsCNGC20-d interacted with GsCDPK29 under salt stress. <i>Environmental and Experimental Botany</i> , 2023, 206, 105185.	2.0	3
4934	The allene oxide synthase gene family in sugarcane and its involvement in disease resistance. <i>Industrial Crops and Products</i> , 2023, 192, 116136.	2.5	9
4935	Avermectin induces cardiac toxicity in early embryonic stage of zebrafish. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2023, 264, 109529.	1.3	6
4936	Embryogenesis of a calanoid copepod analyzed by transcriptomics. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 45, 101054.	0.4	0
4937	A transcriptomic study of "Granny Smith" apple fruit response to x-ray irradiation using RNA-Seq. <i>Scientia Horticulturae</i> , 2023, 311, 111777.	1.7	2
4939	Genetic dissection of the soybean dwarf mutant <i>dm</i> with integrated genomic, transcriptomic and methylomic analyses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
4940	Identification of Liver Fibrosis-Related MicroRNAs in Human Primary Hepatic Stellate Cells Using High-Throughput Sequencing. <i>Genes</i> , 2022, 13, 2201.	1.0	4
4941	Transcriptome Profiling to Identify Genes Involved in Non-Target-Site-Based Resistance to Clodinafop-Propargyl in Asia Minor Bluegrass (<i>Polypogon fugax</i>). <i>Agronomy</i> , 2022, 12, 2998.	1.3	1
4942	Pretreatment of NaCl enhances the drought resistance of cotton by regulating the biosynthesis of carotenoids and abscisic acid. <i>Frontiers in Environmental Science</i> , 0, 10, .	1.5	1
4943	Microscopic and transcriptomic analyses of early events triggered by <i>Candidatus Liberibacter asiaticus</i> in young flushes of HLB-positive citrus trees. <i>Phytopathology</i> , 0, , .	1.1	1
4944	Genetics and Nutrition Drive the Gut Microbiota Succession and Host-Transcriptome Interactions through the Gilthead Sea Bream (<i>Sparus aurata</i>) Production Cycle. <i>Biology</i> , 2022, 11, 1744.	1.3	8
4945	Transcriptome Level Reveals the Triterpenoid Saponin Biosynthesis Pathway of <i>Bupleurum falcatum</i> L.. <i>Genes</i> , 2022, 13, 2237.	1.0	5
4946	Morusin Protected Ruminal Epithelial Cells against Lipopolysaccharide-Induced Inflammation through Inhibiting EGFR-AKT/NF- κ B Signaling and Improving Barrier Functions. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14428.	1.8	1
4947	Comparative transcriptome analysis of wheat in response to corn leaf aphid, <i>Rhopalosiphum maidis</i> F. infestation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
4948	Metabolic and Transcriptional Stress Memory in <i>Sorbus pohuashanensis</i> Suspension Cells Induced by Yeast Extract. <i>Cells</i> , 2022, 11, 3757.	1.8	2
4949	Comparative transcriptomic analysis provides insights into the molecular basis underlying pre-harvest sprouting in rice. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
4950	The influenza-injured lung microenvironment promotes MRSA virulence, contributing to severe secondary bacterial pneumonia. <i>Cell Reports</i> , 2022, 41, 111721.	2.9	8

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4951	Identification and Characterization of Sex-Biased miRNAs in the Golden Pompano (<i>Trachinotus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	1.0	1
4953	A Comprehensive Sequencing Analysis of Testis-Born miRNAs in Immature and Mature Indigenous Wandong Cattle (<i>Bos taurus</i>). <i>Genes</i> , 2022, 13, 2185.	1.0	4
4954	Host transcriptome and microbiome interactions in Holstein cattle under heat stress condition. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
4955	Achog1 is required for the asexual sporulation, stress responses and pigmentation of <i>Aspergillus cristatus</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
4956	Effect of <i>Inonotus obliquus</i> Extract Supplementation on Endurance Exercise and Energy-Consuming Processes through Lipid Transport in Mice. <i>Nutrients</i> , 2022, 14, 5007.	1.7	1
4957	NtbHLH49, a jasmonate-regulated transcription factor, negatively regulates tobacco responses to <i>Phytophthora nicotianae</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
4958	Integrated Transcriptome Analysis Reveals the Crucial mRNAs and miRNAs Related to Fecundity in the Hypothalamus of Yunshang Black Goats during the Luteal Phase. <i>Animals</i> , 2022, 12, 3397.	1.0	0
4959	Insight into the formation of trumpet and needle-type leaf in <i>Ginkgo biloba</i> L. mutant. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
4960	Comparative analysis of fungal communities between herbicide-resistant and -susceptible <i>Alopecurus aequalis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	1
4961	Differential miRNA expression profiles in the bone marrow of Beagle dogs at different stages of <i>Toxocara canis</i> infection. <i>BMC Genomics</i> , 2022, 23, .	1.2	0
4962	Long-lasting impact of chitoooligosaccharide application on strigolactone biosynthesis and fungal accommodation promotes arbuscular mycorrhiza in <i>Medicago truncatula</i> . <i>New Phytologist</i> , 2023, 237, 2316-2331.	3.5	14
4963	Metabolism Difference Is Involved in Mesosulfuron-Methyl Selectivity between <i>Aegilops tauschii</i> and <i>Triticum aestivum</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2023, 71, 186-196.	2.4	0
4965	Leaf transcriptome analysis of <i>Medicago ruthenica</i> revealed its response and adaptive strategy to drought and drought recovery. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	0
4967	Characterization of lodging variation of weedy rice. <i>Journal of Experimental Botany</i> , 2023, 74, 1403-1419.	2.4	1
4968	Genome-Wide Transcriptome Analysis Revealing the Genes Related to Sugar Metabolism in Kernels of Sweet Corn. <i>Metabolites</i> , 2022, 12, 1254.	1.3	1
4969	Usp22 is an intracellular regulator of systemic emergency hematopoiesis. <i>Science Immunology</i> , 2022, 7, .	5.6	3
4970	Transcriptome profiling provides insights into leaf color changes in two <i>Acer palmatum</i> genotypes. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
4971	Oncogenic KRAS alters splicing factor phosphorylation and alternative splicing in lung cancer. <i>BMC Cancer</i> , 2022, 22, .	1.1	1

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4972	Rumen Epithelial Development- and Metabolism-Related Genes Regulate Their Micromorphology and VFAs Mediating Plateau Adaptability at Different Ages in Tibetan Sheep. <i>International Journal of Molecular Sciences</i> , 2022, 23, 16078.	1.8	3
4974	Transcriptome responses of the aphid vector <i>Myzus persicae</i> are shaped by identities of the host plant and the virus. , 0, 2, .		1
4975	Analysis of Breast Cancer Differences between China and Western Countries Based on Radiogenomics. <i>Genes</i> , 2022, 13, 2416.	1.0	1
4976	Transcriptomic profiling of the cold stress and recovery responsiveness of two contrasting Guizhou HE rice genotypes. <i>Genes and Genomics</i> , 2023, 45, 401-412.	0.5	2
4977	DAP5 enables main ORF translation on mRNAs with structured and uORF-containing 5' leaders. <i>Nature Communications</i> , 2022, 13, .	5.8	15
4978	Transcriptomes of Testes at Different Developmental Stages in the <i>Opsariichthys bidens</i> Predict Key Genes for Testis Development and Spermatogenesis. <i>Marine Biotechnology</i> , 2023, 25, 123-139.	1.1	2
4979	Integrative analysis of the transcriptome and metabolome reveals the response mechanism to tomato spotted wilt virus. <i>Horticultural Plant Journal</i> , 2023, 9, 958-970.	2.3	3
4980	A General Signal Pathway to Regulate Multiple Detoxification Genes Drives the Evolution of <i>Helicoverpa armigera</i> Adaptation to Xenobiotics. <i>International Journal of Molecular Sciences</i> , 2022, 23, 16126.	1.8	3
4982	Multispecies comparison of host responses to <i>Fusarium circinatum</i> challenge in tropical pines show consistency in resistance mechanisms. <i>Plant, Cell and Environment</i> , 2023, 46, 1705-1725.	2.8	1
4983	Overexpression of MsSAG113 gene promotes leaf senescence in alfalfa via participating in the hormone regulatory network. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
4984	Transcriptome and metabolome analyses reveal anthocyanins pathways associated with fruit color changes in plum (<i>Prunus salicina</i> Lindl.). <i>PeerJ</i> , 0, 10, e14413.	0.9	4
4985	Identification of miRNA-mRNA regulatory network associated with the glutamatergic system in post-traumatic epilepsy rats. <i>Frontiers in Neurology</i> , 0, 13, .	1.1	5
4986	Influential factors and transcriptome analyses of immature diploid embryo anthocyanin accumulation in maize. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	4
4987	Aging is associated with a systemic length-associated transcriptome imbalance. <i>Nature Aging</i> , 2022, 2, 1191-1206.	5.3	28
4988	The immune-related circRNA-miRNA-mRNA ceRNA regulatory network in the liver of turbot (<i>Scophthalmus maximus</i> L.) induced by <i>Vibrio anguillarum</i> . <i>Fish and Shellfish Immunology</i> , 2023, 132, 108506.	1.6	4
4989	Differentially expressed long noncoding RNAs in RAW264.7 macrophages during <i>Brucella</i> infection and functional analysis on the bacterial intracellular replication. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
4990	Gut epithelial barrier damage caused by dishwasher detergents and rinse aids. <i>Journal of Allergy and Clinical Immunology</i> , 2023, 151, 469-484.	1.5	17
4991	Efficacy and transcriptome analysis of golden pompano (<i>Trachinotus ovatus</i>) immunized with a formalin-inactivated vaccine against <i>Streptococcus iniae</i> . <i>Fish and Shellfish Immunology</i> , 2023, 134, 108489.	1.6	2

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4993	DNA Methylation Variation Is a Possible Mechanism in the Response of <i>Haemaphysalis longicornis</i> to Low-Temperature Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15207.	1.8	3
4994	Comprehensive Transcriptome Analysis of Different Skin Colors to Evaluate Genes Related to the Production of Pigment in Celestial Goldfish. <i>Biology</i> , 2023, 12, 7.	1.3	1
4995	Liver RBFOX2 regulates cholesterol homeostasis via Scarb1 alternative splicing in mice. <i>Nature Metabolism</i> , 2022, 4, 1812-1829.	5.1	12
4997	Transcriptome profiling of male and female <i>Ascaris lumbricoides</i> reproductive tissues. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	2
4998	Integration of High-Throughput Imaging and Multiparametric Metabolic Profiling Reveals a Mitochondrial Mechanism of Tenofovir Toxicity. <i>Function</i> , 2022, 4, .	1.1	3
4999	Transcriptomics reveals the molecular mechanisms of flesh colour differences in eggplant (<i>Solanum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.6	0
5000	Comprehensive identification and analysis of circRNAs during hickory (<i>Carya cathayensis</i> Sarg.) flower bud differentiation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
5001	High throughput sequencing revealed enhanced cell cycle signaling in SLE patients. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
5002	Dynamic Interplay between O ₂ Availability, Growth Rates, and the Transcriptome of <i>Yarrowia lipolytica</i> . <i>Fermentation</i> , 2023, 9, 74.	1.4	0
5003	LncRNA EN-90756 promotes CPB2-induced proliferation and inhibits apoptosis in IPEC-J2 cells by affecting the JAK-STAT signaling pathway activation. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
5004	Comprehensive Analysis of Metabolome and Transcriptome in Fruits and Roots of Kiwifruit. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1299.	1.8	4
5005	The hitchhikersâ€™™ guide to RNA sequencing and functional analysis. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	8
5006	Integrated analysis of transcriptome and microRNAs associated with exogenous calcium-mediated enhancement of hypoxic tolerance in cucumber seedlings (<i>Cucumis sativus</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
5007	S100A9 plays a key role in <i>Clostridium perfringens</i> beta2 toxin-induced inflammatory damage in porcine IPEC-J2 intestinal epithelial cells. <i>BMC Genomics</i> , 2023, 24, .	1.2	0
5008	The <i>in planta</i> gene expression of <i>Austropuccinia psidii</i> in resistant and susceptible <i>Eucalyptus grandis</i> . <i>Phytopathology</i> , 0, , .	1.1	1
5009	Molecular and physiological mechanisms of tea (<i>Camellia sinensis</i> (L.) O. Kuntze) leaf and root in response to nitrogen deficiency. <i>BMC Genomics</i> , 2023, 24, .	1.2	4
5010	Molecular Mechanism of Cold Tolerance of Centipedegrass Based on the Transcriptome. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1265.	1.8	6

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5013	Genome sequencing and resequencing identified three horizontal gene transfers and uncovered the genetic mechanism on the intraspecies adaptive evolution of <i>Gastrodia elata</i> Blume. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
5014	Transcriptome analysis revealed sh2 gene mutation leads reduced zein protein accumulation in maize endosperm. <i>Genetic Resources and Crop Evolution</i> , 2023, 70, 1663-1676.	0.8	0
5015	Host Transcriptome Analysis of <i>Spodoptera frugiperda</i> Larvae Parasitized by <i>Microplitis manilae</i> . <i>Insects</i> , 2023, 14, 100.	1.0	3
5016	Genetic adaptation to pathogens and increased risk of inflammatory disorders in post-Neolithic Europe. <i>Cell Genomics</i> , 2023, 3, 100248.	3.0	19
5017	Comprehensive bulk and single-cell transcriptome profiling give useful insights into the characteristics of osteoarthritis associated synovial macrophages. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
5018	Urate oxidase from tea microbe <i>Colletotrichum camelliae</i> is involved in the caffeine metabolism pathway and plays a role in fungal virulence. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	6
5019	Co-expression analysis of long non-coding RNAs and mRNAs involved in intramuscular fat deposition in Muchuan black-bone chicken. <i>British Poultry Science</i> , 2023, 64, 289-298.	0.8	1
5020	Differentially expressed genes in head kidney of <i>Pelteobagrus fulvidraco</i> following <i>Vibrio cholerae</i> challenge. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
5021	Insights into H ₂ O ₂ -induced signaling in Jurkat cells from analysis of gene expression. <i>Free Radical Research</i> , 0, , 1-11.	1.5	0
5022	Towards understanding the mechanism of n-hexane tolerance in <i>Synechocystis</i> sp. PCC 6803. <i>Chinese Journal of Chemical Engineering</i> , 2023, 59, 128-134.	1.7	0
5023	Integrated transcriptome and proteome revealed that the declined expression of cell cycle-related genes associated with follicular atresia in geese. <i>BMC Genomics</i> , 2023, 24, .	1.2	4
5024	Superior Antioxidant Capacity and Auxin Production Promote Seedling Formation of Rice Seeds under Submergence Stress. <i>Agronomy</i> , 2023, 13, 171.	1.3	0
5025	An atlas of transcribed human cardiac promoters and enhancers reveals an important role of regulatory elements in heart failure. , 2023, 2, 58-75.		7
5026	Full-length transcriptome analysis of two chemotype and functional characterization of genes related to sesquiterpene biosynthesis in <i>Atractylodes lancea</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 225, 1543-1554.	3.6	5
5027	The Prmt5-Vasa module is essential for spermatogenesis in <i>Bombyx mori</i> . <i>PLoS Genetics</i> , 2023, 19, e1010600.	1.5	4
5028	Development and Application of EST-SSR Markers Related to Lead Stress Responses in Kenaf Based on Transcriptome Sequencing Data. <i>Sustainability</i> , 2023, 15, 1514.	1.6	1
5030	Integrated analysis of lncRNA and mRNA for the apoptosis of porcine ovarian granulosa cells after polyphenol resveratrol treatment. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	6

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5031	Ustiloxin A inhibits proliferation of renal tubular epithelial cells in vitro and induces renal injury in mice by disrupting structure and respiratory function of mitochondria. <i>Journal of Hazardous Materials</i> , 2023, 448, 130791.	6.5	3
5032	Identification of aluminum-resistant miRNAs and lncRNAs in <i>Vitis quinquangularis</i> and exploration of the related aluminum-tolerance mechanisms. <i>Environmental and Experimental Botany</i> , 2023, 206, 105194.	2.0	2
5033	Starch granules of the sugar-pathway were eliminated under the stress of PEG-drought compared with Soil-drought. <i>Industrial Crops and Products</i> , 2023, 193, 116158.	2.5	6
5034	Single-cell transcriptome uncovers heterogeneity and immune responses of leukocytes after vaccination with inactivated <i>Edwardsiella tarda</i> in flounder (<i>Paralichthys olivaceus</i>). <i>Aquaculture</i> , 2023, 566, 739238.	1.7	7
5035	Molecular and physiological mechanisms of strigolactones-mediated drought stress in crab apple (<i>Malus hupehensis</i> Rehd.) seedlings. <i>Scientia Horticulturae</i> , 2023, 311, 111800.	1.7	11
5036	Accelerated energy metabolism plays an important role in Heterosis and maternal effect of hybrids bred from southern and northern Suminoe oysters (<i>Crassostrea ariakensis</i>). <i>Aquaculture</i> , 2023, 566, 739214.	1.7	0
5037	Transcriptomic response to GnRH down regulation by RNA interference in clam <i>Ruditapes philippinarum</i> , suggest possible role in reproductive function. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2023, 277, 111367.	0.8	0
5038	Dissection of the Inner Female and Male Cone Differentiation Mechanisms at Different Development Stages in Masson's Pine (<i>Pinus massoniana</i> Lamb.) by RNA-Seq Techniques. <i>Journal of Biobased Materials and Bioenergy</i> , 2022, 16, 668-675.	0.1	0
5039	Transcriptomic Network Analysis Using Exfoliative Cervical Cells Could Discriminate a Potential Risk of Progression to Cancer in HPV-related Cervical Lesions: A Pilot Study. <i>Cancer Genomics and Proteomics</i> , 2023, 20, 75-87.	1.0	2
5040	Integrated transcriptome and methylome analyses reveal the molecular regulation of drought stress in wild strawberry (<i>Fragaria nilgerrensis</i>). <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2
5041	Construction of a Hierarchical Gene Regulatory Network to Reveal the Drought Tolerance Mechanism of Shanxin Poplar. <i>International Journal of Molecular Sciences</i> , 2023, 24, 384.	1.8	3
5042	Starvation Affects the Muscular Morphology, Antioxidant Enzyme Activity, Expression of Lipid Metabolism-Related Genes, and Transcriptomic Profile of Javelin Goby (<i>Synechogobius hasta</i>). <i>Aquaculture Nutrition</i> , 2022, 2022, 1-20.	1.1	7
5043	Transcriptomic and enzymatic analysis reveals the roles of glutamate dehydrogenase in <i>Corynebacterium glutamicum</i> . <i>AMB Express</i> , 2022, 12, .	1.4	1
5044	MoNap1, a Nucleosome Assemble Protein 1, Regulates Growth, Development, and Pathogenicity in <i>Magnaporthe oryzae</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 50.	1.5	0
5045	Identification of Kynurenic Acid-Induced Apoptotic Biomarkers in Gastric Cancer-Derived AGS Cells through Next-Generation Transcriptome Sequencing Analysis. <i>Nutrients</i> , 2023, 15, 193.	1.7	3
5046	OsPPR11 encoding P-type PPR protein that affects group II intron splicing and chloroplast development. <i>Plant Cell Reports</i> , 0, , .	2.8	0
5047	BSR and Full-Length Transcriptome Approaches Identified Candidate Genes for High Seed Ratio in <i>Camellia vietnamensis</i> . <i>Current Issues in Molecular Biology</i> , 2023, 45, 311-326.	1.0	0
5048	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. <i>Cancers</i> , 2023, 15, 259.	1.7	2

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5050	Genetic assimilation of ancestral plasticity during parallel adaptation to zinc contamination in <i>Silene uniflora</i> . <i>Nature Ecology and Evolution</i> , 2023, 7, 414-423.	3.4	3
5051	B1 SINE-binding ZFP266 impedes mouse iPSC generation through suppression of chromatin opening mediated by reprogramming factors. <i>Nature Communications</i> , 2023, 14, .	5.8	7
5052	Microbially produced vitamin B12 contributes to the lipid-lowering effect of silymarin. <i>Nature Communications</i> , 2023, 14, .	5.8	12
5053	Genome-wide identification of the MATE gene family and functional characterization of PbrMATE9 related to anthocyanin in pear. <i>Horticultural Plant Journal</i> , 2023, 9, 1079-1094.	2.3	3
5054	Transcriptional Analysis of Tea Plants (<i>Camellia sinensis</i>) in Response to Salicylic Acid Treatment. <i>Journal of Agricultural and Food Chemistry</i> , 2023, 71, 2377-2389.	2.4	7
5056	Involvement of the E3 ubiquitin ligase Cblb in host defense and evaluation of transcriptome during <i>Trueperella pyogenes</i> infection. <i>Microbes and Infection</i> , 2023, , 105104.	1.0	0
5057	Identification and expression analyses of the olfactory-related genes in different tissues' transcriptome of a predacious soldier beetle, <i>Podabrus annulatus</i> (Coleoptera, Cantharidae). <i>Archives of Insect Biochemistry and Physiology</i> , 2023, 112, .	0.6	3
5058	Comparative analysis of drought responsive transcriptome in <i>Brassica napus</i> genotypes with contrasting drought tolerance under different potassium levels. <i>Euphytica</i> , 2023, 219, .	0.6	2
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