

The Significance of Digital Gene Expression Profiles

Genome Research

7, 986-995

DOI: [10.1101/gr.7.10.986](https://doi.org/10.1101/gr.7.10.986)

Citation Report

#	ARTICLE	IF	CITATIONS
1	An Introduction to High-Throughput Bioinformatics Data. , 2006, , 1-39.		4
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1062	De novo assembly, functional annotation, and marker development of Asian pear (<i>Pyrus pyrifolia</i>) fruit transcriptome through massively parallel sequencing. <i>Genetics and Molecular Research</i> , 2015, 14, 18344-18355.	0.3	1

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1071	Solexa-Sequencing Based Transcriptome Study of Plaice Skin Phenotype in Rex Rabbits (<i>Oryctolagus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.1	13
1072	Transcriptome-Wide Identification of miRNAs and Their Targets from <i>Typha angustifolia</i> by RNA-Seq and Their Response to Cadmium Stress. <i>PLoS ONE</i> , 2015, 10, e0125462.	1.1	20
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1327	The enhancement of tolerance to salt and cold stresses by modifying the redox state and salicylic acid content via the cytosolic malate dehydrogenase gene in transgenic apple plants. <i>Plant Biotechnology Journal</i> , 2016, 14, 1986-1997.	4.1	100
1328	Effects of drought and salt-stresses on gene expression in <i>Caragana korshinskii</i> seedlings revealed by RNA-seq. <i>BMC Genomics</i> , 2016, 17, 200.	1.2	47
1329	Discovery of genes associated with cadmium accumulation from gill of scallop <i>Chlamys farreri</i> based on high-throughput sequencing. <i>Genes and Genomics</i> , 2016, 38, 439-445.	0.5	3
1330	Transcriptome profiling reveals differentially expressed genes associated with wizened flower bud formation in Chinese pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Journal of Horticultural Science and Biotechnology</i> , 2016, 91, 227-235.	0.9	4
1331	Analysis on the transcriptome information of two different wheat mutants and identification of salt-induced differential genes. <i>Biochemical and Biophysical Research Communications</i> , 2016, 473, 1197-1204.	1.0	8
1332	Transcriptional profiling of macrophage and tumor cell interactions in vitro. <i>Genomics Data</i> , 2016, 8, 1-3.	1.3	5
1333	Characterization of Glycolytic Pathway Genes Using RNA-Seq in Developing Kernels of <i>Eucommia ulmoides</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 3712-3731.	2.4	17

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1335	Dynamic integrated analysis of DNA methylation and gene expression profiles in <i>in vivo</i> and <i>in vitro</i> fertilized mouse post-implantation extraembryonic and placental tissues. <i>Molecular Human Reproduction</i> , 2016, 22, 485-498.	1.3	28
1336	Differential gene expression in porcine SK6 cells infected with wild-type and SAP domain-mutant foot-and-mouth disease virus. <i>Virologica Sinica</i> , 2016, 31, 249-257.	1.2	5
1337	Global comparative analysis of expressed genes in ovules and leaves of <i>Ginkgo biloba</i> L.. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	12
1338	Transcriptome de novo assembly and analysis of differentially expressed genes related to cytoplasmic male sterility in cabbage. <i>Plant Physiology and Biochemistry</i> , 2016, 105, 224-232.	2.8	40
1339	Identification of microRNAs involved in chilling response of maize by high-throughput sequencing. <i>Biologia Plantarum</i> , 2016, 60, 251-260.	1.9	4
1340	Comparative transcriptome analysis of fertile and sterile buds from a genetically male sterile line of Chinese cabbage. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2016, 52, 130-139.	0.9	21
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1345	Transcriptome comparison between newly emerged and sexually matured bees of <i>Apis mellifera</i> . <i>Journal of Asia-Pacific Entomology</i> , 2016, 19, 893-897.	0.4	4
1346	Caveolin-1-mediated endocytic pathway is involved in classical swine fever virus Shimen infection of porcine alveolar macrophages. <i>Veterinary Microbiology</i> , 2016, 195, 81-86.	0.8	27
1347	Transcriptional profiling analysis of <i>Penicillium digitatum</i> , the causal agent of citrus green mold, unravels an inhibited ergosterol biosynthesis pathway in response to citral. <i>BMC Genomics</i> , 2016, 17, 599.	1.2	92
1348	Comprehensive transcriptome-based characterization of differentially expressed genes involved in microsporogenesis of radish CMS line and its maintainer. <i>Functional and Integrative Genomics</i> , 2016, 16, 529-543.	1.4	12
1349	Transcriptome analysis of male and female mature gonads of Japanese scallop <i>Patinopecten yessoensis</i> . <i>Genes and Genomics</i> , 2016, 38, 1041-1052.	0.5	18
1350	Data on the expression of cellular lncRNAs in human adenovirus infected cells. <i>Data in Brief</i> , 2016, 8, 1263-1279.	0.5	6
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1353	Identification of microRNAs and their targets in <i>Paulownia fortunei</i> plants free from phytoplasma pathogen after methyl methane sulfonate treatment. <i>Biochimie</i> , 2016, 127, 271-280.	1.3	12
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1372	Transcriptomic analysis of heteromorphic stamens in <i>Cassia bispapsularis</i> L.. <i>Scientific Reports</i> , 2016, 6, 31600.	1.6	3
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1390	Discovery and profiling of microRNAs and their targets in Paulownia 'Yuza' plants via high-throughput sequencing and degradome analysis. Genes and Genomics, 2016, 38, 757-766.	0.5	4
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1428	Transcriptomic analysis of global changes in cytokine expression in mouse spleens following acute <i>Toxoplasma gondii</i> infection. <i>Parasitology Research</i> , 2016, 115, 703-712.	0.6	51
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1458	Genome-wide gene expression patterns in dikaryon of the basidiomycete fungus <i>Pleurotus ostreatus</i> . <i>Brazilian Journal of Microbiology</i> , 2017, 48, 380-390.	0.8	10
1459	miR-29a modulates SCD expression and is regulated in response to a saturated fatty acids diet in juvenile GIFT (<i>Oreochromis niloticus</i>). <i>Journal of Experimental Biology</i> , 2017, 220, 1481-1489.	0.8	17
1460	Comparative transcriptome analysis provides insight into differentially expressed genes related to cytoplasmic male sterility in broccoli (<i>Brassica oleracea</i> var. <i>italica</i>). <i>Scientia Horticulturae</i> , 2017, 217, 234-242.	1.7	18

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1461	Combined analysis of mRNA and miRNA identifies dehydration and salinity responsive key molecular players in citrus roots. <i>Scientific Reports</i> , 2017, 7, 42094.	1.6	44
1462	Expression of microRNAs during female inflorescence development in African oil palm (<i>Elaeis</i>). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i>	0.6	10
1463	Characterization of transcriptome in the Indian meal moth <i>Plodia interpunctella</i> (Lepidoptera:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662</i>	1.0	22
1464	Transcriptome Profiling Reveals the Important Role of Exogenous Nitrogen in Alleviating Cadmium Toxicity in Poplar Plants. <i>Journal of Plant Growth Regulation</i> , 2017, 36, 942-956.	2.8	11
1465	Digital gene expression profiling of the pathogen-resistance mechanism of <i>Oryza sativa</i> 9311 in response to <i>Bacillus amyloliquefaciens</i> FZB42 induction. <i>Biological Control</i> , 2017, 110, 89-97.	1.4	9
1466	Identification of putative flavonoid-biosynthetic genes through transcriptome analysis of Taihe <i>Toona sinensis</i> bud. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	14
1467	Identification of microRNAs expressed in the midgut of <i>Aedes albopictus</i> during dengue infection. <i>Parasites and Vectors</i> , 2017, 10, 63.	1.0	25
1468	Differential expression of a WRKY gene between wild and cultivated soybeans correlates to seed size. <i>Journal of Experimental Botany</i> , 2017, 68, 2717-2729.	2.4	65
1469	Intron retention is regulated by altered MeCP2-mediated splicing factor recruitment. <i>Nature Communications</i> , 2017, 8, 15134.	5.8	92
1470	Environment-dependent regulation of spliceosome activity by the LSM2-8 complex in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2017, 45, 7416-7431.	6.5	36
1471	Genome of <i>Paulownia</i> (<i>Paulownia fortunei</i>) illuminates the related transcripts, miRNA and proteins for salt resistance. <i>Scientific Reports</i> , 2017, 7, 1285.	1.6	13
1472	Fruit quality and differentially expressed genes of winter-harvested pineapple in response to elevated temperature over a short postharvest period. <i>Postharvest Biology and Technology</i> , 2017, 130, 21-27.	2.9	5
1473	Identification and profiling of <i>Cyprinus carpio</i> microRNAs during ovary differentiation by deep sequencing. <i>BMC Genomics</i> , 2017, 18, 333.	1.2	42
1474	Expression profiles of a cytoplasmic male sterile line of <i>Gossypium harknessii</i> and its fertility restorer and maintainer lines revealed by RNA-Seq. <i>Plant Physiology and Biochemistry</i> , 2017, 116, 106-115.	2.8	8
1475	Dietary TiO ₂ particles modulate expression of hormone-related genes in <i>Bombyx mori</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2017, 95, e21397.	0.6	4
1476	Drought responsive microRNAs in two barley cultivars differing in their level of sensitivity to drought stress. <i>Plant Physiology and Biochemistry</i> , 2017, 118, 121-129.	2.8	37
1477	The draft genome of blunt snout bream (<i>Megalobrama amblycephala</i>) reveals the development of intermuscular bone and adaptation to herbivorous diet. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	95
1478	The contrasting microRNA content of a drought tolerant and a drought susceptible wheat cultivar. <i>Journal of Plant Physiology</i> , 2017, 216, 35-43.	1.6	45

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1480	Genetic Subtraction Profiling Identifies Candidate miRNAs Involved in Rice Female Gametophyte Abortion. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2281-2293.	0.8	13
1481	Comparative Transcriptomic Analysis of Vernalization- and Cytokinin-Induced Floral Transition in <i>Dendrobium nobile</i> . <i>Scientific Reports</i> , 2017, 7, 45748.	1.6	22
1482	Identification and expression analysis of WRKY transcription factor genes in response to fungal pathogen and hormone treatments in apple (<i>Malus domestica</i>). <i>Journal of Plant Biology</i> , 2017, 60, 215-230.	0.9	36
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1484	Developmental, chemical and transcriptional characteristics of artificially pollinated and hormone-induced parthenocarpic fruits of <i>Siraitia grosvenorii</i> . <i>RSC Advances</i> , 2017, 7, 12419-12428.	1.7	11
1485	Transcriptomic analysis of two <i>Beauveria bassiana</i> strains grown on cuticle extracts of the silkworm uncovers their different metabolic response at early infection stage. <i>Journal of Invertebrate Pathology</i> , 2017, 145, 45-54.	1.5	23
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1487	Transcriptomic analysis reveals the flooding tolerant mechanism in flooding tolerant line and abscisic acid treated soybean. <i>Plant Molecular Biology</i> , 2017, 93, 479-496.	2.0	35
1488	A novel peptide, 9R-P201, strongly inhibits the viability, proliferation and migration of liver cancer HepG2 cells and induces apoptosis by down-regulation of FoxM1 expression. <i>European Journal of Pharmacology</i> , 2017, 796, 175-189.	1.7	16
1489	Jasmonic Acid Enhances Al-Induced Root Growth Inhibition. <i>Plant Physiology</i> , 2017, 173, 1420-1433.	2.3	79
1490	Comparative analysis of cadmium responsive microRNAs in roots of two <i>Ipomoea aquatica</i> Forsk. cultivars with different cadmium accumulation capacities. <i>Plant Physiology and Biochemistry</i> , 2017, 111, 329-339.	2.8	28
1491	Posttranscriptional Regulation in Adenovirus Infected Cells. <i>Journal of Proteome Research</i> , 2017, 16, 872-888.	1.8	20
1492	De novo transcriptome assembly for pericarp in Litchi <i>chinesis</i> Sonn. cv. Feizixiao and identification of differentially expressed genes in response to Mg Foliar Nutrient. <i>Scientia Horticulturae</i> , 2017, 226, 59-67.	1.7	5
1493	The Ste12-like transcription factor MaSte12 is involved in pathogenicity by regulating the appressorium formation in the entomopathogenic fungus, <i>Metarhizium acridum</i> . <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 8571-8584.	1.7	29
1494	Identification and Functional Analysis of Chitin Synthase A in Oriental Armyworm, <i>Mythimna separata</i> . <i>Proteomics</i> , 2017, 17, 1700165.	1.3	19
1495	Transcriptome analysis of hepatopancreas of <i>Procambarus clarkii</i> challenged with polyriboinosinic polyribocytidylic acid (poly I:C). <i>Fish and Shellfish Immunology</i> , 2017, 71, 144-150.	1.6	28
1496	RNA sequencing analysis of activated macrophages treated with the anti-HIV ABX464 in intestinal inflammation. <i>Scientific Data</i> , 2017, 4, 170150.	2.4	5

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1498	Transcriptomic analysis of flower development in tea (<i>Camellia sinensis</i> (L.)). <i>Gene</i> , 2017, 631, 39-51.	1.0	48
1499	Expression profiles of miRNAs from bovine mammary glands in response to <i>Streptococcus agalactiae</i> -induced mastitis. <i>Journal of Dairy Research</i> , 2017, 84, 300-308.	0.7	46
1500	Transcriptomic analysis of <i>Camellia oleifera</i> in response to drought stress using high throughput RNA-seq. <i>Russian Journal of Plant Physiology</i> , 2017, 64, 728-737.	0.5	6
1501	Histochemical Analyses Reveal That Stronger Intrinsic Defenses in <i>Gossypium barbadense</i> Than in <i>G. hirsutum</i> Are Associated With Resistance to <i>Verticillium dahliae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 984-996.	1.4	65
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1504	Potential factors involved in virulence of <i>Cronobacter sakazakii</i> isolates by comparative transcriptome analysis. <i>Journal of Dairy Science</i> , 2017, 100, 8826-8837.	1.4	13
1505	Effects of toxic <i>Microcystis aeruginosa</i> on the silver carp <i>Hypophthalmichthys molitrix</i> revealed by hepatic RNA-seq and miRNA-seq. <i>Scientific Reports</i> , 2017, 7, 10456.	1.6	7
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1507	Chickpea- <i>Fusarium oxysporum</i> interaction transcriptome reveals differential modulation of plant defense strategies. <i>Scientific Reports</i> , 2017, 7, 7746.	1.6	31
1508	Genotype-dependent regulation of drought-responsive genes in tolerant and sensitive sugarcane cultivars. <i>Gene</i> , 2017, 633, 17-27.	1.0	13
1509	Genome-wide identification of histone H2A and histone variant H2A.Z-interacting proteins by bPPI-seq. <i>Cell Research</i> , 2017, 27, 1258-1274.	5.7	14
1510	Pro- and anti-inflammatory responses of peripheral blood mononuclear cells induced by <i>Staphylococcus aureus</i> and <i>Pseudomonas aeruginosa</i> phages. <i>Scientific Reports</i> , 2017, 7, 8004.	1.6	179
1511	Effect of fluoride treatment on gene expression in tea plant (<i>Camellia sinensis</i>). <i>Scientific Reports</i> , 2017, 7, 9847.	1.6	31
1512	The Combination of RNA and Protein Profiling Reveals the Response to Nitrogen Depletion in <i>Thalassiosira pseudonana</i> . <i>Scientific Reports</i> , 2017, 7, 8989.	1.6	23
1513	Low genetic diversity and functional constraint of miRNA genes participating pollen-pistil interaction in rice. <i>Plant Molecular Biology</i> , 2017, 95, 89-98.	2.0	4
1514	Transcriptome analysis reveals temperature-regulated antiviral response in turbot <i>Scophthalmus maximus</i> . <i>Fish and Shellfish Immunology</i> , 2017, 68, 359-367.	1.6	21

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1516	Integrative analysis of mRNA and miRNA expression profiles in oral lichen planus: preliminary results. <i>Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology</i> , 2017, 124, 390-402.e17.	0.2	22
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1518	Neuron-autonomous transcriptome changes upon ischemia/reperfusion injury. <i>Scientific Reports</i> , 2017, 7, 5800.	1.6	15
1519	Spliceosomal protein <i>eftud2</i> mutation leads to p53-dependent apoptosis in zebrafish neural progenitors. <i>Nucleic Acids Research</i> , 2017, 45, 3422-3436.	6.5	64
1520	PMK-1 p38 MAPK promotes cadmium stress resistance, the expression of SKN-1/Nrf and DAF-16 target genes, and protein biosynthesis in <i>Caenorhabditis elegans</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 1341-1361.	1.0	19
1521	De novo RNA sequencing and analysis of the transcriptome of signalgrass (<i>Urochloa decumbens</i>) roots exposed to aluminum. <i>Plant Growth Regulation</i> , 2017, 83, 157-170.	1.8	23
1522	Comparative transcriptomic evidence for Tween80-enhanced biodegradation of phenanthrene by <i>Sphingomonas</i> sp. GY2B. <i>Science of the Total Environment</i> , 2017, 609, 1161-1171.	3.9	36
1523	Differential expression of genes in HepG2 cells caused by UC001kfo RNAi as shown by RNA-seq. <i>Journal of Huazhong University of Science and Technology [Medical Sciences]</i> , 2017, 37, 510-515.	1.0	2
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1526	A high ratio of IL-12R β 2-positive tumor-infiltrating lymphocytes indicates favorable prognosis in laryngeal cancer. <i>Oral Oncology</i> , 2017, 74, 148-156.	0.8	9
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1530	Transcriptome changes between compatible and incompatible graft combination of <i>Litchi chinensis</i> by digital gene expression profile. <i>Scientific Reports</i> , 2017, 7, 3954.	1.6	46
1531	Transcriptome differences between 20- and 3,000-year-old <i>Platycladus orientalis</i> reveal that ROS are involved in senescence regulation. <i>Electronic Journal of Biotechnology</i> , 2017, 29, 68-77.	1.2	8
1532	Metabolic reprogramming is associated with flavopiridol resistance in prostate cancer DU145 cells. <i>Scientific Reports</i> , 2017, 7, 5081.	1.6	23

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1534	Whole genome duplication enhances the photosynthetic capacity of <i>Chrysanthemum nankingense</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 1247-1256.	1.0	13
1535	Comparative transcriptome analysis on the synthesis pathway of honey bee (<i>Apis mellifera</i>) mandibular gland secretions. <i>Scientific Reports</i> , 2017, 7, 4530.	1.6	35
1536	Transcriptome profiling of cancer and normal tissues from cervical squamous cancer patients by deep sequencing. <i>Molecular Medicine Reports</i> , 2017, 16, 2075-2088.	1.1	17
1537	Deep Super-SAGE transcriptomic analysis of cold acclimation in lentil (<i>Lens culinaris</i> Medik.). <i>BMC Plant Biology</i> , 2017, 17, 111.	1.6	19
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1539	Small RNA sequencing reveals a role for sugarcane miRNAs and their targets in response to <i>Sporisorium scitamineum</i> infection. <i>BMC Genomics</i> , 2017, 18, 325.	1.2	34
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1542	miR-122 promotes hepatic antioxidant defense of genetically improved farmed tilapia (GIFT). <i>Toxicology</i> , 2017, 182, 39-48.	1.9	56
1543	Investigating the mechanisms of glyphosate resistance in goosegrass (<i>Eleusine indica</i> (L.) Gaertn.). <i>Toxicology</i> , 2017, 182, 39-48.	2.8	44
1545	Drought stress-induced changes of microRNAs in diploid and autotetraploid <i>Paulownia tomentosa</i> . <i>Genes and Genomics</i> , 2017, 39, 77-86.	0.5	17
1546	Comparative transcriptome sequencing of the hepatopancreas reveals differentially expressed genes in the precocious juvenile Chinese mitten crab, <i>Eriocheir sinensis</i> (Crustacea: Decapoda). <i>Aquaculture Research</i> , 2017, 48, 3645-3656.	0.9	19
1547	In vitro reprogramming of rat bmMSCs into pancreatic endocrine-like cells. <i>In Vitro Cellular and Developmental Biology - Animal</i> , 2017, 53, 157-166.	0.7	9
1548	Comparison of phytohormone biosynthesis and signal transduction pathways in developing and abortive hazelnut ovules. <i>Plant Growth Regulation</i> , 2017, 81, 147-157.	1.8	23
1549	The C-terminal MIR-containing region in the Pmt1 O-mannosyltransferase restrains sporulation and is dispensable for virulence in <i>Beauveria bassiana</i> . <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1143-1161.	1.7	6
1550	Gene Expression Profiling Stratifies IDH1-Mutant Glioma with Distinct Prognoses. <i>Molecular Neurobiology</i> , 2017, 54, 5996-6005.	1.9	41
1551	Comparative transcriptome analysis of transcription factors in different maize varieties under salt stress conditions. <i>Plant Growth Regulation</i> , 2017, 81, 183-195.	1.8	35

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1553	Differentially expressed gene analysis of <i>Tamarix chinensis</i> provides insights into NaCl-stress response. <i>Trees - Structure and Function</i> , 2017, 31, 645-658.	0.9	13
1554	Illumina-based de novo transcriptome sequencing and analysis of Chinese forest musk deer. <i>Journal of Genetics</i> , 2017, 96, 1033-1040.	0.4	11
1555	Transcriptome profiles reveal cold acclimation and freezing tolerance of susceptible and tolerant hulless barley genotypes. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	16
1556	Biotoxicity of Cry1Ab protein on wolf spider <i>Pardosa pseudoannulata</i> . <i>Ecotoxicology</i> , 2017, 26, 1336-1343.	1.1	4
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1558	Genome-wide expression analysis of transcripts, microRNAs, and the degradome in <i>Paulownia tomentosa</i> under drought stress. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	4
1559	Gene expression variability and the analysis of large-scale RNA-seq studies with the MDSeq. <i>Nucleic Acids Research</i> , 2017, 45, e127-e127.	6.5	35
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1561	Transcriptome Analysis of <i>Hamelia patens</i> (Rubiaceae) Anthers Reveals Candidate Genes for Tapetum and Pollen Wall Development. <i>Frontiers in Plant Science</i> , 2017, 7, 1991.	1.7	8
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1571	Transcriptome and Metabolome Analyses Provide Insights into the Occurrence of Peel Roughing Disorder on Satsuma Mandarin (<i>Citrus unshiu</i> Marc.) Fruit. <i>Frontiers in Plant Science</i> , 2017, 8, 1907.	1.7	10
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1573	Chemosensory genes in the antennal transcriptome of two syrphid species, <i>Episyrphus balteatus</i> and <i>Eupeodes corollae</i> (Diptera: Syrphidae). <i>BMC Genomics</i> , 2017, 18, 586.	1.2	64
1574	Comparative Analysis of the Cytology and Transcriptomes of the Cytoplasmic Male Sterility Line H276A and Its Maintainer Line H276B of Cotton (<i>Gossypium barbadense</i> L.). <i>International Journal of Molecular Sciences</i> , 2017, 18, 2240.	1.8	32
1575	Characterization of the Asiatic Acid Glucosyltransferase, UGT73AH1, Involved in Asiaticoside Biosynthesis in <i>Centella asiatica</i> (L.) Urban. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2630.	1.8	33
1576	Comparative Transcriptome Analysis of <i>Penicillium citrinum</i> Cultured with Different Carbon Sources Identifies Genes Involved in Citrinin Biosynthesis. <i>Toxins</i> , 2017, 9, 69.	1.5	23
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1580	Gibberellic Acid Signaling Is Required to Induce Flowering of <i>Chrysanthemums</i> Grown under Both Short and Long Days. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1259.	1.8	31
1581	The Eukaryote-Like Serine/Threonine Kinase STK Regulates the Growth and Metabolism of Zoonotic <i>Streptococcus suis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 66.	1.8	52
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1583	Transcriptome Analysis of <i>Arabidopsis thaliana</i> in Response to <i>Plasmodiophora brassicae</i> during Early Infection. <i>Frontiers in Microbiology</i> , 2017, 8, 673.	1.5	60
1584	RNA Sequencing Reveals that Endoplasmic Reticulum Stress and Disruption of Membrane Integrity Underlie Dimethyl Trisulfide Toxicity against <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Tropical Race 4. <i>Frontiers in Microbiology</i> , 2017, 8, 1365.	1.5	25
1585	Transcriptome Analysis of Orange Head Chinese Cabbage (<i>Brassica rapa</i> L. ssp. <i>pekinensis</i>) and Molecular Marker Development. <i>International Journal of Genomics</i> , 2017, 2017, 1-8.	0.8	5
1586	Dehydration induced transcriptomic responses in two Tibetan hulless barley (<i>Hordeum vulgare</i> var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	25
1587	Whole Transcriptomic Analysis Provides Insights into Molecular Mechanisms for Toxin Biosynthesis in a Toxic Dinoflagellate <i>Alexandrium catenella</i> (ACHK-T). <i>Toxins</i> , 2017, 9, 213.	1.5	33

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1646	Genome-wide gene expression profiles in response to downy mildew in Chinese cabbage (<i>Brassica rapa</i>) Tj ETQq0 0.0 r gBT /Overlock 10	0.8	10
1647	De novo transcriptome analysis of immune response on cobia (<i>Rachycentron canadum</i>) infected with <i>Photobacterium damsela</i> subsp. <i>piscicida</i> revealed inhibition of complement components and involvement of MyD88-independent pathway. <i>Fish and Shellfish Immunology</i> , 2018, 77, 120-130.	1.6	16
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1662	Transcriptome analysis of <i>Rana chensinensis</i> liver under trichlorfon stress. <i>Ecotoxicology and Environmental Safety</i> , 2018, 147, 487-493.	2.9	21
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1675	Upregulated TSG-6 Expression in ADSCs Inhibits the BV2 Microglia-Mediated Inflammatory Response. <i>BioMed Research International</i> , 2018, 2018, 1-11.	0.9	15
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1691	Transcriptome and gene expression analysis of docosahexaenoic acid producer <i>Schizochytrium</i> sp. under different oxygen supply conditions. <i>Biotechnology for Biofuels</i> , 2018, 11, 249.	6.2	44
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1703	Transcriptome sequencing analysis of two different genotypes of Asian pear reveals potential drought stress genes. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	9
1704	Transcriptome sequencing for identification of diapause-associated genes in fall webworm, <i>Hyphantria cunea</i> Drury. <i>Gene</i> , 2018, 668, 229-236.	1.0	15
1705	Fipronil-induced toxic effects in zebrafish (<i>Danio rerio</i>) larvae by using digital gene expression profiling. <i>Science of the Total Environment</i> , 2018, 639, 550-559.	3.9	22
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1717	FLO Genes Family and Transcription Factor MIG1 Regulate <i>Saccharomyces cerevisiae</i> Biofilm Formation During Immobilized Fermentation. <i>Frontiers in Microbiology</i> , 2018, 9, 1860.	1.5	26
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1719	RNA-seq Analysis Reveals Gene Expression Profiling of Female Fertile and Sterile Ovules of <i>Pinus Tabulaeformis</i> Carr. during Free Nuclear Mitosis of the Female Gametophyte. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2246.	1.8	7
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1722	Comparative Transcriptome Analysis for Understanding Predator-Induced Polyphenism in the Water Flea <i>Daphnia pulex</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 2110.	1.8	20
1723	Determination of multidrug resistance mechanisms in <i>Clostridium perfringens</i> type A isolates using RNA sequencing and 2D-electrophoresis. <i>Brazilian Journal of Medical and Biological Research</i> , 2018, 51, e7044.	0.7	3
1724	Genome-Wide Analysis of Gene and microRNA Expression in Diploid and Autotetraploid <i>Paulownia fortunei</i> (Seem) Hemsl. under Drought Stress by Transcriptome, microRNA, and Degradome Sequencing. <i>Forests</i> , 2018, 9, 88.	0.9	11
1725	Comparative Analysis of MicroRNA Expression in Three <i>Paulownia</i> Species with <i>Phytoplasma</i> Infection. <i>Forests</i> , 2018, 9, 302.	0.9	7
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1728	Seed Transcriptomics Analysis in <i>Camellia oleifera</i> Uncovers Genes Associated with Oil Content and Fatty Acid Composition. <i>International Journal of Molecular Sciences</i> , 2018, 19, 118.	1.8	56
1729	Comparative Digital Gene Expression Analysis of Tissue-Cultured Plantlets of Highly Resistant and Susceptible Banana Cultivars in Response to <i>Fusarium oxysporum</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 350.	1.8	24
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1731	Comparative Transcriptome Analysis of Waterlogging-Sensitive and Waterlogging-Tolerant <i>Chrysanthemum morifolium</i> Cultivars under Waterlogging Stress and Reoxygenation Conditions. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1455.	1.8	44

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1734	Identification of candidate chemosensory genes in <i>Mythimna separata</i> by transcriptomic analysis. <i>BMC Genomics</i> , 2018, 19, 518.	1.2	34
1735	Transcriptome analysis of abscisic acid induced 20E regulation in suspension <i>Ajuga lobata</i> cells. <i>3 Biotech</i> , 2018, 8, 320.	1.1	5
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1737	Whole-transcriptome splicing profiling of E7.5 mouse primary germ layers reveals frequent alternative promoter usage during mouse early embryogenesis. <i>Biology Open</i> , 2018, 7, .	0.6	6
1738	Combined analysis and miRNA expression profiles of the flowering related genes in common wild rice (<i>Oryza rufipogon</i> Griff.). <i>Genes and Genomics</i> , 2018, 40, 835-845.	0.5	5
1739	Acute Hepatopancreatic Necrosis Disease (AHPND) related microRNAs in <i>Litopenaeus vannamei</i> infected with AHPND-causing strain of <i>Vibrio parahaemolyticus</i> . <i>BMC Genomics</i> , 2018, 19, 335.	1.2	29
1740	Transcriptome analysis of adipose tissues from two fat-tailed sheep breeds reveals key genes involved in fat deposition. <i>BMC Genomics</i> , 2018, 19, 338.	1.2	57
1741	Gene co-expression network analysis reveals coordinated regulation of three characteristic secondary biosynthetic pathways in tea plant (<i>Camellia sinensis</i>). <i>BMC Genomics</i> , 2018, 19, 616.	1.2	71
1742	Identification of lncRNAs and Their Functional Network Associated with Chemoresistance in SW1990/GZ Pancreatic Cancer Cells by RNA Sequencing. <i>DNA and Cell Biology</i> , 2018, 37, 839-849.	0.9	25
1743	Detoxification- and Immune-Related Transcriptomic Analysis of Gills from Bay Scallops (<i>Argopecten</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.5	32
1744	Auxin homeostasis and signaling alterations result in the aberrant phenotype in scl mutant of cotton (<i>Gossypium hirsutum</i> L.). <i>Revista Brasileira De Botanica</i> , 2018, 41, 775-784.	0.5	0
1745	De novo transcriptomic assembly and mRNA expression patterns of <i>Botryosphaeria dothidea</i> infection with mycoviruses chrysovirus 1 (BdCV1) and partitivirus 1 (BdPV1). <i>Virology Journal</i> , 2018, 15, 126.	1.4	14
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1748	Comparative performance of the BGISEQ-500 and Illumina HiSeq4000 sequencing platforms for transcriptome analysis in plants. <i>Plant Methods</i> , 2018, 14, 69.	1.9	128
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1751	Brassinosteroids regulate root growth by controlling reactive oxygen species homeostasis and dual effect on ethylene synthesis in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2018, 14, e1007144.	1.5	152
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1753	Exploration of the effect of blue light on microRNAs involved in the accumulation of functional metabolites of longan embryonic calli through RNA-seq. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 1533-1547.	1.7	10
1754	Transcriptional Study Revealed That Boron Supplementation May Alter the Immune-Related Genes Through MAPK Signaling in Ostrich Chick Thymus. <i>Biological Trace Element Research</i> , 2019, 189, 209-223.	1.9	8
1755	ACDtool: a web-server for the generic analysis of large data sets of counts. <i>Bioinformatics</i> , 2019, 35, 170-171.	1.8	5
1756	A unique life cycle transition in the red seaweed <i>Pyropia yezoensis</i> depends on apospory. <i>Communications Biology</i> , 2019, 2, 299.	2.0	27
1757	Genome-Wide Identification of Long Non-Coding RNAs and Their Regulatory Networks Involved in <i>Apis mellifera ligustica</i> Response to <i>Nosema ceranae</i> Infection. <i>Insects</i> , 2019, 10, 245.	1.0	35
1758	Comparative Transcriptome Analysis of Unusual Localized Skin Lesions in Sika Deer (<i>Cervus</i>)	0.9	10
1759	Hyperuricemia is associated with impaired intestinal permeability in mice. <i>American Journal of Physiology - Renal Physiology</i> , 2019, 317, G484-G492.	1.6	45
1760	RNA sequencing analysis of <i>Cymbidium goeringii</i> identifies floral scent biosynthesis related genes. <i>BMC Plant Biology</i> , 2019, 19, 337.	1.6	35
1761	Circular RNA expression profiles in cisplatin-induced acute kidney injury in mice. <i>Epigenomics</i> , 2019, 11, 1191-1207.	1.0	19
1762	Transcriptome analysis of virulence-differentiated <i>Fusarium oxysporum</i> f. sp. <i>cucumerinum</i> isolates during cucumber colonisation reveals pathogenicity profiles. <i>BMC Genomics</i> , 2019, 20, 570.	1.2	13
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1767	P8 nuclear receptor responds to acaricides exposure and regulates transcription of P450 enzyme in the two-spotted spider mite, <i>Tetranychus urticae</i> . <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2019, 224, 108561.	1.3	3

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1769	Core transcriptional signatures of phase change in the migratory locust. <i>Protein and Cell</i> , 2019, 10, 883-901.	4.8	28
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1771	Microcystin-LR Degradation and Gene Regulation of Microcystin-Degrading <i>Novosphingobium</i> sp. THN1 at Different Carbon Concentrations. <i>Frontiers in Microbiology</i> , 2019, 10, 1750.	1.5	14
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1776	Sulfadiazine biodegradation by <i>Phanerochaete chrysosporium</i> : Mechanism and degradation product identification. <i>Chemosphere</i> , 2019, 237, 124418.	4.2	27
1777	Effects of short-time exposure to atrazine on miRNA expression profiles in the gonad of common carp (<i>Cyprinus carpio</i>). <i>BMC Genomics</i> , 2019, 20, 587.	1.2	13
1778	Transcriptome analysis of Korean fir (<i>Abies koreana</i>) in response to elevated carbon dioxide and high temperature. <i>Plant Biotechnology Reports</i> , 2019, 13, 603-612.	0.9	5
1779	The relationship between cuticular lipids and associated gene expression in above ground organs of <i>Thellungiella salsugineum</i> (Pall.) Al-Shehbaz & Warwick. <i>Plant Science</i> , 2019, 287, 110200.	1.7	4
1780	Differential microRNA Expression in Porcine Endometrium Involved in Remodeling and Angiogenesis That Contributes to Embryonic Implantation. <i>Frontiers in Genetics</i> , 2019, 10, 661.	1.1	29
1781	Detoxification, Apoptosis, and Immune Transcriptomic Responses of the Gill Tissue of Bay Scallop Following Exposure to the Algicide Thiazolidinedione 49. <i>Biomolecules</i> , 2019, 9, 310.	1.8	7
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1784	Comparative analysis of biocontrol agent <i>Trichoderma asperellum</i> ACCC30536 transcriptome during its interaction with <i>Populus davidiana</i> A— <i>P. alba</i> var. <i>pyramidalis</i> . <i>Microbiological Research</i> , 2019, 227, 126294.	2.5	15
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1794	Whole solid tumour volume histogram analysis of the apparent diffusion coefficient for differentiating high-grade from low-grade serous ovarian carcinoma: correlation with Ki-67 proliferation status. <i>Clinical Radiology</i> , 2019, 74, 918-925.	0.5	17
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1799	Study on the differential gene expression of elm leaves fed on by <i>Tetraneura akinire</i> Sasaki. <i>Genes and Genomics</i> , 2019, 41, 1505-1516.	0.5	2
1800	Screening for differentially expressed miRNAs in <i>Aedes albopictus</i> (Diptera: Culicidae) exposed to DENV-2 and their effect on replication of DENV-2 in C6/36 cells. <i>Parasites and Vectors</i> , 2019, 12, 44.	1.0	16
1801	<i>Arabidopsis</i> SME1 Regulates Plant Development and Response to Abiotic Stress by Determining Spliceosome Activity Specificity. <i>Plant Cell</i> , 2019, 31, 537-554.	3.1	42
1802	Comparative transcriptome analysis of two selenium-accumulating genotypes of <i>Aegilops tauschii</i> Coss. in response to selenium. <i>BMC Genetics</i> , 2019, 20, 9.	2.7	10
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1806	Genetic control of compound leaf development in the mungbean (<i>Vigna radiata</i> L.). <i>Horticulture Research</i> , 2019, 6, 23.	2.9	22
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1809	Photosynthesis and yield response to elevated CO ₂ , C ₄ plant foxtail millet behaves similarly to C ₃ species. <i>Plant Science</i> , 2019, 285, 239-247.	1.7	26
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1813	Comparative transcriptome analysis reveals resistance-related genes and pathways in <i>Musa acuminata</i> banana 'Guijiao 9' in response to <i>Fusarium</i> wilt. <i>Plant Physiology and Biochemistry</i> , 2019, 141, 83-94.	2.8	44
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1817	Comprehensive analysis of full genome sequence and Bd-milRNA/target mRNAs to discover the mechanism of hypovirulence in <i>Botryosphaeria dothidea</i> strains on pear infection with BdCV1 and BdPV1. <i>IMA Fungus</i> , 2019, 10, 3.	1.7	11
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1823	Identification and Characterization of Salt-Responsive MicroRNAs in <i>Vicia faba</i> by High-Throughput Sequencing. <i>Genes</i> , 2019, 10, 303.	1.0	23
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1826	MADS-box transcription factor <i>Mcm1</i> controls cell cycle, fungal development, cell integrity and virulence in the filamentous insect pathogenic fungus <i>Beauveria bassiana</i> . <i>Environmental Microbiology</i> , 2019, 21, 3392-3416.	1.8	30
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1832	Transcriptome analysis reveals regulatory framework for salt and osmotic tolerance in a succulent xerophyte. <i>BMC Plant Biology</i> , 2019, 19, 88.	1.6	23
1833	Gene expression profiling of ovary identified eggshell proteins regulated by 20-hydroxyecdysone in <i>Bactrocera dorsalis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 30, 206-216.	0.4	7
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1835	Adipose-derived mesenchymal stromal cells improve hemodynamic function in pulmonary arterial hypertension: identification of microRNAs implicated in modulating endothelial function. <i>Cytotherapy</i> , 2019, 21, 416-427.	0.3	8
1836	De novo assembly and characterization of the transcriptome of the northern mauxia shrimp <i>Acetes chinensis</i> . <i>Marine Genomics</i> , 2019, 47, 100672.	0.4	4
1837	Identification and classification of differentially expressed genes in pyrethroid-resistant <i>Culex pipiens pallens</i> . <i>Molecular Genetics and Genomics</i> , 2019, 294, 861-873.	1.0	10
1838	Coordinated expression of vascular endothelial growth factor A and urokinase-type plasminogen activator contributes to classical swine fever virus Shimen infection in macrophages. <i>BMC Veterinary Research</i> , 2019, 15, 82.	0.7	2
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1843	Transcriptome profiling of faba bean (<i>Vicia faba</i> L.) drought-tolerant variety hassawi-2 under drought stress using RNA sequencing. <i>Electronic Journal of Biotechnology</i> , 2019, 39, 15-29.	1.2	19
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1846	Circular RNA expression profiling of granulosa cells in women of reproductive age with polycystic ovary syndrome. <i>Archives of Gynecology and Obstetrics</i> , 2019, 300, 431-440.	0.8	40
1847	Transcriptome Analysis of Dairy Goat Mammary Gland Tissues from Different Lactation Stages. <i>DNA and Cell Biology</i> , 2019, 38, 129-143.	0.9	12
1848	Identification and expression analysis of ceftriaxone resistance-related genes in <i>Neisseria gonorrhoeae</i> integrating RNA-Seq data and qRT-PCR validation. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 16, 202-209.	0.9	19
1849	Transcriptome and Proteome Alternation With Resistance to <i>Bacillus thuringiensis</i> Cry1A δ Toxin in <i>Ostrinia furnacalis</i> . <i>Frontiers in Physiology</i> , 2019, 10, 27.	1.3	16
1850	Genome-wide analysis and identification of the low potassium stress responsive gene SiMYB3 in foxtail millet (<i>Setaria italica</i> L.). <i>BMC Genomics</i> , 2019, 20, 136.	1.2	15
1851	Acaricidal Mechanism of Scopoletin Against <i>Tetranychus cinnabarinus</i> . <i>Frontiers in Physiology</i> , 2019, 10, 164.	1.3	17
1852	Diff isomiRs: Large-scale detection of differential isomiRs for understanding non-coding regulated stress omics in plants. <i>Scientific Reports</i> , 2019, 9, 1406.	1.6	9
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1854	Comparative sialotranscriptome analysis of the rare Chinese cicada <i>Subsalsaltria yangi</i> , with identification of candidate genes related to host-plant adaptation. <i>International Journal of Biological Macromolecules</i> , 2019, 130, 323-332.	3.6	7
1855	Genome-wide discovery and characterization of flower development related long non-coding RNAs in <i>Prunus mume</i> . <i>BMC Plant Biology</i> , 2019, 19, 64.	1.6	36
1856	Molecular Mechanism of Xylogenesis in Moso Bamboo (<i>Phyllostachys edulis</i>) Shoots during Cold Storage. <i>Polymers</i> , 2019, 11, 38.	2.0	9
1857	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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1860	The changing paradigm of intron retention: regulation, ramifications and recipes. <i>Nucleic Acids Research</i> , 2019, 47, 11497-11513.	6.5	90
1861	Transcriptomic Profiling Identifies Candidate Genes Involved in the Salt Tolerance of the Xerophyte <i>Pugionium cornutum</i> . <i>Genes</i> , 2019, 10, 1039.	1.0	9
1862	The Indispensable Role of Histone Methyltransferase PoDot1 in Extracellular Glycoside Hydrolase Biosynthesis of <i>Penicillium oxalicum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2566.	1.5	16
1863	Transcriptional and post-transcriptional responses of diploid and autotetraploid <i>Paulownia tomentosa</i> and <i>Paulownia fortunei</i> under water-deficit condition. <i>Revista Brasileira De Botanica</i> , 2019, 42, 623-641.	0.5	6
1864	Transcriptome Analysis Reveals the Molecular Mechanisms Underlying Adenosine Biosynthesis in Anamorph Strain of Caterpillar Fungus. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	8
1865	Expression profiles of genes regulated by BpIMYB46 in <i>Betula platyphylla</i> . <i>Journal of Forestry Research</i> , 2019, 30, 2267-2276.	1.7	0
1866	<i>Xanthomonas campestris</i> Promotes Diffusible Signal Factor Biosynthesis and Pathogenicity by Utilizing Glucose and Sucrose from Host Plants. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 157-166.	1.4	12
1867	Maternal control of seed weight in rapeseed (<i>Brassica napus</i> L.): the causal link between the size of pod (mother, source) and seed (offspring, sink). <i>Plant Biotechnology Journal</i> , 2019, 17, 736-749.	4.1	37
1868	The genome and transcriptome of <i>Lactococcus lactis</i> ssp. <i>lactis</i> F44 and G423: Insights into adaptation to the acidic environment. <i>Journal of Dairy Science</i> , 2019, 102, 1044-1058.	1.4	10
1869	Single-nucleotide-resolution mapping of DNA gyrase cleavage sites across the <i>Escherichia coli</i> genome. <i>Nucleic Acids Research</i> , 2019, 47, 1373-1388.	6.5	50
1870	Transcriptome sequencing of the gill and barbel of Southern catfish (<i>Silurus meridionalis</i>) revealed immune responses and novel rhamnose-binding lectins (RBLs). <i>Genomics</i> , 2019, 111, 222-230.	1.3	8
1871	Insights into genes encoding respiratory burst oxidase homologs (RBOHs) in rubber tree (<i>Hevea</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 11 2.5 31	1.7	13
1872	<i>In vivo</i> transcriptomic analysis of <i>Beauveria bassiana</i> reveals differences in infection strategies in <i>Galleria mellonella</i> and <i>Plutella xylostella</i> . <i>Pest Management Science</i> , 2019, 75, 1443-1452.	1.7	13
1873	Comparative transcriptome analysis highlights the hormone effects on somatic embryogenesis in <i>Catalpa bungei</i> . <i>Plant Reproduction</i> , 2019, 32, 141-151.	1.3	22
1874	<i>Rh6</i> gene modulates the visual mechanism of host utilization in fruit fly <i>Bactrocera minax</i> . <i>Pest Management Science</i> , 2019, 75, 1621-1629.	1.7	37
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1877	The protein phosphatase gene MaPpt1 acts as a programmer of microcycle conidiation and a negative regulator of UV-B tolerance in <i>Metarhizium acridum</i> . <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1351-1362.	1.7	10
1878	De novo leaf and root transcriptome analysis to explore biosynthetic pathway of Celangulin V in <i>Celastrus angulatus maxim.</i> <i>BMC Genomics</i> , 2019, 20, 7.	1.2	26
1879	Understanding the Resistance Mechanism in <i>Brassica napus</i> to Clubroot Caused by <i>Plasmodiophora brassicae</i> . <i>Phytopathology</i> , 2019, 109, 810-818.	1.1	16
1880	Transcriptomic and proteomic analyses reveal new insights into the regulation of immune pathways during adenovirus type 2 infection. <i>BMC Microbiology</i> , 2019, 19, 15.	1.3	10
1881	Three isoforms of exosomal circPTGR1 promote hepatocellular carcinoma metastasis via the miR449a-MET pathway. <i>EBioMedicine</i> , 2019, 40, 432-445.	2.7	186
1882	Liver transcriptome analysis and de novo annotation of the orange-spotted groupers (<i>Epinephelus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Proteomics, 2019, 29, 264-273.	0.4	29
1883	Transcriptomic de novo analysis of pitaya (<i>Hylocereus polyrhizus</i>) canker disease caused by <i>Neoscytalidium dimidiatum</i> . <i>BMC Genomics</i> , 2019, 20, 10.	1.2	39
1884	Comparative Transcriptome Analysis Reveals an Efficient Mechanism of δ^{\pm} -Linolenic Acid in Tree Peony Seeds. <i>International Journal of Molecular Sciences</i> , 2019, 20, 65.	1.8	25
1885	Transcriptome analysis of strawberry (<i>Fragaria</i> — <i>ananassa</i>) fruits under osmotic stresses and identification of genes related to ascorbic acid pathway. <i>Physiologia Plantarum</i> , 2019, 166, 979-995.	2.6	13
1886	Identification of critical sex-biased genes in <i>Andrias davidianus</i> by de novo transcriptome. <i>Molecular Genetics and Genomics</i> , 2019, 294, 287-299.	1.0	17
1887	Regulation of compound leaf development in mungbean (<i>Vigna radiata</i> L.) by CUP-SHAPED COTYLEDON/NO APICAL MERISTEM (CUC/NAM) gene. <i>Planta</i> , 2019, 249, 765-774.	1.6	39
1888	Transcriptomic responses to low temperature stress in the Nile tilapia, <i>Oreochromis niloticus</i> . <i>Fish and Shellfish Immunology</i> , 2019, 84, 1145-1156.	1.6	73
1889	Differential expression of genes in greenbug (<i>Schizaphis graminum</i> Rondani) treated by imidacloprid and RNA interference. <i>Pest Management Science</i> , 2019, 75, 1726-1733.	1.7	18
1890	Gene transcription profiling of <i>Aspergillus oryzae</i> 3.042 treated with ergosterol biosynthesis inhibitors. <i>Brazilian Journal of Microbiology</i> , 2019, 50, 43-52.	0.8	13
1891	Molecular characterization of anthocyanin and betulinic acid biosynthesis in red and white mulberry fruits using high-throughput sequencing. <i>Food Chemistry</i> , 2019, 279, 364-372.	4.2	28
1892	A Novel R2R3-MYB Transcription Factor Contributes to Petal Blotch Formation by Regulating Organ-Specific Expression of <i>PsCHS</i> in Tree Peony (<i>Paeonia suffruticosa</i>). <i>Plant and Cell Physiology</i> , 2019, 60, 599-611.	1.5	77
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1895	<i>De novo</i> transcriptome combined with spectrophotometry and gas chromatography-mass spectrometer (GC-MS) reveals differentially expressed genes during accumulation of secondary metabolites in purple-leaf tea (<i>Camellia sinensis</i> cv Hongyafoshou). <i>Journal of Horticultural Science and Biotechnology</i> , 2019, 94, 349-367.	0.9	36
1896	The regulatory module MdPUB29-MdbHLH3 connects ethylene biosynthesis with fruit quality in apple. <i>New Phytologist</i> , 2019, 221, 1966-1982.	3.5	88
1897	HT-SuperSAGE of the gut tissue of a Vip3A-resistant <i>Heliothis virescens</i> (Lepidoptera: Noctuidae) strain provides insights into the basis of resistance. <i>Insect Science</i> , 2019, 26, 479-498.	1.5	5
1898	Transcriptome analysis of <i>Oncidium</i> petals provides new insights into the initiation of petal senescence. <i>Journal of Horticultural Science and Biotechnology</i> , 2019, 94, 12-23.	0.9	5
1899	Differential Transcriptome Analysis of Early Postnatal Developing <i>Longissimus Dorsi</i> Muscle from Two Pig Breeds Characterized in Divergent Myofiber Traits and Fatness. <i>Animal Biotechnology</i> , 2019, 30, 63-74.	0.7	16
1900	Response of Chinese fir seedlings to low phosphorus stress and analysis of gene expression differences. <i>Journal of Forestry Research</i> , 2019, 30, 183-192.	1.7	10
1901	Identification of genes related to chlamyospore formation in <i>Clonostachys rosea</i> . <i>MicrobiologyOpen</i> , 2019, 8, e00624.	1.2	14
1902	CRISPR disruption of TCTP gene impaired normal development in the silkworm <i>Bombyx mori</i> . <i>Insect Science</i> , 2019, 26, 973-982.	1.5	10
1903	Lipopolysaccharide induces the differentiation of hepatic progenitor cells into myofibroblasts constitutes the hepatocarcinogenesis-associated microenvironment. <i>Cell Death and Differentiation</i> , 2020, 27, 85-101.	5.0	34
1904	Transcriptome Characterization of Gene Profiling During Early Stage of Nitric Oxide-Induced Adventitious Rooting in Mung Bean Seedlings. <i>Journal of Plant Growth Regulation</i> , 2020, 39, 430-455.	2.8	6
1905	Systematic identification and analysis of heat-stress-responsive lncRNAs, circRNAs and miRNAs with associated co-expression and ceRNA networks in cucumber (<i>Cucumis sativus</i> L.). <i>Physiologia Plantarum</i> , 2020, 168, 736-754.	2.6	90
1906	Comparative morphological and transcriptomic responses of lowland and upland rice to root-zone hypoxia. <i>Environmental and Experimental Botany</i> , 2020, 169, 103916.	2.0	17
1907	Metformin ameliorates stress-induced depression-like behaviors via enhancing the expression of BDNF by activating AMPK/CREB-mediated histone acetylation. <i>Journal of Affective Disorders</i> , 2020, 260, 302-313.	2.0	83
1908	Transcriptome analysis reveals new insights into immune response to hypoxia challenge of large yellow croaker (<i>Larimichthys crocea</i>). <i>Fish and Shellfish Immunology</i> , 2020, 98, 738-747.	1.6	29
1909	Transcription factor BnaA9.WRKY47 contributes to the adaptation of <i>Brassica napus</i> to low boron stress by up-regulating the boric acid channel gene <i>BnaA3.NIP5;1</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 1241-1254.	4.1	47
1910	Contact-dependent delivery of IL-2 by dendritic cells to CD4 T cells in the contraction phase promotes their long-term survival. <i>Protein and Cell</i> , 2020, 11, 108-123.	4.8	4
1911	Comparative analysis of dsRNA-induced lncRNAs in three kinds of insect species. <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 103, e21640.	0.6	13

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1913	A Transcriptomic Analysis of Neuropathic Pain in Rat Dorsal Root Ganglia Following Peripheral Nerve Injury. <i>NeuroMolecular Medicine</i> , 2020, 22, 250-263.	1.8	30
1914	Identifying Vitamin E Biosynthesis Genes in <i>Elaeis guineensis</i> by Genome-Wide Association Study. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 678-685.	2.4	7
1915	Comparative Transcriptomics Reveals Features and Possible Mechanisms of Glucose-Mediated Soil Fungistasis Relief in <i>Arthrobotrys oligospora</i> . <i>Frontiers in Microbiology</i> , 2020, 10, 3143.	1.5	5
1916	Genome-wide methylation and expression profiling identify methylation-associated genes in colorectal cancer. <i>Epigenomics</i> , 2020, 12, 19-36.	1.0	10
1917	Coordination of multiple regulation pathways contributes to the tolerance of a wild citrus species (<i>Citrus ichangensis</i> 2586™) against Huanglongbing. <i>Physiological and Molecular Plant Pathology</i> , 2020, 109, 101457.	1.3	12
1918	Global scale transcriptome analysis reveals differentially expressed genes involve in early somatic embryogenesis in <i>Dimocarpus longan</i> Lour. <i>BMC Genomics</i> , 2020, 21, 4.	1.2	32
1919	Multiple microRNAs control ecdysone signaling in the midgut of <i>Spodoptera litura</i> . <i>Insect Science</i> , 2020, 27, 1208-1223.	1.5	11
1920	Metabolome and transcriptome profiling reveals quality variation and underlying regulation of three ecotypes for <i>Cistanche deserticola</i> . <i>Plant Molecular Biology</i> , 2020, 102, 253-269.	2.0	26
1921	Transcriptomic Analysis Suggests Genes Expressed Stage-Independently and Stage-Dependently Modulating the Wing Dimorphism of the Brown Planthopper. <i>Genes</i> , 2020, 11, 19.	1.0	3
1922	Pharmacological Effects of Novel Peptide Drugs on Allergic Rhinitis at the Small Ribonucleic Acids Level. <i>Frontiers in Genetics</i> , 2020, 11, 560812.	1.1	1
1923	Repression of FGF signaling is responsible for <i>Dnmt3b</i> inhibition and impaired <i>de novo</i> DNA methylation during early development of <i>in vitro</i> fertilized embryos. <i>International Journal of Biological Sciences</i> , 2020, 16, 3085-3099.	2.6	7
1924	Pro-197-Ser Mutation in ALS and High-Level GST Activities: Multiple Resistance to ALS and ACCase Inhibitors in <i>Beckmannia syzigachne</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 572610.	1.7	13
1925	Transcriptome analysis identifies key genes involved in carotenoid biosynthesis in the flesh of red pummelo (<i>Citrus maxima</i>). <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 614-622.	0.5	2
1926	C-type lectin-mediated microbial homeostasis is critical for <i>Helicoverpa armigera</i> larval growth and development. <i>PLoS Pathogens</i> , 2020, 16, e1008901.	2.1	17
1927	The Chromosome Level Genome and Genome-wide Association Study for the Agronomic Traits of <i>Panax Notoginseng</i> . <i>IScience</i> , 2020, 23, 101538.	1.9	34
1928	Comparative transcriptome analysis reveals heat stress-responsive genes and their signalling pathways in lilies (<i>Lilium longiflorum</i> vs. <i>Lilium distichum</i>). <i>PLoS ONE</i> , 2020, 15, e0239605.	1.1	6
1929	<i>Penicillium oxalicum</i> putative methyltransferase Mtr23B has similarities and differences with <i>LaeA</i> in regulating conidium development and glycoside hydrolase gene expression. <i>Fungal Genetics and Biology</i> , 2020, 143, 103445.	0.9	8

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1931	Detection of candidate proteins in the indican biosynthetic pathway of <i>Persicaria tinctoria</i> (<i>Polygonum tinctorium</i>) using protein-protein interactions and transcriptome analyses. Phytochemistry, 2020, 179, 112507.	1.4	3
1932	Alternative splicing of flowering time gene FT is associated with halving of time to flowering in coconut. Scientific Reports, 2020, 10, 11640.	1.6	11
1933	Transcriptomic analysis of flower opening response to relatively low temperatures in <i>Osmanthus fragrans</i> . BMC Plant Biology, 2020, 20, 337.	1.6	8
1934	Transcriptome analysis reveals key information on improving duck yolk lipid contents induced by dietary fish oil or flaxseed oil. Journal of Applied Animal Research, 2020, 48, 192-200.	0.4	0
1935	TWIST1-MicroRNA-10a-MAP3K7 Axis Ameliorates Synovitis of Osteoarthritis in Fibroblast-like Synoviocytes. Molecular Therapy - Nucleic Acids, 2020, 22, 1107-1120.	2.3	9
1936	Temporal salt stress-induced transcriptome alterations and regulatory mechanisms revealed by PacBio long-reads RNA sequencing in <i>Gossypium hirsutum</i> . BMC Genomics, 2020, 21, 838.	1.2	19
1937	Comparative transcriptome analysis of lingonberry (<i>Vaccinium vitis-idaea</i>) provides insights into genes associated with flavonoids metabolism during fruit development. Biotechnology and Biotechnological Equipment, 2020, 34, 1252-1264.	0.5	8
1938	Comparative Transcriptome Analysis of Toxic and Non-Toxic <i>Nassarius</i> Communities and Identification of Genes Involved in TTX-Adaptation. Toxins, 2020, 12, 761.	1.5	6
1939	3 β -Hydroxycholest-5-en-7-one from seahorse alleviates lipopolysaccharide-induced inflammatory responses by downregulating miR-98-5p. Life Sciences, 2020, 258, 118176.	2.0	5
1940	Brain transcriptome study through CRISPR/Cas9 mediated mouse Dip2c gene knock-out. Gene, 2020, 758, 144975.	1.0	17
1941	Based on RNA-Seq analysis identification and expression analysis of Transcription factor-related genes of UV-treatment in postharvest grape fruit. Archives of Biochemistry and Biophysics, 2020, 690, 108471.	1.4	7
1942	The identification of differentially expressed genes in male and female gametophytes of simple thalloid liverwort <i>Pellia endiviifolia</i> sp. B using an RNA-seq approach. Planta, 2020, 252, 21.	1.6	3
1943	Deployment of Genetic and Genomic Tools Toward Gaining a Better Understanding of Rice- <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Interactions for Development of Durable Bacterial Blight Resistant Rice. Frontiers in Plant Science, 2020, 11, 1152.	1.7	41
1944	A basic/helix-loop-helix transcription factor controls leaf shape by regulating auxin signaling in apple. New Phytologist, 2020, 228, 1897-1913.	3.5	16
1945	The protective effect of quercetin on retinal inflammation in mice: the involvement of tumor necrosis factor/nuclear factor- κ B signaling pathways. Food and Function, 2020, 11, 8150-8160.	2.1	9
1946	A Transcriptomic Analysis Reveals Novel Patterns of Gene Expression During 3T3-L1 Adipocyte Differentiation. Frontiers in Molecular Biosciences, 2020, 7, 564339.	1.6	20
1947	HMGR overexpression and interference affect the expression of steroidogenic genes and cholesterol content in bovine intramuscular adipocytes. Scientific Reports, 2020, 10, 16606.	1.6	5

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1950	Analysis of novel siRNA and piRNA and identification of vsiRNA and vpiRNA expressed in the midgut of <i>Aedes albopictus</i> during dengue infection. <i>Entomological Research</i> , 2020, 50, 463-474.	0.6	1
1951	Dysfunction of dimorphic sperm impairs male fertility in the silkworm. <i>Cell Discovery</i> , 2020, 6, 60.	3.1	30
1952	Characterization of the DREBA4-Type Transcription Factor (SIDREBA4), Which Contributes to Heat Tolerance in Tomatoes. <i>Frontiers in Plant Science</i> , 2020, 11, 554520.	1.7	17
1953	Prototype foamy virus downregulates RelB expression to facilitate viral replication. <i>FEBS Open Bio</i> , 2020, 10, 2137-2148.	1.0	7
1954	Proteomic and transcriptomic studies of BGC823 cells stimulated with <i>Helicobacter pylori</i> isolates from gastric MALT lymphoma. <i>PLoS ONE</i> , 2020, 15, e0238379.	1.1	3
1955	Transcriptome sequencing of <i>Coccinella septempunctata</i> adults (Coleoptera: Coccinellidae) feeding on artificial diet and <i>Aphis craccivora</i> . <i>PLoS ONE</i> , 2020, 15, e0236249.	1.1	5
1956	High-throughput sequencing reveals the molecular mechanisms determining the stay-green characteristic in soybeans. <i>Journal of Biosciences</i> , 2020, 45, 1.	0.5	3
1957	Transcriptome Dynamics during Black and White Sesame (<i>Sesamum indicum</i> L.) Seed Development and Identification of Candidate Genes Associated with Black Pigmentation. <i>Genes</i> , 2020, 11, 1399.	1.0	25
1958	Transcriptome Analysis of Ovarian and Uterine Clear Cell Malignancies. <i>Frontiers in Oncology</i> , 2020, 10, 598579.	1.3	12
1959	Digital gene expression profiling analysis of A549 cells cultured with PM10 in moxa smoke. <i>Journal of Traditional Chinese Medical Sciences</i> , 2020, 7, 404-412.	0.1	0
1960	Genome-wide identification of candidate genes related to disease resistance and high biomass in tetraploid <i>Paulownia</i> . <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	1.0	3
1961	Basal-Level Effects of (p)ppGpp in the Absence of Branched-Chain Amino Acids in <i>Actinobacillus pleuropneumoniae</i> . <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	4
1962	Disruption of a C69-Family Cysteine Dipeptidase Gene Enhances Heat Shock and UV-B Tolerances in <i>Metarhizium acridum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 849.	1.5	7
1963	The Biotechnological Potential of the Marine Diatom <i>Skeletonema dohrnii</i> to the Elevated Temperature and pCO ₂ . <i>Marine Drugs</i> , 2020, 18, 259.	2.2	16
1964	Analysis of the Transcriptome of <i>Polygonatum odoratum</i> (Mill.) Druce Uncovers Putative Genes Involved in Isoflavonoid Biosynthesis. <i>Journal of Plant Biology</i> , 2020, 63, 217-228.	0.9	3
1965	The Mitogen-Activated Protein Kinase Gene <i>Crmapk</i> Is Involved in <i>Clonostachys chloroleuca</i> Mycoparasitism. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 902-910.	1.4	11
1966	Transcriptome Analysis Reveals the Flexibility of Cordycepin Network in <i>Cordyceps militaris</i> Activated by L-Alanine Addition. <i>Frontiers in Microbiology</i> , 2020, 11, 577.	1.5	23

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1967	Tree peony variegated flowers show a small insertion in the F3â€™™H gene of the acyanic flower parts. <i>BMC Plant Biology</i> , 2020, 20, 211.	1.6	20
1968	Lipid accumulation and eicosapentaenoic acid distribution in response to nitrogen limitation in microalga <i>Eustigmatos vischeri</i> JHsu-01 (<i>Eustigmatophyceae</i>). <i>Algal Research</i> , 2020, 48, 101910.	2.4	23
1969	Transcriptome analysis of ovarian maturation in a chondrostei Chinese sturgeon <i>Acipenser sinensis</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2020, 334, 280-293.	0.6	6
1970	Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional regulation. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1330-1341.	1.9	16
1971	Improving Azo Dye Decolorization Performance and Halotolerance of <i>Pichia occidentalis</i> A2 by Static Magnetic Field and Possible Mechanisms Through Comparative Transcriptome Analysis. <i>Frontiers in Microbiology</i> , 2020, 11, 712.	1.5	24
1972	Comparing transcriptome expression profiles to reveal the mechanisms of salt tolerance and exogenous glycine betaine mitigation in maize seedlings. <i>PLoS ONE</i> , 2020, 15, e0233616.	1.1	25
1973	Genome-Wide Analysis of Basic Helix-Loop-Helix Transcription Factors to Elucidate Candidate Genes Related to Fruit Ripening and Stress in Banana (<i>Musa acuminata</i> L. AAA Group, cv. Cavendish). <i>Frontiers in Plant Science</i> , 2020, 11, 650.	1.7	15
1974	The Influence of Immune Heterogeneity on the Effectiveness of Immune Checkpoint Inhibitors in Multifocal Hepatocellular Carcinomas. <i>Clinical Cancer Research</i> , 2020, 26, 4947-4957.	3.2	24
1975	Comparative transcriptome analysis of normal and CD44-deleted mouse brain under chronic infection with <i>Toxoplasma gondii</i> . <i>Acta Tropica</i> , 2020, 210, 105589.	0.9	2
1976	Transcriptome analysis reveals molecular strategies in gills and heart of large yellow croaker (<i>Larimichthys crocea</i>) under hypoxia stress. <i>Fish and Shellfish Immunology</i> , 2020, 104, 304-313.	1.6	52
1977	Comparative transcriptome analysis of MeJA-responsive AP2/ERF transcription factors involved in notoginsenosides biosynthesis. <i>3 Biotech</i> , 2020, 10, 290.	1.1	8
1978	Comparative analysis of the ovarian transcriptome reveals novel insights into fertility differences in Large White sows. <i>Genes and Genomics</i> , 2020, 42, 715-725.	0.5	6
1979	Integrated analysis of mRNA and miRNA in testis and cauda epididymidis reveals candidate molecular markers associated with reproduction in Dezhou donkey. <i>Livestock Science</i> , 2020, 234, 103885.	0.6	14
1980	A Transcriptome Analysis Reveals that Hepatic Glycolysis and Lipid Synthesis Are Negatively Associated with Feed Efficiency in DLY Pigs. <i>Scientific Reports</i> , 2020, 10, 9874.	1.6	8
1981	Molecular Mechanism Underlying Mechanical Wounding-Induced Flavonoid Accumulation in <i>Dalbergia odorifera</i> T. Chen, an Endangered Tree That Produces Chinese Rosewood. <i>Genes</i> , 2020, 11, 478.	1.0	17
1982	Heat Stress Factors Expressed during Seed Maturation Differentially Regulate Seed Longevity and Seedling Greening. <i>Plants</i> , 2020, 9, 335.	1.6	6
1983	Long noncoding RNA TANC1 promotes $\hat{3}\hat{1}$ T cells activation by regulating TRAIL expression in cis. <i>Cell and Bioscience</i> , 2020, 10, 15.	2.1	9
1984	UV-B Induces Distinct Transcriptional Re-programing in UVR8-Signal Transduction, Flavonoid, and Terpenoids Pathways in <i>Camellia sinensis</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 234.	1.7	27

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1986	KLF10 is upregulated in osteoarthritis and inhibits chondrocyte proliferation and migration by upregulating <i>Acvr1</i> and suppressing <i>inhibb</i> expression. <i>Acta Histochemica</i> , 2020, 122, 151528.	0.9	8
1987	Integrated Analysis of Large-Scale Omics Data Revealed Relationship Between Tissue Specificity and Evolutionary Dynamics of Small RNAs in Maize (<i>Zea mays</i>). <i>Frontiers in Genetics</i> , 2020, 11, 51.	1.1	7
1988	The response strategies of <i>Colletotrichum gloeosporioides</i> s.s. due to the stress caused by biological control agent <i>Bacillus amyloliquefaciens</i> deciphered by transcriptome analyses. <i>Biological Control</i> , 2020, 150, 104372.	1.4	15
1989	Identification of tRFs and phasiRNAs in tomato (<i>Solanum lycopersicum</i>) and their responses to exogenous abscisic acid. <i>BMC Plant Biology</i> , 2020, 20, 320.	1.6	7
1990	Transcriptomic Analysis of Extracellular RNA Governed by the Endocytic Adaptor Protein Cin1 of <i>Cryptococcus deformeformans</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 256.	1.8	12
1991	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
1992	Identification and sex-biased profiles of candidate olfactory genes in the antennal transcriptome of the parasitoid wasp <i>Cotesia vestalis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 34, 100657.	0.4	18
1993	Discovery and identification of medium-chain fatty acid responsive promoters in <i>Saccharomyces cerevisiae</i> . <i>Engineering in Life Sciences</i> , 2020, 20, 186-196.	2.0	4
1994	RNA sequencing analysis of low temperature and low light intensity-responsive transcriptomes of zucchini (<i>Cucurbita pepo</i> L.). <i>Scientia Horticulturae</i> , 2020, 265, 109263.	1.7	11
1995	Phytochemical and comparative transcriptome analyses reveal different regulatory mechanisms in the terpenoid biosynthesis pathways between <i>Matricaria recutita</i> L. and <i>Chamaemelum nobile</i> L.. <i>BMC Genomics</i> , 2020, 21, 169.	1.2	11
1996	<i>Wolbachia</i> limits pathogen infections through induction of host innate immune responses. <i>PLoS ONE</i> , 2020, 15, e0226736.	1.1	18
1997	Knockdown of GmVQ58 encoding a VQ motif-containing protein enhances soybean resistance to the common cutworm (<i>Spodoptera litura</i> Fabricius). <i>Journal of Experimental Botany</i> , 2020, 71, 3198-3210.	2.4	16
1998	MicroRNA-based recombinant AAV vector assembly improves efficiency of suicide gene transfer in a murine model of lymphoma. <i>Cancer Medicine</i> , 2020, 9, 3188-3201.	1.3	4
1999	AhHDA1-mediated AhGLK1 promoted chlorophyll synthesis and photosynthesis regulates recovery growth of peanut leaves after water stress. <i>Plant Science</i> , 2020, 294, 110461.	1.7	13
2000	Transcriptome analysis of terpenoid biosynthetic genes and simple sequence repeat marker screening in <i>Eucommia ulmoides</i> . <i>Molecular Biology Reports</i> , 2020, 47, 1979-1990.	1.0	13
2001	Metabolic Adaptation to Sulfur of Hyperthermophilic <i>Palaeococcus pacificus</i> DY20341T from Deep-Sea Hydrothermal Sediments. <i>International Journal of Molecular Sciences</i> , 2020, 21, 368.	1.8	8
2002	Transcriptome analysis of <i>Clinopodium gracile</i> (Benth.) Matsum and identification of genes related to Triterpenoid Saponin biosynthesis. <i>BMC Genomics</i> , 2020, 21, 49.	1.2	12

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2004	Transcriptome Analysis Unravels Metabolic and Molecular Pathways Related to Fruit Sac Granulation in a Late-Ripening Navel Orange (<i>Citrus sinensis</i> Osbeck). <i>Plants</i> , 2020, 9, 95.	1.6	26
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2008	Transcriptome sequencing and identification of key callus browning-related genes from petiole callus of tree peony (<i>Paeonia suffruticosa</i> cv. Kao) cultured on media with three browning inhibitors. <i>Plant Physiology and Biochemistry</i> , 2020, 149, 36-49.	2.8	25
2009	Molecular and expression characterization of Toll-like receptor family genes from the <i>Anadara sativa</i> (Bivalvia, Arcidae) transcriptome. <i>Developmental and Comparative Immunology</i> , 2020, 106, 103630.	1.0	7
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2015	Mechanisms Underlying the Rhizosphere-To-Rhizoplane Enrichment of <i>Cellvibrio</i> Unveiled by Genome-Centric Metagenomics and Metatranscriptomics. <i>Microorganisms</i> , 2020, 8, 583.	1.6	14
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2017	Hydroxyecdysone regulates the prophenoloxidase cascade to immunize <i>Metarhizium anisopliae</i> in <i>Locusta migratoria</i> . <i>Pest Management Science</i> , 2020, 76, 3149-3158.	1.7	8
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2264	Transcription analysis of chlorophyll biosynthesis in wildtype and chlorophyll b-lacking rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overlook	0.9	10
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2267	Abiotic Stress-Related Expressed Sequence Tags from the Diploid Strawberry <i>Fragaria vesca</i> f. <i>semperflorens</i> . <i>Plant Genome</i> , 2011, 4, .	1.6	7
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2270	Methotrexate combined with methylprednisolone for the recovery of motor function and differential gene expression in rats with spinal cord injury. <i>Neural Regeneration Research</i> , 2017, 12, 1507.	1.6	13
2271	Novel circular RNAs expressed in brain microvascular endothelial cells after oxygen-glucose deprivation/recovery. <i>Neural Regeneration Research</i> , 2019, 14, 2104.	1.6	21
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2277	Different RNA splicing mechanisms contribute to diverse infective outcome of classical swine fever viruses of differing virulence: insights from the deep sequencing data in swine umbilical vein endothelial cells. <i>PeerJ</i> , 2016, 4, e2113.	0.9	4
2278	Transcriptome analysis reveals the regulation of brassinosteroids on petal growth in <i>Gerbera hybrida</i> . <i>PeerJ</i> , 2017, 5, e3382.	0.9	30
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2280	RNA-Seq analysis of differential gene expression in <i>Betula luminifera</i> xylem during the early stages of tension wood formation. <i>PeerJ</i> , 2018, 6, e5427.	0.9	15
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2292	Functional Genomics in Fungi. , 2004, , 115-128.		0
2293	Gene Expression Profiling. , 0, , .		0
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2328	Flower transcriptome dynamics during nectary development in pepper (<i>Capsicum annuum</i> L.). <i>Genetics and Molecular Biology</i> , 2020, 43, e20180267.	0.6	3
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2337	Deep Sequencing of MicroRNAs in Cancer: Expression Profiling and Its Applications. , 2012, , 523-546.		2
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2534	Transcriptome-Based Weighted Correlation Network Analysis of Maize Leaf Angle Regulation by Exogenous Brassinosteroid. <i>Agronomy</i> , 2022, 12, 1895.	1.3	0
2535	Characterization of Peroxidase and Laccase Gene Families and In Silico Identification of Potential Genes Involved in Upstream Steps of Lignan Formation in Sesame. <i>Life</i> , 2022, 12, 1200.	1.1	4
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2543	Screening of immune-related genes against bacterial infection in <i>Ostrinia furnacalis</i> (Lepidoptera: Tj ETQq1 1 0.784314 rgBT ₀ /Overlook	1.2	0
2544	Evidence that <i>miR168a</i> contributes to salinity tolerance of <i>Brassica rapa</i> L. via mediating melatonin biosynthesis. <i>Physiologia Plantarum</i> , 2022, 174, .	2.6	4
2545	Transcriptional regulation mechanism of flavonoids biosynthesis gene during fruit development in <i>astragalus membranaceus</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
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2560	MINI BODY1, encoding a MATE/DTX family transporter, affects plant architecture in mungbean (<i>Vigna</i>) Tj ETQq0 0 0 rBT /Overlock 10 T	1.7	0
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