

Gene ontology analysis for RNA-seq: accounting for selection bias

Genome Biology

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Citation Report

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1	Use of homologous and heterologous gene expression profiling tools to characterize transcription dynamics during apple fruit maturation and ripening. BMC Plant Biology, 2010, 10, 229.	3.6	79
2	Gene set enrichment; a problem of pathways. Briefings in Functional Genomics, 2010, 9, 385-390.	2.7	9
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6	Differential expression in RNA-seq: A matter of depth. Genome Research, 2011, 21, 2213-2223.	5.5	1,456
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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.	2.2	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.	3.9	11
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1172	Modulation of xenobiotic nuclear receptors in high-fat diet induced non-alcoholic fatty liver disease. <i>Toxicology</i> , 2018, 410, 199-213.	4.2	38
1173	Control of inducible gene expression links cohesin to hematopoietic progenitor self-renewal and differentiation. <i>Nature Immunology</i> , 2018, 19, 932-941.	14.5	175
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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.	4.8	109
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1198	Comparative transcriptome analysis reveals significant metabolic alterations in eri-silkworm (<i>Samia</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.5	12
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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.	2.2	20
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1203	Transcriptome profiling of pumpkin (<i>Cucurbita moschata</i> Duch.) leaves infected with powdery mildew. <i>PLoS ONE</i> , 2018, 13, e0190175.	2.5	51
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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.	8.3	69
1209	Transcriptome Analysis. , 2019, , 792-805.		8
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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.	5.2	20
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1284	Integrative analysis of metabolome and transcriptome reveals anthocyanins biosynthesis regulation in grass species <i>Pennisetum purpureum</i> . <i>Industrial Crops and Products</i> , 2019, 138, 111470.	5.2	27
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.	4.1	12
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1556	Physiological and Transcriptome Analyses of Early Leaf Senescence for <i>ospls1</i> Mutant Rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	4.1	17
1557	Phenotypic and transcriptomic characterization of canine myeloid-derived suppressor cells. <i>Scientific Reports</i> , 2019, 9, 3574.	3.3	26
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1581	Transcriptomic analysis of fetal membranes reveals pathways involved in preterm birth. <i>BMC Medical Genomics</i> , 2019, 12, 53.	1.5	20
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1681	Transcriptomic Analysis of Dark-Induced Senescence in Bermudagrass (<i>Cynodon dactylon</i>). <i>Plants</i> , 2019, 8, 614.	3.5	12
1682	Comparative transcriptomic analysis of the flower induction and development of the Lei bamboo (<i>Phyllostachys violascens</i>). <i>BMC Bioinformatics</i> , 2019, 20, 687.	2.6	14
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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.	6.0	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.	3.6	30
1841	Transcriptional responses of soybean aphids to sublethal insecticide exposure. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 118, 103285.	2.7	11

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1842	Melatonin enhances salt stress tolerance in rubber tree (<i>Hevea brasiliensis</i>) seedlings. <i>Industrial Crops and Products</i> , 2020, 145, 111990.	5.2	27
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.	3.2	5
1844	Skin barrier damage after exposure to paraphenylenediamine. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 619-631.e2.	2.9	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.	8.0	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.	3.9	3
1847	Transcriptional and Functional Programming of Decidual Innate Lymphoid Cells. <i>Frontiers in Immunology</i> , 2019, 10, 3065.	4.8	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.	3.6	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.	1.3	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.	3.6	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.	8.2	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.	2.3	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.	2.4	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.	3.5	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.	11.0	199
1856	Analysis of lncRNA Expression Profile during the Formation of Male Germ Cells in Chickens. <i>Animals</i> , 2020, 10, 1850.	2.3	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.	2.7	4
1858	Alternative Splicing Enhances the Transcriptome Complexity of <i>Liriodendron chinense</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 578100.	3.6	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.	3.5	17

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1860	Transcriptomic and targeted metabolomic analysis identifies genes and metabolites involved in anthocyanin accumulation in tuberous roots of sweetpotato (<i>Ipomoea batatas</i> L.). <i>Plant Physiology and Biochemistry</i> , 2020, 156, 323-332.	5.8	13
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.	2.9	5
1862	Integrative analysis of long non-coding RNA and mRNA in broilers with valgus-varus deformity. <i>PLoS ONE</i> , 2020, 15, e0239450.	2.5	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.	16.2	122
1864	tagHi-C Reveals 3D Chromatin Architecture Dynamics during Mouse Hematopoiesis. <i>Cell Reports</i> , 2020, 32, 108206.	6.4	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.	7.5	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.	2.3	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.	3.5	8
1868	Transcriptome analyses to reveal the dynamic change mechanism of pigeon magnum during one eggâ€­laying cycle. <i>Molecular Reproduction and Development</i> , 2020, 87, 1141-1151.	2.0	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.	3.6	11
1870	Identification of Differentially Methylated Regions Associated with a Knockout of SUV39H1 in Prostate Cancer Cells. <i>Genes</i> , 2020, 11, 1188.	2.4	2
1871	Identification of Candidate Genes Involved in Fruit Ripening and Crispness Retention Through Transcriptome Analyses of a â€­Honeycrispâ€­™ Population. <i>Plants</i> , 2020, 9, 1335.	3.5	11
1872	NOD-like receptors mediate inflammatory lung injury during plateau hypoxia exposure. <i>Journal of Physiological Anthropology</i> , 2020, 39, 32.	2.6	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.	2.2	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.	3.3	10
1875	JMJD3 acts in tandem with KLF4 to facilitate reprogramming to pluripotency. <i>Nature Communications</i> , 2020, 11, 5061.	12.8	24
1876	Transcriptome Analysis of <i>Psacothaea hilaris</i> : De Novo Assembly and Antimicrobial Peptide Prediction. <i>Insects</i> , 2020, 11, 676.	2.2	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.	2.2	8

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1878	Differential expression in leaves of <i>Saccharum</i> genotypes contrasting in biomass production provides evidence of genes involved in carbon partitioning. <i>BMC Genomics</i> , 2020, 21, 673.	2.8	10
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.	3.6	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.	2.1	5
1881	4EHP and GIGYF1/2 Mediate Translation-Coupled Messenger RNA Decay. <i>Cell Reports</i> , 2020, 33, 108262.	6.4	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, .	2.4	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.	2.5	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.	7.5	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.	8.8	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.	2.8	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.	3.5	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.	3.5	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.	2.1	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.	3.2	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.	10.2	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.	2.6	8
1893	Giant Island Mice Exhibit Widespread Gene Expression Changes in Key Metabolic Organs. <i>Genome Biology and Evolution</i> , 2020, 12, 1277-1301.	2.5	1
1894	Global transcriptomic and proteomics analysis of <i>Lactobacillus plantarum</i> Y44 response to 2,2-azobis(2-methylpropionamidine) dihydrochloride (AAPH) stress. <i>Journal of Proteomics</i> , 2020, 226, 103903.	2.4	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.	2.8	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.	2.3	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.	2.8	7
1899	Effect of diflubenzuron on the chitin biosynthesis pathway in <i>Conopomorpha sinensis</i> eggs. <i>Insect Science</i> , 2021, 28, 1061-1075.	3.0	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.	7.1	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.	2.5	11
1902	Transcriptional Profiling of Normal, Stenotic, and Regurgitant Human Aortic Valves. <i>Genes</i> , 2020, 11, 789.	2.4	14
1903	Transcriptome analysis of grape leaves reveals insights into response to heat acclimation. <i>Scientia Horticulturae</i> , 2020, 272, 109554.	3.6	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.	2.9	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.	2.9	9
1906	Characterization of γ -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.	0.6	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.	1.8	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.	2.8	18
1909	Transcriptome Profiling of Abscissic Acid-Related Pathways in SNAC4/9-Silenced Tomato Fruits. <i>Transactions of Tianjin University</i> , 2020, 27, 473.	6.4	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.	1.9	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.	1.0	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.	2.8	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.	1.4	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.	2.1	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.	4.4	32
1916	Interleukin-1 promotes autoimmune neuroinflammation by suppressing endothelial heme oxygenase-1 at the bloodâ€“brain barrier. <i>Acta Neuropathologica</i> , 2020, 140, 549-567.	7.7	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.	3.9	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.	4.1	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.	2.8	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.	2.3	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.	5.1	2
1922	Transcriptomic investigation reveals toxic damage due to tilmicotin and potential resistance against tilmicotin in primary chicken myocardial cells. <i>Poultry Science</i> , 2020, 99, 6355-6370.	3.4	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.	3.6	20
1924	<p></p>Functional Implication of Exosomal miR-217 and miR-23b-3p in the Progression of Prostate Cancer</p><p></p>. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 11595-11606.	2.0	36
1925	Temperature Differentially Affects Gene Expression in Antarctic Thraustochytrid <i>Oblongichytrium</i> sp. RT2316-13. <i>Marine Drugs</i> , 2020, 18, 563.	4.6	9
1926	Identification and Characterization of circRNAs in the Developing Stem Cambium of Poplar Seedlings. <i>Molecular Biology</i> , 2020, 54, 708-718.	1.3	2
1927	MADA: a web service for analysing DNA methylation array data. <i>BMC Bioinformatics</i> , 2020, 21, 403.	2.6	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.	3.6	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.	2.3	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	2.2	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.	2.3	15

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1932	Transcriptome divergence between developmental senescence and premature senescence in <i>Nicotiana tabacum</i> L.. Scientific Reports, 2020, 10, 20556.	3.3	6
1933	Systemic paralogy and function of retinal determination network homologs in arachnids. BMC Genomics, 2020, 21, 811.	2.8	20
1934	RNA-Seq-Based Transcriptomic Analysis of <i>Saccharopolyspora spinosa</i> Revealed the Critical Function of PEP Phosphonomutase in the Replenishment Pathway. Journal of Agricultural and Food Chemistry, 2020, 68, 14660-14669.	5.2	5
1935	Transcriptome analysis of genes related to cadmium absorption and transportation in pepper. Israel Journal of Ecology and Evolution, 2020, 67, 29-38.	0.6	0
1936	Deciphering Novel Antimicrobial Peptides from the Transcriptome of <i>Papilio xuthus</i> . Insects, 2020, 11, 776.	2.2	6
1937	The Tetracentron genome provides insight into the early evolution of eudicots and the formation of vessel elements. Genome Biology, 2020, 21, 291.	8.8	23
1938	Comparative transcriptome analysis in three sorghum (<i>Sorghum bicolor</i>) cultivars reveal genomic basis of differential seed quality. Plant Biosystems, 2022, 156, 232-241.	1.6	3
1939	High-throughput profiling of diapause regulated genes from <i>Trichogramma dendrolimi</i> (Hymenoptera: Tj ETQq1 1 0.784314, 25 BT /Over	2.8	25
1940	Transcriptomic profiles of non-embryogenic and embryogenic callus cells in a highly regenerative upland cotton line (<i>Gossypium hirsutum</i> L.). BMC Developmental Biology, 2020, 20, 25.	2.1	19
1941	Endogenous Auxin Content Contributes to Larger Size of Apple Fruit. Frontiers in Plant Science, 2020, 11, 592540.	3.6	23
1942	Transcriptome analysis reveals mechanism of early ripening in Kyoho grape with hydrogen peroxide treatment. BMC Genomics, 2020, 21, 784.	2.8	29
1943	Osteoporosis Is Characterized by Altered Expression of Exosomal Long Non-coding RNAs. Frontiers in Genetics, 2020, 11, 566959.	2.3	11
1944	Characterization of microRNA-like RNAs associated with sclerotial development in <i>Sclerotinia sclerotiorum</i> . Fungal Genetics and Biology, 2020, 144, 103471.	2.1	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. International Journal of Molecular Sciences, 2020, 21, 8215.	4.1	27
1946	Genome-Wide Analysis Reveals Changes in Long Noncoding RNAs in the Differentiation of Canine BMSCs into Insulin-Producing Cells. International Journal of Molecular Sciences, 2020, 21, 5549.	4.1	5
1947	Uncovering candidate genes responsive to salt stress in <i>Salix matsudana</i> (Koidz) by transcriptomic analysis. PLoS ONE, 2020, 15, e0236129.	2.5	16
1948	Genome-Wide Differential DNA Methylation in Reproductive, Morphological, and Visual System Differences Between Queen Bee and Worker Bee (<i>Apis mellifera</i>). Frontiers in Genetics, 2020, 11, 770.	2.3	14
1949	Integrated physiological, transcriptomic and proteomic analyses revealed molecular mechanism for salt resistance in <i>Solidago canadensis</i> L.. Environmental and Experimental Botany, 2020, 179, 104211.	4.2	19

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1950	Neural innervation as a potential trigger of morphological color change and sexual dimorphism in cichlid fish. <i>Scientific Reports</i> , 2020, 10, 12329.	3.3	23
1951	Parallel reaction monitoring revealed tolerance to drought proteins in weedy rice (<i>Oryza sativa</i> L.). <i>Plant Physiology</i> , 2020, 165, 1074-1084.	3.3	4
1952	Effects of Trace Irrigation at Different Depths on Transcriptome Expression Pattern in Cotton (<i>G.</i>). <i>Transcriptomics</i> , 2020, 9, 10.	1.9	3
1953	The Wheat GENIE3 Network Provides Biologically-Relevant Information in Polyploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3675-3686.	1.8	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.	1.5	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.	10.0	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.	3.1	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.	2.5	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.	2.9	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.	1.7	8
1960	Shedding the Light on <i>Litopenaeus vannamei</i> Differential Muscle and Hepatopancreas Immune Responses in White Spot Syndrome Virus (WSSV) Exposure. <i>Genes</i> , 2020, 11, 805.	2.4	12
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.	3.5	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.	1.8	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.	3.3	24
1964	Collagen Density Modulates the Immunosuppressive Functions of Macrophages. <i>Journal of Immunology</i> , 2020, 205, 1461-1472.	0.8	64
1965	Population variation in miRNAs and isomiRs and their impact on human immunity to infection. <i>Genome Biology</i> , 2020, 21, 187.	8.8	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.	2.9	18
1967	Transcriptomic and Metabolic Responses to a Live-Attenuated <i>Francisella tularensis</i> Vaccine. <i>Vaccines</i> , 2020, 8, 412.	4.4	17

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1968	Utilization of <i>Cratogeomys formosus</i> crude extract for synthesis of ZnO nanosheets: Characterization, biological activities and effects on gene expression of nonmelanoma skin cancer cell. <i>Biomedicine and Pharmacotherapy</i> , 2020, 130, 110552.	5.6	27
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.	4.2	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.	8.0	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.	3.0	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.	1.8	2
1973	Comparative transcriptome analysis reveals ecological adaption of cold tolerance in northward invasion of <i>Alternanthera philoxeroides</i> . <i>BMC Genomics</i> , 2020, 21, 532.	2.8	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.	3.6	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.	3.3	6
1976	Exogenous abscisic acid induces the lipid and flavonoid metabolism of tea plants under drought stress. <i>Scientific Reports</i> , 2020, 10, 12275.	3.3	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.	3.5	32
1978	Transcriptome Profiling across Five Tissues of Giant Panda. <i>BioMed Research International</i> , 2020, 2020, 1-13.	1.9	8
1979	Integration of QTL, Transcriptome and Polymorphism Studies Reveals Candidate Genes for Water Stress Response in Tomato. <i>Genes</i> , 2020, 11, 900.	2.4	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.	7.5	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 / Overlaid. <i>Endocrinology</i> , 2020, 298, 113567.	1.8	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.	2.9	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.	5.8	4
1984	Within-individual phenotypic plasticity in flowers fosters pollination niche shift. <i>Nature Communications</i> , 2020, 11, 4019.	12.8	29
1985	Distinct fibroblast subsets regulate lacteal integrity through YAP/TAZ-induced VEGF-C in intestinal villi. <i>Nature Communications</i> , 2020, 11, 4102.	12.8	36

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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.	4.0	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.	6.0	2
1989	Early emergence of T central memory precursors programs clonal dominance during chronic viral infection. <i>Nature Immunology</i> , 2020, 21, 1563-1573.	14.5	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.	3.3	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.	1.4	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.	3.6	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.	2.8	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.	2.8	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.	2.9	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.	2.4	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.	3.6	17
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1999	Graph-based exploitation of gene ontology using GOxploreR for scrutinizing biological significance. <i>Scientific Reports</i> , 2020, 10, 16672.	3.3	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.	3.3	14
2001	Assessing alveolar rhabdomyosarcoma cell lines as tumor models by comparison of mRNA expression profiles. <i>Gene</i> , 2020, 760, 145025.	2.2	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.	1.8	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.	3.4	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.	4.1	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.	6.3	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.	1.5	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.	3.3	6
2009	Evolutionary Variation in MADS Box Dimerization Affects Floral Development and Protein Abundance in Maize. <i>Plant Cell</i> , 2020, 32, 3408-3424.	6.6	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.	2.5	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.	1.9	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.	3.6	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.	2.4	8
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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.	4.0	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.	3.3	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.	2.7	15
2018	Identification of microRNAs Targeting the Transporter Associated with Antigen Processing TAP1 in Melanoma. <i>Journal of Clinical Medicine</i> , 2020, 9, 2690.	2.4	18
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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.	4.6	9
2021	Transcriptome analysis and comparison reveal divergence between the Mediterranean and the greenhouse whiteflies. <i>PLoS ONE</i> , 2020, 15, e0237744.	2.5	2

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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.	2.4	2
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2038	Sharing a Î²-Glucan Meal: Transcriptomic Eavesdropping on a <i>Bacteroides ovatus</i> - <i>Subdoligranulum variabile</i> - <i>Hungateella hathewayi</i> Consortium. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	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, .	2.4	6
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2052	A Broad Response to Intracellular Long-Chain Polyphosphate in Human Cells. <i>Cell Reports</i> , 2020, 33, 108318.	6.4	33
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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.	1.4	4
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2096	Transcriptomic analyses reveal distinct response of porcine macrophages to <i>Toxoplasma gondii</i> infection. <i>Parasitology Research</i> , 2020, 119, 1819-1828.	1.6	6
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2543	IL-10 signaling reduces survival in mouse models of synucleinopathy. <i>Npj Parkinson's Disease</i> , 2021, 7, 30.	5.3	8
2544	Novel Transcriptome Study and Detection of Metabolic Variations in UV-B-Treated Date Palm (Phoenix) Tj ETQq1 1 0.784314rgBT /Over	4.1	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.	1.8	8
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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.	2.9	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.	2.3	10
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2568	Transcriptome responses of the dinoflagellate <i>Karenia mikimotoi</i> driven by nitrogen deficiency. <i>Harmful Algae</i> , 2021, 103, 101977.	4.8	15
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2577	Cell-type-aware analysis of RNA-seq data. <i>Nature Computational Science</i> , 2021, 1, 253-261.	8.0	12
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2588	Comparative Genomics and Transcriptomics of the Extreme Halophyte <i>Puccinellia tenuiflora</i> Provides Insights Into Salinity Tolerance Differentiation Between Halophytes and Glycophytes. <i>Frontiers in Plant Science</i> , 2021, 12, 649001.	3.6	14
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2696	Identification and functional prediction of long noncoding RNAs related to intramuscular fat content in Laiwu pigs. <i>Animal Bioscience</i> , 2022, 35, 115-125.	2.0	10
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2707	Direct and heritable effects of natural tidal environments on DNA methylation in Pacific oysters (<i>Crassostrea gigas</i>). <i>Environmental Research</i> , 2021, 197, 111058.	7.5	15
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2726	Quantum processor-inspired machine learning in the biomedical sciences. <i>Patterns</i> , 2021, 2, 100246.	5.9	16
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2733	Genomic analyses provide comprehensive insights into the domestication of bast fiber crop ramie (<i>Boehmeria nivea</i>). <i>Plant Journal</i> , 2021, 107, 787-800.	5.7	18
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2745	Transcriptome analysis provides insights into copper toxicology in piebald naked carp (<i>Gymnocypris</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 T 2745	2.8	3
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2748	Gene set enrichment analysis for genome-wide DNA methylation data. <i>Genome Biology</i> , 2021, 22, 173.	8.8	68
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2750	Melatonin Improves Cotton Salt Tolerance by Regulating ROS Scavenging System and Ca ²⁺ + Signal Transduction. <i>Frontiers in Plant Science</i> , 2021, 12, 693690.	3.6	44
2751	Extracellular succinate hyperpolarizes M2 macrophages through SUCNR1/GPR91-mediated Gq signaling. <i>Cell Reports</i> , 2021, 35, 109246.	6.4	61
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2795	Screening and Interaction Analysis Identify Genes Related to Anther Dehiscence in <i>Solanum melongena</i> L.. <i>Frontiers in Plant Science</i> , 2021, 12, 648193.	3.6	4
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2831	Liver-fibrosis-activated transcriptional networks govern hepatocyte reprogramming and intra-hepatic communication. <i>Cell Metabolism</i> , 2021, 33, 1685-1700.e9.	16.2	73
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2938	Transcriptome profiling of farmed rainbow trout (<i>Oncorhynchus mykiss</i>) liver from different sources of dietary zinc. <i>Aquaculture</i> , 2021, 543, 737017.	3.5	4
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3534	Analysis of miRNAs Involved in Mouse Heart Injury Upon Coxsackievirus A2 Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 765445.	3.9	1
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3549	Gene expression alterations from reversible to irreversible stages during coral metamorphosis. <i>Zoological Letters</i> , 2022, 8, 4.	1.3	2
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3556	Comparative analysis of the orange versus yellow petal of rapeseed (<i>Brassica</i>) Tj ETQq1 1 0.784314 rgBT 1 Overlock 10 Tf 50 14	1.9	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.	6.0	10
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3580	De Novo Transcriptome of <i>Mammillaria bombycina</i> (Cactaceae) under In Vitro Conditions and Identification of Glyoxalase Genes. <i>Plants</i> , 2022, 11, 399.	3.5	0
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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.	2.4	14
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3597	Transcriptional regulation of cell growth and reprogramming of systemic response in wheat (<i>Triticum turgidum</i> subsp. <i>durum</i>) seedlings by <i>Bacillus paralicheniformis</i> TRQ65. <i>Planta</i> , 2022, 255, 56.	3.2	8
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3603	Comparative transcriptomics analysis of testicular miRNA from indicine and taurine cattle. <i>Animal Biotechnology</i> , 2022, , 1-11.	1.5	1
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3612	Perturbation of Wnt/ β -catenin signaling and sexual dimorphism in nonâ€alcoholic fatty liver disease. <i>Hepatology Research</i> , 2022, 52, 433-448.	3.4	2
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3615	Identification of sodium homeostasis genes in <i>Camelus bactrianus</i> by whole transcriptome sequencing. FEBS Open Bio, 2022, 12, 864-876.	2.3	0
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3617	Inflammation and convergent placenta gene co-option contributed to a novel reproductive tissue. Current Biology, 2022, 32, 715-724.e4.	3.9	8
3618	Transcriptome Profiling Revealed Basis for Growth Heterosis in Hybrid Tilapia (<i>Oreochromis niloticus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.7	5
3619	Systematic identification and functional analysis of long noncoding RNAs involved in indoxacarb resistance in <i>Spodoptera litura</i> . Insect Science, 2022, 29, 1721-1736.	3.0	10
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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.	4.1	1
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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.	2.4	4
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5131	Transcriptomic and QTL Analysis of Seed Germination Vigor under Low Temperature in Weedy Rice WR04-6. <i>Plants</i> , 2023, 12, 871.	3.5	0
5132	Identification of lncRNAs and Their Regulatory Network Involved in Oil Biosynthesis in Developing Seeds of Yellowhorn (<i>Xanthoceras sorbifolium</i>). <i>Forests</i> , 2023, 14, 407.	2.1	3

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