

Transcript-level expression analysis of RNA-seq experim Ballgown

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Citation Report

#	ARTICLE	IF	CITATIONS
1	RNA sequencing analysis of the developing chicken retina. <i>Scientific Data</i> , 2016, 3, 160117.	2.4	39
2	DUSP11 activity on triphosphorylated transcripts promotes Argonaute association with noncanonical viral microRNAs and regulates steady-state levels of cellular noncoding RNAs. <i>Genes and Development</i> , 2016, 30, 2076-2092.	2.7	46
3	Computational pan-genomics: status, promises and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw089.	3.2	207
4	Protease Inhibitors of Parasitic Flukes: Emerging Roles in Parasite Survival and Immune Defence. <i>Trends in Parasitology</i> , 2017, 33, 400-413.	1.5	31
5	A genetic interaction analysis identifies cancer drivers that modify EGFR dependency. <i>Genes and Development</i> , 2017, 31, 184-196.	2.7	58
6	Genomic Insights into the Evolution of the Nicotine Biosynthesis Pathway in Tobacco. <i>Plant Physiology</i> , 2017, 174, 999-1011.	2.3	97
7	Identification of HDA15-PIF1 as a key repression module directing the transcriptional network of seed germination in the dark. <i>Nucleic Acids Research</i> , 2017, 45, 7137-7150.	6.5	89
8	BioQueue: a novel pipeline framework to accelerate bioinformatics analysis. <i>Bioinformatics</i> , 2017, 33, 3286-3288.	1.8	9
9	Genome graphs and the evolution of genome inference. <i>Genome Research</i> , 2017, 27, 665-676.	2.4	264
10	Comprehensive RNA-seq transcriptomic profiling in the malignant progression of gliomas. <i>Scientific Data</i> , 2017, 4, 170024.	2.4	208
11	Modifications to a <i>LATE MERISTEM IDENTITY1</i> gene are responsible for the major leaf shapes of Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E57-E66.	3.3	96
12	Comprehensive analysis of circRNA expression profiles in humans by RAISE. <i>International Journal of Oncology</i> , 2017, 51, 1625-1638.	1.4	35
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16	Genome-Wide Identification of <i>Medicago</i> Peptides Involved in Macronutrient Responses and Nodulation. <i>Plant Physiology</i> , 2017, 175, 1669-1689.	2.3	101
17	Adult-onset obesity is triggered by impaired mitochondrial gene expression. <i>Science Advances</i> , 2017, 3, e1700677.	4.7	36
18	Alloimmune Responses of Humanized Mice to Human Pluripotent Stem Cell Therapeutics. <i>Cell Reports</i> , 2017, 20, 1978-1990.	2.9	31

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20	The roles of plasticity and evolutionary change in shaping gene expression variation in natural populations of extremophile fish. <i>Molecular Ecology</i> , 2017, 26, 6384-6399.	2.0	33
21	Identification of competing endogenous RNAs of the tumor suppressor gene PTEN: A probabilistic approach. <i>Scientific Reports</i> , 2017, 7, 7755.	1.6	18
22	Cross-Species Y Chromosome Function Between Malaria Vectors of the <i>Anopheles gambiae</i> Species Complex. <i>Genetics</i> , 2017, 207, 729-740.	1.2	18
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29	Transcriptomics reveals multiple resistance mechanisms against cotton leaf curl disease in a naturally immune cotton species, <i>Gossypium arboreum</i> . <i>Scientific Reports</i> , 2017, 7, 15880.	1.6	61
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38	Transcriptomic Studies in Non-Model Plants: Case of <i>Pisum sativum</i> L. and <i>Medicago lupulina</i> L., 2017, .		1
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123	Transcriptomic Analysis for Differentially Expressed Genes in Ovarian Follicle Activation in the Zebrafish. <i>Frontiers in Endocrinology</i> , 2018, 9, 593.	1.5	42
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146	A Guide for Designing and Analyzing RNA-Seq Data. <i>Methods in Molecular Biology</i> , 2018, 1783, 35-80.	0.4	23
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1168	Radiation Impacts Early Atherosclerosis by Suppressing Intimal LDL Accumulation. <i>Circulation Research</i> , 2021, 128, 530-543.	2.0	12
1169	A draft phased assembly of the diploid Cascade hop (<i>Humulus lupulus</i>) genome. <i>Plant Genome</i> , 2021, 14, e20072.	1.6	25
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1173	Genome-wide discovery of natural variation in pre-mRNA splicing and prioritising causal alternative splicing to salt stress response in rice. <i>New Phytologist</i> , 2021, 230, 1273-1287.	3.5	20
1174	Clade III cytokinin response factors share common roles in response to oxidative stress responses linked to cytokinin synthesis. <i>Journal of Experimental Botany</i> , 2021, 72, 3294-3306.	2.4	4
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1176	Lasting consequences of psyllid (<i>Bactericera cockerelli</i> L.) infestation on tomato defense, gene expression, and growth. <i>BMC Plant Biology</i> , 2021, 21, 114.	1.6	5
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1200	Genomic analyses provide insights into peach local adaptation and responses to climate change. <i>Genome Research</i> , 2021, 31, 592-606.	2.4	30
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1207	Genomic insights into the host specific adaptation of the <i>Pneumocystis</i> genus. <i>Communications Biology</i> , 2021, 4, 305.	2.0	23
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1269	Identification and Characterization of Long Non-coding RNAs in the Intestine of Olive Flounder (<i>Paralichthys olivaceus</i>) During <i>Edwardsiella tarda</i> Infection. <i>Frontiers in Immunology</i> , 2021, 12, 623764.	2.2	21
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1312	Antisense RNAs during early vertebrate development are divided in groups with distinct features. <i>Genome Research</i> , 2021, 31, 995-1010.	2.4	7
1313	Chromosome-level genome assembly of burbot (<i>Lota lota</i>) provides insights into the evolutionary adaptations in freshwater. <i>Molecular Ecology Resources</i> , 2021, 21, 2022-2033.	2.2	8
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1320	RNA-Seq Reveals Function of Bta-miR-149-5p in the Regulation of Bovine Adipocyte Differentiation. <i>Animals</i> , 2021, 11, 1207.	1.0	15
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1482	Genome Size Estimation and Full-Length Transcriptome of <i>Sphingonotus tsinlingensis</i> : Genetic Background of a Drought-Adapted Grasshopper. <i>Frontiers in Genetics</i> , 2021, 12, 678625.	1.1	3
1483	Comparative Analysis of Skeletal Muscle DNA Methylation and Transcriptome of the Chicken Embryo at Different Developmental Stages. <i>Frontiers in Physiology</i> , 2021, 12, 697121.	1.3	5
1484	Physiological and Expressional Regulation on Photosynthesis, Starch and Sucrose Metabolism Response to Waterlogging Stress in Peanut. <i>Frontiers in Plant Science</i> , 2021, 12, 601771.	1.7	27
1485	Identification and characterization of amphibian SLC26A5 using RNA-Seq. <i>BMC Genomics</i> , 2021, 22, 564.	1.2	2
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1487	Bioinformatics Pathway Analysis Pipeline for NGS Transcriptome Profile Data on Nasopharyngeal Carcinoma. <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 794, 012115.	0.2	1
1488	Transcriptomal dissection of soybean circadian rhythmicity in two geographically, phenotypically and genetically distinct cultivars. <i>BMC Genomics</i> , 2021, 22, 529.	1.2	2
1489	Adversity in early life and pregnancy are immunologically distinct from total life adversity: macrophage-associated phenotypes in women exposed to interpersonal violence. <i>Translational Psychiatry</i> , 2021, 11, 391.	2.4	16
1490	Metabolomic and transcriptomic profiling reveals distinct nutritional properties of cassavas with different flesh colors. <i>Food Chemistry Molecular Sciences</i> , 2021, 2, 100016.	0.9	10

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1500	Ecotoxicogenomic analysis of zebrafish embryos exposed to triclosan and mixture triclosan and methyl triclosan using suppression subtractive hybridization and next-generation sequencing. <i>Journal of Hazardous Materials</i> , 2021, 414, 125450.	6.5	7
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1504	MRSA strains with distinct accessory genes predominate at different ages in cystic fibrosis. <i>Pediatric Pulmonology</i> , 2021, 56, 2868-2878.	1.0	6
1505	Tissue-specificity of RNA editing in plant: analysis of transcripts from three tobacco (<i>Nicotiana</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 0.98		
1506	Transcriptional regulation of <i>ZIP</i> genes is independent of local zinc status in <i>Brachypodium</i> shoots upon zinc deficiency and resupply. <i>Plant, Cell and Environment</i> , 2021, 44, 3376-3397.	2.8	9
1508	Genome design of hybrid potato. <i>Cell</i> , 2021, 184, 3873-3883.e12.	13.5	112
1510	A Chromosome-Scale Assembly of the Wheat Leaf Rust Pathogen <i>Puccinia triticina</i> Provides Insights Into Structural Variations and Genetic Relationships With Haplotype Resolution. <i>Frontiers in Microbiology</i> , 2021, 12, 704253.	1.5	12
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1512	Co-expression network and comparative transcriptome analysis for fiber initiation and elongation reveal genetic differences in two lines from upland cotton CCR170 RIL population. <i>PeerJ</i> , 2021, 9, e11812.	0.9	9
1513	Identification and expression analysis of lncRNA in seven organs of <i>Rhinopithecus roxellana</i> . <i>Functional and Integrative Genomics</i> , 2021, 21, 543-555.	1.4	2

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1522	A forward genetics approach integrating genome-wide association study and expression quantitative trait locus mapping to dissect leaf development in maize (<i>Zea mays</i>). <i>Plant Journal</i> , 2021, 107, 1056-1071.	2.8	19
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1528	Whole genome sequencing and bulked segregant analysis suggest a new mechanism of amitraz resistance in the citrus red mite, <i>Panonychus citri</i> (Acari: Tetranychidae). <i>Pest Management Science</i> , 2021, 77, 5032-5048.	1.7	6
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1531	Amino acid transporter (AAT) gene family in foxtail millet (<i>Setaria italica</i> L.): widespread family expansion, functional differentiation, roles in quality formation and response to abiotic stresses. <i>BMC Genomics</i> , 2021, 22, 519.	1.2	12
1532	Integrated Genome and Transcriptome Sequencing to Solve a Neuromuscular Puzzle: Miyoshi Muscular Dystrophy and Early Onset Primary Dystonia in Siblings of the Same Family. <i>Frontiers in Genetics</i> , 2021, 12, 672906.	1.1	3
1533	The protective effect and crucial biological pathways analysis of <i>Trametes lactinea</i> mycelium polysaccharides on acute alcoholic liver injury in mice based on transcriptomics and metabolomics. <i>Food Science and Human Wellness</i> , 2021, 10, 480-489.	2.2	7

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1535	An immunogenomic phenotype predicting behavioral treatment response: Toward precision psychiatry for mothers and children with trauma exposure. <i>Brain, Behavior, and Immunity</i> , 2022, 99, 350-362.	2.0	7
1536	The lincRNA XH123 is involved in cotton cold-stress regulation. <i>Plant Molecular Biology</i> , 2021, 106, 521-531.	2.0	20
1537	Genome-wide mapping reveals R-loops associated with centromeric repeats in maize. <i>Genome Research</i> , 2021, 31, 1409-1418.	2.4	37
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1541	The transcription factor PagLBD3 contributes to the regulation of secondary growth in <i>Populus</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 7092-7106.	2.4	10
1542	RNA-seq between asexual archeospores and meiosis-related conchospores in <i>Neopyropia yezoensis</i> using Smart-seq2. <i>Journal of Phycology</i> , 2021, 57, 1648-1658.	1.0	6
1543	Comparative Analysis of PacBio and Oxford Nanopore Sequencing Technologies for Transcriptomic Landscape Identification of <i>Penaeus monodon</i> . <i>Life</i> , 2021, 11, 862.	1.1	7
1544	Cyclic growth of dermal papilla and regeneration of follicular mesenchymal components during feather cycling. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	10
1545	New biomarkers and therapeutic targets of human liver cancer: Transcriptomic findings. <i>BioFactors</i> , 2021, 47, 1016-1031.	2.6	2
1546	The Road to Sorghum Domestication: Evidence From Nucleotide Diversity and Gene Expression Patterns. <i>Frontiers in Plant Science</i> , 2021, 12, 666075.	1.7	6
1547	Integrative Transcriptomic, Lipidomic, and Metabolomic Analysis Reveals Potential Biomarkers of Basal and Luminal Muscle Invasive Bladder Cancer Subtypes. <i>Frontiers in Genetics</i> , 2021, 12, 695662.	1.1	3
1548	NGPF2 triggers synaptic scaling up through ALK-LIMK-cofilin-mediated mechanisms. <i>Cell Reports</i> , 2021, 36, 109515.	2.9	6
1549	Distinct Persistence Fate of <i>Mycobacterium tuberculosis</i> in Various Types of Cells. <i>MSystems</i> , 2021, 6, e0078321.	1.7	4
1550	Differences in transcription regulation of diurnal metabolic support to physiologically contrasting seasonal life-history states in migratory songbirds. <i>Journal of Ornithology</i> , 2022, 163, 199-212.	0.5	5
1551	<i>Prevotella copri</i> increases fat accumulation in pigs fed with formula diets. <i>Microbiome</i> , 2021, 9, 175.	4.9	100

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1555	LncRNA expression profile analysis of Mg ²⁺ -induced osteogenesis by RNA-seq and bioinformatics. <i>Genes and Genomics</i> , 2021, 43, 1247-1257.	0.5	3
1557	Comparative Transcriptome Analysis of <i>Bombyx mori</i> (Lepidoptera) Larval Hemolymph in Response to <i>Autographa californica</i> Nucleopolyhedrovirus in Differentially Resistant Strains. <i>Processes</i> , 2021, 9, 1401.	1.3	6
1558	ESAI regulates meiotic chromosome axis and crossover frequency via acetylating histone H4. <i>Nucleic Acids Research</i> , 2021, 49, 9353-9373.	6.5	19
1559	Evolutionary and Characteristic Analysis of RING-DUF1117 E3 Ubiquitin Ligase Genes in <i>Gossypium</i> Discerning the Role of GhRDUF4D in <i>Verticillium dahliae</i> Resistance. <i>Biomolecules</i> , 2021, 11, 1145.	1.8	13
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1568	Genome-Wide Association Analysis Reveals Loci and Candidate Genes Involved in Fiber Quality Traits Under Multiple Field Environments in Cotton (<i>Gossypium hirsutum</i>). <i>Frontiers in Plant Science</i> , 2021, 12, 695503.	1.7	12
1569	Integration of Molecular Inflammatory Interactome Analyses Reveals Dynamics of Circulating Cytokines and Extracellular Vesicle Long Non-Coding RNAs and mRNAs in Heroin Addicts During Acute and Protracted Withdrawal. <i>Frontiers in Immunology</i> , 2021, 12, 730300.	2.2	8
1570	Retinoic Acid Receptors and the Control of Positional Information in the Regenerating Axolotl Limb. <i>Cells</i> , 2021, 10, 2174.	1.8	3
1571	Early transcriptional responses in <i>Solanum peruvianum</i> and <i>Solanum lycopersicum</i> account for different acclimation processes during water scarcity events. <i>Scientific Reports</i> , 2021, 11, 15961.	1.6	4
1572	Characterization and comparative analysis of transcriptional profiles of porcine colostrum and mature milk at different parities. <i>BMC Genomic Data</i> , 2021, 22, 25.	0.7	3
1573	Mechanism underlying the toxicity of the microplastic fibre transfer in the sea cucumber <i>Apostichopus japonicus</i> . <i>Journal of Hazardous Materials</i> , 2021, 416, 125858.	6.5	10
1574	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
1575	Integrated Analysis of mRNA and Non-coding RNA Transcriptome in Pepper (<i>Capsicum chinense</i>) Hybrid at Seedling and Flowering Stages. <i>Frontiers in Genetics</i> , 2021, 12, 685788.	1.1	15

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1578	Identification and Characterization of Pleiotropic High-Persistence Mutations in the Beta Subunit of the Bacterial RNA Polymerase. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0052221.	1.4	2
1579	Gene expression profiling after LINC00472 overexpression in an NSCLC cell line1. <i>Cancer Biomarkers</i> , 2021, 32, 175-188.	0.8	6
1580	Transcriptomic Analyses of the Adenoma-Carcinoma Sequence Identify Hallmarks Associated With the Onset of Colorectal Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 704531.	1.3	12
1581	Potent prophylactic and therapeutic efficacy of recombinant human ACE2-Fc against SARS-CoV-2 infection in vivo. <i>Cell Discovery</i> , 2021, 7, 65.	3.1	51
1582	Cell Walls Are Remodeled to Alleviate nY₂O₃ Cytotoxicity by Elaborate Regulation of <i>de Novo</i> Synthesis and Vesicular Transport. <i>ACS Nano</i> , 2021, 15, 13166-13177.	7.3	13
1583	<i>ltpr1</i> regulates the formation of anterior eye segment tissues derived from neural crest cells. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	9
1584	Transcriptome based genetic resources from Rabbiteye and Southern Highbush blueberries. <i>Journal of Berry Research</i> , 2021, 11, 363-375.	0.7	0
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1587	Dog colour patterns explained by modular promoters of ancient canid origin. <i>Nature Ecology and Evolution</i> , 2021, 5, 1415-1423.	3.4	24
1588	TCF3 Regulates the Proliferation and Apoptosis of Human Spermatogonial Stem Cells by Targeting PODXL. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 695545.	1.8	8
1589	Key Gene and Functional Pathways Identified in Unexplained Recurrent Spontaneous Abortion Using Targeted RNA Sequencing and Clinical Analysis. <i>Frontiers in Immunology</i> , 2021, 12, 717832.	2.2	10
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1591	Transcriptome profiling provides insights into the molecular mechanisms of maize kernel and silk development. <i>BMC Genomic Data</i> , 2021, 22, 28.	0.7	0
1592	Identifying transcript 5â€²-â€²capped ends in <i>Plasmodium falciparum</i>. <i>PeerJ</i> , 2021, 9, e11983.	0.9	2
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1594	A single amino acid residue substitution in BraA04g017190.3C, a histone methyltransferase, results in premature bolting in Chinese cabbage (<i>Brassica rapa</i> L. ssp. <i>Pekinensis</i>). <i>BMC Plant Biology</i> , 2021, 21, 373.	1.6	3

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1596	Signaling pathway perturbation analysis for assessment of biological impact of cigarette smoke on lung cells. <i>Scientific Reports</i> , 2021, 11, 16715.	1.6	5
1598	The sugar-responsive enteroendocrine neuropeptide F regulates lipid metabolism through glucagon-like and insulin-like hormones in <i>Drosophila melanogaster</i> . <i>Nature Communications</i> , 2021, 12, 4818.	5.8	42
1599	Enhancement of Transgene Expression by Mild Hypothermia Is Promoter Dependent in HEK293 Cells. <i>Life</i> , 2021, 11, 901.	1.1	4
1600	Selection and Evaluation of a Thornless and HLB-Tolerant Bud-Sport of Pummelo Citrus With an Emphasis on Molecular Mechanisms. <i>Frontiers in Plant Science</i> , 2021, 12, 739108.	1.7	8
1601	lncRNA and mRNA sequencing of the left testis in experimental varicocele rats treated with <i>Morinda officinalis</i> polysaccharide. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 1136.	0.8	7
1602	SuMO-Fil: Supervised multi-omic filtering prior to performing network analysis. <i>PLoS ONE</i> , 2021, 16, e0255579.	1.1	3
1603	Assembly of fungal mycelium-carbon nanotube composites and their application in pyrene removal. <i>Journal of Hazardous Materials</i> , 2021, 415, 125743.	6.5	18
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1606	PPFIBP1 induces glioma cell migration and invasion through FAK/Src/JNK signaling pathway. <i>Cell Death and Disease</i> , 2021, 12, 827.	2.7	20
1607	Comprehensive Characterization of Multitissue Expression Landscape, Co-Expression Networks and Positive Selection in Pikeperch. <i>Cells</i> , 2021, 10, 2289.	1.8	4
1609	Transcriptome analysis of oviduct in laying ducks under different stocking densities. <i>British Poultry Science</i> , 2022, 63, 283-290.	0.8	2
1610	Global Transcriptome Profile of the Oleaginous Yeast <i>Saitozyma podzolica</i> DSM 27192 Cultivated in Glucose and Xylose. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 758.	1.5	11
1611	Identification and Characterization of Secondary Wall-Associated NAC Genes and Their Involvement in Hormonal Responses in Tobacco (<i>Nicotiana tabacum</i>). <i>Frontiers in Plant Science</i> , 2021, 12, 712254.	1.7	5
1612	Morphological, physiological, and transcriptional responses to low nitrogen stress in <i>Populus deltoides</i> Marsh. clones with contrasting nitrogen use efficiency. <i>BMC Genomics</i> , 2021, 22, 697.	1.2	3
1613	Genome-Wide DNA Methylation and Hydroxymethylation Changes Revealed Epigenetic Regulation of Neuromodulation and Myelination in Yak Hypothalamus. <i>Frontiers in Genetics</i> , 2021, 12, 592135.	1.1	2
1614	Multiple Variant Calling Pipelines in Wheat Whole Exome Sequencing. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10400.	1.8	1

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1618	Gene Expression Nebulas (GEN): a comprehensive data portal integrating transcriptomic profiles across multiple species at both bulk and single-cell levels. <i>Nucleic Acids Research</i> , 2022, 50, D1016-D1024.	6.5	18
1619	The <i>Candida glabrata</i> Upc2A transcription factor is a global regulator of antifungal drug resistance pathways. <i>PLoS Genetics</i> , 2021, 17, e1009582.	1.5	22
1620	Multiple transcriptomic profiling: potential novel metabolism-related genes predict prepubertal testis damage caused by DEHP exposure. <i>Environmental Science and Pollution Research</i> , 2022, 29, 13478-13490.	2.7	5
1621	Haploid Genome Analysis Reveals a Tandem Cluster of Four HSP20 Genes Involved in the High-Temperature Adaptation of <i>Corioliopsis trogii</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0028721.	1.2	7
1623	Mechanisms of responsiveness to and resistance against trabectedin in murine models of human myxoid liposarcoma. <i>Genomics</i> , 2021, 113, 3439-3448.	1.3	2
1625	In vivo and in vitro transcriptomics meta-analyses reveal that BPA may affect TGF-beta signaling regardless of the toxicology system employed. <i>Environmental Pollution</i> , 2021, 285, 117472.	3.7	4
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1627	Comparative Transcriptomics During Brown Rot Decay in Three Fungi Reveals Strain-Specific Degradative Strategies and Responses to Wood Acetylation. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	1
1628	The Genetic Network of Forkhead Gene Family in Development of Brown Planthoppers. <i>Biology</i> , 2021, 10, 867.	1.3	3
1629	Evolutionary Analysis of OAT Gene Family in River and Swamp Buffalo: Potential Role of SLCO3A1 Gene in Milk Performance. <i>Genes</i> , 2021, 12, 1394.	1.0	4
1630	Comparative Transcriptome Analysis of Chemoreception Organs of <i>Laodelphax striatellus</i> in Response to Rice Stripe Virus Infection. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10299.	1.8	2
1631	Spatial variation in gene expression of Tasmanian devil facial tumors despite minimal host transcriptomic response to infection. <i>BMC Genomics</i> , 2021, 22, 698.	1.2	6
1632	Transcriptome and Proteome Analysis Revealed Key Pathways Regulating Final Stage of Oocyte Maturation of the Turkey (<i>Meleagris gallopavo</i>). <i>International Journal of Molecular Sciences</i> , 2021, 22, 10589.	1.8	1
1633	The Natural Antisense Transcript <i>DONE40</i> Derived from the lncRNA <i>ENOD40</i> Locus Interacts with SET Domain Protein ASHR3 During Inception of Symbiosis in <i>Arachis hypogaea</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1057-1070.	1.4	11
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1858	The histone modification reader ZCWPW1 links histone methylation to PRDM9-induced double-strand break repair. <i>ELife</i> , 2020, 9, .	2.8	34
1859	Nuclear receptor Ftz-f1 promotes follicle maturation and ovulation partly via bHLH/PAS transcription factor Sim. <i>ELife</i> , 2020, 9, .	2.8	26
1860	Serotonin signaling by maternal neurons upon stress ensures progeny survival. <i>ELife</i> , 2020, 9, .	2.8	33
1861	Centromere deletion in <i>Cryptococcus deuterogattii</i> leads to neocentromere formation and chromosome fusions. <i>ELife</i> , 2020, 9, .	2.8	22
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2050	Weighted gene coexpression network analysis reveals ESR1, FLNA and Furin as hub genes for DEHP-induced prepubertal testicular injury. <i>Reproductive Toxicology</i> , 2021, 106, 115-125.	1.3	4
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2058	Comprehensive Analysis of Differentially Expressed mRNA, Non-coding RNA, and Their Competitive Endogenous RNA Network of Pacific Oyster <i>Crassostrea gigas</i> With Different Glycogen Content Between Different Environments. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	1
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2089	A susceptibility biomarker identification strategy based on significantly differentially expressed ceRNA triplets for ischemic cardiomyopathy. <i>Bioscience Reports</i> , 2020, 40, .	1.1	3
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2115	Integrative genome-wide analysis of dopaminergic neuron-specific PARIS expression in <i>Drosophila</i> dissects recognition of multiple PPAR- β associated gene regulation. <i>Scientific Reports</i> , 2021, 11, 21500.	1.6	8
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2141	Effect of oxLDL on transcriptional expression of human lens epithelial cells. <i>International Journal of Clinical and Experimental Pathology</i> , 2020, 13, 655-663.	0.5	1
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2165	Global identification and integrated analysis of heat-responsive long non-coding RNAs in contrasting rice cultivars. <i>Theoretical and Applied Genetics</i> , 2022, 135, 833-852.	1.8	7
2167	Genome-wide differences in gene expression and alternative splicing in developing embryo and endosperm, and between F1 hybrids and their parental pure lines in sorghum. <i>Plant Molecular Biology</i> , 2022, 108, 1-14.	2.0	2
2169	Genomic and Transcriptomic Profiling of Brain Metastases. <i>Cancers</i> , 2021, 13, 5598.	1.7	0
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2200	Circular RNA Expression and Regulation Profiling in Testicular Tissues of Immature and Mature Wandong Cattle (<i>Bos taurus</i>). <i>Frontiers in Genetics</i> , 2021, 12, 685541.	1.1	4

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2228	Genome-wide identification of lipases in silkworm (<i>Bombyx mori</i>) and their spatio-temporal expression in larval midgut. <i>Gene</i> , 2022, 813, 146121.	1.0	4
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2257	Comprehensive Detoxification Mechanism Assessment of Red Imported Fire Ant (<i>Solenopsis invicta</i>) against Indoxacarb. <i>Molecules</i> , 2022, 27, 870.	1.7	21
2259	Genetic Aberrations and Interaction of <i>NEK2</i> and <i>TP53</i> Accelerate Aggressiveness of Multiple Myeloma. <i>Advanced Science</i> , 2022, 9, e2104491.	5.6	13
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2264	Understanding of Waggle Dance in the Honey Bee (<i>Apis mellifera</i>) from the Perspective of Long Non-Coding RNA. <i>Insects</i> , 2022, 13, 111.	1.0	4
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2277	The Preservation of PPAR ^{Î³} Genome Duplicates in Some Teleost Lineages: Insights into Lipid Metabolism and Xenobiotic Exploitation. <i>Genes</i> , 2022, 13, 107.	1.0	5
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2286	Transcriptional effects of electroporation on <i>Echinococcus multilocularis</i> primary cell culture. <i>Parasitology Research</i> , 2022, 121, 1155-1168.	0.6	2
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2299	Cherry Blossom Forecast Based on Transcriptome of Floral Organs Approaching Blooming in the Flowering Cherry (<i>Cerasus</i> Å— <i>yedoensis</i>) Cultivar Å“Somei-YoshinoÅ“™. <i>Frontiers in Plant Science</i> , 2022, 13, 802203.	1.7	6

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2319	Transcriptome Profiling Unravels the Involvement of Phytohormones in Tomato Resistance to the Tomato Yellow Leaf Curl Virus (TYLCV). <i>Horticulturae</i> , 2022, 8, 143.	1.2	3
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2471	Genome-wide analysis of the long noncoding RNAs and mRNAs involved in flower bud development of <i>Eucommia ulmoides</i> Oliver. <i>Scientia Horticulturae</i> , 2022, 300, 111038.	1.7	4
2472	Chromosome-scale <i>Cerasus humilis</i> genome assembly reveals gene family evolution and possible genomic basis of calcium accumulation in fruits. <i>Scientia Horticulturae</i> , 2022, 299, 111012.	1.7	5
2473	Integrative analysis of the miRNA-mRNA regulation network in hemocytes of <i>Penaeus vannamei</i> following <i>Vibrio alginolyticus</i> infection. <i>Developmental and Comparative Immunology</i> , 2022, 131, 104390.	1.0	7
2474	Transcriptomic and metabolomic analysis reveals the potential mechanisms underlying the improvement of β -carotene and torulene production in <i>Rhodospiridiobolus colostri</i> under low temperature treatment. <i>Food Research International</i> , 2022, 156, 111158.	2.9	16
2475	Integrated lipidomic and transcriptomic analysis reveals triacylglycerol accumulation in castor bean seedlings under heat stress. <i>Industrial Crops and Products</i> , 2022, 180, 114702.	2.5	7
2476	Genome-wide transcriptional profiling and functional analysis reveal miR-330-MAPK15 axis involving in cellular responses to deoxynivalenol exposure. <i>Chemosphere</i> , 2022, 298, 134199.	4.2	3
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2480	Inhibition Molecular Mechanism of the Novel Fungicidal N-(Naphthalen-1-yl) phenazine-1-carboxamide against <i>Rhizoctonia solani</i> . <i>Agronomy</i> , 2021, 11, 2532.	1.3	3

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2482	Subgenome Bias and Temporal Postponement of Gene Expression Contributes to the Distinctions of Fiber Quality in <i>Gossypium</i> Species. <i>Frontiers in Plant Science</i> , 2021, 12, 819679.	1.7	5
2483	Muscle transcriptome analysis reveal candidate genes and pathways related to fat and lipid metabolism in Yunling cattle. <i>Animal Biotechnology</i> , 2021, , 1-8.	0.7	4
2484	Sly-miR159 regulates fruit morphology by modulating GA biosynthesis in tomato. <i>Plant Biotechnology Journal</i> , 2022, 20, 833-845.	4.1	19
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2486	FOXO3 regulates a common genomic program in aging and glioblastoma stem cells. <i>Aging and Cancer</i> , 2021, 2, 137-159.	0.5	3
2487	DPPA2 and DPPA4 are dispensable for mouse zygotic genome activation and pre-implantation development. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	17
2488	Transcriptome-Wide m6A Analysis Provides Novel Insights Into Testicular Development and Spermatogenesis in Xia-Nan Cattle. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 791221.	1.8	7
2489	Sequencing of Argonaute-bound microRNA/mRNA hybrids reveals regulation of the unfolded protein response by microRNA-320a. <i>PLoS Genetics</i> , 2021, 17, e1009934.	1.5	9
2490	Establishment and Characterization of FusionRed Stable Transfected Canine Prostate Adenocarcinoma and Transitional Cell Carcinoma Cells. <i>In Vivo</i> , 2022, 36, 170-179.	0.6	1
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2494	Genome-wide analysis uncovers tomato leaf lncRNAs transcriptionally active upon <i>Pseudomonas syringae</i> pv. tomato challenge. <i>Scientific Reports</i> , 2021, 11, 24523.	1.6	8
2495	Transcriptome comparative analysis of ovarian follicles reveals the key genes and signaling pathways implicated in hen egg production. <i>BMC Genomics</i> , 2021, 22, 899.	1.2	16
2496	Identification of genes related to growth traits from transcriptome profiles of duck breast muscle tissue. <i>Animal Biotechnology</i> , 2021, , 1-8.	0.7	0
2497	Genome-wide association and selective sweep analyses reveal genetic loci for FCR of egg production traits in ducks. <i>Genetics Selection Evolution</i> , 2021, 53, 98.	1.2	7
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2500	Adhesion GPCR GPR56 Expression Profiling in Human Tissues. <i>Cells</i> , 2021, 10, 3557.	1.8	6
2501	Nuclear NAD ⁺ -biosynthetic enzyme NMNAT1 facilitates development and early survival of retinal neurons. <i>ELife</i> , 2021, 10, .	2.8	11
2503	Transcriptome analysis and potential mechanisms of bovine oocytes under seasonal heat stress. <i>Animal Biotechnology</i> , 2023, 34, 1179-1195.	0.7	1
2504	The Mevalonate Pathway Is Important for Growth, Spore Production, and the Virulence of <i>Phytophthora sojae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, .	1.5	5
2505	Deciphering Evolutionary Dynamics of WRKY I Genes in Rosaceae Species. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	0
2506	Transcriptomic and metabolomic changes triggered by <i>Macrosiphum rosivorum</i> in rose (<i>Rosa</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502	1.2	3
2507	An MD-2-related lipid-recognition protein is required for insect reproduction and integument development. <i>Open Biology</i> , 2021, 11, 210170.	1.5	1
2508	Transcriptomic analysis reveals that non-forage or forage fiber source promotes rumen development through different metabolic processes in lambs. <i>Animal Biotechnology</i> , 2023, 34, 1058-1071.	0.7	2
2510	Quantitative Trait Loci and Transcriptome Analysis Reveal Genetic Basis of Fiber Quality Traits in CCR170 RIL Population of <i>Gossypium hirsutum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 753755.	1.7	5
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2514	Circular RNA, microRNA and Protein Profiles of the Longissimus Dorsi of Germany ZIKA and Sichuan White Rabbits. <i>Frontiers in Genetics</i> , 2021, 12, 777232.	1.1	2
2515	<scp>LncRNA</scp>-mediated <scp>ceRNA</scp> networks provide novel potential biomarkers for peanut drought tolerance. <i>Physiologia Plantarum</i> , 2022, 174, e13610.	2.6	10
2516	Phenotypic Switching and Filamentation in <i>Candida haemulonii</i> , an Emerging Opportunistic Pathogen of Humans. <i>Microbiology Spectrum</i> , 2021, 9, e0077921.	1.2	7
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2523	Potential contribution of intrinsic developmental stability toward body plan conservation. <i>BMC Biology</i> , 2022, 20, 82.	1.7	6
2524	Med23 supports angiogenesis and maintains vascular integrity through negative regulation of angiotensin II expression. <i>Communications Biology</i> , 2022, 5, 374.	2.0	0
2525	Management of prostate cancer by targeting 3 β HSD1 after enzalutamide and abiraterone treatment. <i>Cell Reports Medicine</i> , 2022, 3, 100608.	3.3	11
2526	Comparative transcriptomic analysis of two <i>Cucumis melo</i> var. <i>saccharinus</i> germplasm differing in fruit physical and chemical characteristics. <i>BMC Plant Biology</i> , 2022, 22, 193.	1.6	4
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2529	Astroblastomas exhibit radial glia stem cell lineages and differential expression of imprinted and X-inactivation escape genes. <i>Nature Communications</i> , 2022, 13, 2083.	5.8	3
2530	Natural herbicidal alkaloid berberine regulates the expression of <i>thalianol</i> and <i>marneral</i> gene clusters in <i>Arabidopsis thaliana</i> . <i>Pest Management Science</i> , 2022, , .	1.7	2
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2533	Network Pharmacology and Comparative Transcriptome Reveals Biotargets and Mechanisms of Curcumin Treating Lung Adenocarcinoma Patients With COVID-19. <i>Frontiers in Nutrition</i> , 2022, 9, 870370.	1.6	13
2535	A Chromosome-Level Genome of the Camphor Tree and the Underlying Genetic and Climatic Factors for Its Top-Geophytism. <i>Frontiers in Plant Science</i> , 2022, 13, 827890.	1.7	9
2536	Multidimensional Gene Regulatory Landscape of Motor Organ Pulvinus in the Model Legume <i>Medicago truncatula</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 4439.	1.8	5
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2539	Transcriptomic analysis provides insights into the growth and maturation of ovarian follicles in the ricefield eel (<i>Monopterus albus</i>). <i>Aquaculture</i> , 2022, 555, 738251.	1.7	7
2540	Long-lasting effects of lipopolysaccharide on the reproduction and splenic transcriptome of hens and their offspring. <i>Ecotoxicology and Environmental Safety</i> , 2022, 237, 113527.	2.9	2

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3039	Transcriptome analysis of fasudil treatment in the APP ^{swe} /PSEN1 ^{dE9} transgenic (APP/PS1) mice model of Alzheimer's disease. <i>Scientific Reports</i> , 2022, 12, 6625.	1.6	8
3040	Meiotic cDNA libraries reveal gene truncations and mitochondrial proteins important for competitive fitness in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2022, , .	1.2	0
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3043	24 ^{nt} phasiRNAs move from tapetal to meiotic cells in maize anthers. <i>New Phytologist</i> , 2022, 235, 488-501.	3.5	15
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3047	Lessons learned about the biology and genomics of <i>Diaphorina citri</i> infection with <i>Candidatus Liberibacter asiaticus</i> by integrating new and archived organ-specific transcriptome data. <i>GigaScience</i> , 2022, 11, .	3.3	5
3048	Inheritance of social dominance is associated with global sperm DNA methylation in inbred male mice. <i>Environmental Epigenetics</i> , 0, , .	0.9	0
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3050	Differential Long Non-Coding RNA Expression Analysis in Chronic Non-Atrophic Gastritis, Gastric Mucosal Intraepithelial Neoplasia, and Gastric Cancer Tissues. <i>Frontiers in Genetics</i> , 2022, 13, 833857.	1.1	2
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3052	Transcriptome and metabolome analyses reveal new insights into chlorophyll, photosynthesis, metal ion and phenylpropanoids related pathways during sugarcane ratoon chlorosis. <i>BMC Plant Biology</i> , 2022, 22, 222.	1.6	5
3053	Graphene-Mediated Antioxidant Enzyme Activity and Respiration in Plant Roots. <i>ACS Agricultural Science and Technology</i> , 2022, 2, 646-660.	1.0	8
3054	Effect of Humantenine on mRNA m6A Modification and Expression in Human Colon Cancer Cell Line HCT116. <i>Genes</i> , 2022, 13, 781.	1.0	9
3055	Screening of candidate genes associated with high titer production of oncolytic measles virus based on systems biology approach. <i>Virus Genes</i> , 2022, , 1.	0.7	0
3056	Reduced adhesion of aged intestinal stem cells contributes to an accelerated clonal drift. <i>Life Science Alliance</i> , 2022, 5, e202201408.	1.3	2
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3061	Long Noncoding RNA Expression Profiles Elucidate the Potential Roles of lncRNA- XR_003496198 in Duck Hepatitis A Virus Type 1 Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 858537.	1.8	3
3062	Pitaya Genome and Multiomics Database (PGMD): A Comprehensive and Integrative Resource of <i>Selenicereus undatus</i> . <i>Genes</i> , 2022, 13, 745.	1.0	16
3064	Hepatic GSK3 β -Dependent CRY1 Degradation Contributes to Diabetic Hyperglycemia. <i>Diabetes</i> , 2022, 71, 1373-1387.	0.3	10
3065	Enhancer transcription detected in the nascent transcriptomic landscape of bread wheat. <i>Genome Biology</i> , 2022, 23, 109.	3.8	14
3066	Discovery and functional assessment of a novel adipocyte population driven by intracellular Wnt/ β -catenin signaling in mammals. <i>ELife</i> , 2022, 11, .	2.8	5
3067	Integrative Analysis of lncRNA-miRNA-mRNA Regulatory Network Reveals the Key lncRNAs Implicated Potentially in the Differentiation of Adipocyte in Goats. <i>Frontiers in Physiology</i> , 2022, 13, .	1.3	4
3068	Genome-Wide Analyses of MADS-Box Genes in <i>Humulus lupulus</i> L. Reveal Potential Participation in Plant Development, Floral Architecture, and Lupulin Gland Metabolism. <i>Plants</i> , 2022, 11, 1237.	1.6	7
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3070	Pervasive male-biased expression throughout the germline-specific regions of the sea lamprey genome supports key roles in sex differentiation and spermatogenesis. <i>Communications Biology</i> , 2022, 5, 434.	2.0	5
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3072	Thiamine functions as a key activator for modulating plant health and broad-spectrum tolerance in cotton. <i>Plant Journal</i> , 2022, 111, 374-390.	2.8	11
3073	Identification and Clarification of VrCYCA1: A Key Genic Male Sterility-Related Gene in Mungbean by Multi-Omics Analysis. <i>Agriculture (Switzerland)</i> , 2022, 12, 686.	1.4	2
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3075	The miR319/TaGAMYB3 module regulates plant architecture and improves grain yield in common wheat (<i>Triticum aestivum</i>). <i>New Phytologist</i> , 2022, 235, 1515-1530.	3.5	12
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3077	ISL2 is a putative tumor suppressor whose epigenetic silencing reprograms the metabolism of pancreatic cancer. <i>Developmental Cell</i> , 2022, 57, 1331-1346.e9.	3.1	9
3078	Integrated lipidomics and RNA sequencing analysis reveal novel changes during 3T3-L1 cell adipogenesis. <i>PeerJ</i> , 2022, 10, e13417.	0.9	4

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3079	Genome-Wide Identification and Transcriptional Expression Profiles of PP2C in the Barley (<i>Hordeum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	2
3080	RNA-Seq Analysis Reveals Expression Regulatory Divergence of W-Linked Genes between Two Contrasting Chicken Breeds. <i>Animals</i> , 2022, 12, 1218.	1.0	0
3081	Transcriptome Analysis Using RNA Sequencing for Finding Genes Related to Fiber in Cotton: A Review. , 0, , .		0
3082	Divergence in the ABA gene regulatory network underlies differential growth control. <i>Nature Plants</i> , 2022, 8, 549-560.	4.7	19
3083	Screening of Bovine Tissue-Specific Expressed Genes and Identification of Genetic Variation Within an Adipose Tissue-Specific lncRNA Gene. <i>Frontiers in Veterinary Science</i> , 2022, 9, .	0.9	3
3084	Adiponectin receptors sustain haematopoietic stem cells throughout adulthood by protecting them from inflammation. <i>Nature Cell Biology</i> , 2022, 24, 697-707.	4.6	15
3085	Transcriptome Sequencing to Identify Important Genes and lncRNAs Regulating Abdominal Fat Deposition in Ducks. <i>Animals</i> , 2022, 12, 1256.	1.0	3
3086	Transcriptomic and Metabolomic Response to High Light in the Charophyte Alga <i>Klebsormidium nitens</i> . <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	6
3087	Physiological and transcriptional responses of the ectomycorrhizal fungus <i>Cenococcum geophilum</i> to salt stress. <i>Mycorrhiza</i> , 2022, 32, 327-340.	1.3	6
3088	Integrated transcriptome and endogenous hormone analysis provides new insights into callus proliferation in <i>Osmanthus fragrans</i> . <i>Scientific Reports</i> , 2022, 12, 7609.	1.6	5
3089	miR-29a-5p Inhibits Prenatal Hair Placode Formation Through Targeting EDAR by ceRNA Regulatory Network. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	0
3090	Population-Scale Polymorphic Short Tandem Repeat Provides an Alternative Strategy for Allele Mining in Cotton. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	0
3091	Dynamic Transcriptome Profiling Reveals lncRNA-Centred Regulatory Networks in the Modulation of Pluripotency. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	1
3092	Integrated analysis of lncRNAs and mRNAs by RNA-Seq in secondary hair follicle development and cycling (anagen, catagen and telogen) of Jiangnan cashmere goat (<i>Capra hircus</i>). <i>BMC Veterinary Research</i> , 2022, 18, 167.	0.7	7
3093	Comparative Transcriptional Analysis of Two Contrasting Rice Genotypes in Response to Salt Stress. <i>Agronomy</i> , 2022, 12, 1163.	1.3	2
3094	Transcriptomic profiling of <i>Trypanosoma congolense</i> mouthpart parasites from naturally infected flies. <i>Parasites and Vectors</i> , 2022, 15, 152.	1.0	1
3095	Global changes in gene expression related to <i>Opisthorchis felineus</i> liver fluke infection reveal temporal heterogeneity of a mammalian host response. <i>Food and Waterborne Parasitology</i> , 2022, 27, e00159.	1.1	10
3096	Comparative transcriptomic analysis unveils a network of energy reallocation in <i>Litopenaeus vannamei</i> responsive to heat-stress. <i>Ecotoxicology and Environmental Safety</i> , 2022, 238, 113600.	2.9	10

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3098	TRY intron2 determined its expression in inflorescence activated by SPL9 and MADS-box genes in <i>Arabidopsis</i> . <i>Plant Science</i> , 2022, 321, 111311.	1.7	6
3099	Transcriptomic Diversity of <i>Solanum tuberosum</i> Varieties: A Drive towards Future Analysis of Its Polyploidy Genome. , 2021, 11, .		0
3100	PRDM1 Drives Human Primary T Cell Hyporesponsiveness by Altering the T Cell Transcriptome and Epigenome. <i>Frontiers in Immunology</i> , 2022, 13, 879501.	2.2	4
3101	The Comparative Survey of Coordinated Regulation of Steroidogenic Pathway in Japanese Flounder (<i>Paralichthys olivaceus</i>) and Chinese Tongue Sole (<i>Cynoglossus semilaevis</i>). <i>International Journal of Molecular Sciences</i> , 2022, 23, 5520.	1.8	5
3102	Complex Ecotype Dynamics Evolve in Response to Fluctuating Resources. <i>MBio</i> , 2022, 13, e0346721.	1.8	7
3103	Th1 cytokines synergize to change gene expression and promote corticosteroid insensitivity in pediatric airway smooth muscle. <i>Respiratory Research</i> , 2022, 23, 126.	1.4	4
3104	Transcriptome-Wide Characterization of Seed Aging in Rice: Identification of Specific Long-Lived mRNAs for Seed Longevity. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	4
3105	An Integrated Regulatory Network of mRNAs, microRNAs, and lncRNAs Involved in Nitrogen Metabolism of Moso Bamboo. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	2
3106	The Rice <i>ILI2</i> Locus Is a Bidirectional Target of the African <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Major Transcription Activator-like Effector <i>TalC</i> but Does Not Contribute to Disease Susceptibility. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5559.	1.8	1
3107	High-Quality Genome Assembly of <i>Olea europaea</i> subsp. <i>cuspidata</i> Provides Insights Into Its Resistance to Fungal Diseases in the Summer Rain Belt in East Asia. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	5
3108	A retrotransposon storm marks clinical phenoconversion to late-onset Alzheimer's disease. <i>GeroScience</i> , 2022, 44, 1525-1550.	2.1	12
3109	<i>Hoxb5</i> reprogrammes murine multipotent blood progenitors into haematopoietic stem cell-like cells. <i>Cell Proliferation</i> , 2022, 55, e13235.	2.4	3
3110	Phase II Clinical Trial of Eribulin-Gemcitabine Combination Therapy in Previously Treated Patients With Advanced Liposarcoma or Leiomyosarcoma. <i>Clinical Cancer Research</i> , 2022, 28, 3225-3234.	3.2	5
3111	Embryonic vascular establishment requires protein C receptor-expressing endothelial progenitors. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	4
3112	Construction of the miRNA-mRNA regulatory networks for both the cartilage formation and remodel zones in the antler tip in sika deer (<i>Cervus nippon</i>). <i>Animal Production Science</i> , 2022, , .	0.6	0
3115	Genome-wide identification and association analysis for virus-responsive lncRNAs in rice (<i>Oryza sativa</i>) Tj ETQq0 0 Q rgBT /Overlock 10 T	1.8	2
3117	Genome-wide association study of eigenvectors provides genetic insights into selective breeding for tomato metabolites. <i>BMC Biology</i> , 2022, 20, .	1.7	7

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3118	Understanding the Underlying Molecular Mechanisms of Meiotic Arrest during In Vitro Spermatogenesis in Rat Prepubertal Testicular Tissue. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5893.	1.8	3
3119	Transcriptome analysis reveals fluid shear stress (FSS) and atherosclerosis pathway as a candidate molecular mechanism of short-term low salinity stress tolerance in abalone. <i>BMC Genomics</i> , 2022, 23, .	1.2	8
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3121	An isogenic cell line panel for sequence-based screening of targeted anticancer drugs. <i>IScience</i> , 2022, 25, 104437.	1.9	2
3122	Sulfur limitation boosts more starch accumulation than nitrogen or phosphorus limitation in duckweed (<i>Spirodela polyrhiza</i>). <i>Industrial Crops and Products</i> , 2022, 185, 115098.	2.5	9
3123	Dynamicity of Histone H3K27ac and H3K27me3 Modifications Regulate the Cold-Responsive Gene Expression in <i>Oryza Sativa</i> L. Ssp. <i>Indica</i> . <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
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3125	Responses to Flooding Stress in Quinoa Seedlings Based on Metabolomic and Transcriptomic Analysis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3126	The mechanism by which hyperbaric oxygen treatment alleviates spinal cord injury: genome-wide transcriptome analysis. <i>Neural Regeneration Research</i> , 2022, 17, 2737.	1.6	8
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3132	Maize ZmBES1/BZR1-3 and -9 Transcription Factors Negatively Regulate Drought Tolerance in Transgenic <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 6025.	1.8	11
3133	Ethylene Promotes Expression of the Appressorium- and Pathogenicity-Related Genes via GPCR- and MAPK-Dependent Manners in <i>Colletotrichum gloeosporioides</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 570.	1.5	6
3134	Retinoic acid induced meiosis initiation in female germline stem cells by remodelling three-dimensional chromatin structure. <i>Cell Proliferation</i> , 0, , .	2.4	2
3135	The Short-Day Cycle Induces Intestinal Epithelial Purine Metabolism Imbalance and Hepatic Disfunctions in Antibiotic-Mediated Gut Microbiota Perturbation Mice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6008.	1.8	3
3137	Identification and Regulatory Network Analysis of Genes Related to Reproductive Performance in the Hypothalamus and Pituitary of Angus Cattle. <i>Genes</i> , 2022, 13, 965.	1.0	1
3138	Spatial and Temporal Development of Müller Glial Cells in hiPSC-Derived Retinal Organoids Facilitates the Cell Enrichment and Transcriptome Analysis. <i>Frontiers in Cellular Neuroscience</i> , 0, 16, .	1.8	6

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3141	<i>Plasmodium</i> manipulates the expression of host long non-coding RNA during red blood cell intracellular infection. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	8
3142	Effects of tryptophan and phenylalanine on tryptophol production in <i>Saccharomyces cerevisiae</i> revealed by transcriptomic and metabolomic analyses. <i>Journal of Microbiology</i> , 2022, 60, 832-842.	1.3	3
3143	The H3K27M mutation alters stem cell growth, epigenetic regulation, and differentiation potential. <i>BMC Biology</i> , 2022, 20, .	1.7	10
3144	Cross-Species Analysis Reveals Co-Expressed Genes Regulating Antler Development in Cervidae. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
3145	Identification of Protein Isoforms Using Reference Databases Built from Long and Short Read RNA-Sequencing. <i>Journal of Proteome Research</i> , 2022, 21, 1628-1639.	1.8	4
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3150	Transcriptome-Wide m6A Methylome and m6A-Modified Gene Analysis in Asthma. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	4
3151	Comparative transcriptome analysis elucidates positive physiological effects of foliar application of pyraclostrobin on tomato (<i>Solanum lycopersicum</i> L.). <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 971-986.	1.4	3
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3155	Whole-Transcriptome Analysis Reveals Autophagy Is Involved in Early Senescence of zj-es Mutant Rice. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	1
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3157	Expression rewiring and methylation of non-coding RNAs involved in rhizome phenotypic variations of lotus ecotypes. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2848-2860.	1.9	1
3159	Jasmonate signaling and remodeling of cell wall metabolism induced by boron deficiency in pea shoots. <i>Environmental and Experimental Botany</i> , 2022, 201, 104947.	2.0	14
3160	Comparative Transcriptome Analysis Reveals the Adaptation Mechanism to High Salinity in <i>Litopenaeus vannamei</i> . <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	4

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3175	Spatiotemporal Regulation of a Single Adaptively Evolving<i>Trans</i>-Regulatory Element Contributes to Spermatogenetic Expression Divergence in<i>Drosophila</i>. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	2
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3178	Comparative Genomic Analyses Provide Insight Into the Pathogenicity of <i>Metschnikowia bicuspidata</i> LNES0119. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	7
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3180	Transcriptome and Metabolome Analysis of Upland Cotton (<i>Gossypium hirsutum</i>) Seed Pretreatment with MgSO ₄ in Response to Salinity Stress. <i>Life</i> , 2022, 12, 921.	1.1	5
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3182	Perirenal adipose afferent nerves sustain pathological high blood pressure in rats. <i>Nature Communications</i> , 2022, 13, .	5.8	12

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3186	Identification and functional annotation of long intergenic non-coding RNAs in Brassicaceae. <i>Plant Cell</i> , 2022, 34, 3233-3260.	3.1	22
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3189	Dual function of SF3B2 on chromatin and RNA to regulate transcription in head and neck squamous cell carcinoma. <i>Cell and Bioscience</i> , 2022, 12, .	2.1	1
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3204	De novo assembly provides new insights into the evolution of <i>Elaeagnus angustifolia</i> L.. <i>Plant Methods</i> , 2022, 18, .	1.9	3
3205	Activation of plant immunity by exposure to dinitrogen pentoxide gas generated from air using plasma technology. <i>PLoS ONE</i> , 2022, 17, e0269863.	1.1	4
3206	Maternal binge alcohol consumption leads to distinctive acute perturbations in embryonic cardiac gene expression profiles. <i>Alcoholism: Clinical and Experimental Research</i> , 0, , .	1.4	1
3207	Ploidy Variation and Spontaneous Haploid-Diploid Switching of <i>Candida glabrata</i> Clinical Isolates. <i>MSphere</i> , 2022, 7, .	1.3	3
3208	Transcriptome Profiling of Transposon-Derived Long Non-coding RNAs Response to Hormone in Strawberry Fruit Development. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
3209	Integrated Metabolomics and Transcriptome Analyses Unveil Pathways Involved in Sugar Content and Rind Color of Two Sugarcane Varieties. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	11
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3213	Genetic analysis and identification of VrFRO8, a salt tolerance-related gene in mungbean. <i>Gene</i> , 2022, 836, 146658.	1.0	5
3214	Activation of thermogenesis pathways in testis of diet-induced obesity mice. <i>Reproductive Biology</i> , 2022, 22, 100652.	0.9	1
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3216	TRIM37 Augments AP-2 ^β Transcriptional Activity and Cellular Localization via K63-linked Ubiquitination to Drive Breast Cancer Progression. <i>International Journal of Biological Sciences</i> , 2022, 18, 4316-4328.	2.6	4
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3224	Single-cell transcriptomic analysis identifies an immune-prone population in erythroid precursors during human ontogenesis. <i>Nature Immunology</i> , 2022, 23, 1109-1120.	7.0	30
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3227	Maternal obesity induces liver lipid accumulation of offspring through the lncRNA Lockd/mTOR autophagy pathway. <i>Molecular Genetics and Genomics</i> , 2022, 297, 1277-1287.	1.0	3
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3229	Comparative Transcriptome Profiling Reveals the Genes Involved in Storage Root Expansion in Sweetpotato (<i>Ipomoea batatas</i> (L.) Lam.). <i>Genes</i> , 2022, 13, 1156.	1.0	3
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3233	Complex regulatory role of DNA methylation in caste- and age-specific expression of a termite. <i>Open Biology</i> , 2022, 12, .	1.5	6
3234	Starch Phosphorylase 2 is essential for cellular carbohydrate partitioning in maize. <i>Journal of Integrative Plant Biology</i> , 0, , .	4.1	1
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3237	Chromosome-scale assembly and annotation of the perennial ryegrass genome. <i>BMC Genomics</i> , 2022, 23, .	1.2	17
3238	Transcriptome Dynamics of an Oyster Larval Response to a Conspecific Cue-Mediated Settlement Induction in the Pacific Oyster <i>Crassostrea gigas</i> . <i>Diversity</i> , 2022, 14, 559.	0.7	3
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3242	Comparative Physiological and Transcriptome Analysis Provide Insights into the Response of <i>Cenococcum geophilum</i> , an Ectomycorrhizal Fungus to Cadmium Stress. <i>Journal of Fungi (Basel)</i> , Tj ETQq1 1 0.78434 4 rgBT 10 Overlo		
3244	Transcriptomic analysis of starch accumulation patterns in different glutinous sorghum seeds. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
3246	Xylem Transcriptome Analysis in Contrasting Wood Phenotypes of <i>Eucalyptus urophylla</i> × <i>tereticornis</i> Hybrids. <i>Forests</i> , 2022, 13, 1102.	0.9	2
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3248	Growing Maize Root: Lectins Involved in Consecutive Stages of Cell Development. <i>Plants</i> , 2022, 11, 1799.	1.6	0
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3254	Physiological responses and adaptations to high methane production in Japanese Black cattle. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
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3261	Transcriptional networks regulating suberin and lignin in endodermis link development and ABA response. <i>Plant Physiology</i> , 2022, 190, 1165-1181.	2.3	16
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3264	DNA Methylome and LncRNAome Analysis Provide Insights Into Mechanisms of Genome-Dosage Effects in Autotetraploid Cassava. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
3265	Genome-wide identification and expression analysis of mitogen-activated protein kinase (<sc>MAPK</sc>) genes in response to salinity stress in channel catfish (<i>Ictalurus punctatus</i>). <i>Journal of Fish Biology</i> , 2022, 101, 972-984.	0.7	3
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3267	Dynamics of histone H3K27ac and H3K27me3 modifications regulate the cold-responsive gene expression in <i>Oryza sativa</i> L. ssp. indica. <i>Genomics</i> , 2022, 114, 110433.	1.3	10
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3270	Effective Mechanisms for Improving Seed Oil Production in Pennycress (<i>Thlaspi arvense</i> L.) Highlighted by Integration of Comparative Metabolomics and Transcriptomics. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
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3302	Grade follicles transcriptional profiling analysis in different laying stages in chicken. <i>BMC Genomics</i> , 2022, 23, .	1.2	10

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3398	Tissue-Specific Transcriptomes Outline Halophyte Adaptive Strategies in the Gray Mangrove (<i>Avicennia</i>) Tj ETQq0 0,0 rgBT /Oylock 10 1.3 3		
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3433	Steroidogenic Effects of Salinity Change on the Hypothalamus-Pituitary-Gonad (HPG) Axis of Male Chinese Sea Bass (<i>Lateolabrax maculatus</i>). <i>International Journal of Molecular Sciences</i> , 2022, 23, 10905.	1.8	1
3434	Comparative transcriptome meta-analysis reveals a set of genes involved in the responses to multiple pathogens in maize. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
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3482	Triploid production and performance in hybrid grouper (<i>Epinephelus fuscoguttatus</i> × <i>Epinephelus</i>) Tj ETQq0,0 0 rgBT ₁ /Overlock	1.7	1
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3501	BPL3 binds the long non-coding RNA <i>nalncFL7</i> to suppress <i>FORKED-LIKE7</i> and modulate HAI1-mediated MPK3/6 dephosphorylation in plant immunity. <i>Plant Cell</i> , 2023, 35, 598-616.	3.1	14
3502	Transcriptomic Analysis to Unravel Potential Pathways and Genes Involved in Pecan (<i>Carya</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 To 2022, 23, 11621.	1.8	4
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3504	Characterization of Glossy Spike Mutants and Identification of Candidate Genes Regulating Cuticular Wax Synthesis in Barley (<i>Hordeum vulgare</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 13025.	1.8	0
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3517	<i>ZmCCT10</i> -delayed photoperiod sensitivity regulates natural variation in the arithmetical formation of male germinal cells in maize. <i>New Phytologist</i> , 0, , .	3.5	1
3518	Determination of physiological, biochemical and molecular interactions between Fraser's <i>Photinia</i> (<i>Photinia</i> - <i>fraseri</i> Dress.) and its endophytic bacterium PGB_invit. <i>Plant Cell, Tissue and Organ Culture</i> , 2022, 151, 631-649.	1.2	2

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3524	A Comparison of the Flavonoid Biosynthesis Mechanisms of <i>Dendrobium</i> Species by Analyzing the Transcriptome and Metabolome. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11980.	1.8	9
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3531	De novo genome assembly and annotation of <i>Holothuria scabra</i> (Jaeger, 1833) from nanopore sequencing reads. <i>Genes and Genomics</i> , 2022, 44, 1487-1498.	0.5	3
3532	Common but Nonpersistent Acquisitions of Plant Viruses by Plant-Associated Fungi. <i>Viruses</i> , 2022, 14, 2279.	1.5	13
3534	Allele-specific expression and chromatin accessibility contribute to heterosis in tea plants (<i>Camellia sinensis</i>). <i>Plant Journal</i> , 2022, 112, 1194-1211.	2.8	17
3535	Physiological and transcriptomic responses to starvation in the corallivorous crown-of-thorn starfish. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	2
3536	Identification and functional analysis of m6A in the mammary gland tissues of dairy goats at the early and peak lactation stages. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	3
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3538	Identification of long non-coding RNA-microRNA-mRNA regulatory modules and their potential roles in drought stress response in wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
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3552	Extracellular fluid viscosity enhances cell migration and cancer dissemination. <i>Nature</i> , 2022, 611, 365-373.	13.7	94
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3555	L-threonine promotes healthspan by expediting ferritin-dependent ferroptosis inhibition in <i>C. elegans</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	18
3556	TeaPVs: a comprehensive genomic variation database for tea plant (<i>Camellia sinensis</i>). <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2
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3559	Three-Dimensional Bio-Printed Autologous Omentum Patch Ameliorates Unilateral Ureteral Obstruction-Induced Renal Fibrosis. <i>Tissue Engineering - Part C: Methods</i> , 2022, 28, 672-682.	1.1	3
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3562	An integrative analysis of lncRNAs and mRNAs highlights the potential roles of lncRNAs in the process of follicle selection in Taihang chickens. <i>Theriogenology</i> , 2023, 195, 122-130.	0.9	1
3563	Host-microbiota interactions play a crucial role in oyster adaptation to rising seawater temperature in summer. <i>Environmental Research</i> , 2023, 216, 114585.	3.7	7
3564	Transcriptome analysis reveals the mechanism of caffeic acid-grafted-chitosan/poly(lactic acid) film packaging to delay quality deterioration in postharvest <i>Agaricus bisporus</i> . <i>Scientia Horticulturae</i> , 2023, 309, 111647.	1.7	4
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3569	<sc>CRISPR</sc>/Cas9-mediated methoprene-tolerant 1 knockout results in precocious metamorphosis of beet armyworm (<i>Spodoptera exigua</i>) only at the late larval stage. <i>Insect Molecular Biology</i> , 2023, 32, 132-142.	1.0	3
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3574	Cancer cell-intrinsic XBP1 drives immunosuppressive reprogramming of intratumoral myeloid cells by promoting cholesterol production. <i>Cell Metabolism</i> , 2022, 34, 2018-2035.e8.	7.2	29
3575	Unraveling the Pathobiological Role of the Fungal KEOPS Complex in <i>Cryptococcus neoformans</i> . <i>MBio</i> , 2022, 13, .	1.8	3
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3578	Transcriptome analysis of gonads and brain of giant freshwater prawn (<i>Macrobrachium rosenbergii</i>): screening and validation of genes related to germ cell development. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
3579	Defining newly formed and tissue-resident bone marrow-derived macrophages in adult mice based on lysozyme expression. , 2022, 19, 1333-1346.		5
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3582	Transcriptome analysis of differentially expressed circRNAs miRNAs and mRNAs during the challenge of coccidiosis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
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