Salmon provides fast and bias-aware quantification of t

Nature Methods

14, 417-419

DOI: 10.1038/nmeth.4197

Citation Report

#	Article	IF	Citations
2	The reactivity of hydrazine with photosystem II strongly depends on the redox state of the water oxidizing system. FEBS Letters, 1990, 277, 141-146.	2.8	43
3	Chromosomal dynamics predicted by an elastic network model explains genome-wide accessibility and long-range couplings. Nucleic Acids Research, 2017, 45, 3663-3673.	14.5	24
4	Severe acute dehydration in a desert rodent elicits a transcriptional response that effectively prevents kidney injury. American Journal of Physiology - Renal Physiology, 2017, 313, F262-F272.	2.7	37
5	A high quality Arabidopsis transcriptome for accurate transcript-level analysis of alternative splicing. Nucleic Acids Research, 2017, 45, 5061-5073.	14.5	262
6	Benchmarking of RNA-sequencing analysis workflows using whole-transcriptome RT-qPCR expression data. Scientific Reports, 2017, 7, 1559.	3.3	247
7	Assessment of engineered cells using CellNet and RNA-seq. Nature Protocols, 2017, 12, 1089-1102.	12.0	41
8	Reference standards for next-generation sequencing. Nature Reviews Genetics, 2017, 18, 473-484.	16.3	194
9	Bioinformatic analysis of bacteria and host cell dual RNA-sequencing experiments. Briefings in Bioinformatics, 2018, 19, 1115-1129.	6.5	16
10	YY1 Haploinsufficiency Causes an Intellectual Disability Syndrome Featuring Transcriptional and Chromatin Dysfunction. American Journal of Human Genetics, 2017, 100, 907-925.	6.2	125
11	Neuromedin B Expression Defines the Mouse Retrotrapezoid Nucleus. Journal of Neuroscience, 2017, 37, 11744-11757.	3.6	61
12	Mammalian APE1 controls miRNA processing and its interactome is linked to cancer RNA metabolism. Nature Communications, 2017, 8, 797.	12.8	107
13	Genomeâ€wide characterization of differential transcript usage in Arabidopsis thaliana. Plant Journal, 2017, 92, 1218-1231.	5.7	31
14	Barley SIX-ROWED SPIKE3 encodes a putative Jumonji C-type H3K9me2/me3 demethylase that represses lateral spikelet fertility. Nature Communications, 2017, 8, 936.	12.8	78
15	Extensive gene tree discordance and hemiplasy shaped the genomes of North American columnar cacti. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12003-12008.	7.1	90
16	Research Techniques Made Simple: Bioinformatics for Genome-Scale Biology. Journal of Investigative Dermatology, 2017, 137, e163-e168.	0.7	14
17	A heterochromatin-dependent transcription machinery drives piRNA expression. Nature, 2017, 549, 54-59.	27.8	213
18	De novo transcriptome assembly for the spiny mouse (Acomys cahirinus). Scientific Reports, 2017, 7, 8996.	3.3	37
19	Long noncoding RNAs in the model species Brachypodium distachyon. Scientific Reports, 2017, 7, 11252.	3.3	51

#	Article	IF	Citations
20	A three enzyme system to generate the Strychnos alkaloid scaffold from a central biosynthetic intermediate. Nature Communications, 2017, 8, 316.	12.8	117
21	Repression of Stress-Induced LINE-1 Expression Protects Cancer Cell Subpopulations from Lethal Drug Exposure. Cancer Cell, 2017, 32, 221-237.e13.	16.8	177
22	Cell-Type-Specific Translation Profiling Reveals a Novel Strategy for Treating Fragile X Syndrome. Neuron, 2017, 95, 550-563.e5.	8.1	81
23	Six-Rowed Spike3 (VRS3) Is a Histone Demethylase That Controls Lateral Spikelet Development in Barley. Plant Physiology, 2017, 174, 2397-2408.	4.8	62
24	Characterization of the human thyroid epigenome. Journal of Endocrinology, 2017, 235, 153-165.	2.6	8
25	Cytoplasmic polyadenylation-mediated translational control of maternal mRNAs directs maternal to zygotic transition. Development (Cambridge), 2017, 145, .	2.5	46
26	Single-cell RNA-sequencing uncovers transcriptional states and fate decisions in haematopoiesis. Nature Communications, 2017, 8, 2045.	12.8	147
27	Put3 Positively Regulates Proline Utilization in Candida albicans. MSphere, 2017, 2, .	2.9	17
28	Accurate assembly of transcripts through phase-preserving graph decomposition. Nature Biotechnology, 2017, 35, 1167-1169.	17.5	162
29	RNA polymerase III limits longevity downstream of TORC1. Nature, 2017, 552, 263-267.	27.8	83
30	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. Nature Communications, 2017, 8, 59.	12.8	225
31	Customized workflow development and data modularization concepts for RNA-Sequencing and metatranscriptome experiments. Journal of Biotechnology, 2017, 261, 85-96.	3.8	16
32	Quark enables semi-reference-based compression of RNA-seq data. Bioinformatics, 2017, 33, 3380-3386.	4.1	4
33	Integration of quantitated expression estimates from polyA-selected and rRNA-depleted RNA-seq libraries. BMC Bioinformatics, 2017, 18, 301.	2.6	40
34	A hypothesis-driven approach to assessing significance of differences in RNA expression levels among specific groups of genes. Current Plant Biology, 2017, 11-12, 46-51.	4.7	4
35	Evaluation and comparison of computational tools for RNA-seq isoform quantification. BMC Genomics, 2017, 18, 583.	2.8	137
36	Transcriptome analyses reveal SR45 to be a neutral splicing regulator and a suppressor of innate immunity in Arabidopsis thaliana. BMC Genomics, 2017, 18, 772.	2.8	64
37	A Dramatic Difference in Global Gene Expression between TCDD-Treated Atlantic Tomcod Larvae from the Resistant Hudson River and a Nearby Sensitive Population. Genome Biology and Evolution, 2017, 9, 2251-2264.	2.5	2

#	Article	IF	Citations
38	Practical Data Processing Approach for RNA Sequencing of Microorganisms. , 2017, , .		0
39	RNAâ€seq: Applications and Best Practices. , 0, , .		17
40	Elucidating the Role of Host Long Non-Coding RNA during Viral Infection: Challenges and Paths Forward. Vaccines, 2017, 5, 37.	4.4	12
41	A high-resolution mRNA expression time course of embryonic development in zebrafish. ELife, 2017, 6, .	6.0	257
42	Integrative genomic analyses for identification and prioritization of long non-coding RNAs associated with autism. PLoS ONE, 2017, 12, e0178532.	2.5	32
43	Stochastic principles governing alternative splicing of RNA. PLoS Computational Biology, 2017, 13, e1005761.	3.2	16
44	RNA-Seq differential expression analysis: An extended review and a software tool. PLoS ONE, 2017, 12, e0190152.	2.5	451
45	DE-kupl: exhaustive capture of biological variation in RNA-seq data through k-mer decomposition. Genome Biology, 2017, 18, 243.	8.8	33
46	RNA sequencing identifies novel non-coding RNA and exon-specific effects associated with cigarette smoking. BMC Medical Genomics, 2017, 10, 58.	1.5	48
47	stageR: a general stage-wise method for controlling the gene-level false discovery rate in differential expression and differential transcript usage. Genome Biology, 2017, 18, 151.	8.8	97
48	SuperTranscripts: a data driven reference for analysis and visualisation of transcriptomes. Genome Biology, 2017, 18, 148.	8.8	79
49	Extensive transcriptomic and epigenomic remodelling occurs during Arabidopsis thaliana germination. Genome Biology, 2017, 18, 172.	8.8	163
50	Splatter: simulation of single-cell RNA sequencing data. Genome Biology, 2017, 18, 174.	8.8	626
51	Alignment-free sequence comparison: benefits, applications, and tools. Genome Biology, 2017, 18, 186.	8.8	371
52	Adaptation of iCLIP to plants determines the binding landscape of the clock-regulated RNA-binding protein AtGRP7. Genome Biology, 2017, 18, 204.	8.8	87
53	Central nervous system transcriptome of Biomphalaria alexandrina, an intermediate host for schistosomiasis. BMC Research Notes, 2017, 10, 729.	1.4	11
54	Evolutionary loss of melanogenesis in the tunicate Molgula occulta. EvoDevo, 2017, 8, 11.	3.2	38
55	Local sequence and sequencing depth dependent accuracy of RNA-seq reads. BMC Bioinformatics, 2017, 18, 364.	2.6	8

#	Article	IF	Citations
56	Gene length and detection bias in single cell RNA sequencing protocols. F1000Research, 2017, 6, 595.	1.6	76
57	Improved data-driven likelihood factorizations for transcript abundance estimation. Bioinformatics, 2017, 33, i142-i151.	4.1	23
58	Identification of long non-coding RNA in the horse transcriptome. BMC Genomics, 2017, 18, 511.	2.8	30
59	Genome-wide CRISPR-Cas9 Screen Identifies Leukemia-Specific Dependence on a Pre-mRNA Metabolic Pathway Regulated by DCPS. Cancer Cell, 2018, 33, 386-400.e5.	16.8	99
60	AltHapAlignR: improved accuracy of RNA-seq analyses through the use of alternative haplotypes. Bioinformatics, 2018, 34, 2401-2408.	4.1	27
61	Inborn Errors of RNA Lariat Metabolism in Humans with Brainstem Viral Infection. Cell, 2018, 172, 952-965.e18.	28.9	92
62	An ancient family of lytic polysaccharide monooxygenases with roles in arthropod development and biomass digestion. Nature Communications, 2018, 9, 756.	12.8	192
63	Bias, robustness and scalability in single-cell differential expression analysis. Nature Methods, 2018, 15, 255-261.	19.0	592
64	EAF2 and p53 Co-Regulate STAT3 Activation in Prostate Cancer. Neoplasia, 2018, 20, 351-363.	5.3	16
65	Gene expression differs in susceptible and resistant amphibians exposed to Batrachochytrium dendrobatidis. Royal Society Open Science, 2018, 5, 170910.	2.4	37
66	Introduction to Singleâ€Cell RNA Sequencing. Current Protocols in Molecular Biology, 2018, 122, e57.	2.9	115
67	Using Minimum Path Cover to Boost Dynamic Programming on DAGs: Co-linear Chaining Extended. Lecture Notes in Computer Science, 2018, , 105-121.	1.3	13
68	Novel sequencing technologies to support industrial biotechnology. FEMS Microbiology Letters, 2018, 365, .	1.8	15
69	Tracking the NGS revolution: managing life science research on shared high-performance computing clusters. GigaScience, 2018, 7, .	6.4	8
70	Research in Computational Molecular Biology. Lecture Notes in Computer Science, 2018, , .	1.3	0
71	Spatiotemporal heterogeneity and patterning of developing renal blood vessels. Angiogenesis, 2018, 21, 617-634.	7.2	55
72	Environment-dependent striatal gene expression in the BACHD rat model for Huntington disease. Scientific Reports, 2018, 8, 5803.	3.3	10
73	Human ADAR1 Prevents Endogenous RNA from Triggering Translational Shutdown. Cell, 2018, 172, 811-824.e14.	28.9	375

#	Article	IF	Citations
74	Scikit-ribo Enables Accurate Estimation and Robust Modeling of Translation Dynamics at Codon Resolution. Cell Systems, 2018, 6, 180-191.e4.	6.2	41
75	Cyanophage-encoded lipid desaturases: oceanic distribution, diversity and function. ISME Journal, 2018, 12, 343-355.	9.8	23
76	FreePSI: an alignment-free approach to estimating exon-inclusion ratios without a reference transcriptome. Nucleic Acids Research, 2018, 46, e11-e11.	14.5	3
77	Functionally Conserved Noncoding Regulators of Cardiomyocyte Proliferation and Regeneration in Mouse and Human. Circulation Genomic and Precision Medicine, 2018, 11, e001805.	3.6	14
78	Highâ€‰throughput identification of <scp>RNA</scp> nuclear enrichment sequences. EMBO Journal, 2018, 37, .	7.8	99
79	Brain Transcriptome Databases: A User's Guide. Journal of Neuroscience, 2018, 38, 2399-2412.	3.6	68
80	The Ancient Origins of Neural Substrates for Land Walking. Cell, 2018, 172, 667-682.e15.	28.9	76
81	A Non-canonical BCOR-PRC1.1 Complex Represses Differentiation Programs in Human ESCs. Cell Stem Cell, 2018, 22, 235-251.e9.	11.1	80
82	Comparative analysis of high butanol tolerance and production in clostridia. Biotechnology Advances, 2018, 36, 721-738.	11.7	46
83	Effect of Plasmid Design and Type of Integration Event on Recombinant Protein Expression in Pichia pastoris. Applied and Environmental Microbiology, 2018, 84, .	3.1	54
84	High-dimensional single-cell analysis predicts response to anti-PD-1 immunotherapy. Nature Medicine, 2018, 24, 144-153.	30.7	564
85	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. Nature Genetics, 2018, 50, 172-174.	21.4	156
86	Impact of cycling cells and cell cycle regulation on Hydra regeneration. Developmental Biology, 2018, 433, 240-253.	2.0	28
87	Outlier detection for improved differential splicing quantification from RNA-Seq experiments with replicates. Bioinformatics, 2018, 34, 1488-1497.	4.1	35
88	The Expanding Landscape of Alternative Splicing Variation in Human Populations. American Journal of Human Genetics, 2018, 102, 11-26.	6.2	290
89	High-quality assembly of Dermatophagoides pteronyssinus genome and transcriptome reveals a wide range of novel allergens. Journal of Allergy and Clinical Immunology, 2018, 141, 2268-2271.e8.	2.9	34
90	Rapid genome shrinkage in a self-fertile nematode reveals sperm competition proteins. Science, 2018, 359, 55-61.	12.6	102
91	The fractured landscape of RNA-seq alignment: the default in our STARs. Nucleic Acids Research, 2018, 46, 5125-5138.	14.5	17

#	Article	IF	Citations
92	Missing enzymes in the biosynthesis of the anticancer drug vinblastine in Madagascar periwinkle. Science, 2018, 360, 1235-1239.	12.6	279
93	Uncovering the molecular mechanisms of lignocellulose digestion in shipworms. Biotechnology for Biofuels, 2018, 11, 59.	6.2	42
94	Shifting metabolic priorities among key protistan taxa within and below the euphotic zone. Environmental Microbiology, 2018, 20, 2865-2879.	3.8	32
95	The Amount of Nitrogen Used for Photosynthesis Modulates Molecular Evolution in Plants. Molecular Biology and Evolution, 2018, 35, 1616-1625.	8.9	37
96	Advances in Transcriptomics. Circulation Research, 2018, 122, 1200-1220.	4.5	38
97	Neurotransmitter Switching Coupled to Î²-Adrenergic Signaling in Sympathetic Neurons in Prehypertensive States. Hypertension, 2018, 71, 1226-1238.	2.7	27
98	Long intergenic non-coding RNAs have an independent impact on survival in multiple myeloma. Leukemia, 2018, 32, 2626-2635.	7.2	48
99	Automated brightfield morphometry of 3D organoid populations by OrganoSeg. Scientific Reports, 2018, 8, 5319.	3.3	92
100	Genome Sequencing and RNA-Motif Analysis Reveal Novel Damaging Noncoding Mutations in Human Tumors. Molecular Cancer Research, 2018, 16, 1112-1124.	3.4	18
101	Dissecting the Functional Consequences of De Novo DNA Methylation Dynamics in Human Motor Neuron Differentiation and Physiology. Cell Stem Cell, 2018, 22, 559-574.e9.	11.1	53
102	How does temperature affect splicing events? Isoform switching of splicing factors regulates splicing of LATE ELONGATED HYPOCOTYL (LHY). Plant, Cell and Environment, 2018, 41, 1539-1550.	5.7	25
103	Genome-wide analyses using UK Biobank data provide insights into the genetic architecture of osteoarthritis. Nature Genetics, 2018, 50, 549-558.	21.4	223
105	The impact of single-cell RNA sequencing on understanding the functional organization of the immune system. Briefings in Functional Genomics, 2018, 17, 265-272.	2.7	30
106	The transcriptome, extracellular proteome and active secretome of agroinfiltrated Nicotiana benthamiana uncover a large, diverse protease repertoire. Plant Biotechnology Journal, 2018, 16, 1068-1084.	8.3	54
107	Transcriptional Response of Respiratory Epithelium to Nontuberculous Mycobacteria. American Journal of Respiratory Cell and Molecular Biology, 2018, 58, 241-252.	2.9	37
108	Single Cell Resolution of Human Hematoendothelial Cells Defines Transcriptional Signatures of Hemogenic Endothelium. Stem Cells, 2018, 36, 206-217.	3.2	24
109	Induced pluripotent stem cells derived from human amnion in chemically defined conditions. Cell Cycle, 2018, 17, 330-347.	2.6	4
110	Transcriptional Profiles of Secondary Metabolite Biosynthesis Genes and Cytochromes in the Leaves of Four Papaver Species. Data, 2018, 3, 55.	2.3	7

#	Article	IF	Citations
111	MIA. , 2018, , .		1
112	iDEP: an integrated web application for differential expression and pathway analysis of RNA-Seq data. BMC Bioinformatics, 2018, 19, 534.	2.6	803
113	RF/6A Chorioretinal Cells Do Not Display Key Endothelial Phenotypes. , 2018, 59, 5795.		18
114	Towards Selective-Alignment. , 2018, , .		5
115	PiGx: reproducible genomics analysis pipelines with GNU Guix. GigaScience, 2018, 7, .	6.4	66
116	Investigation of the skeletal muscle transcriptome in lambs fed Î² adrenergic agonists and subjected to heat stress for 21 d1. Translational Animal Science, 2018, 2, S53-S56.	1.1	11
117	Paean: A parallel transcriptome quantification tool combining gene expression and alternative splicing events using GPU. , 2018, , .		0
118	ASGAL: aligning RNA-Seq data to a splicing graph to detect novel alternative splicing events. BMC Bioinformatics, 2018, 19, 444.	2.6	26
119	A de novo transcriptome assembly of the zebra bullhead shark, Heterodontus zebra. Scientific Data, 2018, 5, 180197.	5.3	11
120	Single sample scoring of molecular phenotypes. BMC Bioinformatics, 2018, 19, 404.	2.6	286
121	Simulation-based benchmarking of isoform quantification in single-cell RNA-seq. Genome Biology, 2018, 19, 191.	8.8	25
122	Single-cell transcriptional analysis reveals ILC-like cells in zebrafish. Science Immunology, 2018, 3, .	11.9	103
123	A chromosomeâ€scale assembly of the model desiccation tolerant grass Oropetium thomaeum. Plant Direct, 2018, 2, e00096.	1.9	39
124	RAS P21 Protein Activator 3 (RASA3) Specifically Promotes Pathogenic T Helper 17 Cell Generation by Repressing T-Helper-2-Cell-Biased Programs. Immunity, 2018, 49, 886-898.e5.	14.3	15
125	Comprehensive evaluation of RNA-seq analysis pipelines in diploid and polyploid species. GigaScience, 2018, 7, .	6.4	23
126	Improved reference genome of Aedes aegypti informs arbovirus vector control. Nature, 2018, 563, 501-507.	27.8	426
127	The crowns have eyes: multiple opsins found in the eyes of the crown-of-thorns starfish Acanthaster planci. BMC Evolutionary Biology, 2018, 18, 168.	3.2	13
128	Empirical assessment of the impact of sample number and read depth on RNA-Seq analysis workflow performance. BMC Bioinformatics, 2018, 19, 423.	2.6	48

#	Article	IF	Citations
129	Versican is differentially regulated in the adventitial and medial layers of human vein grafts. PLoS ONE, 2018, 13, e0204045.	2.5	4
130	Reproducible bioinformatics project: a community for reproducible bioinformatics analysis pipelines. BMC Bioinformatics, 2018, 19, 349.	2.6	49
131	The proto CpG island methylator phenotype of sessile serrated adenomas/polyps. Epigenetics, 2018, 13, 1088-1105.	2.7	21
132	Integrated systems analysis reveals conserved gene networks underlying response to spinal cord injury. ELife, 2018, 7, .	6.0	29
133	PI3KÎ±/Î´ inhibition promotes anti-tumor immunity through direct enhancement of effector CD8+ T-cell activity. , 2018, 6, 158.		62
134	Building a Science Gateway For Processing and Modeling Sequencing Data Via Apache Airavata. , 2018, 2018, .		4
135	Unraveling inter-species differences in hagfish slime skein deployment. Journal of Experimental Biology, 2018, 221, .	1.7	6
136	Casein Kinase II Phosphorylation of Spt6 Enforces Transcriptional Fidelity by Maintaining Spn1-Spt6 Interaction. Cell Reports, 2018, 25, 3476-3489.e5.	6.4	20
137	Cluster oligonucleotide signatures for rapid identification by sequencing. BMC Bioinformatics, 2018, 19, 395.	2.6	7
138	RNAâ€“Protein Interactions Prevent Long RNA Duplex Formation: Implications for the Design of RNA-Based Therapeutics. Molecules, 2018, 23, 3329.	3.8	0
139	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. F1000Research, 2018, 7, 952.	1.6	87
140	Integrative system biology analyses of CRISPR-edited iPSC-derived neurons and human brains reveal deficiencies of presynaptic signaling in FTLD and PSP. Translational Psychiatry, 2018, 8, 265.	4.8	47
141	Daphnia galeata responds to the exposure to an ichthyosporean gut parasite by down-regulation of immunity and lipid metabolism. BMC Genomics, 2018, 19, 932.	2.8	9
142	CHESS: a new human gene catalog curated from thousands of large-scale RNA sequencing experiments reveals extensive transcriptional noise. Genome Biology, 2018, 19, 208.	8.8	263
143	RORÎ± controls inflammatory state of human macrophages. PLoS ONE, 2018, 13, e0207374.	2.5	50
144	Different iron storage strategies among bloom-forming diatoms. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E12275-E12284.	7.1	61
145	Modeling and analysis of RNAâ€seq data: a review from a statistical perspective. Quantitative Biology, 2018, 6, 195-209.	0.5	49
146	A prognostic mRNA expression signature of four 16q24.3 genes in radio(chemo)therapyâ€treated head and neck squamous cell carcinoma (HNSCC). Molecular Oncology, 2018, 12, 2085-2101.	4.6	21

#	Article	IF	Citations
147	Regulatory mechanisms of incomplete huntingtin mRNA splicing. Nature Communications, 2018, 9, 3955.	12.8	55
148	Heterogeneity of Ly6G⁺Ly6C⁺Myeloid-Derived Suppressor Cell Infiltrates during Staphylococcus aureus Biofilm Infection. Infection and Immunity, 2018, 86, .	2.2	35
149	DNA Methylation by Restriction Modification Systems Affects the Global Transcriptome Profile in Borrelia burgdorferi. Journal of Bacteriology, 2018, 200, .	2.2	30
150	Highly efficient genome editing via CRISPRâ€“Cas9 in human pluripotent stem cells is achieved by transient BCL-XL overexpression. Nucleic Acids Research, 2018, 46, 10195-10215.	14.5	93
151	HSRA: Hadoop-based spliced read aligner for RNA sequencing data. PLoS ONE, 2018, 13, e0201483.	2.5	12
152	A stably self-renewing adult blood-derived induced neural stem cell exhibiting patternability and epigenetic rejuvenation. Nature Communications, 2018, 9, 4047.	12.8	49
153	In-Depth Venome of the Brazilian Rattlesnake Crotalus durissus terrificus: An Integrative Approach Combining Its Venom Gland Transcriptome and Venom Proteome. Journal of Proteome Research, 2018, 17, 3941-3958.	3.7	24
154	Cell-specific proteome analyses of human bone marrow reveal molecular features of age-dependent functional decline. Nature Communications, 2018, 9, 4004.	12.8	71
155	Rhinoceros beetle horn development reveals deep parallels with dung beetles. PLoS Genetics, 2018, 14, e1007651.	3.5	45
156	Mixed-species RNA-seq for elucidation of non-cell-autonomous control of gene transcription. Nature Protocols, 2018, 13, 2176-2199.	12.0	21
157	Epigenomic map of human liver reveals principles of zonated morphogenic and metabolic control. Nature Communications, 2018, 9, 4150.	12.8	65
158	PRP4KA, a Putative Spliceosomal Protein Kinase, Is Important for Alternative Splicing and Development in Arabidopsis thaliana. Genetics, 2018, 210, 1267-1285.	2.9	20
159	Microtubule Acetylation Is Required for Mechanosensation in Drosophila. Cell Reports, 2018, 25, 1051-1065.e6.	6.4	47
160	TransAtlasDB: an integrated database connecting expression data, metadata and variants. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	2
161	Progranulin reduces insoluble TDP-43 levels, slows down axonal degeneration and prolongs survival in mutant TDP-43 mice. Molecular Neurodegeneration, 2018, 13, 55.	10.8	38
162	Single Cell Gene Expression to Understand the Dynamic Architecture of the Heart. Frontiers in Cardiovascular Medicine, 2018, 5, 167.	2.4	16
163	Adapting the Smart-seq2 Protocol for Robust Single Worm RNA-seq. Bio-protocol, 2018, 8, .	0.4	29
164	The microRNA-29/PGC1Î± regulatory axis is critical for metabolic control of cardiac function. PLoS Biology, 2018, 16, e2006247.	5.6	42

#	Article	IF	Citations
165	Gene expression variability across cells and species shapes innate immunity. Nature, 2018, 563, 197-202.	27.8	165
166	Targeted cleavage of nad6 mRNA induced by a modified pentatricopeptide repeat protein in plant mitochondria. Communications Biology, 2018, 1, 166.	4.4	39
167	Bioinformatics: Sequences, Structures, Phylogeny. , 2018, , .		0
168	Temporal autoregulation during human PU.1 locus SubTAD formation. Blood, 2018, 132, 2643-2655.	1.4	12
170	Innate Immunity Activation and RNAi Interplay in Citrus Exocortis Viroidâ€"Tomato Pathosystem. Viruses, 2018, 10, 587.	3.3	23
171	N-methyladenine DNA Modification in Glioblastoma. Cell, 2018, 175, 1228-1243.e20.	28.9	236
172	Towards reconstructing the ancestral brain gene-network regulating caste differentiation in ants. Nature Ecology and Evolution, 2018, 2, 1782-1791.	7.8	40
173	Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy and Tools. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	3.0	14
174	The m6A-methylase complex recruits TREX and regulates mRNA export. Scientific Reports, 2018, 8, 13827.	3.3	89
175	RNAâ€seq: Basic Bioinformatics Analysis. Current Protocols in Molecular Biology, 2018, 124, e68.	2.9	44
176	FLOWERING LOCUS T3 Controls Spikelet Initiation But Not Floral Development. Plant Physiology, 2018, 178, 1170-1186.	4.8	44
177	Circular <scp>RNA</scp>s: Methodological challenges and perspectives in cardiovascular diseases. Journal of Cellular and Molecular Medicine, 2018, 22, 5176-5187.	3.6	54
178	MetaWRAPâ€"a flexible pipeline for genome-resolved metagenomic data analysis. Microbiome, 2018, 6, 158.	11.1	1,098
179	Integrative Brain Transcriptome Analysis Reveals Region-Specific and Broad Molecular Changes in Shank3-Overexpressing Mice. Frontiers in Molecular Neuroscience, 2018, 11, 250.	2.9	44
180	Key regulators of lipid metabolism drive endocrine resistance in invasive lobular breast cancer. Breast Cancer Research, 2018, 20, 106.	5.0	69
181	Methylation of Structured RNA by the m6A Writer METTL16 Is Essential for Mouse Embryonic Development. Molecular Cell, 2018, 71, 986-1000.e11.	9.7	250
182	Computational tools to unmask transposable elements. Nature Reviews Genetics, 2018, 19, 688-704.	16.3	173
183	Dynamics of microbial populations mediating biogeochemical cycling in a freshwater lake. Microbiome, 2018, 6, 165.	11.1	40

#	Article	IF	Citations
184	Transcriptomic insights on the virulence-controlling CsrA, BadR, RpoN, and RpoS regulatory networks in the Lyme disease spirochete. PLoS ONE, 2018, 13, e0203286.	2.5	26
185	Efficient and Accurate Quantitative Profiling of Alternative Splicing Patterns of Any Complexity on a Laptop. Molecular Cell, 2018, 72, 187-200.e6.	9.7	121
186	Quantitative single-cell transcriptomics. Briefings in Functional Genomics, 2018, 17, 220-232.	2.7	50
187	Fine needle aspirates of kidneys: a promising tool for RNA sequencing in native and transplanted kidneys. BMC Nephrology, 2018, 19, 221.	1.8	7
188	Terminal exon characterization with TECtool reveals an abundance of cell-specific isoforms. Nature Methods, 2018, 15, 832-836.	19.0	27
189	T-cell transcriptomics from peripheral blood highlights differences between polymyositis and dermatomyositis patients. Arthritis Research and Therapy, 2018, 20, 188.	3.5	21
190	Umap and Bismap: quantifying genome and methylome mappability. Nucleic Acids Research, 2018, 46, e120.	14.5	94
191	Detection of HPV E7 Transcription atÂSingle-Cell Resolution in Epidermis. Journal of Investigative Dermatology, 2018, 138, 2558-2567.	0.7	19
192	Modulation of the transcriptomic profile of the R2C tumor Leydig cell line by the adipose tissue derived hormone leptin. Reproductive Biology, 2018, 18, 440-449.	1.9	2
193	A Dynamic Co-expression Map of Early Inflorescence Development in Setaria viridis Provides a Resource for Gene Discovery and Comparative Genomics. Frontiers in Plant Science, 2018, 9, 1309.	3.6	19
194	Rapid and precise alignment of raw reads against redundant databases with KMA. BMC Bioinformatics, 2018, 19, 307.	2.6	433
195	Metabolic and Transcriptional Modules Independently Diversify Plasma Cell Lifespan and Function. Cell Reports, 2018, 24, 2479-2492.e6.	6.4	103
196	Follow up of a robust meta-signature to identify Zika virus infection in Aedes aegypti: another brick in the wall. Memorias Do Instituto Oswaldo Cruz, 2018, 113, e180053.	1.6	4
197	Genome-Guided Transcriptomics, DNA-Protein Interactions, and Variant Calling. , 2018, , .		0
198	Mechanisms of establishment and functional significance of DNA demethylation during erythroid differentiation. Blood Advances, 2018, 2, 1833-1852.	5.2	15
199	Comparative Transcriptome Profiling Analysis of Red- and White-Fleshed Strawberry (FragariaÃ—ananassa) Provides New Insight into the Regulation of the Anthocyanin Pathway. Plant and Cell Physiology, 2018, 59, 1844-1859.	3.1	48
200	From Tissues to Cell Types and Back: Single-Cell Gene Expression Analysis of Tissue Architecture. Annual Review of Biomedical Data Science, 2018, 1, 29-51.	6.5	91
201	Rapid and Dynamic Alternative Splicing Impacts the Arabidopsis Cold Response Transcriptome. Plant Cell, 2018, 30, 1424-1444.	6.6	294

#	Article	IF	Citations
202	Current and Future Methods for mRNA Analysis: A Drive Toward Single Molecule Sequencing. Methods in Molecular Biology, 2018, 1783, 209-241.	0.9	46
203	Gene Expression Analysis. Methods in Molecular Biology, 2018, , .	0.9	3
204	Computational identification and validation of alternative splicing in ZSF1 rat RNA-seq data, a preclinical model for type 2 diabetic nephropathy. Scientific Reports, 2018, 8, 7624.	3.3	10
205	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. Nucleic Acids Research, 2018, 46, W537-W544.	14.5	3,003
206	The exonâ€“intron gene structure upstream of the initiation codon predicts translation efficiency. Nucleic Acids Research, 2018, 46, 4575-4591.	14.5	23
207	Extrapolation of significant genes and transcriptional regulatory networks involved in Zea mays in response in UV-B stress. Genes and Genomics, 2018, 40, 973-990.	1.4	22
208	Big Data Technologies for DNA Sequencing. , 2018, , 1-6.		1
209	Discovery of UDP-Glycosyltransferases and BAHD-Acyltransferases Involved in the Biosynthesis of the Antidiabetic Plant Metabolite Montbretin A. Plant Cell, 2018, 30, 1864-1886.	6.6	41
210	Transcriptional profiling of stellate ganglia from normotensive and spontaneously hypertensive rat strains. Scientific Data, 2018, 5, 180123.	5.3	9
211	Identifying core biological processes distinguishing human eye tissues with precise systems-level gene expression analyses and weighted correlation networks. Human Molecular Genetics, 2018, 27, 3325-3339.	2.9	46
212	Uncovering pseudotemporal trajectories with covariates from single cell and bulk expression data. Nature Communications, 2018, 9, 2442.	12.8	80
213	Guidelines for RNA-seq projects: applications and opportunities in non-model decapod crustacean species. Hydrobiologia, 2018, 825, 5-27.	2.0	13
214	Two Tabersonine 6,7-Epoxidases Initiate Lochnericine-Derived Alkaloid Biosynthesis in Catharanthus roseus. Plant Physiology, 2018, 177, 1473-1486.	4.8	34
215	Minimizing Clonal Variation during Mammalian Cell Line Engineering for Improved Systems Biology Data Generation. ACS Synthetic Biology, 2018, 7, 2148-2159.	3.8	51
216	Organoid cultures recapitulate esophageal adenocarcinoma heterogeneity providing a model for clonality studies and precision therapeutics. Nature Communications, 2018, 9, 2983.	12.8	206
217	Draft genome assembly of the invasive cane toad, Rhinella marina. GigaScience, 2018, 7, .	6.4	60
218	Non-parent of Origin Expression of Numerous Effector Genes Indicates a Role of Gene Regulation in Host Adaption of the Hybrid Triticale Powdery Mildew Pathogen. Frontiers in Plant Science, 2018, 9, 49.	3.6	33
219	Pathogenic tau-induced piRNA depletion promotes neuronal death through transposable element dysregulation in neurodegenerative tauopathies. Nature Neuroscience, 2018, 21, 1038-1048.	14.8	201

#	Article	IF	Citations
220	Application of Transcriptomics to Compare the Carbohydrate Active Enzymes That Are Expressed by Diverse Genera of Anaerobic Fungi to Degrade Plant Cell Wall Carbohydrates. Frontiers in Microbiology, 2018, 9, 1581.	3.5	58
221	RNA-Seq Data Analysis, Applications and Challenges. Comprehensive Analytical Chemistry, 2018, 82, 71-106.	1.3	9
222	Functional aspects of meningeal lymphatics in ageing and Alzheimerâ€™s disease. Nature, 2018, 560, 185-191.	27.8	839
223	Molecular Portrait of Hypoxia in Breast Cancer: A Prognostic Signature and Novel HIF-Regulated Genes. Molecular Cancer Research, 2018, 16, 1889-1901.	3.4	68
224	ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers. BMC Bioinformatics, 2018, 19, 234.	2.6	81
225	A single cell transcriptional portrait of embryoid body differentiation and comparison to progenitors of the developing embryo. Stem Cell Research, 2018, 31, 201-215.	0.7	16
226	Limitations of alignment-free tools in total RNA-seq quantification. BMC Genomics, 2018, 19, 510.	2.8	64
227	Single Cell RNA Sequencing of Rare Immune Cell Populations. Frontiers in Immunology, 2018, 9, 1553.	4.8	94
228	Environmental Enrichment Prevents Transcriptional Disturbances Induced by Alpha-Synuclein Overexpression. Frontiers in Cellular Neuroscience, 2018, 12, 112.	3.7	30
229	Hypothesis on monochromatic vision in scorpionflies questioned by new transcriptomic data. Scientific Reports, 2018, 8, 9872.	3.3	7
230	Genetic variants associated with Alzheimerâ€™s disease confer different cerebral cortex cell-type population structure. Genome Medicine, 2018, 10, 43.	8.2	62
231	MHC proteins confer differential sensitivity to CTLA-4 and PD-1 blockade in untreated metastatic melanoma. Science Translational Medicine, 2018, 10, .	12.4	425
232	A promoter interaction map for cardiovascular disease genetics. ELife, 2018, 7, .	6.0	120
233	The Splicing Factor RNA-Binding Fox Protein 1 Mediates the Cellular Immune Response in Drosophila melanogaster. Journal of Immunology, 2018, 201, 1154-1164.	0.8	11
234	Ranking genome-wide correlation measurements improves microarray and RNA-seq based global and targeted co-expression networks. Scientific Reports, 2018, 8, 10885.	3.3	73
235	Benchmarking differential expression analysis tools for RNA-Seq: normalization-based vs. log-ratio transformation-based methods. BMC Bioinformatics, 2018, 19, 274.	2.6	48
236	Functional Characterization of the Osteoarthritis Genetic Risk Residing at ALDH1A2 Identifies rs12915901 as a Key Target Variant. Arthritis and Rheumatology, 2018, 70, 1577-1587.	5.6	45
237	Widespread epigenomic, transcriptomic and proteomic differences between hip osteophytic and articular chondrocytes in osteoarthritis. Rheumatology, 2018, 57, 1481-1489.	1.9	19

#	Article	IF	Citations
238	Ubiquitin-related genes are differentially expressed in isogenic lines contrasting for pericarp cell size and grain weight in hexaploid wheat. BMC Plant Biology, 2018, 18, 22.	3.6	29
239	De novo assembly of the complex genome of Nippostrongylus brasiliensis using MinION long reads. BMC Biology, 2018, 16, 6.	3.8	35
240	Antisense suppression of the nonsense mediated decay factor Upf3b as a potential treatment for diseases caused by nonsense mutations. Genome Biology, 2018, 19, 4.	8.8	39
241	SUPPA2: fast, accurate, and uncertainty-aware differential splicing analysis across multiple conditions. Genome Biology, 2018, 19, 40.	8.8	408
242	Sequencing Plant Genomes. Progress in Botany Fortschritte Der Botanik, 2018, , 109-193.	0.3	4
243	Grouper: graph-based clustering and annotation for improved de novo transcriptome analysis. Bioinformatics, 2018, 34, 3265-3272.	4.1	12
244	A Spatiotemporal DNA Endoploidy Map of the Arabidopsis Root Reveals Roles for the Endocycle in Root Development and Stress Adaptation. Plant Cell, 2018, 30, 2330-2351.	6.6	107
245	Isolation and differential transcriptome of vascular smooth muscle cells and mid-capillary pericytes from the rat brain. Scientific Reports, 2018, 8, 12272.	3.3	55
246	Epigenetic dysregulation of naive CD4+ T-cell activation genes in childhood food allergy. Nature Communications, 2018, 9, 3308.	12.8	71
247	Dppa2/4 Facilitate Epigenetic Remodeling during Reprogramming to Pluripotency. Cell Stem Cell, 2018, 23, 396-411.e8.	11.1	61
248	Studying Smaller and Neglected Organisms in Modern Evolutionary Venomics Implementing RNASeq (Transcriptomics)â€"A Critical Guide. Toxins, 2018, 10, 292.	3.4	26
249	Gene expression profiling reveals deepâ€sea coral response to the Deepwater Horizon oil spill. Molecular Ecology, 2018, 27, 4066-4077.	3.9	24
250	IL-1Î² inflammatory response driven by primary breast cancer prevents metastasis-initiating cell colonization. Nature Cell Biology, 2018, 20, 1084-1097.	10.3	122
251	A radiomics approach to assess tumour-infiltrating CD8 cells and response to anti-PD-1 or anti-PD-L1 immunotherapy: an imaging biomarker, retrospective multicohort study. Lancet Oncology, The, 2018, 19, 1180-1191.	10.7	811
252	Initial B Cell Activation Induces Metabolic Reprogramming and Mitochondrial Remodeling. IScience, 2018, 5, 99-109.	4.1	205
253	RNA Sequencing (RNA-Seq) Reveals Extremely Low Levels of Reticulocyte-Derived Globin Gene Transcripts in Peripheral Blood From Horses (Equus caballus) and Cattle (Bos taurus). Frontiers in Genetics, 2018, 9, 278.	2.3	13
254	Regulation of the Î²-cell inflammasome and contribution to stress-induced cellular dysfunction and apoptosis. Molecular and Cellular Endocrinology, 2018, 478, 106-114.	3.2	19
255	Fibroblastic reticular cells initiate immune responses in visceral adipose tissues and secure peritoneal immunity. Science Immunology, 2018, 3, .	11.9	44

#	Article	IF	Citations
256	Transcriptome Sequencing Approaches to Elucidate Hostâ€“Microbe Interactions in Opportunistic Human Fungal Pathogens. Current Topics in Microbiology and Immunology, 2018, 422, 193-235.	1.1	8
257	Isoform-Level Interpretation of High-Throughput Proteomics Data Enabled by Deep Integration with RNA-seq. Journal of Proteome Research, 2018, 17, 3431-3444.	3.7	23
258	Metabolic Capability and Phylogenetic Diversity of Mono Lake during a Bloom of the Eukaryotic Phototroph Picocystis sp. Strain ML. Applied and Environmental Microbiology, 2018, 84, .	3.1	18
259	Adipose transcriptome analysis provides novel insights into molecular regulation of prolonged fasting in northern elephant seal pups. Physiological Genomics, 2018, 50, 495-503.	2.3	15
260	RNA Sequencing Reveals Novel Transcripts from Sympathetic Stellate Ganglia During Cardiac Sympathetic Hyperactivity. Scientific Reports, 2018, 8, 8633.	3.3	12
261	Genome-wide identification and analysis of A-to-I RNA editing events in bovine by transcriptome sequencing. PLoS ONE, 2018, 13, e0193316.	2.5	27
262	In silico read normalization using set multi-cover optimization. Bioinformatics, 2018, 34, 3273-3280.	4.1	8
263	Dgcr8 deletion in the primitive heart uncovered novel microRNA regulating the balance of cardiac-vascular gene program. Protein and Cell, 2019, 10, 327-346.	11.0	14
264	Toward fast and accurate SNP genotyping from whole genome sequencing data for bedside diagnostics. Bioinformatics, 2019, 35, 415-420.	4.1	24
265	De novo transcriptomic analysis of the oleaginous alga Botryococcus braunii AC768 (Chlorophyta). Journal of Applied Phycology, 2019, 31, 255-267.	2.8	3
266	PAX8 activates metabolic genes via enhancer elements in Renal Cell Carcinoma. Nature Communications, 2019, 10, 3739.	12.8	49
267	Molecular mechanisms of lineage decisions in metabolite-specific T cells. Nature Immunology, 2019, 20, 1244-1255.	14.5	74
268	A Heterochromatin-Specific RNA Export Pathway Facilitates piRNA Production. Cell, 2019, 178, 964-979.e20.	28.9	81
269	Physiological status of silver carp (Hypophthalmichthys molitrix) in the Illinois River: An assessment of fish at the leading edge of the invasion front. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 32, 100614.	1.0	11
270	The conserved histone chaperone LINâ€53 is required for normal lifespan and maintenance of muscle integrity in Caenorhabditis elegans. Aging Cell, 2019, 18, e13012.	6.7	13
271	Comparative transcriptomic analysis illuminates the host-symbiont interactions in the deep-sea mussel Bathymodiolus platifrons. Deep-Sea Research Part I: Oceanographic Research Papers, 2019, 151, 103082.	1.4	16
272	Reproducible changes in the gut microbiome suggest a shift in microbial and host metabolism during spaceflight. Microbiome, 2019, 7, 113.	11.1	67
273	Performance of gene expression analyses using de novo assembled transcripts in polyploid species. Bioinformatics, 2019, 35, 4314-4320.	4.1	10

#	Article	IF	Citations
274	Regulation of Pituitary Cocaine- and Amphetamine-Regulated Transcript Expression and Secretion by Hypothalamic Gonadotropin-Releasing Hormone in Chickens. Frontiers in Physiology, 2019, 10, 882.	2.8	6
275	Allelic Imbalance of Recurrently Mutated Genes in Acute Myeloid Leukaemia. Scientific Reports, 2019, 9, 11796.	3.3	9
276	Sex Differences in Adrenal Bmal1 Deletionâ€“Induced Augmentation of Glucocorticoid Responses to Stress and ACTH in Mice. Endocrinology, 2019, 160, 2215-2229.	2.8	8
277	A Computational Analysis of Alternative Splicing across Mammalian Tissues Reveals Circadian and Ultradian Rhythms in Splicing Events. International Journal of Molecular Sciences, 2019, 20, 3977.	4.1	26
278	Assessing Transcriptional Responses to Light by the Dinoflagellate Symbiodinium. Microorganisms, 2019, 7, 261.	3.6	7
280	TrxG Complex Catalytic and Non-catalytic Activity Play Distinct Roles in Pancreas Progenitor Specification and Differentiation. Cell Reports, 2019, 28, 1830-1844.e6.	6.4	10
281	The MS4A gene cluster is a key modulator of soluble TREM2 and Alzheimerâ€™s disease risk. Science Translational Medicine, 2019, 11, .	12.4	170
282	Yanagi: Fast and interpretable segment-based alternative splicing and gene expression analysis. BMC Bioinformatics, 2019, 20, 421.	2.6	3
283	Strategies among phytoplankton in response to alleviation of nutrient stress in a subtropical gyre. ISME Journal, 2019, 13, 2984-2997.	9.8	13
284	A comprehensive examination of Nanopore native RNA sequencing for characterization of complex transcriptomes. Nature Communications, 2019, 10, 3359.	12.8	164
285	Somatic evolution and global expansion of an ancient transmissible cancer lineage. Science, 2019, 365, .	12.6	58
286	Defects of mitochondrial RNA turnover lead to the accumulation of double-stranded RNA in vivo. PLoS Genetics, 2019, 15, e1008240.	3.5	40
287	Natural Variation in TBP-ASSOCIATED FACTOR 4b Controls Meiotic Crossover and Germline Transcription in Arabidopsis. Current Biology, 2019, 29, 2676-2686.e3.	3.9	25
288	RNA sequencing: the teenage years. Nature Reviews Genetics, 2019, 20, 631-656.	16.3	1,192
289	Nonparametric expression analysis using inferential replicate counts. Nucleic Acids Research, 2019, 47, e105-e105.	14.5	54
290	Divergent lnc <scp>RNA MYMLR</scp> regulates <scp>MYC</scp> by eliciting <scp>DNA</scp> looping and promoterâ€enhancer interaction. EMBO Journal, 2019, 38, e98441.	7.8	24
291	Chlamydia trachomatis. Methods in Molecular Biology, 2019, , .	0.9	1
292	Class IIa HDACs regulate learning and memory through dynamic experience-dependent repression of transcription. Nature Communications, 2019, 10, 3469.	12.8	34

#	Article	IF	Citations
293	The nascent RNA binding complex SFiNX licenses piRNA-guided heterochromatin formation. Nature Structural and Molecular Biology, 2019, 26, 720-731.	8.2	75
294	Ferredoxin5 Deletion Affects Metabolism of Algae during the Different Phases of Sulfur Deprivation. Plant Physiology, 2019, 181, 426-441.	4.8	3
295	Differential gene expression analysis of symbiotic and aposymbiotic Exaiptasia anemones under immune challenge with Vibrio coralliilyticus. Ecology and Evolution, 2019, 9, 8279-8293.	1.9	10
296	Dual RNA-Seq of Chlamydia and Host Cells. Methods in Molecular Biology, 2019, 2042, 123-135.	0.9	7
297	Combination Olaparib and Temozolomide in Relapsed Small-Cell Lung Cancer. Cancer Discovery, 2019, 9, 1372-1387.	9.4	158
298	Systematic identification and characterization of Aedes aegypti long noncoding RNAs (lncRNAs). Scientific Reports, 2019, 9, 12147.	3.3	34
299	Heterozygous loss of Srp72 in mice is not associated with major hematological phenotypes. European Journal of Haematology, 2019, 103, 319-328.	2.2	5
300	The RNA exosome nuclease complex regulates human embryonic stem cell differentiation. Journal of Cell Biology, 2019, 218, 2564-2582.	5.2	35
301	Conservation, acquisition, and functional impact of sex-biased gene expression in mammals. Science, 2019, 365, .	12.6	152
302	PadR-type repressors controlling production of a non-canonical FtsW/RodA homologue and other trans-membrane proteins. Scientific Reports, 2019, 9, 10023.	3.3	9
303	In-Vitro and In-Vivo Establishment and Characterization of Bioluminescent Orthotopic Chemotherapy-Resistant Human Osteosarcoma Models in NSG Mice. Cancers, 2019, 11, 997.	3.7	10
304	NF-Y controls fidelity of transcription initiation at gene promoters through maintenance of the nucleosome-depleted region. Nature Communications, 2019, 10, 3072.	12.8	53
305	Minnow: a principled framework for rapid simulation of dscRNA-seq data at the read level. Bioinformatics, 2019, 35, i136-i144.	4.1	17
306	MEK Inhibition Targets Cancer Stem Cells and Impedes Migration of Pancreatic Cancer CellsIn VitroandIn Vivo. Stem Cells International, 2019, 2019, 1-11.	2.5	11
307	High-Throughput Sequence Analysis of Peripheral T-Cell Lymphomas Indicates Subtype-Specific Viral Gene Expression Patterns and Immune Cell Microenvironments. MSphere, 2019, 4, .	2.9	13
308	MRE11A Isoform Expression Associated with Outcome Following Radiotherapy in Muscle-Invasive Bladder Cancer does not Alter Cell Survival and DNA Double-Strand Break Repair Following Ionising Radiation. Bladder Cancer, 2019, 5, 147-157.	0.4	2
309	Data Analysis in Single-Cell RNA-Seq. , 2019, , 419-432.		0
310	Mechanisms of vascular permeability and remodeling associated with hemarthrosis in factor VIIIâ€deficient mice. Journal of Thrombosis and Haemostasis, 2019, 17, 1815-1826.	3.8	11

#	Article	IF	Citations
311	Toxins from scratch? Diverse, multimodal gene origins in the predatory robber fly Dasypogon diadema indicate a dynamic venom evolution in dipteran insects. GigaScience, 2019, 8, .	6.4	25
312	De novo European eel transcriptome provides insights into the evolutionary history of duplicated genes in teleost lineages. PLoS ONE, 2019, 14, e0218085.	2.5	41
313	Global donor and acceptor splicing site kinetics in human cells. ELife, 2019, 8, .	6.0	51
314	Altered differentiation is central to HIV-specific CD4+ T cell dysfunction in progressive disease. Nature Immunology, 2019, 20, 1059-1070.	14.5	84
315	Restoration of histone acetylation ameliorates disease and metabolic abnormalities in a FUS mouse model. Acta Neuropathologica Communications, 2019, 7, 107.	5.2	61
316	Pan-cancer Convergence to a Small-Cell Neuroendocrine Phenotype that Shares Susceptibilities with Hematological Malignancies. Cancer Cell, 2019, 36, 17-34.e7.	16.8	119
317	Alterations in Wnt- and/or STAT3 signaling pathways and the immune microenvironment during metastatic progression. Oncogene, 2019, 38, 5942-5958.	5.9	10
318	Early Life Stress Restricts Translational Reactivity in CA3 Neurons Associated With Altered Stress Responses in Adulthood. Frontiers in Behavioral Neuroscience, 2019, 13, 157.	2.0	39
319	A combined epigenome- and transcriptome-wide association study of the oral masticatory mucosa assigns CYP1B1 a central role for epithelial health in smokers. Clinical Epigenetics, 2019, 11, 105.	4.1	21
320	Role of miRâ€214 in regulation of Î²â€catenin and the malignant phenotype of melanoma. Molecular Carcinogenesis, 2019, 58, 1974-1984.	2.7	13
321	Transcriptomics of a KDELR1 knockout cell line reveals modulated cell adhesion properties. Scientific Reports, 2019, 9, 10611.	3.3	7
322	The transcriptome of Darwinâ€™s bark spider silk glands predicts proteins contributing to dragline silk toughness. Communications Biology, 2019, 2, 275.	4.4	46
323	Relative Abundance of Transcripts (RATs): Identifying differential isoform abundance from RNA-seq. F1000Research, 2019, 8, 213.	1.6	20
324	Transcriptome profiling of interaction effects of soybean cyst nematodes and soybean aphids on soybean. Scientific Data, 2019, 6, 133.	5.3	13
325	Eye in a Disk: eyeIntegration Human Pan-Eye and Body Transcriptome Database Version 1.0. , 2019, 60, 3236.		31
326	Computational approaches for characterizing the tumor immune microenvironment. Immunology, 2019, 158, 70-84.	4.4	30
327	Largeâ€scale potential <scp>RNA</scp> editing profiling in different adult chicken tissues. Animal Genetics, 2019, 50, 460-474.	1.7	12
328	Lack of long-term acclimation in Antarctic encrusting species suggests vulnerability to warming. Nature Communications, 2019, 10, 3383.	12.8	21

#	Article	IF	Citations
329	Novel cell adhesion/migration pathways are predictive markers of HDAC inhibitor resistance in cutaneous T cell lymphoma. EBioMedicine, 2019, 46, 170-183.	6.1	26
330	MAPCap allows high-resolution detection and differential expression analysis of transcription start sites. Nature Communications, 2019, 10, 3219.	12.8	16
331	The Lyme disease spirochete's BpuR DNA/RNAâ€binding protein is differentially expressed during the mammalâ€“tick infectious cycle, which affects translation of the SodA superoxide dismutase. Molecular Microbiology, 2019, 112, 973-991.	2.5	11
332	Acute suppression of insulin resistance-associated hepatic miR-29 in vivo improves glycemic control in adult mice. Physiological Genomics, 2019, 51, 379-389.	2.3	33
333	Exogenous RNAi mechanisms contribute to transcriptome adaptation by phased siRNA clusters in Paramecium. Nucleic Acids Research, 2019, 47, 8036-8049.	14.5	21
334	Novel insights into endogenous RNA viral elements in Ixodes scapularis and other arbovirus vector genomes. Virus Evolution, 2019, 5, vez010.	4.9	34
335	Cooperation Between the Inflammation and Coagulation Systems Promotes the Survival of Circulating Tumor Cells in Renal Cell Carcinoma Patients. Frontiers in Oncology, 2019, 9, 504.	2.8	31
336	FGFR4 overexpression and hotspot mutations in metastatic ER+ breast cancer are enriched in the lobular subtype. Npj Breast Cancer, 2019, 5, 19.	5.2	46
337	Single-cell RNA-seq variant analysis for exploration of genetic heterogeneity in cancer. Scientific Reports, 2019, 9, 9524.	3.3	19
338	Comparative Transcriptomic Analysis of Temozolomide Resistant Primary GBM Stem-Like Cells and Recurrent GBM Identifies Up-Regulation of the Carbonic Anhydrase CA2 Gene as Resistance Factor. Cancers, 2019, 11, 921.	3.7	20
339	Glial Î±â€synuclein promotes neurodegeneration characterized by a distinct transcriptional program in vivo. Glia, 2019, 67, 1933-1957.	4.9	27
340	A Stromal Niche Defined by Expression of the Transcription Factor WT1 Mediates Programming and Homeostasis of Cavity-Resident Macrophages. Immunity, 2019, 51, 119-130.e5.	14.3	105
341	Halophilic microbial community compositional shift after a rare rainfall in the Atacama Desert. ISME Journal, 2019, 13, 2737-2749.	9.8	62
342	Modular one-pot assembly of CRISPR arrays enables library generation and reveals factors influencing crRNA biogenesis. Nature Communications, 2019, 10, 2948.	12.8	75
343	Alternative cleavage and polyadenylation in health and disease. Nature Reviews Genetics, 2019, 20, 599-614.	16.3	305
344	Spatiotemporal Patterning of Zygotic Genome Activation in a Model Vertebrate Embryo. Developmental Cell, 2019, 49, 852-866.e7.	7.0	54
345	Transcriptional profiling of the zebrafish proximal tubule. American Journal of Physiology - Renal Physiology, 2019, 317, F478-F488.	2.7	17
346	High Concentration of Low-Density Lipoprotein Results in Disturbances in Mitochondrial Transcription and Functionality in Endothelial Cells. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-12.	4.0	8

#	Article	IF	Citations
347	Immune and environmentâ€driven gene expression during invasion: An ecoâ€immunological application of RNAâ€Seq. Ecology and Evolution, 2019, 9, 6708-6721.	1.9	16
348	Narrow leaf 1 (NAL1) regulates leaf shape by affecting cell expansion in rice (Oryza sativa L.). Biochemical and Biophysical Research Communications, 2019, 516, 957-962.	2.1	28
349	Dephosphorylation of HDAC4 by PP2A-BÎ´ unravels a new role for the HDAC4/MEF2 axis in myoblast fusion. Cell Death and Disease, 2019, 10, 512.	6.3	9
350	Single-cell RNA sequencing of a European and an African lymphoblastoid cell line. Scientific Data, 2019, 6, 112.	5.3	23
351	Alternating EM algorithm for a bilinear model in isoform quantification from RNA-seq data. Bioinformatics, 2020, 36, 805-812.	4.1	8
352	Transcriptome profiling of mouse samples using nanopore sequencing of cDNA and RNA molecules. Scientific Reports, 2019, 9, 14908.	3.3	90
353	Super-enhancer-guided mapping of regulatory networks controlling mouse trophoblast stem cells. Nature Communications, 2019, 10, 4749.	12.8	45
354	Improved gene co-expression network quality through expression dataset down-sampling and network aggregation. Scientific Reports, 2019, 9, 14431.	3.3	26
355	Romanticism of Numbers: Hamilton, Jefferson, and the Sublime. American Literary History, 2019, 31, 619-638.	0.3	2
356	The Lineage Determining Factor GRHL2 Collaborates with FOXA1 to Establish a Targetable Pathway in Endocrine Therapy-Resistant Breast Cancer. Cell Reports, 2019, 29, 889-903.e10.	6.4	40
357	Molecular evolution in immune genes across the avian tree of life. Parasitology Open, 2019, 5, .	0.9	3
358	Microprojection arrays applied to skin generate mechanical stress, induce an inflammatory transcriptome and cell death, and improve vaccine-induced immune responses. Npj Vaccines, 2019, 4, 41.	6.0	23
359	Genome-Wide Distribution of Nascent Transcripts in Sperm DNA, Products of a Late Wave of General Transcription. Cells, 2019, 8, 1196.	4.1	6
360	The caudate nucleus undergoes dramatic and unique transcriptional changes in human prodromal Huntingtonâ€™s disease brain. BMC Medical Genomics, 2019, 12, 137.	1.5	36
361	Hippocampal Subregions Express Distinct Dendritic Transcriptomes that Reveal Differences in Mitochondrial Function in CA2. Cell Reports, 2019, 29, 522-539.e6.	6.4	61
362	A TBR1-K228E Mutation Induces Tbr1 Upregulation, Altered Cortical Distribution of Interneurons, Increased Inhibitory Synaptic Transmission, and Autistic-Like Behavioral Deficits in Mice. Frontiers in Molecular Neuroscience, 2019, 12, 241.	2.9	25
363	Proteases and nucleases across midgut tissues of Nezara viridula (Hemiptera:Pentatomidae) display distinct activity profiles that are conserved through life stages. Journal of Insect Physiology, 2019, 119, 103965.	2.0	17
364	Histone lysine demethylase KDM4B regulates the alternative splicing of the androgen receptor in response to androgen deprivation. Nucleic Acids Research, 2019, 47, 11623-11636.	14.5	30

#	Article	IF	Citations
365	Active and Repressed Chromatin Domains Exhibit Distinct Nucleosome Segregation during DNA Replication. Cell, 2019, 179, 953-963.e11.	28.9	116
366	Exercise reduces inflammatory cell production and cardiovascular inflammation via instruction of hematopoietic progenitor cells. Nature Medicine, 2019, 25, 1761-1771.	30.7	157
367	Immunological observations and transcriptomic analysis of trimesterâ€specific fullâ€term placentas from three Zika virusâ€infected women. Clinical and Translational Immunology, 2019, 8, e01082.	3.8	20
368	Viral Infections Exacerbate FUS-ALS Phenotypes in iPSC-Derived Spinal Neurons in a Virus Species-Specific Manner. Frontiers in Cellular Neuroscience, 2019, 13, 480.	3.7	19
369	The Guild. Literary Imagination, 2019, 21, 313-314.	0.0	0
370	A Subset of Olfactory Sensory Neurons Express Forkhead Box J1-Driven eGFP. Chemical Senses, 2019, 44, 663-671.	2.0	4
371	ILF3 contributes to the establishment of the antiviral type I interferon program. Nucleic Acids Research, 2020, 48, 116-129.	14.5	20
372	Development of a high-productivity, halophilic, thermotolerant microalga Picochlorum renovo. Communications Biology, 2019, 2, 388.	4.4	58
373	Transcriptomic analysis reveals flavonoid biosynthesis of Syringa oblata Lindl. in response to different light intensity. BMC Plant Biology, 2019, 19, 487.	3.6	21
374	B Cells and T Follicular Helper Cells Mediate Response to Checkpoint Inhibitors in High Mutation Burden Mouse Models of Breast Cancer. Cell, 2019, 179, 1191-1206.e21.	28.9	291
375	Therapeutic potential of N-acetylcysteine in acrylamide acute neurotoxicity in adult zebrafish. Scientific Reports, 2019, 9, 16467.	3.3	17
376	Genomic dissection of an extended phenotype: Oak galling by a cynipid gall wasp. PLoS Genetics, 2019, 15, e1008398.	3.5	44
377	Building gene regulatory networks from scATAC-seq and scRNA-seq using Linked Self Organizing Maps. PLoS Computational Biology, 2019, 15, e1006555.	3.2	56
378	The Mithralog EC-7072 Induces Chronic Lymphocytic Leukemia Cell Death by Targeting Tonic B-Cell Receptor Signaling. Frontiers in Immunology, 2019, 10, 2455.	4.8	4
379	AIDE: annotation-assisted isoform discovery with high precision. Genome Research, 2019, 29, 2056-2072.	5.5	10
380	Freeâ€living and symbiotic lifestyles of a thermotolerant coral endosymbiont display profoundly distinct transcriptomes under both stable and heat stress conditions. Molecular Ecology, 2019, 28, 5265-5281.	3.9	40
381	Large-scale analysis of the cassava transcriptome reveals the impact of cold stress on alternative splicing. Journal of Experimental Botany, 2020, 71, 422-434.	4.8	27
382	Reconstruction of the Functional Ecosystem in the High Light, Low Temperature Union Glacier Region, Antarctica. Frontiers in Microbiology, 2019, 10, 2408.	3.5	19

#	Article	IF	Citations
383	Genome-wide CRISPR Screens in T Helper Cells Reveal Pervasive Crosstalk between Activation and Differentiation. Cell, 2019, 176, 882-896.e18.	28.9	135
384	Genome-wide characterization and evolutionary analysis of heat shock transcription factors (HSFs) to reveal their potential role under abiotic stresses in radish (Raphanus sativus L.). BMC Genomics, 2019, 20, 772.	2.8	23
385	Malpighian tubules of caterpillars: blending RNAseq and physiology to reveal regional functional diversity and novel epithelial ion transport control mechanisms. Journal of Experimental Biology, 2019, 222, .	1.7	8
386	Selection of suitable reference genes for gene expression studies in myxosporean (Myxozoa, Cnidaria) parasites. Scientific Reports, 2019, 9, 15073.	3.3	10
387	Metagenomic Analysis of the Diversity of DNA Viruses in the Surface and Deep Sea of the South China Sea. Frontiers in Microbiology, 2019, 10, 1951.	3.5	34
388	Unique transcriptional and protein-expression signature in human lung tissue-resident NK cells. Nature Communications, 2019, 10, 3841.	12.8	79
389	Sin3a regulates the developmental progression through morulaâ€toâ€blastocyst transition via Hdacl. FASEB Journal, 2019, 33, 12541-12553.	0.5	13
390	Gene Expression Predicts Histological Severity and Reveals Distinct Molecular Profiles of Nonalcoholic Fatty Liver Disease. Scientific Reports, 2019, 9, 12541.	3.3	106
391	Efficient and specific oligo-based depletion of rRNA. Scientific Reports, 2019, 9, 12281.	3.3	44
392	Associated Bacteria Affect Sexual Reproduction by Altering Gene Expression and Metabolic Processes in a Biofilm Inhabiting Diatom. Frontiers in Microbiology, 2019, 10, 1790.	3.5	21
393	Immune gene regulation in the gut during metamorphosis in a holo- versus a hemimetabolous insect. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190073.	4.0	32
394	Comprehensive characterization of circular RNAs in ~â€‰1000 human cancer cell lines. Genome Medicine, 2019, 11, 55.	8.2	116
395	Fungal Physiology and Immunopathogenesis. Current Topics in Microbiology and Immunology, 2019, , .	1.1	4
396	Transcriptome analysis to characterize the genes related to gonad growth and fatty acid metabolism in the sea urchin Strongylocentrotus intermedius. Genes and Genomics, 2019, 41, 1397-1415.	1.4	9
397	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. Cell, 2019, 178, 1465-1477.e17.	28.9	144
398	Natural resistance to Fasciola hepatica (Trematoda) in Pseudosuccinea columella snails: A review from literature and insights from comparative â€œomicâ€•analyses. Developmental and Comparative Immunology, 2019, 101, 103463.	2.3	10
399	Single-Cell Analysis of Human Mononuclear Phagocytes Reveals Subset-Defining Markers and Identifies Circulating Inflammatory Dendritic Cells. Immunity, 2019, 51, 573-589.e8.	14.3	336
400	Catabolism of Alkylphenols in Rhodococcus via a Meta-Cleavage Pathway Associated With Genomic Islands. Frontiers in Microbiology, 2019, 10, 1862.	3.5	14

#	Article	IF	Citations
401	UVB-Induced Tumor Heterogeneity Diminishes Immune Response in Melanoma. Cell, 2019, 179, 219-235.e21.	28.9	270
402	Fibrogenic Activity of MECP2 Is Regulated by Phosphorylation in Hepatic Stellate Cells. Gastroenterology, 2019, 157, 1398-1412.e9.	1.3	27
403	Targeting interferon signaling and CTLA-4 enhance the therapeutic efficacy of anti-PD-1 immunotherapy in preclinical model of HPV+ oral cancer. , 2019, 7, 252.		57
404	Genetic determinants of cellular addiction to DNA polymerase theta. Nature Communications, 2019, 10, 4286.	12.8	106
405	Enhanced CRISPR-based DNA demethylation by Casilio-ME-mediated RNA-guided coupling of methylcytosine oxidation and DNA repair pathways. Nature Communications, 2019, 10, 4296.	12.8	41
406	Physical and Functional Compartmentalization of Archaeal Chromosomes. Cell, 2019, 179, 165-179.e18.	28.9	62
407	Differentiation but not ALS mutations in FUS rewires motor neuron metabolism. Nature Communications, 2019, 10, 4147.	12.8	41
408	Identification of Î²â€catenin target genes in colorectal cancer by interrogating gene fitness screening data. Oncology Letters, 2019, 18, 3769-3777.	1.8	5
409	Comparison between transcriptomic responses to short-term stress exposures of a common Holarctic and endemic Lake Baikal amphipods. BMC Genomics, 2019, 20, 712.	2.8	17
410	Equine Fetal, Adult, and Embryonic Stem Cell-Derived Tenocytes Are All Immune Privileged but Exhibit Different Immune Suppressive Properties In Vitro. Stem Cells and Development, 2019, 28, 1413-1423.	2.1	8
411	Differential Gene Expression in Articular Cartilage and Subchondral Bone of Neonatal and Adult Horses. Genes, 2019, 10, 745.	2.4	4
412	Transcriptome analysis of hemocytes from the white shrimp Litopenaeus vannamei with the injection of dopamine. Fish and Shellfish Immunology, 2019, 94, 497-509.	3.6	21
413	De novo transcriptome assembly and analysis of the freshwater araphid diatom Fragilaria radians, Lake Baikal. Scientific Data, 2019, 6, 183.	5.3	14
414	Melanin Concentrating Hormone Signaling Deficits in Schizophrenia: Association with Memory and Social Impairments and Abnormal Sensorimotor Gating. International Journal of Neuropsychopharmacology, 2020, 23, 53-65.	2.1	11
415	Telescope: Characterization of the retrotranscriptome by accurate estimation of transposable element expression. PLoS Computational Biology, 2019, 15, e1006453.	3.2	99
416	Genome-Wide Identification of Splicing Quantitative Trait Loci (sQTLs) in Diverse Ecotypes of Arabidopsis thaliana. Frontiers in Plant Science, 2019, 10, 1160.	3.6	19
417	Identification and characterization of an IgG sequence variant with an 11 kDa heavy chain C-terminal extension using a combination of mass spectrometry and high-throughput sequencing analysis. MAbs, 2019, 11, 1452-1463.	5.2	9
418	Estrogen Signaling Drives Ciliogenesis in Human Endometrial Organoids. Endocrinology, 2019, 160, 2282-2297.	2.8	60

#	Article	IF	Citations
419	Causes and Consequences of A Glutamine Induced Normoxic HIF1 Activity for the Tumor Metabolism. International Journal of Molecular Sciences, 2019, 20, 4742.	4.1	19
420	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	6.2	45
421	Cytosolic Phospholipase A2 Alpha Regulates TLR Signaling and Migration in Metastatic 4T1 Cells. International Journal of Molecular Sciences, 2019, 20, 4800.	4.1	13
422	The RNA Helicase DDX6 Controls Cellular Plasticity by Modulating P-Body Homeostasis. Cell Stem Cell, 2019, 25, 622-638.e13.	11.1	82
423	Transcriptome sequencing reveals phagocytosis as the main immune response in the pathogen-challenged sea urchin Strongylocentrotus intermedius. Fish and Shellfish Immunology, 2019, 94, 780-791.	3.6	14
424	Single-Cell Transcriptome Analysis of Uniparental Embryos Reveals Parent-of-Origin Effects on Human Preimplantation Development. Cell Stem Cell, 2019, 25, 697-712.e6.	11.1	61
425	TNFR2 induced priming of the inflammasome leads to a RIPK1-dependent cell death in the absence of XIAP. Cell Death and Disease, 2019, 10, 700.	6.3	25
426	KLF4 is involved in the organization and regulation of pluripotency-associated three-dimensional enhancer networks. Nature Cell Biology, 2019, 21, 1179-1190.	10.3	122
427	A field guide for the compositional analysis of any-omics data. GigaScience, 2019, 8, .	6.4	187
428	Widespread interâ€individual gene expression variability in Arabidopsis thaliana. Molecular Systems Biology, 2019, 15, e8591.	7.2	55
429	Proteogenomics Uncovers Critical Elements of Host Response in Bovine Soft Palate Epithelial Cells Following In Vitro Infection with Foot-And-Mouth Disease Virus. Viruses, 2019, 11, 53.	3.3	13
430	Using ATAC-seq and RNA-seq to increase resolution in GRN connectivity. Methods in Cell Biology, 2019, 151, 115-126.	1.1	19
431	Targeted expression profiling by RNA-Seq improves detection of cellular dynamics during pregnancy and identifies a role for T cells in term parturition. Scientific Reports, 2019, 9, 848.	3.3	46
432	Digoxin, an Overlooked Agonist of RORÎ³/RORÎ³T. Frontiers in Pharmacology, 2018, 9, 1460.	3.5	19
433	Aurantimycin resistance genes contribute to survival of Listeria monocytogenes during life in the environment. Molecular Microbiology, 2019, 111, 1009-1024.	2.5	16
434	Identification and Characterization of Mitogen-Activated Protein Kinase (MAPK) Genes in Sunflower (Helianthus annuus L.). Plants, 2019, 8, 28.	3.5	21
435	Transcriptomics of Arabidopsis sperm cells at single-cell resolution. Plant Reproduction, 2019, 32, 29-38.	2.2	23
436	The Histone H3K4 Demethylase JMJ16 Represses Leaf Senescence in Arabidopsis. Plant Cell, 2019, 31, 430-443.	6.6	89

#	Article	IF	Citations
437	Predicting drug response of tumors from integrated genomic profiles by deep neural networks. BMC Medical Genomics, 2019, 12, 18.	1.5	123
438	Single-Cell Transcriptomics of Regulatory T Cells Reveals Trajectories of Tissue Adaptation. Immunity, 2019, 50, 493-504.e7.	14.3	352
439	Regulation of Growth and Flavonoid Formation of Tea Plants (Camellia sinensis) by Blue and Green Light. Journal of Agricultural and Food Chemistry, 2019, 67, 2408-2419.	5.2	56
440	Transcript Abundance Estimation and the Laminar Packing Problem. Lecture Notes in Computer Science, 2019, , 203-211.	1.3	0
441	Identification of Genes Differentially Expressed in Simvastatinâ€Induced Alveolar Bone Formation. JBMR Plus, 2019, 3, e10122.	2.7	9
442	The AvrPm3-Pm3 effector-NLR interactions control both race-specific resistance and host-specificity of cereal mildews on wheat. Nature Communications, 2019, 10, 2292.	12.8	103
443	Singleâ€Cell RNAâ€seq: Introduction to Bioinformatics Analysis. Current Protocols in Molecular Biology, 2019, 127, e92.	2.9	10
444	Microcystin-LR-regulated transcriptome dynamics in ZFL cells. Aquatic Toxicology, 2019, 212, 222-232.	4.0	11
445	Multi omics analysis of fibrotic kidneys in two mouse models. Scientific Data, 2019, 6, 92.	5.3	26
446	Zebrafish macroH2A variants have distinct embryo localization and function. Scientific Reports, 2019, 9, 8632.	3.3	5
447	Robust elimination of genome-damaged cells safeguards against brain somatic aneuploidy following Knl1 deletion. Nature Communications, 2019, 10, 2588.	12.8	35
448	Interferon Signaling Is Diminished with Age and Is Associated with Immune Checkpoint Blockade Efficacy in Triple-Negative Breast Cancer. Cancer Discovery, 2019, 9, 1208-1227.	9.4	81
449	GR and LSD1/KDM1A-Targeted Gene Activation Requires Selective H3K4me2 Demethylation at Enhancers. Cell Reports, 2019, 27, 3522-3532.e3.	6.4	23
450	Description of strongly heat-inducible heat shock protein 70 transcripts from Baikal endemic amphipods. Scientific Reports, 2019, 9, 8907.	3.3	7
451	Transcriptome Kinetics of Saccharomyces cerevisiae in Response to Viral Killer Toxin K1. Frontiers in Microbiology, 2019, 10, 1102.	3.5	5
452	Transcriptome analyses suggest minimal effects of Shank3 dosage on directional gene expression changes in the mouse striatum. Animal Cells and Systems, 2019, 23, 270-274.	2.2	14
453	Physical and Molecular Landscapes of Mouse Glioma Extracellular Vesicles Define Heterogeneity. Cell Reports, 2019, 27, 3972-3987.e6.	6.4	46
454	IL-10-Dependent Crosstalk between Murine Marginal Zone B Cells, Macrophages, and CD8Î±+ Dendritic Cells Promotes Listeria monocytogenes Infection. Immunity, 2019, 51, 64-76.e7.	14.3	25

#	Article	IF	Citations
455	Effect of de novo transcriptome assembly on transcript quantification. Scientific Reports, 2019, 9, 8304.	3.3	36
456	Bridging the gap between reference and real transcriptomes. Genome Biology, 2019, 20, 112.	8.8	38
457	Genomics and data science: an application within an umbrella. Genome Biology, 2019, 20, 109.	8.8	46
458	NG-meta-profiler: fast processing of metagenomes using NGLess, a domain-specific language. Microbiome, 2019, 7, 84.	11.1	42
459	The aryl hydrocarbon receptor is a tumor suppressorâ€"like gene in glioblastoma. Journal of Biological Chemistry, 2019, 294, 11342-11353.	3.4	33
460	CYFIP1 overexpression increases fear response in mice but does not affect social or repetitive behavioral phenotypes. Molecular Autism, 2019, 10, 25.	4.9	17
461	Transcriptomics of host-specific interactions in natural populations of the parasitic plant purple witchweed (Striga hermonthica). Weed Science, 2019, 67, 397-411.	1.5	16
462	Longitudinal comparative transcriptomics reveals unique mechanisms underlying extended healthspan in bats. Nature Ecology and Evolution, 2019, 3, 1110-1120.	7.8	70
463	Coupling Genome-wide Transcriptomics and Developmental Toxicity Profiles in Zebrafish to Characterize Polycyclic Aromatic Hydrocarbon (PAH) Hazard. International Journal of Molecular Sciences, 2019, 20, 2570.	4.1	39
464	Uncovering the cellular and humoral immune responses of Antheraea pernyi hemolymph to Antheraea pernyi nucleopolyhedrovirus infection by transcriptome analysis. Journal of Invertebrate Pathology, 2019, 166, 107205.	3.2	9
465	Type I and II PRMTs regulate catabolic as well as detoxifying processes in Aspergillus nidulans. Fungal Genetics and Biology, 2019, 129, 86-100.	2.1	5
466	Stk40 deletion elevates c-JUN protein level and impairs mesoderm differentiation. Journal of Biological Chemistry, 2019, 294, 9959-9972.	3.4	5
467	The Oncogene ECT2 Contributes to a Hyperplastic, Proliferative Lung Epithelial Cell Phenotype in Idiopathic Pulmonary Fibrosis. American Journal of Respiratory Cell and Molecular Biology, 2019, 61, 713-726.	2.9	15
468	GREIN: An Interactive Web Platform for Re-analyzing GEO RNA-seq Data. Scientific Reports, 2019, 9, 7580.	3.3	126
469	Establishment of porcine and human expanded potential stem cells. Nature Cell Biology, 2019, 21, 687-699.	10.3	261
470	Ruminal microbiome-host crosstalk stimulates the development of the ruminal epithelium in a lamb model. Microbiome, 2019, 7, 83.	11.1	116
471	Regional Heterogeneity in Gene Expression, Regulation, and Coherence in the Frontal Cortex and Hippocampus across Development and Schizophrenia. Neuron, 2019, 103, 203-216.e8.	8.1	158
472	The transcriptomic response to a short day to long day shift in leaves of the reference legume Medicago truncatula. PeerJ, 2019, 7, e6626.	2.0	17

#	Article	IF	Citations
473	A perfusion bioreactor-based 3D model of the subarachnoid space based on a meningeal tissue construct. Fluids and Barriers of the CNS, 2019, 16, 17.	5.0	8
474	Transcriptome profiling of induced susceptibility effects on soybeanâ€“soybean aphid (Hemiptera:) Tj ETQq1 1 0.784314 rgBT /Overlock	1.4	8
475	Cloning of a COBL gene determining brittleness in diploid wheat using a MapRseq approach. Plant Science, 2019, 285, 141-150.	3.6	12
476	Macroevolutionary patterns in overexpression of tyrosine: An antiâ€herbivore defence in a speciose tropical tree genus, Inga (Fabaceae). Journal of Ecology, 2019, 107, 1620-1632.	4.0	21
477	Polychromic Reporter Mice Reveal Unappreciated Innate Lymphoid Cell Progenitor Heterogeneity and Elusive ILC3 Progenitors in Bone Marrow. Immunity, 2019, 51, 104-118.e7.	14.3	94
478	Arginine vasotocin (AVT)/mesotocin (MT) receptors in chickens: Evidence for the possible involvement of AVT-AVPR1 signaling in the regulation of oviposition and pituitary prolactin expression. General and Comparative Endocrinology, 2019, 281, 91-104.	1.8	19
479	ARMOR: An <u>A</u>utomated <u>R</u>eproducible <u>MO</u>dular Workflow for Preprocessing and Differential Analysis of <u>R</u>NA-seq Data. G3: Genes, Genomes, Genetics, 2019, 9, 2089-2096.	1.8	44
480	Targeted, High-Resolution RNA Sequencing of Non-coding Genomic Regions Associated With Neuropsychiatric Functions. Frontiers in Genetics, 2019, 10, 309.	2.3	28
481	Fat bodyâ€specific vitellogenin expression regulates host-seeking behaviour in the mosquito Aedes albopictus. PLoS Biology, 2019, 17, e3000238.	5.6	22
482	High OGT activity is essential for MYC-driven proliferation of prostate cancer cells. Theranostics, 2019, 9, 2183-2197.	10.0	58
483	Addressing confounding artifacts in reconstruction of gene co-expression networks. Genome Biology, 2019, 20, 94.	8.8	68
484	Stem Cell Proliferation Is Kept in Check by the Chromatin Regulators Kismet/CHD7/CHD8 and Trr/MLL3/4. Developmental Cell, 2019, 49, 556-573.e6.	7.0	25
485	RNA sequencing reveals MMP2 and TGFB1 downregulation in LRRK2 G2019S Parkinson's iPSC-derived astrocytes. Neurobiology of Disease, 2019, 129, 56-66.	4.4	55
486	FastqPuri: high-performance preprocessing of RNA-seq data. BMC Bioinformatics, 2019, 20, 226.	2.6	26
487	Computational Methods for Mapping, Assembly and Quantification for Coding and Non-coding Transcripts. Computational and Structural Biotechnology Journal, 2019, 17, 628-637.	4.1	25
488	Obesity-Associated Hypermetabolism and Accelerated Senescence of Bone Marrow Stromal Stem Cells Suggest a Potential Mechanism for Bone Fragility. Cell Reports, 2019, 27, 2050-2062.e6.	6.4	86
489	Cytomegalovirus Infection Drives Avidity Selection of Natural Killer Cells. Immunity, 2019, 50, 1381-1390.e5.	14.3	42
490	Distinct modes of cell competition shape mammalian tissue morphogenesis. Nature, 2019, 569, 497-502.	27.8	112

#	Article	IF	Citations
491	Snf2 controls pulcherriminic acid biosynthesis and antifungal activity of the biocontrol yeast Metschnikowia pulcherrima. Molecular Microbiology, 2019, 112, 317-332.	2.5	64
492	Developmental Apoptosis Promotes a Disease-Related Gene Signature and Independence from CSF1R Signaling in Retinal Microglia. Cell Reports, 2019, 27, 2002-2013.e5.	6.4	53
493	Integrated Analysis of Transcriptomic, miRNA and Proteomic Changes of a Novel Hybrid Yellow Catfish Uncovers Key Roles for miRNAs in Heterosis. Molecular and Cellular Proteomics, 2019, 18, 1437-1453.	3.8	30
494	Accumulating computational resource usage of genomic data analysis workflow to optimize cloud computing instance selection. GigaScience, 2019, 8, .	6.4	8
495	A chromosomeâ€level genome of black rockfish, Sebastes schlegelii, provides insights into the evolution of live birth. Molecular Ecology Resources, 2019, 19, 1309-1321.	4.8	44
496	RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis. Annual Review of Biomedical Data Science, 2019, 2, 139-173.	6.5	101
497	Novel gene regulatory networks identified in response to nitro-conjugated linoleic acid in human endothelial cells. Physiological Genomics, 2019, 51, 224-233.	2.3	15
498	De novo transcriptome assembly: A comprehensive cross-species comparison of short-read RNA-Seq assemblers. GigaScience, 2019, 8, .	6.4	150
499	Tracking transcriptomic responses to endogenous and exogenous variation in cetaceans in the Southern California Bight. , 2019, 7, coz018.		8
500	Corrupted coordination of epigenetic modifications leads to diverging chromatin states and transcriptional heterogeneity in CLL. Nature Communications, 2019, 10, 1874.	12.8	63
501	De Novo Transcriptome Assembly and Functional Annotation in Five Species of Bats. Scientific Reports, 2019, 9, 6222.	3.3	23
502	RNA Sequencing Analyses of Gene Expression during Epstein-Barr Virus Infection of Primary B Lymphocytes. Journal of Virology, 2019, 93, .	3.4	71
503	Expression estimation and eQTL mapping for HLA genes with a personalized pipeline. PLoS Genetics, 2019, 15, e1008091.	3.5	75
504	GSK2801, a BAZ2/BRD9 Bromodomain Inhibitor, Synergizes with BET Inhibitors to Induce Apoptosis in Triple-Negative Breast Cancer. Molecular Cancer Research, 2019, 17, 1503-1518.	3.4	39
505	TAF5L and TAF6L Maintain Self-Renewal of Embryonic Stem Cells via the MYC Regulatory Network. Molecular Cell, 2019, 74, 1148-1163.e7.	9.7	36
506	A Clinically Applicable Gene-Expression Classifier Reveals Intrinsic and Extrinsic Contributions to Consensus Molecular Subtypes in Primary and Metastatic Colon Cancer. Clinical Cancer Research, 2019, 25, 4431-4442.	7.0	40
507	Nexilin Is a New Component of Junctional Membrane Complexes Required for Cardiac T-Tubule Formation. Circulation, 2019, 140, 55-66.	1.6	41
508	CENTRORADIALIS Interacts with FLOWERING LOCUS T-Like Genes to Control Floret Development and Grain Number. Plant Physiology, 2019, 180, 1013-1030.	4.8	40

#	Article	IF	Citations
509	RIG-I Activation by a Designer Short RNA Ligand Protects Human Immune Cells against Dengue Virus Infection without Causing Cytotoxicity. Journal of Virology, 2019, 93, .	3.4	11
510	A highly expressed intestinal cysteine protease of Ancylostoma ceylanicum protects vaccinated hamsters from hookworm infection. PLoS Neglected Tropical Diseases, 2019, 13, e0007345.	3.0	11
511	A Single-Cell RNA Sequencing Profiles the Developmental Landscape of Arabidopsis Root. Molecular Plant, 2019, 12, 648-660.	8.3	317
512	Distinct Requirements of CHD4 during B Cell Development and Antibody Response. Cell Reports, 2019, 27, 1472-1486.e5.	6.4	11
513	Selenium Drives a Transcriptional Adaptive Program to Block Ferroptosis and Treat Stroke. Cell, 2019, 177, 1262-1279.e25.	28.9	576
514	Origin and differentiation trajectories of fibroblastic reticular cells in the splenic white pulp. Nature Communications, 2019, 10, 1739.	12.8	73
515	Multiple Differentially Methylated Regions Specific to Keratoconus Explain Known Keratoconus Linkage Loci. , 2019, 60, 1501.		15
516	Myocardial differentiation is dependent upon endocardial signaling during early cardiogenesis in vitro. Development (Cambridge), 2019, 146, .	2.5	9
518	A Bioinformatic Toolkit for Single-Cell mRNA Analysis. Methods in Molecular Biology, 2019, 1979, 433-455.	0.9	2
519	The Transcriptional Landscape of Mareka€™s Disease Virus in Primary Chicken B Cells Reveals Novel Splice Variants and Genes. Viruses, 2019, 11, 264.	3.3	29
520	No direct effect of SGLT2 activity on glucagon secretion. Diabetologia, 2019, 62, 1011-1023.	6.3	58
521	Analyzing the 3D chromatin organization coordinating with gene expression regulation in B-cell lymphoma. BMC Medical Genomics, 2019, 11, 127.	1.5	13
522	Regulation of fiber-specific actin expression by the Drosophila SRF ortholog Blistered. Development (Cambridge), 2019, 146, .	2.5	4
523	Biosynthesis and Signal Transduction of ABA, JA, and BRs in Response to Drought Stress of Kentucky Bluegrass. International Journal of Molecular Sciences, 2019, 20, 1289.	4.1	59
524	Regeneration associated transcriptional signature of retinal microglia and macrophages. Scientific Reports, 2019, 9, 4768.	3.3	82
525	Dynamics of Wnt activity on the acquisition of ectoderm potency in epiblast stem cells. Development (Cambridge), 2019, 146, .	2.5	18
526	Transcriptomic analysis of differentially expressed genes in the oriental armyworm Mythimna separata Walker at different temperatures. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 30, 186-195.	1.0	3
527	Oxygen induces the expression of invasion and stress response genes in the anaerobic salmon parasite Spironucleus salmonicida. BMC Biology, 2019, 17, 19.	3.8	9

#	Article	IF	Citations
528	Transcriptomic Analysis of High Fat Diet Fed Mouse Brain Cortex. Frontiers in Genetics, 2019, 10, 83.	2.3	37
529	Regnase-1-mediated post-transcriptional regulation is essential for hematopoietic stem and progenitor cell homeostasis. Nature Communications, 2019, 10, 1072.	12.8	19
530	Promiscuous terpene synthases from Prunella vulgaris highlight the importance of substrate and compartment switching in terpene synthase evolution. New Phytologist, 2019, 223, 323-335.	7.3	26
531	TGIF transcription factors repress acetyl CoA metabolic gene expression and promote intestinal tumor growth. Genes and Development, 2019, 33, 388-402.	5.9	16
532	A modular analysis of microglia gene expression, insights into the aged phenotype. BMC Genomics, 2019, 20, 164.	2.8	24
533	Revealing cellular and molecular transitions in neonatal germ cell differentiation using Single-cell RNA sequencing. Development (Cambridge), 2019, 146, .	2.5	20
534	Comparative transcriptomic analysis reveal the regulation mechanism underlying MeJA-induced accumulation of alkaloids in Dendrobium officinale. Journal of Plant Research, 2019, 132, 419-429.	2.4	43
535	Distinct phenotype of CD4+ T cells driving celiac disease identified in multiple autoimmune conditions. Nature Medicine, 2019, 25, 734-737.	30.7	112
536	RNA-sequencing in ophthalmology research: considerations for experimental design and analysis. Therapeutic Advances in Ophthalmology, 2019, 11, 251584141983546.	1.4	6
537	Species-specific enhancement of enterohemorrhagic E. coli pathogenesis mediated by microbiome metabolites. Microbiome, 2019, 7, 43.	11.1	102
538	Slide-seq: A scalable technology for measuring genome-wide expression at high spatial resolution. Science, 2019, 363, 1463-1467.	12.6	1,396
539	Combined Transcriptome and Proteome Analysis of Immortalized Human Keratinocytes Expressing Human Papillomavirus 16 (HPV16) Oncogenes Reveals Novel Key Factors and Networks in HPV-Induced Carcinogenesis. MSphere, 2019, 4, .	2.9	23
540	Investigating the Biological Relevance of In Vitro -Identified Putative Packaging Signals at the 5â€² Terminus of Satellite Tobacco Necrosis Virus 1 Genomic RNA. Journal of Virology, 2019, 93, .	3.4	9
541	Separation of breast cancer and organ microenvironment transcriptomes in metastases. Breast Cancer Research, 2019, 21, 36.	5.0	36
542	Extracellular vesicles induce minimal hepatotoxicity and immunogenicity. Nanoscale, 2019, 11, 6990-7001.	5.6	118
543	Overexpression of Nudt7 decreases bile acid levels and peroxisomal fatty acid oxidation in the liver. Journal of Lipid Research, 2019, 60, 1005-1019.	4.2	11
544	Contaminant Exposure Linked to Cellular and Endocrine Biomarkers in Southern California Bottlenose Dolphins. Environmental Science & Technology, 2019, 53, 3811-3822.	10.0	15
545	CYPs in different families are involved in the divergent regio-specific epoxidation of alkenyl sex pheromone precursors in moths. Insect Biochemistry and Molecular Biology, 2019, 108, 9-15.	2.7	11

#	Article	IF	Citations
546	Holistic optimization of an RNA-seq workflow for multi-threaded environments. Bioinformatics, 2019, 35, 4173-4175.	4.1	4
547	Developmental Dieldrin Exposure Alters DNA Methylation at Genes Related to Dopaminergic Neuron Development and Parkinsonâ€™s Disease in Mouse Midbrain. Toxicological Sciences, 2019, 169, 593-607.	3.1	33
548	Bioinformatics applied to biotechnology: A review towards bioenergy research. Biomass and Bioenergy, 2019, 123, 195-224.	5.7	17
549	RNA-Sequencing of Umbilical Cord Blood to Investigate Spontaneous Preterm Birth: A Pilot Study. AJP Reports, 2019, 09, e60-e66.	0.7	2
550	Integrative genomic analysis of peritoneal malignant mesothelioma: understanding a case with extraordinary chemotherapy response. Journal of Physical Education and Sports Management, 2019, 5, a003566.	1.2	6
551	Acoel genome reveals the regulatory landscape of whole-body regeneration. Science, 2019, 363, .	12.6	125
553	Juvenility-associated lncRNA Gm14230 maintains cellular juvenescence. Journal of Cell Science, 2019, 132, .	2.0	4
554	CANTATAdb 2.0: Expanding the Collection of Plant Long Noncoding RNAs. Methods in Molecular Biology, 2019, 1933, 415-429.	0.9	71
555	Analyzing Mechanisms of Metastatic Cancer Cell Adhesive Phenotype Leveraging Preparative Adhesion Chromatography Microfluidic. Advanced Biology, 2019, 3, e1800328.	3.0	9
556	Leishmania. Methods in Molecular Biology, 2019, , .	0.9	1
557	Cos-Seq: A High-Throughput Gain-of-Function Screen for Drug Resistance Studies in Leishmania. Methods in Molecular Biology, 2019, 1971, 141-167.	0.9	6
558	Basal expression of interferon regulatory factor 1 drives intrinsic hepatocyte resistance to multiple RNA viruses. Nature Microbiology, 2019, 4, 1096-1104.	13.3	69
559	Alevin efficiently estimates accurate gene abundances from dscRNA-seq data. Genome Biology, 2019, 20, 65.	8.8	195
560	Placenta Transcriptome Profiling in Intrauterine Growth Restriction (IUGR). International Journal of Molecular Sciences, 2019, 20, 1510.	4.1	53
561	Transcriptome sequencing to unravel the molecular mechanisms underlying the cuticle liquefaction of Antheraea pernyi following Antheraea pernyi nucleopolyhedrovirus challenge. Molecular Immunology, 2019, 109, 108-115.	2.2	6
562	Systems Metabolic Engineering Meets Machine Learning: A New Era for Dataâ€Đriven Metabolic Engineering. Biotechnology Journal, 2019, 14, e1800416.	3.5	45
563	Neofunctionalisation of basic helixâ^'loopâ^'helix proteins occurred when embryophytes colonised the land. New Phytologist, 2019, 223, 993-1008.	7.3	18
564	Alternative splicing, RNA-seq and drug discovery. Drug Discovery Today, 2019, 24, 1258-1267.	6.4	55

#	Article	IF	Citations
565	Differential isoform expression and alternative splicing in sex determination in mice. BMC Genomics, 2019, 20, 202.	2.8	23
566	Transcriptome analysis reveals novel insights in air-breathing magur catfish (Clarias magur) in response to high environmental ammonia. Gene, 2019, 703, 35-49.	2.2	25
567	Diverse aromatic-degrading bacteria present in a highly enriched autotrophic nitrifying sludge. Science of the Total Environment, 2019, 666, 245-251.	8.0	39
569	X-ray irradiation induces subtle changes in the genome-wide distribution of DNA hydroxymethylation with opposing trends in genic and intergenic regions. Epigenetics, 2019, 14, 81-93.	2.7	8
570	Transcriptome, proteome and draft genome of Euglena gracilis. BMC Biology, 2019, 17, 11.	3.8	98
571	Investigating the potential of body fluid identification using the Oxford Nanopore MinION. Australian Journal of Forensic Sciences, 2019, 51, S27-S30.	1.2	2
572	Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. MSystems, 2019, 4, .	3.8	40
573	Combined single-cell profiling of expression and DNA methylation reveals splicing regulation and heterogeneity. Genome Biology, 2019, 20, 30.	8.8	61
574	Evolution of cnidarian transâ€defensins: Sequence, structure and exploration of chemical space. Proteins: Structure, Function and Bioinformatics, 2019, 87, 551-560.	2.6	20
575	MicroRNA-375 Suppresses the Growth and Invasion of Fibrolamellar Carcinoma. Cellular and Molecular Gastroenterology and Hepatology, 2019, 7, 803-817.	4.5	34
576	Toxicity of perfluorooctane sulfonate on Phanerochaete chrysosporium: Growth, pollutant degradation and transcriptomics. Ecotoxicology and Environmental Safety, 2019, 174, 66-74.	6.0	25
577	Cold-Dependent Expression and Alternative Splicing of Arabidopsis Long Non-coding RNAs. Frontiers in Plant Science, 2019, 10, 235.	3.6	70
578	Sparse Dynamic Programming on DAGs with Small Width. ACM Transactions on Algorithms, 2019, 15, 1-21.	1.0	16
579	Antigen Receptor Sequence Reconstruction and Clonality Inference from scRNA-Seq Data. Methods in Molecular Biology, 2019, 1935, 223-249.	0.9	8
580	Bcl9 and Pygo synergise downstream of Apc to effect intestinal neoplasia in FAP mouse models. Nature Communications, 2019, 10, 724.	12.8	31
581	Phototactic tails: Evolution and molecular basis of a novel sensory trait in sea snakes. Molecular Ecology, 2019, 28, 2013-2028.	3.9	15
582	Tissue-Specific Transcriptomes Reveal Gene Expression Trajectories in Two Maturing Skin Epithelial Layers in Zebrafish Embryos. G3: Genes, Genomes, Genetics, 2019, 9, 3439-3452.	1.8	14
583	Non-Coding Mutations in Urothelial Bladder Cancer: Biological and Clinical Relevance and Potential Utility as Biomarkers. Bladder Cancer, 2019, 5, 263-272.	0.4	10

#	Article	IF	Citations
584	Transcriptomics analysis of â€˜Cabernet Sauvignonâ€™ berry skins from Reno and Bordeaux in the late stages of ripening. Acta Horticulturae, 2019, , 353-360.	0.2	1
585	Benchmark of long non-coding RNA quantification for RNA sequencing of cancer samples. GigaScience, 2019, 8, .	6.4	32
586	The global transcriptomic signature in sinonasal tissues reveals roles for tissue type and chronic rhinosinusitis disease phenotype. Rhinology, 2020, 58, 273-283.	1.3	8
587	Exploring the RNA Gap for Improving Diagnostic Yield in Primary Immunodeficiencies. Frontiers in Genetics, 2019, 10, 1204.	2.3	3
588	Next generation sequencing and proteomics in plant virology: how is Colombia doing?. Acta Biologica Colombiana, 2019, 24, 423-438.	0.4	3
589	Single-Cell RNA Sequencing of Plant-Associated Bacterial Communities. Frontiers in Microbiology, 2019, 10, 2452.	3.5	10
590	DIANA-LncBase v3: indexing experimentally supported miRNA targets on non-coding transcripts. Nucleic Acids Research, 2020, 48, D101-D110.	14.5	137
591	Transcriptome analysis identifies genes related to the waxy coating on blueberry fruit in two northern-adapted rabbiteye breeding populations. BMC Plant Biology, 2019, 19, 460.	3.6	22
592	MiR-29 Regulates de novo Lipogenesis in the Liver and Circulating Triglyceride Levels in a Sirt1-Dependent Manner. Frontiers in Physiology, 2019, 10, 1367.	2.8	12
593	Prolyl hydroxylase substrate adenylosuccinate lyase is an oncogenic driver in triple negative breast cancer. Nature Communications, 2019, 10, 5177.	12.8	27
594	RaNA-Seq: interactive RNA-Seq analysis from FASTQ files to functional analysis. Bioinformatics, 2020, 36, 1955-1956.	4.1	64
595	Quantitative classification of chromatin dynamics reveals regulators of intestinal stem cell differentiation. Development (Cambridge), 2020, 147, .	2.5	15
596	Decapping Enzyme NUDT12 Partners with BLMH for Cytoplasmic Surveillance of NAD-Capped RNAs. Cell Reports, 2019, 29, 4422-4434.e13.	6.4	30
597	Integrative Analysis of Axolotl Gene Expression Data from Regenerative and Wound Healing Limb Tissues. Scientific Reports, 2019, 9, 20280.	3.3	27
598	Cloud accelerated alignment and assembly of full-length single-cell RNA-seq data using Falco. BMC Genomics, 2019, 20, 927.	2.8	2
599	Transcriptome assembly from long-read RNA-seq alignments with StringTie2. Genome Biology, 2019, 20, 278.	8.8	897
600	Longitudinal immune characterization of syngeneic tumor models to enable model selection for immune oncology drug discovery. , 2019, 7, 328.		65
601	QTL and Transcriptomic Analyses Implicate Cuticle Transcription Factor SHINE as a Source of Natural Variation for Epidermal Traits in Cucumber Fruit. Frontiers in Plant Science, 2019, 10, 1536.	3.6	12

#	Article	IF	Citations
602	The Hyaluronidase, TMEM2, Promotes ER Homeostasis and Longevity Independent of the UPRER. Cell, 2019, 179, 1306-1318.e18.	28.9	87
603	Transposable element expression in tumors is associated with immune infiltration and increased antigenicity. Nature Communications, 2019, 10, 5228.	12.8	154
604	Functional Enhancers Shape Extrachromosomal Oncogene Amplifications. Cell, 2019, 179, 1330-1341.e13.	28.9	206
605	Fibroblastic Reticular Cells Control Conduit Matrix Deposition during Lymph Node Expansion. Cell Reports, 2019, 29, 2810-2822.e5.	6.4	58
606	Is geographical variation driving the transcriptomic responses to multiple stressors in the kelp Saccharina latissima?. BMC Plant Biology, 2019, 19, 513.	3.6	14
607	Hostâ€“Symbiont Interactions in Deep-Sea Chemosymbiotic Vesicomyid Clams: Insights From Transcriptome Sequencing. Frontiers in Marine Science, 2019, 6, .	2.5	17
608	ERG Controls B Cell Development by Promoting Igh V-to-DJ Recombination. Cell Reports, 2019, 29, 2756-2769.e6.	6.4	7
609	Detecting, Categorizing, and Correcting Coverage Anomalies of RNA-Seq Quantification. Cell Systems, 2019, 9, 589-599.e7.	6.2	5
610	Organ transcriptomes of the lucinid clam Loripes orbiculatus (Poli, 1791) provide insights into their specialised roles in the biology of a chemosymbiotic bivalve. BMC Genomics, 2019, 20, 820.	2.8	13
611	Dynamics of activating and repressive histone modifications in Drosophila neural stem cell lineages and brain tumors. Development (Cambridge), 2019, 146, .	2.5	7
612	Dynamic Changes of DNA Methylation and Transcriptome Expression in Porcine Ovaries during Aging. BioMed Research International, 2019, 2019, 1-15.	1.9	9
613	Molecular subtyping improves prognostication of Stage 2 colorectal cancer. BMC Cancer, 2019, 19, 1155.	2.6	13
614	Temperature Modulates Sex-Biased Gene Expression in the Gametophytes of the Kelp Saccharina latissima. Frontiers in Marine Science, 2019, 6, .	2.5	16
615	HIV elite control is associated with reduced TRAILshort expression. Aids, 2019, 33, 1757-1763.	2.2	5
616	Neoantigen Fitness Model Predicts Lower Immune Recognition of Cutaneous Squamous Cell Carcinomas Than Actinic Keratoses. Frontiers in Immunology, 2019, 10, 2799.	4.8	9
617	DeepShape: estimating isoform-level ribosome abundance and distribution with Ribo-seq data. BMC Bioinformatics, 2019, 20, 678.	2.6	6
618	Epigenetic therapy of myelodysplastic syndromes connects to cellular differentiation independently of endogenous retroelement derepression. Genome Medicine, 2019, 11, 86.	8.2	20
620	Brain Banks Spur New Frontiers in Neuropsychiatric Research and Strategies for Analysis and Validation. Genomics, Proteomics and Bioinformatics, 2019, 17, 402-414.	6.9	12

#	Article	IF	Citations
621	Investigating the energy crisis in Alzheimer disease using transcriptome study. Scientific Reports, 2019, 9, 18509.	3.3	23
622	Primary Cilia Signaling Promotes Axonal Tract Development and Is Disrupted in Joubert Syndrome-Related Disorders Models. Developmental Cell, 2019, 51, 759-774.e5.	7.0	75
623	BaRTv1.0: an improved barley reference transcript dataset to determine accurate changes in the barley transcriptome using RNA-seq. BMC Genomics, 2019, 20, 968.	2.8	50
624	Comparative Analysis of Strategies for De Novo Transcriptome Assembly in Prokaryotes: Streptomyces clavuligerus as a Case Study. High-Throughput, 2019, 8, 20.	4.4	1
625	Profiles of Long Non-Coding RNAs and mRNA Expression in Human Macrophages Regulated by Interleukin-27. International Journal of Molecular Sciences, 2019, 20, 6207.	4.1	12
626	A computationally inspired in-vivo approach identifies a link between amygdalar transcriptional heterogeneity, socialization and anxiety. Translational Psychiatry, 2019, 9, 336.	4.8	22
627	QuantSeq. 3â€² Sequencing combined with Salmon provides a fast, reliable approach for high throughput RNA expression analysis. Scientific Reports, 2019, 9, 18895.	3.3	33
628	An atlas of cortical circular RNA expression in Alzheimer disease brains demonstrates clinical and pathological associations. Nature Neuroscience, 2019, 22, 1903-1912.	14.8	242
629	Monocytes and Monocyte-Derived Antigen-Presenting Cells Have Distinct Gene Signatures in Experimental Model of Multiple Sclerosis. Frontiers in Immunology, 2019, 10, 2779.	4.8	18
630	The majority of A-to-I RNA editing is not required for mammalian homeostasis. Genome Biology, 2019, 20, 268.	8.8	68
631	A Galaxy-based training resource for single-cell RNA-sequencing quality control and analyses. GigaScience, 2019, 8, .	6.4	4
632	Severe type I interferonopathy and unrestrained interferon signaling due to a homozygous germline mutation in STAT2. Science Immunology, 2019, 4, .	11.9	80
633	Environmental influences on RNA processing: Biochemical, molecular and genetic regulators of cellular response. Wiley Interdisciplinary Reviews RNA, 2019, 10, e1503.	6.4	31
634	Costimulation through TLR2 Drives Polyfunctional CD8+ T Cell Responses. Journal of Immunology, 2019, 202, 714-723.	0.8	51
635	Transcriptomic analysis of the Malpighian tubules of Trichoplusia ni: Clues to mechanisms for switching from ion secretion to ion reabsorption in the distal ileac plexus. Journal of Insect Physiology, 2019, 112, 73-89.	2.0	15
636	Genomics of forest trees. Advances in Botanical Research, 2019, 89, 1-37.	1.1	4
637	Human Breast Cancer Xenograft Model Implicates Peroxisome Proliferatorâ€“activated Receptor Signaling as Driver of Cancer-induced Muscle Fatigue. Clinical Cancer Research, 2019, 25, 2336-2347.	7.0	18
638	RNA splicing analysis in genomic medicine. International Journal of Biochemistry and Cell Biology, 2019, 108, 61-71.	2.8	21

#	Article	IF	Citations
639	SUPT4H1 Depletion Leads to a Global Reduction in RNA. Cell Reports, 2019, 26, 45-53.e4.	6.4	15
640	Method to Synchronize Cell Cycle of Human Pluripotent Stem Cells without Affecting Their Fundamental Characteristics. Stem Cell Reports, 2019, 12, 165-179.	4.8	35
641	Comprehensive identification of RNAâ€“protein interactions in any organism using orthogonal organic phase separation (OOPS). Nature Biotechnology, 2019, 37, 169-178.	17.5	247
642	Understanding the transition from water to land: Insights from multi-omic analyses of the perivitelline fluid of apple snail eggs. Journal of Proteomics, 2019, 194, 79-88.	2.4	11
643	RNA-Seq Reveals Flavonoid Biosynthesis-Related Genes in Pecan (Carya illinoinensis) Kernels. Journal of Agricultural and Food Chemistry, 2019, 67, 148-158.	5.2	33
644	A test metric for assessing single-cell RNA-seq batch correction. Nature Methods, 2019, 16, 43-49.	19.0	278
645	Elevated CO₂ impairs olfactoryâ€mediated neural and behavioral responses and gene expression in oceanâ€phase coho salmon (Oncorhynchus kisutch). Global Change Biology, 2019, 25, 963-977.	9.5	77
646	Retrograde BMP signaling activates neuronal gene expression through widespread deployment of a conserved BMP-responsivecis-regulatoryactivation element. Nucleic Acids Research, 2019, 47, 679-699.	14.5	13
647	LimoRhyde: A Flexible Approach for Differential Analysis of Rhythmic Transcriptome Data. Journal of Biological Rhythms, 2019, 34, 5-18.	2.6	61
648	Proteins Altered by Surgical Weight Loss Highlight Biomarkers of Insulin Resistance in the Community. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 107-115.	2.4	20
649	Expression of seven carbonic anhydrases in red alga Gracilariopsis chorda and their subcellular localization in a heterologous system, Arabidopsis thaliana. Plant Cell Reports, 2019, 38, 147-159.	5.6	11
650	Target (MexB)- and Efflux-Based Mechanisms Decreasing the Effectiveness of the Efflux Pump Inhibitor D13-9001 in Pseudomonas aeruginosa PAO1: Uncovering a New Role for MexMN-OprM in Efflux of Î²-Lactams and a Novel Regulatory Circuit (MmnRS) Controlling MexMN Expression. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	14
651	Enhancing responsiveness of pancreatic cancer cells to gemcitabine treatment under hypoxia by heme oxygenase-1 inhibition. Translational Research, 2019, 207, 56-69.	5.0	35
652	Tissue-specific differences in metabolites and transcripts contribute to the heterogeneity of ricinoleic acid accumulation in Ricinus communis L. (castor) seeds. Metabolomics, 2019, 15, 6.	3.0	21
653	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. Blood, 2019, 133, 1313-1324.	1.4	172
654	IL-1Î² Inflammatory Cytokine-Induced TP63 Isoform â^†NP63Î± Signaling Cascade Contributes to Cisplatin Resistance in Human Breast Cancer Cells. International Journal of Molecular Sciences, 2019, 20, 270.	4.1	34
655	Workflow Development for the Functional Characterization of ncRNAs. Methods in Molecular Biology, 2019, 1912, 111-132.	0.9	7
656	Alignment-free approaches for predicting novel Nuclear Mitochondrial Segments (NUMTs) in the human genome. Gene, 2019, 691, 141-152.	2.2	14

#	Article	IF	Citations
657	Neuronal brain-region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric trait heritability. Nature Neuroscience, 2019, 22, 307-316.	14.8	120
658	ALS-implicated protein TDP-43 sustains levels of STMN2, a mediator of motor neuron growth and repair. Nature Neuroscience, 2019, 22, 167-179.	14.8	353
659	Whole rumen metagenome sequencing allows classifying and predicting feed efficiency and intake levels in cattle. Scientific Reports, 2019, 9, 11.	3.3	108
660	Macrophage Phosphoproteome Analysis Reveals MINCLE-dependent and -independent Mycobacterial Cord Factor Signaling. Molecular and Cellular Proteomics, 2019, 18, 669-685.	3.8	20
661	Revisiting avian â€˜missingâ€™ genes from de novo assembled transcripts. BMC Genomics, 2019, 20, 4.	2.8	36
662	Ocean warming combined with lower omega-3 nutritional availability impairs the cardio-respiratory function of a marine fish. Journal of Experimental Biology, 2019, 222, .	1.7	10
663	Transcriptome profiling reveals key roles of phagosome and NOD-like receptor pathway in spotting diseased Strongylocentrotus intermedius. Fish and Shellfish Immunology, 2019, 84, 521-531.	3.6	27
664	Heavy-tailed prior distributions for sequence count data: removing the noise and preserving large differences. Bioinformatics, 2019, 35, 2084-2092.	4.1	1,085
665	TPMCalculator: one-step software to quantify mRNA abundance of genomic features. Bioinformatics, 2019, 35, 1960-1962.	4.1	149
666	Computational analysis of alternative splicing in plant genomes. Gene, 2019, 685, 186-195.	2.2	9
667	Global analysis of RNA metabolism using bio-orthogonal labeling coupled with next-generation RNA sequencing. Methods, 2019, 155, 88-103.	3.8	8
668	Solving for X: Evidence for sexâ€specific autism biomarkers across multiple transcriptomic studies. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 377-389.	1.7	8
669	Novel microRNAs are associated with population divergence in transcriptional response to thermal stress in an intertidal copepod. Molecular Ecology, 2019, 28, 584-599.	3.9	13
670	A common transcriptomic program acquired in the thymus defines tissue residency of MAIT and NKT subsets. Journal of Experimental Medicine, 2019, 216, 133-151.	8.5	145
671	Transcriptome profiles reveal new regulatory factors of anthocyanin accumulation in a novel purple-colored cherry tomato cultivar Jinling Moyu. Plant Growth Regulation, 2019, 87, 9-18.	3.4	8
672	Histone deacetylase inhibitor targets CD123/CD47-positive cells and reverse chemoresistance phenotype in acute myeloid leukemia. Leukemia, 2019, 33, 931-944.	7.2	39
673	Upstream analysis of alternative splicing: a review of computational approaches to predict context-dependent splicing factors. Briefings in Bioinformatics, 2019, 20, 1358-1375.	6.5	53
674	Alterations in sperm long RNA contribute to the epigenetic inheritance of the effects of postnatal trauma. Molecular Psychiatry, 2020, 25, 2162-2174.	7.9	130

#	Article	IF	Citations
675	The transcriptome landscapes of ovary and three oviduct segments during chicken (Gallus gallus) egg formation. Genomics, 2020, 112, 243-251.	2.9	42
676	Towards a deeper annotation of human lncRNAs. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194385.	1.9	12
677	Multiplexed primer extension sequencing: A targeted RNA-seq method that enables high-precision quantitation of mRNA splicing isoforms and rare pre-mRNA splicing intermediates. Methods, 2020, 176, 34-45.	3.8	8
678	Sulforaphane Bioavailability and Chemopreventive Activity in Men Presenting for Biopsy of the Prostate Gland: A Randomized Controlled Trial. Nutrition and Cancer, 2020, 72, 74-87.	2.0	41
679	Next-generation transcriptome assembly and analysis: Impact of ploidy. Methods, 2020, 176, 14-24.	3.8	20
680	Identification and characterization of long non-coding RNAs in muscle sclerosis of grass carp, Ctenopharyngodon idellus fed with faba bean meal. Aquaculture, 2020, 516, 734521.	3.5	9
681	A high-quality cucumber genome assembly enhances computational comparative genomics. Molecular Genetics and Genomics, 2020, 295, 177-193.	2.1	30
682	Expression of galactinol synthase from Ammopiptanthus nanus in tomato improves tolerance to cold stress. Journal of Experimental Botany, 2020, 71, 435-449.	4.8	29
683	Using R and Bioconductor in Clinical Genomics and Transcriptomics. Journal of Molecular Diagnostics, 2020, 22, 3-20.	2.8	77
684	Transcriptional Profiling of the Murine Airway Response to Acute Ozone Exposure. Toxicological Sciences, 2020, 173, 114-130.	3.1	25
686	Genomic, transcriptomic, and proteomic insights into the symbiosis of deep-sea tubeworm holobionts. ISME Journal, 2020, 14, 135-150.	9.8	41
687	Responses of the kelp Saccharina latissima (Phaeophyceae) to the warming Arctic: from physiology to transcriptomics. Physiologia Plantarum, 2020, 168, 5-26.	5.2	33
688	Acute social isolation alters neurogenomic state in songbird forebrain. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23311-23316.	7.1	25
689	The TMEM106B FTLD-protective variant, rs1990621, is also associated with increased neuronal proportion. Acta Neuropathologica, 2020, 139, 45-61.	7.7	51
690	Mapping RNA-seq reads to transcriptomes efficiently based on learning to hash method. Computers in Biology and Medicine, 2020, 116, 103539.	7.0	8
691	RNA Expression Profiling of Lymphoepithelioma-Like Carcinoma of the Bladder Reveals a Basal-Like Molecular Subtype. American Journal of Pathology, 2020, 190, 134-144.	3.8	13
692	Transcriptome-level effects of the model organic pollutant phenanthrene and its solvent acetone in three amphipod species. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2020, 33, 100630.	1.0	2
693	Magnesium prevents vascular calcification inÂKlotho deficiency. Kidney International, 2020, 97, 487-501.	5.2	50

#	Article	IF	Citations
694	Exploring lithiumâ€™s transcriptional mechanisms of action in bipolar disorder: a multi-step study. Neuropsychopharmacology, 2020, 45, 947-955.	5.4	24
695	Organoid Cultures as Preclinical Models of Nonâ€“Small Cell Lung Cancer. Clinical Cancer Research, 2020, 26, 1162-1174.	7.0	148
696	L1EM: a tool for accurate locus specific LINE-1 RNA quantification. Bioinformatics, 2020, 36, 1167-1173.	4.1	31
697	MX 2 is a novel regulator of cell cycle in melanoma cells. Pigment Cell and Melanoma Research, 2020, 33, 446-457.	3.3	11
698	Vegetative desiccation tolerance in the resurrection plant XerophytaÂhumilis has not evolved through reactivation of the seed canonical LAFL regulatory network. Plant Journal, 2020, 101, 1349-1367.	5.7	19
699	Inferring biosynthetic and gene regulatory networks from Artemisia annua RNA sequencing data on a credit card-sized ARM computer. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194429.	1.9	12
700	Mycovirus-Induced Hypervirulence of Leptosphaeria biglobosa Enhances Systemic Acquired Resistance to Leptosphaeria maculans in Brassica napus. Molecular Plant-Microbe Interactions, 2020, 33, 98-107.	2.6	29
701	In situ metabolic activities of uncultivated Ferrovum sp. CARN8 evidenced by metatranscriptomic analysis. Research in Microbiology, 2020, 171, 37-43.	2.1	7
702	Ferritin Light Chain (FTL) competes with long noncoding RNA Linc00467 for miR-133b binding site to regulate chemoresistance and metastasis of colorectal cancer. Carcinogenesis, 2020, 41, 467-477.	2.8	33
703	Heritable temporal gene expression patterns correlate with metabolomic seed content in developing hexaploid oat seed. Plant Biotechnology Journal, 2020, 18, 1211-1222.	8.3	19
704	AP2/ERF Transcription Factors Integrate Age and Wound Signals for Root Regeneration. Plant Cell, 2020, 32, 226-241.	6.6	100
705	A Single-Step, High-Dose Selection Scheme Reveals Distinct Mechanisms of Acquired Resistance to Oncogenic Kinase Inhibition in Cancer Cells. Cancer Research, 2020, 80, 79-90.	0.9	4
706	The transcriptomic responses of C 4 grasses to subambient CO 2 and low light are largely species specific and only refined by photosynthetic subtype. Plant Journal, 2020, 101, 1170-1184.	5.7	5
707	Comparative genomeâ€scale analysis of Pichia pastoris variants informs selection of an optimal base strain. Biotechnology and Bioengineering, 2020, 117, 543-555.	3.3	34
708	Egg perivitelline fluid proteome of a freshwater snail: Insight into the transition from aquatic to terrestrial egg deposition. Rapid Communications in Mass Spectrometry, 2020, 34, e8605.	1.5	5
709	Singleâ€cell RNA sequencing reveals chemokine selfâ€feeding of myeloma cells promotes extramedullary metastasis. FEBS Letters, 2020, 594, 452-465.	2.8	20
710	The transcription factor FOXM1 regulates the balance between proliferation and aberrant differentiation in head and neck squamous cell carcinoma. Journal of Pathology, 2020, 250, 107-119.	4.5	11
711	New insights into diosgenin biosynthesis pathway and its regulation in <scp>Trigonella foenumâ€graecum</scp> L.. Phytochemical Analysis, 2020, 31, 229-241.	2.4	27

#	Article	IF	Citations
712	Modeling Between-Study Heterogeneity for Improved Replicability in Gene Signature Selection and Clinical Prediction. Journal of the American Statistical Association, 2020, 115, 1125-1138.	3.1	11
713	At the nexus of three kingdoms: the genome of the mycorrhizal fungus Gigaspora margarita provides insights into plant, endobacterial and fungal interactions. Environmental Microbiology, 2020, 22, 122-141.	3.8	84
714	Transcriptome of Tetranychus urticae embryos reveals insights into Wolbachiaâ€induced cytoplasmic incompatibility. Insect Molecular Biology, 2020, 29, 193-204.	2.0	14
715	What a Difference a Gene Makes: Identification of Virulence Factors of Cowpox Virus. Journal of Virology, 2020, 94, .	3.4	6
716	Transcription and Activity of Digestive Enzymes of Nezara viridula Maintained on Different Plant Diets. Frontiers in Physiology, 2019, 10, 1553.	2.8	12
717	Analysis of NAC Domain Transcription Factor Genes of Tectona grandis L.f. Involved in Secondary Cell Wall Deposition. Genes, 2020, 11, 20.	2.4	14
718	A Model of Hormonal Regulation of Stamen Abortion during Pre-Meiosis of Litsea cubeba. Genes, 2020, 11, 48.	2.4	12
719	The basic helixâ€loopâ€helix transcription factor TCF4 impacts brain architecture as well as neuronal morphology and differentiation. European Journal of Neuroscience, 2020, 51, 2219-2235.	2.6	16
720	Evidence in support of chromosomal sex influencing plasma based metabolome vs APOE genotype influencing brain metabolome profile in humanized APOE male and female mice. PLoS ONE, 2020, 15, e0225392.	2.5	25
721	Alternative splicing programming of axon formation. Wiley Interdisciplinary Reviews RNA, 2020, 11, e1585.	6.4	23
722	Transcript profiling for regulation of sweet potato skin color in Sushu8 and its mutant Zhengshu20. Plant Physiology and Biochemistry, 2020, 148, 1-9.	5.8	9
723	The nucleolar protein NOP2 is required for nucleolar maturation and ribosome biogenesis during preimplantation development in mammals. FASEB Journal, 2020, 34, 2715-2729.	0.5	22
724	The transcriptome data from the leaves of four Papaver species captured at the plant's three developmental life cycles. Data in Brief, 2020, 28, 104955.	1.0	2
725	Identifying suitable tools for variant detection and differential gene expression using RNA-seq data. Genomics, 2020, 112, 2166-2172.	2.9	8
726	Human gain-of-function STAT1 mutation disturbs IL-17 immunity in mice. International Immunology, 2020, 32, 259-272.	4.0	20
727	Characterizing the nuclear and cytoplasmic transcriptomes in developing and mature human cortex uncovers new insight into psychiatric disease gene regulation. Genome Research, 2020, 30, 1-11.	5.5	29
728	Interindividual Heterogeneity of SGLT2 Expression and Function in Human Pancreatic Islets. Diabetes, 2020, 69, 902-914.	0.6	42
729	dSreg: a Bayesian model to integrate changes in splicing and RNA-binding protein activity. Bioinformatics, 2020, 36, 2134-2141.	4.1	1

#	Article	IF	Citations
730	Platform-integrated mRNA isoform quantification. Bioinformatics, 2020, 36, 2466-2473.	4.1	5
731	Angiotensin peptide synthesis and cyclic nucleotide modulation in sympathetic stellate ganglia. Journal of Molecular and Cellular Cardiology, 2020, 138, 234-243.	1.9	6
732	Discovery of a first-in-class EZH2 selective degrader. Nature Chemical Biology, 2020, 16, 214-222.	8.0	148
733	TBCRC 032 IB/II Multicenter Study: Molecular Insights to AR Antagonist and PI3K Inhibitor Efficacy in Patients with AR+ Metastatic Triple-Negative Breast Cancer. Clinical Cancer Research, 2020, 26, 2111-2123.	7.0	91
734	Macrophage-tumor cell interaction promotes ATRT progression and chemoresistance. Acta Neuropathologica, 2020, 139, 913-936.	7.7	24
735	Host-Informed Expression of CRISPR Guide RNA for Genomic Engineering in Komagataella phaffii. ACS Synthetic Biology, 2020, 9, 26-35.	3.8	40
736	Ptpn6 inhibits caspase-8- and Ripk3/Mlkl-dependent inflammation. Nature Immunology, 2020, 21, 54-64.	14.5	33
737	Omics Playground: a comprehensive self-service platform for visualization, analytics and exploration of Big Omics Data. NAR Genomics and Bioinformatics, 2020, 2, lqz019.	3.2	35
738	Enteroendocrine Progenitor Cellâ€“Enriched miR-7 Regulates Intestinal Epithelial Proliferation in an Xiap-Dependent Manner. Cellular and Molecular Gastroenterology and Hepatology, 2020, 9, 447-464.	4.5	11
739	B Cell Synovitis and Clinical Phenotypes in Rheumatoid Arthritis: Relationship to Disease Stages and Drug Exposure. Arthritis and Rheumatology, 2020, 72, 714-725.	5.6	33
740	Effective and Accurate Gene Silencing by a Recombinant AAV-Compatible MicroRNA Scaffold. Molecular Therapy, 2020, 28, 422-430.	8.2	20
741	Genomic landscape and genetic manipulation of the black soldier fly Hermetia illucens, a natural waste recycler. Cell Research, 2020, 30, 50-60.	12.0	136
742	Photosystem II 22kDa protein level â€•a prerequisite for excess lightâ€inducible memory, crossâ€tolerance to UVâ€Ć and regulation of electrical signalling. Plant, Cell and Environment, 2020, 43, 649-661.	5.7	23
743	Modeling population heterogeneity from microbial communities to immune response in cells. Cellular and Molecular Life Sciences, 2020, 77, 415-432.	5.4	5
744	Subdivision of Light Signaling Networks Contributes to Partitioning of C₄ Photosynthesis. Plant Physiology, 2020, 182, 1297-1309.	4.8	8
745	Small Molecules Produced by Commensal Staphylococcus epidermidis Disrupt Formation of Biofilms by Staphylococcus aureus. Applied and Environmental Microbiology, 2020, 86, .	3.1	25
746	Factorial study of the RNA-seq computational workflow identifies biases as technical gene signatures. NAR Genomics and Bioinformatics, 2020, 2, lqaa043.	3.2	4
747	Ocean acidification induces distinct transcriptomic responses across life history stages of the sea urchin Heliocidaris erythrogramma. Molecular Ecology, 2020, 29, 4618-4636.	3.9	14

#	Article	IF	Citations
748	Global gene expression profile under low-temperature conditions in the brain of the grass carp (Ctenopharyngodon idellus). PLoS ONE, 2020, 15, e0239730.	2.5	6
749	Transcriptomic and Epigenomic Dynamics of Honey Bees in Response to Lethal Viral Infection. Frontiers in Genetics, 2020, 11, 566320.	2.3	16
750	Changes in Metabolism and Proteostasis Drive Aging Phenotype in Aplysia californica Sensory Neurons. Frontiers in Aging Neuroscience, 2020, 12, 573764.	3.4	8
751	Deletion in the Bardetâ€“Biedl Syndrome Gene TTC8 Results in a Syndromic Retinal Degeneration in Dogs. Genes, 2020, 11, 1090.	2.4	6
752	Fibronectin Gene Up-regulation by Arnica montana in Human Macrophages: Validation by Real-Time Polymerase Chain Reaction Assay. Homeopathy, 2020, 109, 140-145.	1.0	5
753	MED19 Regulates Adipogenesis and Maintenance of White Adipose Tissue Mass by Mediating PPARÎ³-Dependent Gene Expression. Cell Reports, 2020, 33, 108228.	6.4	18
754	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. Scientific Data, 2020, 7, 326.	5.3	40
755	Tissue-specific and interferon-inducible expression of nonfunctional ACE2 through endogenous retroelement co-option. Nature Genetics, 2020, 52, 1294-1302.	21.4	82
756	Reduced stress defence responses contribute to the higher toxicity of a pesticide under warming. Molecular Ecology, 2020, 29, 4735-4748.	3.9	10
757	Identification of Fusarium solani f. sp. pisi (Fsp) Responsive Genes in Pisum sativum. Frontiers in Genetics, 2020, 11, 950.	2.3	9
758	Transcriptional Programs Underlying Cold Acclimation of Common Carp (Cyprinus carpio L.). Frontiers in Genetics, 2020, 11, 556418.	2.3	15
759	Comparative transcriptome analysis of eyestalk from the white shrimp Litopenaeus vannamei after the injection of dopamine. Gene, 2020, 763, 145115.	2.2	7
760	SOX1 Is Required for the Specification of Rostral Hindbrain Neural Progenitor Cells from Human Embryonic Stem Cells. IScience, 2020, 23, 101475.	4.1	6
761	RNA-Seq identifies condition-specific biological signatures of ischemia-reperfusion injury in the human kidney. BMC Nephrology, 2020, 21, 398.	1.8	14
762	Comparative Transcriptomics and Co-Expression Networks Reveal Tissue- and Genotype-Specific Responses of qDTYs to Reproductive-Stage Drought Stress in Rice (Oryza sativa L.). Genes, 2020, 11, 1124.	2.4	13
763	Development of an ObLiGaRe Doxycycline Inducible Cas9 system for pre-clinical cancer drug discovery. Nature Communications, 2020, 11, 4903.	12.8	65
764	A Thalamic Orphan Receptor Drives Variability in Short-Term Memory. Cell, 2020, 183, 522-536.e19.	28.9	24
765	Loss of UTX/KDM6A and the activation of FGFR3 converge to regulate differentiation gene-expression programs in bladder cancer. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25732-25741.	7.1	26

#	Article	IF	Citations
766	A Small-RNA-Mediated Feedback Loop Maintains Proper Levels of 22G-RNAs in C.Âelegans. Cell Reports, 2020, 33, 108279.	6.4	7
767	Identification of Long Noncoding RNAs Involved in Differentiation and Survival of Vascular Smooth Muscle Cells. Molecular Therapy - Nucleic Acids, 2020, 22, 209-221.	5.1	15
768	Comparative eye and liver differentially expressed genes reveal monochromatic vision and cancer resistance in the shortfin mako shark (Isurus oxyrinchus). Genomics, 2020, 112, 4817-4826.	2.9	4
769	TPR is required for the efficient nuclear export of mRNAs and lncRNAs from short and intron-poor genes. Nucleic Acids Research, 2020, 48, 11645-11663.	14.5	34
770	The cytoplasmic SYNCRIP mRNA interactome of mammalian neurons. RNA Biology, 2021, 18, 1-13.	3.1	3
771	Infantile fibrosarcomaâ€“like tumor driven by novel RBPMS-MET fusion consolidated with cabozantinib. Journal of Physical Education and Sports Management, 2020, 6, a005645.	1.2	17
772	Terminus enables the discovery of data-driven, robust transcript groups from RNA-seq data. Bioinformatics, 2020, 36, i102-i110.	4.1	11
773	Differential expression in leaves of Saccharum genotypes contrasting in biomass production provides evidence of genes involved in carbon partitioning. BMC Genomics, 2020, 21, 673.	2.8	10
774	Target Enrichment Enables the Discovery of lncRNAs with Somatic Mutations or Altered Expression in Paraffin-Embedded Colorectal Cancer Samples. Cancers, 2020, 12, 2844.	3.7	7
775	Local intracerebral inhibition of IRE1 by MKC8866 sensitizes glioblastoma to irradiation/chemotherapy in vivo. Cancer Letters, 2020, 494, 73-83.	7.2	32
776	COMPOSITUM 1 contributes to the architectural simplification of barley inflorescence via meristem identity signals. Nature Communications, 2020, 11, 5138.	12.8	37
777	Autophagic protein ULK1 regulates FOXM1 signalling in human hepatoma cells. Biochemical and Biophysical Research Communications, 2020, 532, 570-575.	2.1	3
778	Chd8 haploinsufficiency impairs early brain development and protein homeostasis later in life. Molecular Autism, 2020, 11, 74.	4.9	19
779	The Mammalian Cap-Specific m6Am RNA Methyltransferase PCIF1 Regulates Transcript Levels in Mouse Tissues. Cell Reports, 2020, 32, 108038.	6.4	50
780	Uptake, translocation and toxicity of chlorinated polyfluoroalkyl ether potassium sulfonate (F53B) and chromium co-contamination in water spinach (Ipomoea aquatica Forsk). Environmental Pollution, 2020, 266, 115385.	7.5	18
781	iMOKA: k-mer based software to analyze large collections of sequencing data. Genome Biology, 2020, 21, 261.	8.8	8
782	Transcriptome Analysis Shows Activation of Stress and Defense Responses by Silencing of Chlorophyll Biosynthetic Enzyme CHLI in Transgenic Tobacco. International Journal of Molecular Sciences, 2020, 21, 7044.	4.1	2
783	Noninvasive Early Identification of Therapeutic Benefit from Immune Checkpoint Inhibition. Cell, 2020, 183, 363-376.e13.	28.9	206

#	Article	IF	Citations
784	Î¼DamID: A Microfluidic Approach for Joint Imaging and Sequencing of Protein-DNA Interactions in Single Cells. Cell Systems, 2020, 11, 354-366.e9.	6.2	15
785	Cell-intrinsic Fgf signaling contributes to primordial germ cell homing in zebrafish. Theriogenology, 2020, 158, 424-431.	2.1	5
786	Impact of oxytetracycline on anaerobic wastewater treatment and mitigation using enhanced hydrolysis pretreatment. Water Research, 2020, 187, 116408.	11.3	39
787	Posttranscriptional regulation of human endogenous retroviruses by RNA-binding motif protein 4, RBM4. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26520-26530.	7.1	11
788	VIRTUS: a pipeline for comprehensive virus analysis from conventional RNA-seq data. Bioinformatics, 2021, 37, 1465-1467.	4.1	12
789	An OTX2-PAX3 signaling axis regulates Group 3 medulloblastoma cell fate. Nature Communications, 2020, 11, 3627.	12.8	21
790	A universal and independent synthetic DNA ladder for the quantitative measurement of genomic features. Nature Communications, 2020, 11, 3609.	12.8	7
791	Daphnia magna modifies its gene expression extensively in response to caloric restriction revealing a novel effect on haemoglobin isoform preference. Molecular Ecology, 2020, 29, 3261-3276.	3.9	5
792	MYB30 Orchestrates Systemic Reactive Oxygen Signaling and Plant Acclimation. Plant Physiology, 2020, 184, 666-675.	4.8	54
793	A Bayesian framework for inter-cellular information sharing improves dscRNA-seq quantification. Bioinformatics, 2020, 36, i292-i299.	4.1	13
794	Complete Biosynthesis of the Anti-Diabetic Plant Metabolite Montbretin A. Plant Physiology, 2020, 184, 97-109.	4.8	18
795	The response of the melanized yeast Exophiala dermatitidis to gamma radiation exposure. Environmental Microbiology, 2020, 22, 1310-1326.	3.8	17
796	Sponge microbiome stability during environmental acquisition of highly specific photosymbionts. Environmental Microbiology, 2020, 22, 3593-3607.	3.8	20
797	Correlates of clinical benefit from immunotherapy and targeted therapy in metastatic renal cell carcinoma: comprehensive genomic and transcriptomic analysis. , 2020, 8, e000953.		32
798	HBA-DEALS: accurate and simultaneous identification of differential expression and splicing using hierarchical Bayesian analysis. Genome Biology, 2020, 21, 171.	8.8	7
799	Glycogen accumulation, central carbon metabolism, and aging of hematopoietic stem and progenitor cells. Scientific Reports, 2020, 10, 11597.	3.3	12
800	Profiling and quantification of pluripotency reprogramming reveal that WNT pathways and cell morphology have to be reprogramed extensively. Heliyon, 2020, 6, e04035.	3.2	9
801	Modeling Hypoxia-Induced Neuropathies Using a Fast and Scalable Human Motor Neuron Differentiation System. Stem Cell Reports, 2020, 14, 1033-1043.	4.8	10

#	Article	IF	Citations
802	Transcriptomic Profiling Identifies Novel Hepatic and Intestinal Genes Following Chronic Plus Binge Ethanol Feeding in Mice. Digestive Diseases and Sciences, 2020, 65, 3592-3604.	2.3	11
803	Cell Types Promoting Goosebumps Form a Niche to Regulate Hair Follicle Stem Cells. Cell, 2020, 182, 578-593.e19.	28.9	81
804	Metagenomic Profiling of Ocular Surface Microbiome Changes in Meibomian Gland Dysfunction. , 2020, 61, 22.		27
805	Motor cortex transcriptome reveals microglial key events in amyotrophic lateral sclerosis. Neurology: Neuroimmunology and NeuroInflammation, 2020, 7, .	6.0	54
806	Co-Expression Networks for Causal Gene Identification Based on RNA-Seq Data of Corynebacterium pseudotuberculosis. Genes, 2020, 11, 794.	2.4	3
807	Dibenzazepine promotes cochlear supporting cell proliferation and hair cell regeneration in neonatal mice. Cell Proliferation, 2020, 53, e12872.	5.3	5
808	Data Processing for RNA/DNA Sequencing. , 2020, , 507-514.		0
809	Human endogenous retrovirus-K mRNA expression and genomic alignment data in hepatoblastoma. Data in Brief, 2020, 31, 105895.	1.0	4
810	Physiological dynamics of chemosynthetic symbionts in hydrothermal vent snails. ISME Journal, 2020, 14, 2568-2579.	9.8	17
811	Transcriptional responses in Parascaris univalens after in vitro exposure to ivermectin, pyrantel citrate and thiabendazole. Parasites and Vectors, 2020, 13, 342.	2.5	17
812	Concentrations of persistent organic pollutants in maternal plasma and epigenome-wide placental DNA methylation. Clinical Epigenetics, 2020, 12, 103.	4.1	49
813	Genomic signals found using RNA sequencing show signatures of selection and subtle population differentiation in walleye (Sander vitreus) in a large freshwater ecosystem. Ecology and Evolution, 2020, 10, 7173-7188.	1.9	13
814	Initial responses of the trapâ€crop, Solanum sisymbriifolium, to Globodera pallida invasions. Plant Genome, 2020, 13, e20016.	2.8	2
815	De novo assembly and analysis of the transcriptome of the Dermacentor marginatus genes differentially expressed after blood-feeding and long-term starvation. Parasites and Vectors, 2020, 13, 563.	2.5	9
816	Reduced Mitochondrial Apoptotic Priming Drives Resistance to BH3 Mimetics in Acute Myeloid Leukemia. Cancer Cell, 2020, 38, 872-890.e6.	16.8	80
817	Crosstalk between microglia and patient-derived glioblastoma cells inhibit invasion in a three-dimensional gelatin hydrogel model. Journal of Neuroinflammation, 2020, 17, 346.	7.2	21
818	CD103+CD8+ TRM Cells Accumulate in Tumors of Anti-PD-1-Responder Lung Cancer Patients and Are Tumor-Reactive Lymphocytes Enriched with Tc17. Cell Reports Medicine, 2020, 1, 100127.	6.5	70
819	ADAM22/LGI1 complex as a new actionable target for breast cancer brain metastasis. BMC Medicine, 2020, 18, 349.	5.5	8

#	Article	IF	Citations
820	Tissue-specific Transcriptome analysis reveals lignocellulose synthesis regulation in elephant grass (Pennisetum purpureum Schum). BMC Plant Biology, 2020, 20, 528.	3.6	5
821	Longitudinal Characterization of Transcriptomic, Functional, and Morphological Features in Human iPSC-Derived Neurons and Their Application to Investigate Translational Progranulin Disease Biology. Frontiers in Aging Neuroscience, 2020, 12, 576678.	3.4	3
822	Prospects for Clinical Development of Stat5 Inhibitor IST5-002: High Transcriptomic Specificity in Prostate Cancer and Low Toxicity In Vivo. Cancers, 2020, 12, 3412.	3.7	3
823	The Mosaic Architecture of NRPS-PKS in the Arbuscular Mycorrhizal Fungus Gigaspora margarita Shows a Domain With Bacterial Signature. Frontiers in Microbiology, 2020, 11, 581313.	3.5	8
824	Unique maternal immune and functional microbial profiles during prenatal stress. Scientific Reports, 2020, 10, 20288.	3.3	26
825	Systemic paralogy and function of retinal determination network homologs in arachnids. BMC Genomics, 2020, 21, 811.	2.8	20
826	Genome plasticity in Paramecium bursaria revealed by population genomics. BMC Biology, 2020, 18, 180.	3.8	16
827	Identifying Genes Involved in Alkaloid Biosynthesis in Vinca minor through Transcriptomics and Gene Co-Expression Analysis. Biomolecules, 2020, 10, 1595.	4.0	12
828	Persistent or Transient Human Î² Cell Dysfunction Induced by Metabolic Stress: Specific Signatures and Shared Gene Expression with Type 2 Diabetes. Cell Reports, 2020, 33, 108466.	6.4	65
829	BMP signaling: at the gate between activated melanocyte stem cells and differentiation. Genes and Development, 2020, 34, 1713-1734.	5.9	35
830	Systematic comparison and assessment of RNA-seq procedures for gene expression quantitative analysis. Scientific Reports, 2020, 10, 19737.	3.3	99
831	Comprehensive analysis of cutaneous and uveal melanoma liver metastases. , 2020, 8, e001501.		40
832	Sarcolipin Exhibits Abundant RNA Transcription and Minimal Protein Expression in Horse Gluteal Muscle. Veterinary Sciences, 2020, 7, 178.	1.7	1
833	Quick, Coordinated and Authentic Reprogramming of Ribosome Biogenesis during iPSC Reprogramming. Cells, 2020, 9, 2484.	4.1	7
834	Transcriptome and regulatory maps of decidua-derived stromal cells inform gene discovery in preterm birth. Science Advances, 2020, 6, .	10.3	31
835	Increased biological relevance of transcriptome analyses in human skeletal muscle using a model-specific pipeline. BMC Bioinformatics, 2020, 21, 548.	2.6	7
836	Targeted mutagenesis of âˆ†5 and âˆ†6 fatty acyl desaturases induce dysregulation of lipid metabolism in Atlantic salmon (Salmo salar). BMC Genomics, 2020, 21, 805.	2.8	8
837	Telomere Length Dynamics and DNA Damage Responses Associated with Long-Duration Spaceflight. Cell Reports, 2020, 33, 108457.	6.4	48

#	Article	IF	Citations
838	SCUBE1 Controls BMPR2-Relevant Pulmonary Endothelial Function. JACC Basic To Translational Science, 2020, 5, 1073-1092.	4.1	8
839	Differential gene expression analysis reveals pathways important in early post-traumatic osteoarthritis in an equine model. BMC Genomics, 2020, 21, 843.	2.8	7
840	RNA sequencing: new technologies and applications in cancer research. Journal of Hematology and Oncology, 2020, 13, 166.	17.0	229
841	A Customizable Analysis Flow in Integrative Multi-Omics. Biomolecules, 2020, 10, 1606.	4.0	14
842	Transcriptomic Regulations Underlying Pair-bond Formation and Maintenance in the Socially Monogamous Male and Female Prairie Vole. Biological Psychiatry, 2020, 91, 141-151.	1.3	14
843	Personalized B cell response to the Lactobacillus rhamnosus GG probiotic in healthy human subjects: a randomized trial. Gut Microbes, 2020, 12, 1854639.	9.8	5
844	SITC cancer immunotherapy resource document: a compass in the land of biomarker discovery. , 2020, 8, e000705.		20
845	SARS-CoV-2 Receptor Angiotensin I-Converting Enzyme Type 2 (ACE2) Is Expressed in Human Pancreatic Î²-Cells and in the Human Pancreas Microvasculature. Frontiers in Endocrinology, 2020, 11, 596898.	3.5	144
846	Group 3 Innate Lymphoid Cells Program a Distinct Subset of IL-22BP-Producing Dendritic Cells Demarcating Solitary Intestinal Lymphoid Tissues. Immunity, 2020, 53, 1015-1032.e8.	14.3	41
847	Next-generation diagnostics for precision oncology: Preanalytical considerations, technical challenges, and available technologies. Seminars in Cancer Biology, 2022, 84, 3-15.	9.6	12
848	Molecular signatures of the rediae, cercariae and adult stages in the complex lifeÂcycles of parasitic flatworms (Digenea: Psilostomatidae). Parasites and Vectors, 2020, 13, 559.	2.5	4
849	The Impact of the Deepwater Horizon Oil Spill upon Lung Healthâ€"Mouse Model-Based RNA-Seq Analyses. International Journal of Environmental Research and Public Health, 2020, 17, 5466.	2.6	4
850	Identifying Improved Sites for Heterologous Gene Integration Using ATAC-seq. ACS Synthetic Biology, 2020, 9, 2515-2524.	3.8	13
851	DOCK3 is a dosage-sensitive regulator of skeletal muscle and Duchenne muscular dystrophy-associated pathologies. Human Molecular Genetics, 2020, 29, 2855-2871.	2.9	10
852	Scion genotypes exert long distance control over rootstock transcriptome responses to low phosphate in grafted grapevine. BMC Plant Biology, 2020, 20, 367.	3.6	17
853	Transcription of carbonyl reductase 1 is regulated by DNA topoisomerase II beta. FEBS Letters, 2020, 594, 3395-3405.	2.8	3
854	Variants in SCAF4 Cause a Neurodevelopmental Disorder and Are Associated with Impaired mRNA Processing. American Journal of Human Genetics, 2020, 107, 544-554.	6.2	13
855	Efflux pump activity potentiates the evolution of antibiotic resistance across S. aureus isolates. Nature Communications, 2020, 11, 3970.	12.8	79

#	Article	IF	Citations
856	A guide to human microbiome research: study design, sample collection, and bioinformatics analysis. Chinese Medical Journal, 2020, 133, 1844-1855.	2.3	55
857	CD163⁺cytokine-producing cDC2 stimulate intratumoral type 1 T cell responses in HPV16-induced oropharyngeal cancer. , 2020, 8, e001053.		26
858	The biosynthesis of the antiâ€microbial diterpenoid leubethanol in Leucophyllum frutescens proceeds via an allâ€cis prenyl intermediate. Plant Journal, 2020, 104, 693-705.	5.7	15
859	Comparative Analysis of Microbial Community Structure and Function in the Gut of Wild and Captive Amur Tiger. Frontiers in Microbiology, 2020, 11, 1665.	3.5	39
860	Enzymatic RNA Biotinylation for Affinity Purification and Identification of RNAâ€“Protein Interactions. ACS Chemical Biology, 2020, 15, 2247-2258.	3.4	9
861	The Meningioma Enhancer Landscape Delineates Novel Subgroups and Drives Druggable Dependencies. Cancer Discovery, 2020, 10, 1722-1741.	9.4	30
862	Reference genome and transcriptome informed by the sex chromosome complement of the sample increase ability to detect sex differences in gene expression from RNA-Seq data. Biology of Sex Differences, 2020, 11, 42.	4.1	31
863	Insights into the evolution of symbiosis gene copy number and distribution from a chromosome-scaleLotus japonicusGifu genome sequence. DNA Research, 2020, 27, .	3.4	35
864	Genome-wide analysis and transcript profiling of PSKR gene family members in Oryza sativa. PLoS ONE, 2020, 15, e0236349.	2.5	14
865	Shedding the Light on Litopenaeus vannamei Differential Muscle and Hepatopancreas Immune Responses in White Spot Syndrome Virus (WSSV) Exposure. Genes, 2020, 11, 805.	2.4	12
866	Regulatory T Cells Play a Role in a Subset of Idiopathic Preterm Labor/Birth and Adverse Neonatal Outcomes. Cell Reports, 2020, 32, 107874.	6.4	71
867	A large-scale binding and functional map of human RNA-binding proteins. Nature, 2020, 583, 711-719.	27.8	667
868	Thermostable small-molecule inhibitor of angiogenesis and vascular permeability that suppresses a pERK-FosB/Î”FosBâ€“VCAM-1 axis. Science Advances, 2020, 6, eaaz7815.	10.3	16
869	Resistance Mechanisms ofSaccharomyces cerevisiaeto Commercial Formulations of Glyphosate Involve DNA Damage Repair, the Cell Cycle, and the Cell Wall Structure. G3: Genes, Genomes, Genetics, 2020, 10, 2043-2056.	1.8	9
870	A PIANO (Proper, Insufficient, Aberrant, and NO Reprogramming) Response to the Yamanaka Factors in the Initial Stages of Human iPSC Reprogramming. International Journal of Molecular Sciences, 2020, 21, 3229.	4.1	7
871	Regenerative Reprogramming of the Intestinal Stem Cell State via Hippo Signaling Suppresses Metastatic Colorectal Cancer. Cell Stem Cell, 2020, 27, 590-604.e9.	11.1	112
872	Modulating electrophysiology of motor neural networks via optogenetic stimulation during neurogenesis and synaptogenesis. Scientific Reports, 2020, 10, 12460.	3.3	8
873	Pathogenic Tau Causes a Toxic Depletion of Nuclear Calcium. Cell Reports, 2020, 32, 107900.	6.4	23

#	Article	IF	Citations
874	Placental genomic and epigenomic signatures associated with infant birth weight highlight mechanisms involved in collagen and growth factor signaling. Reproductive Toxicology, 2020, 96, 221-230.	2.9	16
875	Meta-analysis of mouse transcriptomic studies supports a context-dependent astrocyte reaction in acute CNS injury versus neurodegeneration. Journal of Neuroinflammation, 2020, 17, 227.	7.2	56
876	Metagenomic approach reveals the fate of antibiotic resistance genes in a temperature-raising anaerobic digester treating municipal sewage sludge. Journal of Cleaner Production, 2020, 277, 123504.	9.3	41
877	Illuminating the impact of diel vertical migration on visual gene expression in deepâ€sea shrimp. Molecular Ecology, 2020, 29, 3494-3510.	3.9	14
878	Cancer Cell Acid Adaptation Gene Expression Response Is Correlated to Tumor-Specific Tissue Expression Profiles and Patient Survival. Cancers, 2020, 12, 2183.	3.7	19
879	Immunomodulation of intracranial melanoma in response to blood-tumor barrier opening with focused ultrasound. Theranostics, 2020, 10, 8821-8833.	10.0	25
880	Human Tumor-Infiltrating MAIT Cells Display Hallmarks of Bacterial Antigen Recognition in Colorectal Cancer. Cell Reports Medicine, 2020, 1, 100039.	6.5	32
881	Concomitant DNA methylation and transcriptome signatures define epidermal responses to acute solar UV radiation. Scientific Reports, 2020, 10, 12918.	3.3	9
882	The Asp298Asn polymorphism of melanocortinâ€4 receptor (MC4R) in pigs: evidence for its potential effects on MC4R constitutive activity and cell surface expression. Animal Genetics, 2020, 51, 694-706.	1.7	15
883	Transcriptional Response of Osmolyte Synthetic Pathways and Membrane Transporters in a Euryhaline Diatom During Longâ€term Acclimation to a Salinity Gradient. Journal of Phycology, 2020, 56, 1712-1728.	2.3	16
884	Genome-wide Screening Identifies SFMBT1 as an Oncogenic Driver in Cancer with VHL Loss. Molecular Cell, 2020, 77, 1294-1306.e5.	9.7	41
885	Partitioning of MLX-Family Transcription Factors to Lipid Droplets Regulates Metabolic Gene Expression. Molecular Cell, 2020, 77, 1251-1264.e9.	9.7	78
886	The RNA exosome shapes the expression of key protein-coding genes. Nucleic Acids Research, 2020, 48, 8509-8528.	14.5	12
887	H/ACA snoRNA levels are regulated during stem cell differentiation. Nucleic Acids Research, 2020, 48, 8686-8703.	14.5	22
888	Integrated analysis of mRNA and miRNA expression profiles reveals muscle growth differences between fast- and slow-growing king ratsnakes (Elaphe carinata). Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2020, 248-249, 110482.	1.6	1
889	Early pregnancy dyslipidemia is associated with placental DNA methylation at loci relevant for cardiometabolic diseases. Epigenomics, 2020, 12, 921-934.	2.1	12
890	Elucidating the fundamental fibrotic processes driving abdominal adhesion formation. Nature Communications, 2020, 11, 4061.	12.8	52
891	The transcription factor scleraxis differentially regulates gene expression in tenocytes isolated at different developmental stages. Mechanisms of Development, 2020, 163, 103635.	1.7	9

#	Article	IF	Citations
892	Cooperation Between Distinct Cancer Driver Genes Underlies Intertumor Heterogeneity in Hepatocellular Carcinoma. Gastroenterology, 2020, 159, 2203-2220.e14.	1.3	47
893	BrassicaEDB: A Gene Expression Database for Brassica Crops. International Journal of Molecular Sciences, 2020, 21, 5831.	4.1	44
894	Altered rRNA processing disrupts nuclear RNA homeostasis via competition for the poly(A)-binding protein Nab2. Nucleic Acids Research, 2020, 48, 11675-11694.	14.5	13
895	Single-cell RNA profiling links ncRNAs to spatiotemporal gene expression during C. elegans embryogenesis. Scientific Reports, 2020, 10, 18863.	3.3	2
896	Single-cell strand sequencing of a macaque genome reveals multiple nested inversions and breakpoint reuse during primate evolution. Genome Research, 2020, 30, 1680-1693.	5.5	16
897	Transcriptomic Profiling of Mouse Brain During Acute and Chronic Infections by Toxoplasma gondii Oocysts. Frontiers in Microbiology, 2020, 11, 570903.	3.5	10
898	Insights from RNA-Seq analysis of Alzheimer's data suggest upregulation of GPCRs. Gene Reports, 2020, 21, 100921.	0.8	1
899	Burn resuscitation strategy influences the gut microbiota-liver axis in swine. Scientific Reports, 2020, 10, 15655.	3.3	13
900	B cell tolerance and antibody production to the celiac disease autoantigen transglutaminase 2. Journal of Experimental Medicine, 2020, 217, .	8.5	38
901	De novo transcriptome assembly from the gonads of a scleractinian coral, Euphyllia ancora: molecular mechanisms underlying scleractinian gametogenesis. BMC Genomics, 2020, 21, 732.	2.8	14
902	Comprehensive evaluation of differentially expressed non-coding RNAs identified during macrophage activation. Molecular Immunology, 2020, 128, 98-105.	2.2	2
903	Application of compound material alleviates saline and alkaline stress in cotton leaves through regulation of the transcriptome. BMC Plant Biology, 2020, 20, 462.	3.6	12
904	Increased RNA editing in maternal immune activation model of neurodevelopmental disease. Nature Communications, 2020, 11, 5236.	12.8	24
905	Multi-omic studies on missense PLG variants in families with otitis media. Scientific Reports, 2020, 10, 15035.	3.3	4
906	Histone Loaders CAF1 and HIRA Restrict Epstein-Barr Virus B-Cell Lytic Reactivation. MBio, 2020, 11, .	4.1	17
907	A clinically validated human capillary blood transcriptome test for global systems biology studies. BioTechniques, 2020, 69, 289-301.	1.8	15
908	Deciphering the Infectious Process of Colletotrichum lupini in Lupin through Transcriptomic and Proteomic Analysis. Microorganisms, 2020, 8, 1621.	3.6	18
909	A cell-of-origin epigenetic tracer reveals clinically distinct subtypes of high-grade serous ovarian cancer. Genome Medicine, 2020, 12, 94.	8.2	11

#	Article	IF	Citations
910	Rapid Lentiviral Vector Producer Cell Line Generation Using a Single DNA Construct. Molecular Therapy - Methods and Clinical Development, 2020, 19, 47-57.	4.1	24
911	Longitudinal epitranscriptome profiling reveals the crucial role of N6-methyladenosine methylation in porcine prenatal skeletal muscle development. Journal of Genetics and Genomics, 2020, 47, 466-476.	3.9	36
912	â€œReprogram Enablementâ€•as an Assay for Identifying Early Oncogenic Pathways by Their Ability to Allow Neoplastic Cells to Reacquire an Epiblast State. Stem Cell Reports, 2020, 15, 761-775.	4.8	5
913	Coxiella burnetii replicates in Galleria mellonella hemocytes and transcriptome mapping reveals in vivo regulated genes. Virulence, 2020, 11, 1268-1278.	4.4	9
914	Re-evaluation of human BDCA-2+ DC during acute sterile skin inflammation. Journal of Experimental Medicine, 2020, 217, .	8.5	29
915	Physiological expression and function of the MDR1 transporter in cytotoxic T lymphocytes. Journal of Experimental Medicine, 2020, 217, .	8.5	27
916	IL-33 promotes anemia during chronic inflammation by inhibiting differentiation of erythroid progenitors. Journal of Experimental Medicine, 2020, 217, .	8.5	23
917	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. GigaScience, 2020, 9, .	6.4	14
918	Skipped Over: Tuning Natural Killer Cells Toward HIV Through Alternative Splicing. AIDS Research and Human Retroviruses, 2020, 36, 969-972.	1.1	0
919	Systemic Mesenchymal Stem Cell Treatment Mitigates Structural and Functional Retinal Ganglion Cell Degeneration in a Mouse Model of Multiple Sclerosis. Translational Vision Science and Technology, 2020, 9, 16.	2.2	19
920	Transcriptional and immunohistological assessment of immune infiltration in pancreatic cancer. PLoS ONE, 2020, 15, e0238380.	2.5	16
921	Transcriptomic Changes Resulting From STK32B Overexpression Identify Pathways Potentially Relevant to Essential Tremor. Frontiers in Genetics, 2020, 11, 813.	2.3	11
922	Potassium starvation induces autophagy in yeast. Journal of Biological Chemistry, 2020, 295, 14189-14202.	3.4	8
923	microRNA-seq of cartilage reveals an overabundance of miR-140-3p which contains functional isomiRs. Rna, 2020, 26, 1575-1588.	3.5	17
924	CXCR3 and Cognate Ligands are Associated with Immune Cell Alteration and Aggressiveness of Pancreatic Ductal Adenocarcinoma. Clinical Cancer Research, 2020, 26, 6051-6063.	7.0	14
925	LSTrAP-Crowd: prediction of novel components of bacterial ribosomes with crowd-sourced analysis of RNA sequencing data. BMC Biology, 2020, 18, 114.	3.8	8
926	Trem2 promotes anti-inflammatory responses in microglia and is suppressed under pro-inflammatory conditions. Human Molecular Genetics, 2020, 29, 3224-3248.	2.9	76
927	A role for microRNAs in the epigenetic control of sexually dimorphic gene expression in the human placenta. Epigenomics, 2020, 12, 1543-1558.	2.1	18

#	Article	IF	Citations
928	Changes in H3K27ac at Gene Regulatory Regions in Porcine Alveolar Macrophages Following LPS or PolyIC Exposure. Frontiers in Genetics, 2020, 11, 817.	2.3	23
929	Skeletal muscle and cardiac transcriptomics of a regionally endothermic fish, the Pacific bluefin tuna, Thunnus orientalis. BMC Genomics, 2020, 21, 642.	2.8	2
930	Neuroprotective activity of ursodeoxycholic acid in CHMP2B models of frontotemporal dementia. Neurobiology of Disease, 2020, 144, 105047.	4.4	13
931	Disruption of ruminal homeostasis by malnutrition involved in systemic ruminal microbiota-host interactions in a pregnant sheep model. Microbiome, 2020, 8, 138.	11.1	30
932	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. Cell, 2020, 182, 1474-1489.e23.	28.9	126
933	Intratumoral Cancer Chemotherapy with a Carrier-Based Immunogenic Cell-Death Eliciting Platinum (IV) Agent. Molecular Pharmaceutics, 2020, 17, 4334-4345.	4.6	14
934	Molecular correlates of cisplatin-based chemotherapy response in muscle invasive bladder cancer by integrated multi-omics analysis. Nature Communications, 2020, 11, 4858.	12.8	124
935	SMRT- and Illumina-based RNA-seq analyses unveil the ginsinoside biosynthesis and transcriptomic complexity in Panax notoginseng. Scientific Reports, 2020, 10, 15310.	3.3	10
936	Ironâ€“Sulfur Cluster Protein NITROGEN FIXATION S-LIKE1 and Its Interactor FRATAXIN Function in Plant Immunity. Plant Physiology, 2020, 184, 1532-1548.	4.8	13
937	Transcriptional analysis of cleft palate in TGFÎ²3 mutant mice. Scientific Reports, 2020, 10, 14940.	3.3	4
938	Readthrough of stop codons under limiting ABCE1 concentration involves frameshifting and inhibits nonsense-mediated mRNA decay. Nucleic Acids Research, 2020, 48, 10259-10279.	14.5	28
939	Bacterial Genome Wide Association Studies (bGWAS) and Transcriptomics Identifies Cryptic Antimicrobial Resistance Mechanisms in Acinetobacter baumannii. Frontiers in Public Health, 2020, 8, 451.	2.7	9
940	Viral Perturbation of Alternative Splicing of a Host Transcript Benefits Infection. Plant Physiology, 2020, 184, 1514-1531.	4.8	11
941	Global transcriptomic responses orchestrate difenoconazole resistance in Penicillium spp. causing blue mold of stored apple fruit. BMC Genomics, 2020, 21, 574.	2.8	8
942	Explorative Combined Lipid and Transcriptomic Profiling of Substantia Nigra and Putamen in Parkinsonâ€™s Disease. Cells, 2020, 9, 1966.	4.1	29
943	Alteration of genome folding via contact domain boundary insertion. Nature Genetics, 2020, 52, 1076-1087.	21.4	35
944	Cancer-specific CTCF binding facilitates oncogenic transcriptional dysregulation. Genome Biology, 2020, 21, 247.	8.8	70
945	Revealing the Impact of Structural Variants in Multiple Myeloma. Blood Cancer Discovery, 2020, 1, 258-273.	5.0	81

#	Article	IF	Citations
946	The gene expression network regulating queen brain remodeling after insemination and its parallel use in ants with reproductive workers. Science Advances, 2020, 6, .	10.3	12
947	Molecular Footprints of the Immune Assault on Pancreatic Beta Cells in Type 1 Diabetes. Frontiers in Endocrinology, 2020, 11, 568446.	3.5	19
948	Systematic analysis of the <scp>IL</scp> â€17 receptor signalosome reveals a robust regulatory feedback loop. EMBO Journal, 2020, 39, e104202.	7.8	16
949	Impact of Transposable Elements on Methylation and Gene Expression across Natural Accessions of Brachypodium distachyon. Genome Biology and Evolution, 2020, 12, 1994-2001.	2.5	20
950	Alignment and mapping methodology influence transcript abundance estimation. Genome Biology, 2020, 21, 239.	8.8	96
951	The SLC25A42 Transcript Is a Biomarker for Fetal Reprogramming in Response to Placental Insufficiency in Preterm Newborns Under 32 Weeks Gestationâ€"A Pilot Study. Frontiers in Pediatrics, 2020, 8, 459.	1.9	4
952	Mutagenomics: A Rapid, High-Throughput Method to Identify Causative Mutations from a Genetic Screen. Plant Physiology, 2020, 184, 1658-1673.	4.8	6
953	Identifying Conserved Functional Gene Modules Underlying the Dynamic Regulation of Tea Plant Development and Secondary Metabolism. Journal of Agricultural and Food Chemistry, 2020, 68, 11026-11037.	5.2	4
954	Developmentally regulated activation of defense allows for rapid inhibition of infection in age-related resistance to Phytophthora capsici in cucumber fruit. BMC Genomics, 2020, 21, 628.	2.8	13
955	NusG controls transcription pausing and RNA polymerase translocation throughout the Bacillus subtilis genome. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21628-21636.	7.1	38
956	Deadly Proteomes: A Practical Guide to Proteotranscriptomics of Animal Venoms. Proteomics, 2020, 20, e1900324.	2.2	26
957	BAF60a Deficiency in Vascular Smooth Muscle Cells Prevents Abdominal Aortic Aneurysm by Reducing Inflammation and Extracellular Matrix Degradation. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 40, 2494-2507.	2.4	31
958	Developmental Methylome of the Medicinal Plant Catharanthus roseus Unravels the Tissue-Specific Control of the Monoterpene Indole Alkaloid Pathway by DNA Methylation. International Journal of Molecular Sciences, 2020, 21, 6028.	4.1	14
959	Widespread Aberrant Alternative Splicing despite Molecular Remission in Chronic Myeloid Leukaemia Patients. Cancers, 2020, 12, 3738.	3.7	10
960	Toll-Like Receptor 7 Is Required for Lacrimal Gland Autoimmunity and Type 1 Diabetes Development in Male Nonobese Diabetic Mice. International Journal of Molecular Sciences, 2020, 21, 9478.	4.1	11
961	Gene expression data support the hypothesis that Isoetes rootlets are true roots and not modified leaves. Scientific Reports, 2020, 10, 21547.	3.3	9
962	Spinal cord stimulation using differential target multiplexed programming modulates neural cell-specific transcriptomes in an animal model of neuropathic pain. Molecular Pain, 2020, 16, 174480692096436.	2.1	30
963	ideal: an R/Bioconductor package for interactive differential expression analysis. BMC Bioinformatics, 2020, 21, 565.	2.6	23

#	Article	IF	Citations
964	NSs, the Silencing Suppressor of Tomato Spotted Wilt Orthotospovirus, Interferes With JA-Regulated Host Terpenoids Expression to Attract Frankliniella occidentalis. Frontiers in Microbiology, 2020, 11, 590451.	3.5	7
965	Differentially Expressed Genes Shared by Two Distinct Cytoplasmic Male Sterility (CMS) Types of Silene vulgaris Suggest the Importance of Oxidative Stress in Pollen Abortion. Cells, 2020, 9, 2700.	4.1	6
966	Roundup causes embryonic development failure and alters metabolic pathways and gut microbiota functionality in non-target species. Microbiome, 2020, 8, 170.	11.1	27
967	Evidence for the placenta-brain axis: multi-omic kernel aggregation predicts intellectual and social impairment in children born extremely preterm. Molecular Autism, 2020, 11, 97.	4.9	26
968	Nanopore RNA Sequencing Revealed Long Non-Coding and LTR Retrotransposon-Related RNAs Expressed at Early Stages of Triticale SEED Development. Plants, 2020, 9, 1794.	3.5	16
969	3D RNA-seq: a powerful and flexible tool for rapid and accurate differential expression and alternative splicing analysis of RNA-seq data for biologists. RNA Biology, 2021, 18, 1574-1587.	3.1	58
970	Hydrogen-Oxidizing Bacteria Are Abundant in Desert Soils and Strongly Stimulated by Hydration. MSystems, 2020, 5, .	3.8	38
971	Transcriptomic Responses to Darkness and the Survival Strategy of the Kelp Saccharina latissima in the Early Polar Night. Frontiers in Marine Science, 2020, 7, .	2.5	5
972	Transcriptomic Bioinformatic Analyses of Atria Uncover Involvement of Pathways Related to Strain and Post-translational Modification of Collagen in Increased Atrial Fibrillation Vulnerability in Intensely Exercised Mice. Frontiers in Physiology, 2020, 11, 605671.	2.8	8
973	Deletion of the Aspergillus niger Pro-Protein Processing Protease Gene kexB Results in a pH-Dependent Morphological Transition during Submerged Cultivations and Increases Cell Wall Chitin Content. Microorganisms, 2020, 8, 1918.	3.6	5
974	Comparative transcriptome profiling of two sweetpotato cultivars with contrasting flooding stress tolerance levels. Plant Biotechnology Reports, 2020, 14, 743-756.	1.5	8
975	Comparative transcriptome analysis unveils the adaptative mechanisms of Scedosporium apiospermum to the microenvironment encountered in the lungs of patients with cystic fibrosis. Computational and Structural Biotechnology Journal, 2020, 18, 3468-3483.	4.1	9
976	Transcriptomic response of Gordonia sp. strain NB4-1Y when provided with 6:2 fluorotelomer sulfonamidoalkyl betaine or 6:2 fluorotelomer sulfonate as sole sulfur source. Biodegradation, 2020, 31, 407-422.	3.0	8
977	Divergent Role for STAT5 in the Adaptive Responses of Natural Killer Cells. Cell Reports, 2020, 33, 108498.	6.4	32
978	Temporal unsnarling of brainâ€™s acute neuroinflammatory transcriptional profiles reveals panendothelitis as the earliest event preceding microgliosis. Molecular Psychiatry, 2021, 26, 3905-3919.	7.9	28
979	Transfer RNA fragments replace microRNA regulators of the cholinergic poststroke immune blockade. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32606-32616.	7.1	37
980	Differential transcriptomics in sarcoidosis lung and lymph node granulomas with comparisons to pathogen-specific granulomas. Respiratory Research, 2020, 21, 321.	3.6	17
981	Extensive nuclear gyration and pervasive non-genic transcription during primordial germ cell development in zebrafish. Development (Cambridge), 2021, 148, .	2.5	4

#	Article	IF	Citations
982	Transcriptome Analysis of Alternative Splicing Events Induced by Arbuscular Mycorrhizal Fungi (Rhizophagus irregularis) in Pea (Pisum sativum L.) Roots. Plants, 2020, 9, 1700.	3.5	10
983	Functional Contexts of Adipose and Gluteal Muscle Tissue Gene Co-expression Networks in the Domestic Horse. Integrative and Comparative Biology, 2023, 63, 238-249.	2.0	1
984	In Vivo Validation of Alternative FDXR Transcripts in Human Blood in Response to Ionizing Radiation. International Journal of Molecular Sciences, 2020, 21, 7851.	4.1	24
985	Transcriptome Sequencing of the Striped Cucumber Beetle, Acalymma vittatum (F.), Reveals Numerous Sex-Specific Transcripts and Xenobiotic Detoxification Genes. BioTech, 2020, 9, 21.	2.6	7
986	Deep conservation of the enhancer regulatory code in animals. Science, 2020, 370, .	12.6	89
987	Junctional Localization of Septin 2 Is Required for Organization of Junctional Proteins in Static Endothelial Monolayers. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 346-359.	2.4	9
988	PRPS-ST: A Protocol-Agnostic Self-training Method for Gene Expressionâ€“Based Classification of Blood Cancers. Blood Cancer Discovery, 2020, 1, 244-257.	5.0	4
989	Cis-acting lnc-eRNA SEELA directly binds histone H4 to promote histone recognition and leukemia progression. Genome Biology, 2020, 21, 269.	8.8	17
990	Transcriptomics reveals specific molecular mechanisms underlying transgenerational immunity in Manduca sexta. Ecology and Evolution, 2020, 10, 11251-11261.	1.9	6
991	Yeast Viral Killer Toxin K1 Induces Specific Host Cell Adaptions via Intrinsic Selection Pressure. Applied and Environmental Microbiology, 2020, 86, .	3.1	8
992	The Multifunctional Long-Distance Movement Protein of Pea Enation Mosaic Virus 2 Protects Viral and Host Transcripts from Nonsense-Mediated Decay. MBio, 2020, 11, .	4.1	23
993	Organoid-Transplant Model Systems to Study the Effects of Obesity on the Pancreatic Carcinogenesis in vivo. Frontiers in Cell and Developmental Biology, 2020, 8, 308.	3.7	8
994	Single-cell RNA counting at allele and isoform resolution using Smart-seq3. Nature Biotechnology, 2020, 38, 708-714.	17.5	399
995	Feeding exogenous dsRNA interferes with endogenous sRNA accumulation in Paramecium. DNA Research, 2020, 27, .	3.4	4
996	The Paralogous Transcription Factors Stp1 and Stp2 of Candida albicans Have Distinct Functions in Nutrient Acquisition and Host Interaction. Infection and Immunity, 2020, 88, .	2.2	14
997	Whole-Blood RNA Profiles Associated with Pulmonary Arterial Hypertension and Clinical Outcome. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 586-594.	5.6	45
998	Improving Gene Annotation of the Peanut Genome by Integrated Proteogenomics Workflow. Journal of Proteome Research, 2020, 19, 2226-2235.	3.7	7
999	Sequencing the serotonergic neuron translatome reveals a new role for Fkbp5 in stress. Molecular Psychiatry, 2020, 26, 4742-4753.	7.9	15

#	Article	IF	Citations
1000	Integrated single-cell and bulk gene expression and ATAC-seq reveals heterogeneity and early changes in pathways associated with resistance to cetuximab in HNSCC-sensitive cell lines. British Journal of Cancer, 2020, 123, 101-113.	6.4	38
1001	The cell line A-to-I RNA editing catalogue. Nucleic Acids Research, 2020, 48, 5849-5858.	14.5	47
1002	SCOPE: A Normalization and Copy-Number Estimation Method for Single-Cell DNA Sequencing. Cell Systems, 2020, 10, 445-452.e6.	6.2	55
1003	Oxidosqualene cyclases involved in the biosynthesis of triterpenoids in Quercus suber cork. Scientific Reports, 2020, 10, 8011.	3.3	19
1004	CITED4 Protects Against Adverse Remodeling in Response to Physiological and Pathological Stress. Circulation Research, 2020, 127, 631-646.	4.5	29
1005	The Histone Variant MacroH2A1 Regulates Key Genes for Myogenic Cell Fusion in a Splice-Isoform Dependent Manner. Cells, 2020, 9, 1109.	4.1	9
1006	Genome-wide transcriptome analysis reveals equine embryonic stem cell-derived tenocytes resemble fetal, not adult tenocytes. Stem Cell Research and Therapy, 2020, 11, 184.	5.5	6
1007	Transcriptome analysis reveals metabolic regulation mechanism of microalga Chlorella pyrenoidosa in response to the mixed culture with yeast Yarrowia lipolytica. Journal of Applied Phycology, 2020, 32, 2841-2849.	2.8	5
1008	The Biosynthesis of Main Taste Compounds Is Coordinately Regulated by miRNAs and Phytohormones in Tea Plant (Camellia sinensis). Journal of Agricultural and Food Chemistry, 2020, 68, 6221-6236.	5.2	26
1009	Highâ€throughput profiling reveals perturbation of endoplasmic reticulum stressâ€related genes in atherosclerosis induced by highâ€cholesterol diet and the protective role of vitamin E. BioFactors, 2020, 46, 653-664.	5.4	7
1010	An Acyl-CoA N-Acyltransferase Regulates Meristem Phase Change and Plant Architecture in Barley. Plant Physiology, 2020, 183, 1088-1109.	4.8	26
1011	The Dark Side of Orchid Symbiosis: Can Tulasnella calospora Decompose Host Tissues?. International Journal of Molecular Sciences, 2020, 21, 3139.	4.1	22
1012	Assessment of Transcriptomic and Apical Responses of Daphnia magna Exposed to a Polyethylene Microplastic in a 21â€d Chronic Study. Environmental Toxicology and Chemistry, 2020, 39, 1578-1589.	4.3	19
1013	MtSSPdb: The Medicago truncatula Small Secreted Peptide Database. Plant Physiology, 2020, 183, 399-413.	4.8	40
1014	High-resolution profile of transcriptomes reveals a role of alternative splicing for modulating response to nitrogen in maize. BMC Genomics, 2020, 21, 353.	2.8	21
1015	A human lung tumor microenvironment interactome identifies clinically relevant cell-type cross-talk. Genome Biology, 2020, 21, 107.	8.8	33
1016	Deactivation of Glutaminolysis Sensitizes PIK3CA-Mutated Colorectal Cancer Cells to Aspirin-Induced Growth Inhibition. Cancers, 2020, 12, 1097.	3.7	9
1017	The Sophisticated Transcriptional Response Governed by Transposable Elements in Human Health and Disease. International Journal of Molecular Sciences, 2020, 21, 3201.	4.1	8

#	Article	IF	Citations
1018	Transcriptional analysis of the multiple Sry genes and developmental program at the onset of testis differentiation in the rat. Biology of Sex Differences, 2020, 11, 28.	4.1	5
1019	Active Notch signaling is required for arm regeneration in a brittle star. PLoS ONE, 2020, 15, e0232981.	2.5	16
1020	Incomplete Freundâ€™s adjuvant reduces arginase and enhances Th1 dominance, TLR signaling and CD40 ligand expression in the vaccine site microenvironment. , 2020, 8, e000544.		13
1021	Identification of nasal mucosa markers for forensic mRNA body fluid determination. Forensic Science International: Genetics, 2020, 48, 102317.	3.1	8
1022	CD49f Is a Novel Marker of Functional and Reactive Human iPSC-Derived Astrocytes. Neuron, 2020, 107, 436-453.e12.	8.1	115
1023	A Novel Screening Approach for the Dissection of Cellular Regulatory Networks of NF-Î²B Using Arrayed CRISPR gRNA Libraries. SLAS Discovery, 2020, 25, 618-633.	2.7	4
1024	Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. Nature Communications, 2020, 11, 2718.	12.8	53
1025	Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional regulation. Computational and Structural Biotechnology Journal, 2020, 18, 1330-1341.	4.1	16
1026	TGF-Î²1-Licensed Murine MSCs Show Superior Therapeutic Efficacy in Modulating Corneal Allograft Immune Rejection InÂVivo. Molecular Therapy, 2020, 28, 2023-2043.	8.2	38
1027	Shedding Light on the Transcriptomic Dark Matter in Biological Psychiatry: Role of Long Noncoding RNAs in D-cycloserine-Induced Fear Extinction in Posttraumatic Stress Disorder. OMICS A Journal of Integrative Biology, 2020, 24, 352-369.	2.0	7
1028	Reducing Aspergillus fumigatus Virulence through Targeted Dysregulation of the Conidiation Pathway. MBio, 2020, 11, .	4.1	18
1029	Trans-ethnic meta-analysis of genome-wide association studies identifies maternal ITPR1 as a novel locus influencing fetal growth during sensitive periods in pregnancy. PLoS Genetics, 2020, 16, e1008747.	3.5	13
1030	Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?. PLoS Pathogens, 2020, 16, e1008421.	4.7	318
1032	Complex Analysis of Retroposed Genesâ€™ Contribution to Human Genome, Proteome and Transcriptome. Genes, 2020, 11, 542.	2.4	8
1033	Microbiota-Induced Type I Interferons Instruct a Poised Basal State of Dendritic Cells. Cell, 2020, 181, 1080-1096.e19.	28.9	139
1034	The BCL-2 pathway preserves mammalian genome integrity by eliminating recombination-defective oocytes. Nature Communications, 2020, 11, 2598.	12.8	16
1035	High-resolution annotation of the mouse preimplantation embryo transcriptome using long-read sequencing. Nature Communications, 2020, 11, 2653.	12.8	17
1036	De Novo Transcriptome Sequencing of Serangium japonicum (Coleoptera: Coccinellidae) and Application of Two Assembled Unigenes. G3: Genes, Genomes, Genetics, 2020, 10, 247-254.	1.8	0

#	Article	IF	Citations
1037	Linking Virus Discovery to Immune Responses Visualized during Zebrafish Infections. Current Biology, 2020, 30, 2092-2103.e5.	3.9	29
1038	Changes in the Oligodendrocyte Progenitor Cell Proteome with Ageing. Molecular and Cellular Proteomics, 2020, 19, 1281-1302.	3.8	53
1039	Chromosomal-Level Genome Assembly of the Sea Urchin Lytechinus variegatus Substantially Improves Functional Genomic Analyses. Genome Biology and Evolution, 2020, 12, 1080-1086.	2.5	41
1040	Distinct immune evasion in <scp>APOBEC</scp>â€enriched, <scp>HPV</scp>â€negative <scp>HNSCC</scp>. International Journal of Cancer, 2020, 147, 2293-2302.	5.1	10
1041	MKRN2 Physically Interacts with GLE1 to Regulate mRNA Export and Zebrafish Retinal Development. Cell Reports, 2020, 31, 107693.	6.4	11
1042	Transcript expression-aware annotation improves rare variant interpretation. Nature, 2020, 581, 452-458.	27.8	142
1043	USP37 promotes deubiquitination of HIF2Î± in kidney cancer. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13023-13032.	7.1	24
1044	Quantitative analysis of Y-Chromosome gene expression across 36 human tissues. Genome Research, 2020, 30, 860-873.	5.5	56
1045	Ageâ€dependent expression of cancerâ€related genes in a longâ€lived seabird. Evolutionary Applications, 2020, 13, 1708-1718.	3.1	5
1046	Virus-induced genetics revealed by multidimensional precision medicine transcriptional workflow applicable to COVID-19. Physiological Genomics, 2020, 52, 255-268.	2.3	21
1047	Ciliary proteins specify the cell inflammatory response by tuning NFÎºB signaling, independently of primary cilia. Journal of Cell Science, 2020, 133, .	2.0	20
1048	A myelin basic protein fragment induces sexually dimorphic transcriptome signatures of neuropathic pain in mice. Journal of Biological Chemistry, 2020, 295, 10807-10821.	3.4	15
1049	Ampliconic Genes on the Great Ape Y Chromosomes: Rapid Evolution of Copy Number but Conservation of Expression Levels. Genome Biology and Evolution, 2020, 12, 842-859.	2.5	13
1050	Resource: A multiâ€species multiâ€timepoint transcriptome database and webpage for the pineal gland and retina. Journal of Pineal Research, 2020, 69, e12673.	7.4	16
1051	Highly specific multiplexed RNA imaging in tissues with split-FISH. Nature Methods, 2020, 17, 689-693.	19.0	65
1052	Machine learning analyses of methylation profiles uncovers tissueâ€specific gene expression patterns in wheat. Plant Genome, 2020, 13, e20027.	2.8	13
1053	Handling multi-mapped reads in RNA-seq. Computational and Structural Biotechnology Journal, 2020, 18, 1569-1576.	4.1	44
1054	Novel genetic features of human and mouse Purkinje cell differentiation defined by comparative transcriptomics. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15085-15095.	7.1	25

#	Article	IF	Citations
1055	Metabolic mechanisms of Coilia nasus in the natural food intake state during migration. Genomics, 2020, 112, 3294-3305.	2.9	9
1056	Core Binding Factors are essential for ovulation, luteinization, and female fertility in mice. Scientific Reports, 2020, 10, 9921.	3.3	10
1057	BCALM (AC099524.1) Is a Human B Lymphocyteâ€“Specific Long Noncoding RNA That Modulates B Cell Receptorâ€“Mediated Calcium Signaling. Journal of Immunology, 2020, 205, 595-607.	0.8	15
1058	Measuring and interpreting transposable element expression. Nature Reviews Genetics, 2020, 21, 721-736.	16.3	211
1059	Pervasive changes of mRNA splicing in upf1 -deficient zebrafish identify rpl10a as a regulator of T cell development. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15799-15808.	7.1	9
1060	The fungal NADPH oxidase is an essential element for the molecular dialog between Trichoderma and Arabidopsis. Plant Journal, 2020, 103, 2178-2192.	5.7	28
1061	CSI NGS Portal: An Online Platform for Automated NGS Data Analysis and Sharing. International Journal of Molecular Sciences, 2020, 21, 3828.	4.1	19
1062	Three-dimensional bioprinted glioblastoma microenvironments model cellular dependencies and immune interactions. Cell Research, 2020, 30, 833-853.	12.0	149
1063	Differential miRNAs expression pattern of irradiated breast cancer cell lines is correlated with radiation sensitivity. Scientific Reports, 2020, 10, 9054.	3.3	18
1064	A mouse model that is immunologically tolerant to reporter and modifier proteins. Communications Biology, 2020, 3, 273.	4.4	9
1065	Various modes of HP1a interactions with the euchromatic chromosome arms in Drosophila ovarian somatic cells. Chromosoma, 2020, 129, 201-214.	2.2	6
1066	Skeletal muscle reprogramming by breast cancer regardless of treatment history or tumor molecular subtype. Npj Breast Cancer, 2020, 6, 18.	5.2	16
1067	Systems Genetics for Mechanistic Discovery in Heart Diseases. Circulation Research, 2020, 126, 1795-1815.	4.5	8
1068	DNA methylation loci in placenta associated with birthweight and expression of genes relevant for early development and adult diseases. Clinical Epigenetics, 2020, 12, 78.	4.1	28
1069	GluN2D-mediated excitatory drive onto medial prefrontal cortical PV+ fast-spiking inhibitory interneurons. PLoS ONE, 2020, 15, e0233895.	2.5	25
1070	GC-AG Introns Features in Long Non-coding and Protein-Coding Genes Suggest Their Role in Gene Expression Regulation. Frontiers in Genetics, 2020, 11, 488.	2.3	17
1071	Differential gene expression of Plasmodium homocircumflexum (lineage pCOLL4) across two experimentally infected passerine bird species. Genomics, 2020, 112, 2857-2865.	2.9	14
1072	Correction of amyotrophic lateral sclerosis related phenotypes in induced pluripotent stem cell-derived motor neurons carrying a hexanucleotide expansion mutation in C9orf72 by CRISPR/Cas9 genome editing using homology-directed repair. Human Molecular Genetics, 2020, 29, 2200-2217.	2.9	39

#	Article	IF	Citations
1073	Whole transcriptome analysis of multiple Sclerosis patients reveals active inflammatory profile in relapsing patients and downregulation of neurological repair pathways in secondary progressive cases. Multiple Sclerosis and Related Disorders, 2020, 44, 102243.	2.0	9
1074	CT Irradiation-induced Changes of Gene Expression within Peripheral Blood Cells. Health Physics, 2020, 119, 44-51.	0.5	9
1075	Animal biosynthesis of complex polyketides in a photosynthetic partnership. Nature Communications, 2020, 11, 2882.	12.8	38
1076	Shifting evolutionary sands: transcriptome characterization of the Aptostichus atomarius species complex. BMC Evolutionary Biology, 2020, 20, 68.	3.2	1
1077	Stromal beta-catenin activation impacts nephron progenitor differentiation in the developing kidney and may contribute to Wilms tumor. Development (Cambridge), 2020, 147, .	2.5	16
1078	Somatic Gain of KRAS Function in the Endothelium Is Sufficient to Cause Vascular Malformations That Require MEK but Not PI3K Signaling. Circulation Research, 2020, 127, 727-743.	4.5	68
1079	Meta-analysis of transcriptomic variation in T-cell populations reveals both variable and consistent signatures of gene expression and splicing. Rna, 2020, 26, 1320-1333.	3.5	20
1080	Impaired Expression of Chloroplast HSP90C Chaperone Activates Plant Defense Responses with a Possible Link to a Disease-Symptom-Like Phenotype. International Journal of Molecular Sciences, 2020, 21, 4202.	4.1	9
1081	Transcriptome, Spliceosome and Editome Expression Patterns of the Porcine Endometrium in Response to a Single Subclinical Dose of Salmonella Enteritidis Lipopolysaccharide. International Journal of Molecular Sciences, 2020, 21, 4217.	4.1	9
1082	Recurrent horizontal transfer identifies mitochondrial positive selection in a transmissible cancer. Nature Communications, 2020, 11, 3059.	12.8	18
1083	Transcriptome data of temporal and cingulate cortex in the Rett syndrome brain. Scientific Data, 2020, 7, 192.	5.3	9
1084	Transcriptomeâ€Wide Regulation of Key Developmental Pathways in the Mouse Neural Tube by Prenatal Alcohol Exposure. Alcoholism: Clinical and Experimental Research, 2020, 44, 1540-1550.	2.4	6
1085	Functional impairment of cortical AMPA receptors in schizophrenia. Schizophrenia Research, 2022, 249, 25-37.	2.0	20
1086	iPSCs from people with MS can differentiate into oligodendrocytes in a homeostatic but not an inflammatory milieu. PLoS ONE, 2020, 15, e0233980.	2.5	28
1087	Gray whale transcriptome reveals longevity adaptations associated with DNA repair and ubiquitination. Aging Cell, 2020, 19, e13158.	6.7	27
1088	Complete Mitochondrial Genomes and Bacterial Metagenomic Data From Two Species of Parasitic Avian Nasal-Mites (Rhinonyssidae: Mesostigmata). Frontiers in Ecology and Evolution, 2020, 8, .	2.2	6
1089	Loss of Arid1a Promotes Neuronal Survival Following Optic Nerve Injury. Frontiers in Cellular Neuroscience, 2020, 14, 131.	3.7	4
1090	RNA-seq Reveals Differentially Expressed Genes between Two indica Inbred Rice Genotypes Associated with Drought-Yield QTLs. Agronomy, 2020, 10, 621.	3.0	21

#	Article	IF	Citations
1091	Asian Zika Virus Isolate Significantly Changes the Transcriptional Profile and Alternative RNA Splicing Events in a Neuroblastoma Cell Line. Viruses, 2020, 12, 510.	3.3	25
1092	Transcriptional metaâ€analysis of regulatory B cells. European Journal of Immunology, 2020, 50, 1757-1769.	2.9	15
1093	Metagenomic analysis reveals antibiotic resistance genes in the bovine rumen. Microbial Pathogenesis, 2020, 149, 104350.	2.9	13
1094	Genetic and transcriptional dissection of resistance to Claviceps purpurea in the durum wheat cultivar Greenshank. Theoretical and Applied Genetics, 2020, 133, 1873-1886.	3.6	16
1095	Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. Nature Methods, 2020, 17, 414-421.	19.0	48
1096	An NMF-based approach to discover overlooked differentially expressed gene regions from single-cell RNA-seq data. NAR Genomics and Bioinformatics, 2020, 2, lqz020.	3.2	5
1097	Pattern of alternative splicing different associated with difference in rooting depth in rice. Plant and Soil, 2020, 449, 233-248.	3.7	4
1098	BANDITS: Bayesian differential splicing accounting for sample-to-sample variability and mapping uncertainty. Genome Biology, 2020, 21, 69.	8.8	17
1099	Dynamic transcriptomic changes of goat abomasal mucosa in response to Haemonchus contortus infection. Veterinary Research, 2020, 51, 44.	3.0	20
1100	Effects of High-Dose Ionizing Radiation in Human Gene Expression: A Meta-Analysis. International Journal of Molecular Sciences, 2020, 21, 1938.	4.1	8
1101	Identification of genes involved in male sterility in wheat (Triticum aestivum ÂL.) which could be used in a genic hybrid breeding system. Plant Direct, 2020, 4, e00201.	1.9	13
1102	Full-length transcript characterization of SF3B1 mutation in chronic lymphocytic leukemia reveals downregulation of retained introns. Nature Communications, 2020, 11, 1438.	12.8	273
1103	Profiling gene expression in the human dentate gyrus granule cell layer reveals insights into schizophrenia and its genetic risk. Nature Neuroscience, 2020, 23, 510-519.	14.8	67
1104	RASflow: an RNA-Seq analysis workflow with Snakemake. BMC Bioinformatics, 2020, 21, 110.	2.6	38
1105	CuAS: a database of annotated transcripts generated by alternative splicing in cucumbers. BMC Plant Biology, 2020, 20, 119.	3.6	8
1106	RNAi pathways repress reprogramming of C. elegans germ cells during heat stress. Nucleic Acids Research, 2020, 48, 4256-4273.	14.5	32
1107	Mitochondrial metabolism is central for response and resistance of Saccharomyces cerevisiae to exposure to a glyphosate-based herbicide. Environmental Pollution, 2020, 262, 114359.	7.5	7
1108	Identification of Structural Variation in Chimpanzees Using Optical Mapping and Nanopore Sequencing. Genes, 2020, 11, 276.	2.4	14

#	Article	IF	Citations
1109	Evolutionary and Molecular Characterization of liver-enriched gene 1. Scientific Reports, 2020, 10, 4262.	3.3	3
1110	LncRNAs in molluscan and mammalian stages of parasitic schistosomes are developmentally-regulated and coordinately expressed with protein-coding genes. RNA Biology, 2020, 17, 805-815.	3.1	14
1111	Sirt2-associated transcriptome modifications in cisplatin-induced neuronal injury. BMC Genomics, 2020, 21, 192.	2.8	4
1112	Evaluation of Seven Different RNA-Seq Alignment Tools Based on Experimental Data from the Model Plant Arabidopsis thaliana. International Journal of Molecular Sciences, 2020, 21, 1720.	4.1	29
1113	Novel insights into viral infection and oncogenesis from koala retrovirus (KoRV) infection of HEK293T cells. Gene, 2020, 733, 144366.	2.2	5
1114	Exploring the overlap between rheumatoid arthritis susceptibility loci and long non-coding RNA annotations. PLoS ONE, 2020, 15, e0223939.	2.5	2
1115	Osteopontin and iCD8Î± Cells Promote Intestinal Intraepithelial Lymphocyte Homeostasis. Journal of Immunology, 2020, 204, 1968-1981.	0.8	10
1116	Tools for the analysis of high-dimensional single-cell RNA sequencing data. Nature Reviews Nephrology, 2020, 16, 408-421.	9.6	80
1117	A satellite repeat-derived piRNA controls embryonic development of Aedes. Nature, 2020, 580, 274-277.	27.8	90
1118	Rapalog-Mediated Repression of Tribbles Pseudokinase 3 Regulates Pre-mRNA Splicing. Cancer Research, 2020, 80, 2190-2203.	0.9	4
1119	Emergence of an evolutionary innovation: Gene expression differences associated with the transition between oviparity and viviparity. Molecular Ecology, 2020, 29, 1315-1327.	3.9	16
1120	HNF1A recruits KDM6A to activate differentiated acinar cell programs that suppress pancreatic cancer. EMBO Journal, 2020, 39, e102808.	7.8	44
1121	Impact of the gut microbiota on the m6A epitranscriptome of mouse cecum and liver. Nature Communications, 2020, 11, 1344.	12.8	59
1122	Integrated multi-omics framework of the plant response to jasmonic acid. Nature Plants, 2020, 6, 290-302.	9.3	145
1123	Anthoceros genomes illuminate the origin of land plants and the unique biology of hornworts. Nature Plants, 2020, 6, 259-272.	9.3	225
1124	Light organ photosensitivity in deep-sea shrimp may suggest a novel role in counterillumination. Scientific Reports, 2020, 10, 4485.	3.3	14
1125	Novel insights into cardiac regeneration based on differential fetal and adult ovine heart transcriptomic analysis. American Journal of Physiology - Heart and Circulatory Physiology, 2020, 318, H994-H1007.	3.2	11
1126	The structure, functional evolution, and evolutionary trajectories of the H+-PPase gene family in plants. BMC Genomics, 2020, 21, 195.	2.8	7

#	Article	IF	Citations
1127	Molecular and genetic regulation of pig pancreatic islet cell development. Development (Cambridge), 2020, 147, .	2.5	21
1128	Metabolic effects of bezafibrate in mitochondrial disease. EMBO Molecular Medicine, 2020, 12, e11589.	6.9	45
1129	Dynamic Alternative Splicing During Mouse Preimplantation Embryo Development. Frontiers in Bioengineering and Biotechnology, 2020, 8, 35.	4.1	17
1130	Alveolar Macrophage Chromatin Is Modified to Orchestrate Host Response to Mycobacterium bovis Infection. Frontiers in Genetics, 2019, 10, 1386.	2.3	19
1131	Therapeutic potential of KLF2-induced exosomal microRNAs in pulmonary hypertension. Nature Communications, 2020, 11, 1185.	12.8	52
1132	A RING-Type E3 Ubiquitin Ligase, OsGW2, Controls Chlorophyll Content and Dark-Induced Senescence in Rice. International Journal of Molecular Sciences, 2020, 21, 1704.	4.1	20
1133	Mitochondrial stress is relayed to the cytosol by an OMA1â€“DELE1â€“HRI pathway. Nature, 2020, 579, 427-432.	27.8	343
1134	Sketching algorithms for genomic data analysis and querying in a secure enclave. Nature Methods, 2020, 17, 295-301.	19.0	35
1135	Genome-wide identification and characterisation of Aquaporins in Nicotiana tabacum and their relationships with other Solanaceae species. BMC Plant Biology, 2020, 20, 266.	3.6	27
1136	Molecular analysis of Chinese oesophageal squamous cell carcinoma identifies novel subtypes associated with distinct clinical outcomes. EBioMedicine, 2020, 57, 102831.	6.1	11
1137	Quantification of translation uncovers the functions of the alternative transcriptome. Nature Structural and Molecular Biology, 2020, 27, 717-725.	8.2	35
1138	The unfolded protein response regulates hepatic autophagy by sXBP1-mediated activation of TFEB. Autophagy, 2021, 17, 1841-1855.	9.1	61
1139	Terpene Synthases and Terpene Variation in Cannabis sativa. Plant Physiology, 2020, 184, 130-147.	4.8	52
1140	Transcriptome and cell wall degrading enzyme-related gene analysis of Pestalotiopsis neglecta in response to sodium pheophorbide a. Pesticide Biochemistry and Physiology, 2020, 169, 104639.	3.6	5
1141	A molecular basis for neurofibroma-associated skeletal manifestations in NF1. Genetics in Medicine, 2020, 22, 1786-1793.	2.4	12
1142	Environmental Enrichment Improved Learning and Memory, Increased Telencephalic Cell Proliferation, and Induced Differential Gene Expression in Colossoma macropomum. Frontiers in Pharmacology, 2020, 11, 840.	3.5	11
1143	Nonsenseâ€mediated decay factor SMG7 sensitizes cells to TNFÎ±â€induced apoptosis via CYLD tumor suppressor and the noncoding oncogene Pvt1. Molecular Oncology, 2020, 14, 2420-2435.	4.6	8
1144	Roxadustat for Anemia in Patients with Chronic Kidney Disease. New England Journal of Medicine, 2020, 383, e3.	27.0	10

#	Article	IF	Citations
1145	Distinctive Growth and Transcriptional Changes of the Diatom Seminavis robusta in Response to Quorum Sensing Related Compounds. Frontiers in Microbiology, 2020, 11, 1240.	3.5	21
1146	Quantile normalization of single-cell RNA-seq read counts without unique molecular identifiers. Genome Biology, 2020, 21, 160.	8.8	25
1147	A clinically and genomically annotated nerve sheath tumor biospecimen repository. Scientific Data, 2020, 7, 184.	5.3	19
1148	Identification of a potential non-coding RNA biomarker signature for amyotrophic lateral sclerosis. Brain Communications, 2020, 2, fcaa053.	3.3	34
1149	RNA-Seq of three free-living flatworm species suggests rapid evolution of reproduction-related genes. BMC Genomics, 2020, 21, 462.	2.8	12
1150	Multi-tissue epigenetic analysis of the osteoarthritis susceptibility locus mapping to the plectin gene PLEC. Osteoarthritis and Cartilage, 2020, 28, 1448-1458.	1.3	25
1151	Identification and characterization of long noncoding RNAs and their association with acquisition of blood meal in Culex quinquefasciatus. Insect Science, 2021, 28, 917-928.	3.0	9
1152	Comparative analysis of single-cell transcriptomics in human and zebrafish oocytes. BMC Genomics, 2020, 21, 471.	2.8	14
1153	Identification of Novel Molecular Markers of Human Th17 Cells. Cells, 2020, 9, 1611.	4.1	27
1154	Singleâ€Cell RNA Sequencing for Precision Oncology: Current State-of-Art. Journal of the Indian Institute of Science, 2020, 100, 579-588.	1.9	9
1155	Extracellular Acidosis and mTOR Inhibition Drive the Differentiation of Human Monocyte-Derived Dendritic Cells. Cell Reports, 2020, 31, 107613.	6.4	42
1156	A New High-Quality Draft Genome Assembly of the Chinese Cordyceps Ophiocordyceps sinensis. Genome Biology and Evolution, 2020, 12, 1074-1079.	2.5	20
1157	Patient-derived tumor-like cell clusters for drug testing in cancer therapy. Science Translational Medicine, 2020, 12, .	12.4	39
1158	Cardiolipin is required for membrane docking of mitochondrial ribosomes and protein synthesis. Journal of Cell Science, 2020, 133, .	2.0	21
1159	A Genomic Cluster Containing Novel and Conserved Genes is Associated with Cichlid Fish Dental Developmental Convergence. Molecular Biology and Evolution, 2020, 37, 3165-3174.	8.9	12
1160	RNA sequencing analysis of the human retina and associated ocular tissues. Scientific Data, 2020, 7, 199.	5.3	10
1161	Mitochondrial CLPP2 Assists Coordination and Homeostasis of Respiratory Complexes. Plant Physiology, 2020, 184, 148-164.	4.8	26
1162	VviERF6Ls: an expanded clade in Vitis responds transcriptionally to abiotic and biotic stresses and berry development. BMC Genomics, 2020, 21, 472.	2.8	6

#	Article	IF	Citations
1163	Nutlin-Induced Apoptosis Is Specified by a Translation Program Regulated by PCBP2 and DHX30. Cell Reports, 2020, 30, 4355-4369.e6.	6.4	18
1164	A conditional mouse expressing an activating mutation in <scp>NRF2</scp> displays hyperplasia of the upper gastrointestinal tract and decreased white adipose tissue. Journal of Pathology, 2020, 252, 125-137.	4.5	16
1165	Differential expression of polyamine biosynthetic pathways in skin lesions and in plasma reveals distinct profiles in diffuse cutaneous leishmaniasis. Scientific Reports, 2020, 10, 10543.	3.3	9
1166	Y Chromosome LncRNA Are Involved in Radiation Response of Male Nonâ€“Small Cell Lung Cancer Cells. Cancer Research, 2020, 80, 4046-4057.	0.9	21
1167	Dual RNA-seq of Orientia tsutsugamushi informs on host-pathogen interactions for this neglected intracellular human pathogen. Nature Communications, 2020, 11, 3363.	12.8	39
1168	The Seminavis robusta genome provides insights into the evolutionary adaptations of benthic diatoms. Nature Communications, 2020, 11, 3320.	12.8	55
1169	CASC3 promotes transcriptome-wide activation of nonsense-mediated decay by the exon junction complex. Nucleic Acids Research, 2020, 48, 8626-8644.	14.5	35
1170	The regulatory landscape of early maize inflorescence development. Genome Biology, 2020, 21, 165.	8.8	32
1171	Expression of genes involved in phagocytosis in uncultured heterotrophic flagellates. Limnology and Oceanography, 2020, 65, S149.	3.1	19
1172	IGF1-mediated human embryonic stem cell self-renewal recapitulates the embryonic niche. Nature Communications, 2020, 11, 764.	12.8	41
1173	Opportunities and challenges in long-read sequencing data analysis. Genome Biology, 2020, 21, 30.	8.8	1,536
1174	Meta-Analysis of Hypoxic Transcriptomes from Public Databases. Biomedicines, 2020, 8, 10.	3.2	39
1175	Read Mapping and Transcript Assembly: A Scalable and High-Throughput Workflow for the Processing and Analysis of Ribonucleic Acid Sequencing Data. Frontiers in Genetics, 2019, 10, 1361.	2.3	20
1176	Comparative Transcriptome Analysis of Two Cucumber Cultivars with Different Sensitivity to Cucumber Mosaic Virus Infection. Pathogens, 2020, 9, 145.	2.8	13
1177	Estrogen receptor alpha (ERÎ±)â€“mediated coregulator binding and gene expression discriminates the toxic ERÎ± agonist diethylstilbestrol (DES) from the endogenous ERÎ± agonist 17Î²-estradiol (E2). Cell Biology and Toxicology, 2020, 36, 417-435.	5.3	10
1178	De novo transcriptome assembly and sex-biased gene expression in the gonads of Amur catfish (Silurus) Tj ETQq1 1 0.784314 rgBT /Ov	2.9	17
1179	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. PLoS Computational Biology, 2020, 16, e1007664.	3.2	165
1180	Integrative Analysis Identifies Candidate Tumor Microenvironment and Intracellular Signaling Pathways that Define Tumor Heterogeneity in NF1. Genes, 2020, 11, 226.	2.4	11

#	Article	IF	Citations
1181	The epidermis coordinates thermoresponsive growth through the phyB-PIF4-auxin pathway. Nature Communications, 2020, 11, 1053.	12.8	72
1182	Comprehensive transcriptomic profiling reveals SOX7 as an early regulator of angiogenesis in hypoxic human endothelial cells. Journal of Biological Chemistry, 2020, 295, 4796-4808.	3.4	15
1183	Context-Dependent Gene Regulation by Homeodomain Transcription Factor Complexes Revealed by Shape-Readout Deficient Proteins. Molecular Cell, 2020, 78, 152-167.e11.	9.7	26
1184	Deep phenotyping of peripheral tissue facilitates mechanistic disease stratification in sporadic Parkinsonâ€™s disease. Progress in Neurobiology, 2020, 187, 101772.	5.7	35
1185	Wolfram syndrome 1 gene regulates pathways maintaining beta-cell health and survival. Laboratory Investigation, 2020, 100, 849-862.	3.7	34
1186	In situ dissection of domain boundaries affect genome topology and gene transcription in Drosophila. Nature Communications, 2020, 11, 894.	12.8	31
1187	Functionally distinct subgroups of oligodendrocyte precursor cells integrate neural activity and execute myelin formation. Nature Neuroscience, 2020, 23, 363-374.	14.8	154
1188	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. Genome Biology, 2020, 21, 38.	8.8	74
1189	Regulatory Dynamics of Tet1 and Oct4 Resolve Stages of Global DNA Demethylation and Transcriptomic Changes in Reprogramming. Cell Reports, 2020, 30, 2150-2169.e9.	6.4	9
1190	Characteristics, dynamic changes, and prognostic significance of TCR repertoire profiling in patients with renal cell carcinoma. Journal of Pathology, 2020, 251, 26-37.	4.5	18
1191	The Adipocyte Acquires a Fibroblast-Like Transcriptional Signature in Response to a High Fat Diet. Scientific Reports, 2020, 10, 2380.	3.3	49
1192	Transcriptional profiling of human macrophages during infection withBordetella pertussis. RNA Biology, 2020, 17, 731-742.	3.1	15
1193	Identification of universal and cell-type specific p53 DNA binding. BMC Molecular and Cell Biology, 2020, 21, 5.	2.0	14
1194	Parkinsonâ€™s disease-related Leucine-rich repeat kinase 2 modulates nuclear morphology and genomic stability in striatal projection neurons during aging. Molecular Neurodegeneration, 2020, 15, 12.	10.8	26
1195	Symbiotic lifestyle triggers drastic changes in the gene expression of the algal endosymbiont Breviolum minutum (Symbiodiniaceae). Ecology and Evolution, 2020, 10, 451-466.	1.9	33
1196	Combined HER3-EGFR score in triple-negative breast cancer provides prognostic and predictive significance superior to individual biomarkers. Scientific Reports, 2020, 10, 3009.	3.3	34
1197	Inducement and cultivation of novel red Cyclocarya paliurus callus and its unique morphological and metabolic characteristics. Industrial Crops and Products, 2020, 147, 112266.	5.2	12
1198	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. Nature Communications, 2020, 11, 810.	12.8	235

#	Article	IF	Citations
1199	Differential DNA Methylation in Placenta Associated With Maternal Blood Pressure During Pregnancy. Hypertension, 2020, 75, 1117-1124.	2.7	20
1200	A CRISPR/Cas13-based approach demonstrates biological relevance of vlinc class of long non-coding RNAs in anticancer drug response. Scientific Reports, 2020, 10, 1794.	3.3	49
1201	iSeqQC: a tool for expression-based quality control in RNA sequencing. BMC Bioinformatics, 2020, 21, 56.	2.6	15
1202	The intermediate proteasome is constitutively expressed in pancreatic beta cells and upregulated by stimulatory, low concentrations of interleukin 1Â². PLoS ONE, 2020, 15, e0222432.	2.5	13
1203	Yap suppresses T-cell function and infiltration in the tumor microenvironment. PLoS Biology, 2020, 18, e3000591.	5.6	58
1204	TP63 isoform expression is linked with distinct clinical outcomes in cancer. EBioMedicine, 2020, 51, 102561.	6.1	25
1205	Single-cell transcriptional diversity is a hallmark of developmental potential. Science, 2020, 367, 405-411.	12.6	557
1206	Four glial cells regulate ER stress resistance and longevity via neuropeptide signaling in C. elegans. Science, 2020, 367, 436-440.	12.6	92
1207	Reproducibility of Methods to Detect Differentially Expressed Genes from Single-Cell RNA Sequencing. Frontiers in Genetics, 2019, 10, 1331.	2.3	58
1208	Tentacle Transcriptomes of the Speckled Anemone (Actiniaria: Actiniidae: Oulactis sp.): Venom-Related Components and Their Domain Structure. Marine Biotechnology, 2020, 22, 207-219.	2.4	19
1209	The ability to manipulate ROS metabolism in pepper may affect aphid virulence. Horticulture Research, 2020, 7, 6.	6.3	10
1210	VISTA is a checkpoint regulator for naÃ¯ve T cell quiescence and peripheral tolerance. Science, 2020, 367, .	12.6	156
1211	Gene Expression Signatures Identify Novel Therapeutics for Metastatic Pancreatic Neuroendocrine Tumors. Clinical Cancer Research, 2020, 26, 2011-2021.	7.0	40
1212	FilTar: using RNA-Seq data to improve microRNA target prediction accuracy in animals. Bioinformatics, 2020, 36, 2410-2416.	4.1	3
1214	Characterization of Insect Immune Systems from Genomic Data. Springer Protocols, 2020, , 3-34.	0.3	4
1215	Transcriptome-wide-scale-predicted dsRNAs potentially involved in RNA homoeostasis are remarkably excluded from genes with no/very low expression in all developmental stages. RNA Biology, 2020, 17, 554-570.	3.1	2
1216	Genome assembly and characterization of a complex zfBED-NLR gene-containing disease resistance locus in Carolina Gold Select rice with Nanopore sequencing. PLoS Genetics, 2020, 16, e1008571.	3.5	112
1217	Identification of ADPKD-Related Genes and Pathways in Cells Overexpressing PKD2. Genes, 2020, 11, 122.	2.4	5

#	Article	IF	Citations
1218	Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs. Nature Communications, 2020, 11, 462.	12.8	96
1219	A sense of place: transcriptomics identifies environmental signatures in Cabernet Sauvignon berry skins in the late stages of ripening. BMC Plant Biology, 2020, 20, 41.	3.6	20
1220	Transcriptome Analysis of Pineal Glands in the Mouse Model of Alzheimerâ€™s Disease. Frontiers in Molecular Neuroscience, 2019, 12, 318.	2.9	8
1221	Adenosine Signaling Is Prognostic for Cancer Outcome and Has Predictive Utility for Immunotherapeutic Response. Clinical Cancer Research, 2020, 26, 2176-2187.	7.0	54
1222	Systemic HIV and SIV latency reversal via non-canonical NF-Î²B signalling in vivo. Nature, 2020, 578, 160-165.	27.8	210
1223	Targeting redox metabolism: the perfect storm induced by acrylamide poisoning in the brain. Scientific Reports, 2020, 10, 312.	3.3	14
1224	Single-Cell Analysis Uncovers a Vast Diversity in Intracellular Viral Defective Interfering RNA Content Affecting the Large Cell-to-Cell Heterogeneity in Influenza A Virus Replication. Viruses, 2020, 12, 71.	3.3	22
1225	ZmIBH1-1 regulates plant architecture in maize. Journal of Experimental Botany, 2020, 71, 2943-2955.	4.8	39
1226	Involvement of Glutathione Depletion in Selective Cytotoxicity of Oridonin to p53-Mutant Esophageal Squamous Carcinoma Cells. Frontiers in Oncology, 2020, 9, 1525.	2.8	21
1227	Ovarian Transcriptomic Analyses in the Urban Human Health Pest, the Western Black Widow Spider. Genes, 2020, 11, 87.	2.4	1
1228	An internal deletion of ADAR rescued by MAVS deficiency leads to a minute phenotype. Nucleic Acids Research, 2020, 48, 3286-3303.	14.5	39
1229	The RNA degradome: a precious resource for deciphering RNA processing and regulation codes in plants. RNA Biology, 2020, 17, 1223-1227.	3.1	5
1230	Intron retention is a hallmark and spliceosome represents a therapeutic vulnerability in aggressive prostate cancer. Nature Communications, 2020, 11, 2089.	12.8	83
1231	Clinical presentation and differential splicing of SRSF2, U2AF1 and SF3B1 mutations in patients with acute myeloid leukemia. Leukemia, 2020, 34, 2621-2634.	7.2	31
1232	Transcriptome analysis and metabolic profiling reveal the key role of carotenoids in the petal coloration of Liriodendron tulipifera. Horticulture Research, 2020, 7, 70.	6.3	47
1233	Transcriptional Upregulation of NLRC5 by Radiation Drives STING- and Interferon-Independent MHC-I Expression on Cancer Cells and T Cell Cytotoxicity. Scientific Reports, 2020, 10, 7376.	3.3	45
1234	Identification of differentially expressed circulating exosomal lncRNAs in IgA nephropathy patients. BMC Immunology, 2020, 21, 16.	2.2	19
1235	Effect of Transgenesis on mRNA and miRNA Profiles in Cucumber Fruits Expressing Thaumatin II. Genes, 2020, 11, 334.	2.4	7

#	Article	IF	Citations
1236	Venom gland transcriptome from Heloderma horridum horridum by high-throughput sequencing. Toxicon, 2020, 180, 62-78.	1.6	6
1237	Transcriptomic analysis of brain tissues identifies a role for CCAAT enhancer binding protein Î² in HIV-associated neurocognitive disorder. Journal of Neuroinflammation, 2020, 17, 112.	7.2	15
1238	Multiomics Analyses Identify Genes and Pathways Relevant to Essential Tremor. Movement Disorders, 2020, 35, 1153-1162.	3.9	11
1239	Transcriptomics Applied to Rice Grain Quality. , 2020, , 445-472.		1
1240	Plasmodesmata play a critical role in promoting the germination of floral buds in Ilex verticillata. Plant Growth Regulation, 2020, 91, 349-357.	3.4	3
1241	Detailed Molecular and Immune Marker Profiling of Archival Prostate Cancer Samples Reveals an Inverse Association between TMPRSS2:ERG Fusion Status and Immune Cell Infiltration. Journal of Molecular Diagnostics, 2020, 22, 652-669.	2.8	6
1242	Overexpression of LiTPS2 from a cultivar of lily (Lilium â€˜Siberiaâ€™) enhances the monoterpenoids content in tobacco flowers. Plant Physiology and Biochemistry, 2020, 151, 391-399.	5.8	24
1243	Short-term organoid culture for drug sensitivity testing of high-grade serous carcinoma. Gynecologic Oncology, 2020, 157, 783-792.	1.4	46
1244	A genome-wide identification, characterization and functional analysis of salt-related long non-coding RNAs in non-model plant Pistacia vera L. using transcriptome high throughput sequencing. Scientific Reports, 2020, 10, 5585.	3.3	25
1245	RNAmut: robust identification of somatic mutations in acute myeloid leukemia using RNA-sequencing. Haematologica, 2020, 105, e290-e293.	3.5	13
1246	De novo Assembly of Transcriptomes From a B73 Maize Line Introgressed With a QTL for Resistance to Gray Leaf Spot Disease Reveals a Candidate Allele of a Lectin Receptor-Like Kinase. Frontiers in Plant Science, 2020, 11, 191.	3.6	9
1247	Effects of A2E-Induced Oxidative Stress on Retinal Epithelial Cells: New Insights on Differential Gene Response and Retinal Dystrophies. Antioxidants, 2020, 9, 307.	5.1	46
1248	Ex Vivo Organoid Cultures Reveal the Importance of the Tumor Microenvironment for Maintenance of Colorectal Cancer Stem Cells. Cancers, 2020, 12, 923.	3.7	37
1249	Analysis of the Circadian Regulation of Cancer Hallmarks by a Cross-Platform Study of Colorectal Cancer Time-Series Data Reveals an Association with Genes Involved in Huntingtonâ€™s Disease. Cancers, 2020, 12, 963.	3.7	15
1250	Transcriptomic Prediction of Pig Liver-Enriched Gene 1 Functions in a Liver Cell Line. Genes, 2020, 11, 412.	2.4	1
1251	Gene Expression Profiling of Corpus luteum Reveals Important Insights about Early Pregnancy in Domestic Sheep. Genes, 2020, 11, 415.	2.4	15
1252	LSTrAP-Cloud: A User-Friendly Cloud Computing Pipeline to Infer Coexpression Networks. Genes, 2020, 11, 428.	2.4	12
1253	Cellular life from the three domains and viruses are transcriptionally active in a hypersaline desert community. Environmental Microbiology, 2021, 23, 3401-3417.	3.8	20

#	Article	IF	Citations
1254	Comprehensive Analysis of HERV Transcriptome in HIV+ Cells: Absence of HML2 Activation and General Downregulation of Individual HERV Loci. Viruses, 2020, 12, 481.	3.3	9
1255	Flow-induced Reorganization of Laminin-integrin Networks Within the Endothelial Basement Membrane Uncovered by Proteomics. Molecular and Cellular Proteomics, 2020, 19, 1179-1192.	3.8	14
1256	Vargas: heuristic-free alignment for assessing linear and graph read aligners. Bioinformatics, 2020, 36, 3712-3718.	4.1	17
1257	Hotspots of Aberrant Enhancer Activity in Fibrolamellar Carcinoma Reveal Candidate Oncogenic Pathways and Therapeutic Vulnerabilities. Cell Reports, 2020, 31, 107509.	6.4	28
1258	Loss of MBNL1 induces RNA misprocessing in the thymus and peripheral blood. Nature Communications, 2020, 11, 2022.	12.8	15
1259	HLA class-I and class-II restricted neoantigen loads predict overall survival in breast cancer. OncoImmunology, 2020, 9, 1744947.	4.6	26
1260	Myeloid-Derived Suppressor Cell Subsets Drive Glioblastoma Growth in a Sex-Specific Manner. Cancer Discovery, 2020, 10, 1210-1225.	9.4	138
1261	MYC Controls the Epstein-Barr Virus Lytic Switch. Molecular Cell, 2020, 78, 653-669.e8.	9.7	67
1262	A seven-membered cell wall related transglycosylase gene family in Aspergillus niger is relevant for cell wall integrity in cell wall mutants with reduced Î±-glucan or galactomannan. Cell Surface, 2020, 6, 100039.	3.0	15
1263	Why does sulfate inhibit selenate reduction: Molybdenum deprivation from Mo-dependent selenate reductase. Water Research, 2020, 178, 115832.	11.3	16
1264	More Accurate Transcript Assembly via Parameter Advising. Journal of Computational Biology, 2020, 27, 1181-1189.	1.6	6
1265	Genome elimination mediated by gene expression from a selfish chromosome. Science Advances, 2020, 6, eaaz9808.	10.3	48
1266	Computational Oncology in the Multi-Omics Era: State of the Art. Frontiers in Oncology, 2020, 10, 423.	2.8	59
1267	Regenerative Metaplastic Clones in COPD Lung Drive Inflammation and Fibrosis. Cell, 2020, 181, 848-864.e18.	28.9	94
1268	Small-Molecule PAPD5 Inhibitors Restore Telomerase Activity in Patient Stem Cells. Cell Stem Cell, 2020, 26, 896-909.e8.	11.1	57
1269	Deciphering the transcriptomic landscape of tumor-infiltrating CD8 lymphocytes in B16 melanoma tumors with single-cell RNA-Seq. OncoImmunology, 2020, 9, 1737369.	4.6	42
1270	Differential Expression of Immune Genes between Two Closely Related Beetle Species with Different Immunocompetence following Attack by Asecodes parviclava. Genome Biology and Evolution, 2020, 12, 522-534.	2.5	6
1271	Mobile genomics: tools and techniques for tackling transposons. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190345.	4.0	39

#	Article	IF	Citations
1272	Incapacitating effects of fungal coinfection in a novel pathogen system. Molecular Ecology, 2020, 29, 3173-3186.	3.9	20
1273	Constitutive Activation of RAS/MAPK Pathway Cooperates with Trisomy 21 and Is Therapeutically Exploitable in Down Syndrome B-cell Leukemia. Clinical Cancer Research, 2020, 26, 3307-3318.	7.0	28
1274	Modulation of neuroglial interactions using differential target multiplexed spinal cord stimulation in an animal model of neuropathic pain. Molecular Pain, 2020, 16, 174480692091805.	2.1	52
1275	Common gene expression signatures in Parkinsonâ€™s disease are driven by changes in cell composition. Acta Neuropathologica Communications, 2020, 8, 55.	5.2	38
1276	Misuse of RPKM or TPM normalization when comparing across samples and sequencing protocols. Rna, 2020, 26, 903-909.	3.5	215
1277	The inducible Î²5i proteasome subunit contributes to proinsulin degradation in GRP94-deficient Î²-cells and is overexpressed in type 2 diabetes pancreatic islets. American Journal of Physiology - Endocrinology and Metabolism, 2020, 318, E892-E900.	3.5	7
1278	The application of RNA sequencing for the diagnosis and genomic classification of pediatric acute lymphoblastic leukemia. Blood Advances, 2020, 4, 930-942.	5.2	52
1279	The barley stripe mosaic virus expression system reveals the wheat C2H2 zinc finger protein TaZFP1B as a key regulator of drought tolerance. BMC Plant Biology, 2020, 20, 144.	3.6	26
1280	Impact of phages on soil bacterial communities and nitrogen availability under different assembly scenarios. Microbiome, 2020, 8, 52.	11.1	82
1281	A Collection of Pre-mRNA Splicing Mutants in Arabidopsis thaliana. G3: Genes, Genomes, Genetics, 2020, 10, 1983-1996.	1.8	21
1282	De novo Sequencing and Analysis of Salvia hispanica Tissue-Specific Transcriptome and Identification of Genes Involved in Terpenoid Biosynthesis. Plants, 2020, 9, 405.	3.5	11
1283	Stromal Cells Covering Omental Fat-Associated Lymphoid Clusters Trigger Formation of Neutrophil Aggregates to Capture Peritoneal Contaminants. Immunity, 2020, 52, 700-715.e6.	14.3	53
1284	Ribosome profiling at isoform level reveals evolutionary conserved impacts of differential splicing on the proteome. Nature Communications, 2020, 11, 1768.	12.8	28
1285	Homoeologous gene expression and co-expression network analyses and evolutionary inference in allopolyploids. Briefings in Bioinformatics, 2021, 22, 1819-1835.	6.5	23
1286	A practical guide to amplicon and metagenomic analysis of microbiome data. Protein and Cell, 2021, 12, 315-330.	11.0	376
1287	The ASXL1-G643W variant accelerates the development of CEBPA mutant acute myeloid leukemia. Haematologica, 2021, 106, 1000-1007.	3.5	9
1288	The selective PPAR-delta agonist seladelpar reduces ethanol-induced liver disease by restoring gut barrier function and bile acid homeostasis in mice. Translational Research, 2021, 227, 1-14.	5.0	13
1289	Ultraconserved long non-coding RNA uc.112 is highly expressed in childhood T versus B-cell acute lymphoblastic leukemia. Hematology, Transfusion and Cell Therapy, 2021, 43, 28-34.	0.2	15

#	Article	IF	Citations
1290	Small molecule TCS21311 can replace BMP7 and facilitate cell proliferation in inÂvitro expansion culture of nephron progenitor cells. Biochemical and Biophysical Research Communications, 2021, 558, 231-238.	2.1	2
1291	Functional divergence of diacylglycerol acyltransferases in the unicellular green alga Haematococcus pluvialis. Journal of Experimental Botany, 2021, 72, 510-524.	4.8	13
1292	Amoeba Genome Reveals Dominant Host Contribution to Plastid Endosymbiosis. Molecular Biology and Evolution, 2021, 38, 344-357.	8.9	23
1293	Fibroblastâ€derived ILâ€33 is dispensable for lymph node homeostasis but critical for CD8 Tâ€cell responses to acute and chronic viral infection. European Journal of Immunology, 2021, 51, 76-90.	2.9	24
1294	A Fibrosisâ€Independent Hepatic Transcriptomic Signature Identifies Drivers of Disease Progression in Primary Sclerosing Cholangitis. Hepatology, 2021, 73, 1105-1116.	7.3	14
1295	Shark: fishing relevant reads in an RNA-Seq sample. Bioinformatics, 2021, 37, 464-472.	4.1	8
1296	Requirement of Bccip for the Regeneration of Intestinal Progenitors. American Journal of Pathology, 2021, 191, 66-78.	3.8	2
1297	BP4RNAseq: a babysitter package for retrospective and newly generated RNA-seq data analyses using both alignment-based and alignment-free quantification method. Bioinformatics, 2021, 37, 1319-1321.	4.1	64
1298	Installation of C₄ photosynthetic pathway enzymes in rice using a single construct. Plant Biotechnology Journal, 2021, 19, 575-588.	8.3	78
1299	The RNA m6A Reader YTHDF2 Maintains Oncogene Expression and Is a Targetable Dependency in Glioblastoma Stem Cells. Cancer Discovery, 2021, 11, 480-499.	9.4	218
1300	Rova-T enhances the anti-tumor activity of anti-PD1 in a murine model of small cell lung cancer with endogenous Dll3 expression. Translational Oncology, 2021, 14, 100883.	3.7	12
1301	Non-canonical Targets of HIF1a Impair Oligodendrocyte Progenitor Cell Function. Cell Stem Cell, 2021, 28, 257-272.e11.	11.1	25
1302	Chromatin interactions in differentiating keratinocytes reveal novel atopic dermatitisâ€“ and psoriasis-associated genes. Journal of Allergy and Clinical Immunology, 2021, 147, 1742-1752.	2.9	18
1303	Transcriptional response of human articular chondrocytes treated with fibronectin fragments: an in vitro model of the osteoarthritis phenotype. Osteoarthritis and Cartilage, 2021, 29, 235-247.	1.3	17
1304	The transcriptomic response of adult salmon lice (Lepeophtheirus salmonis) to reduced salinity. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 37, 100778.	1.0	5
1305	Immunophenotyping in pemphigus reveals a TH17/TFH17 cellâ€“dominated immune response promoting desmoglein1/3-specific autoantibody production. Journal of Allergy and Clinical Immunology, 2021, 147, 2358-2369.	2.9	44
1306	Compartmentalized evolution of hepatitis B virus contributes differently to the prognosis of hepatocellular carcinoma. Carcinogenesis, 2021, 42, 461-470.	2.8	11
1307	The XPB Subunit of the TFIIH Complex Plays a Critical Role in HIV-1 Transcription, and XPB Inhibition by Spironolactone Prevents HIV-1 Reactivation from Latency. Journal of Virology, 2021, 95, .	3.4	10

#	Article	IF	Citations
1308	Histamine-4 receptor antagonist ameliorates Parkinson-like pathology in the striatum. Brain, Behavior, and Immunity, 2021, 92, 127-138.	4.1	20
1309	Comparative transcriptome profiling reveals that brassinosteroid-mediated lignification plays an important role in garlic adaption to salt stress. Plant Physiology and Biochemistry, 2021, 158, 34-42.	5.8	26
1310	RNA Sequencing Reveals Diverse Functions of Amniotic Fluid Neutrophils and Monocytes/Macrophages in Intra-Amniotic Infection. Journal of Innate Immunity, 2021, 13, 63-82.	3.8	29
1311	Establishment and characterization of a coldâ€sensitive neural cell line from the brain of tilapia (<scp>Oreochromis niloticus</scp>). Journal of Fish Biology, 2021, 98, 842-854.	1.6	5
1313	Intercellular Mitochondria Transfer to Macrophages Regulates White Adipose Tissue Homeostasis and Is Impaired in Obesity. Cell Metabolism, 2021, 33, 270-282.e8.	16.2	160
1314	Clinical Validation of a Machine-learningâ€“derived Signature Predictive of Outcomes from First-line Oxaliplatin-based Chemotherapy in Advanced Colorectal Cancer. Clinical Cancer Research, 2021, 27, 1174-1183.	7.0	28
1315	Identification of Dominant Transcripts in Oxidative Stress Response by a Full-Length Transcriptome Analysis. Molecular and Cellular Biology, 2021, 41, .	2.3	7
1316	A highly differentiated region of wheat chromosome 7AL encodes a Pm1a immune receptor that recognizes its corresponding AvrPm1a effector from Blumeria graminis. New Phytologist, 2021, 229, 2812-2826.	7.3	72
1317	Gene Regulatory Network Analysis and Engineering Directs Development and Vascularization of Multilineage Human Liver Organoids. Cell Systems, 2021, 12, 41-55.e11.	6.2	59
1318	Transcriptome-wide changes associated with the reproductive behaviour of male guppies exposed to 17Î±-ethinyl estradiol. Environmental Pollution, 2021, 270, 116286.	7.5	5
1319	Genome- and transcriptome-wide association studies provide insights into the genetic basis of natural variation of seed oil content in Brassica napus. Molecular Plant, 2021, 14, 470-487.	8.3	107
1320	Transcriptional behavior of the HIV-1 promoter in context of the BACH2 prominent proviral integration gene. Virus Research, 2021, 293, 198260.	2.2	3
1321	Responses of functional miRNA-mRNA regulatory modules to a high-fat diet in the liver of hybrid yellow catfish (Pelteobagrus fulvidraco Ã— P. vachelli). Genomics, 2021, 113, 1207-1220.	2.9	7
1322	Limits to the cellular control of sequestered cryptophyte prey in the marine ciliate Mesodinium rubrum. ISME Journal, 2021, 15, 1056-1072.	9.8	15
1323	Genomeâ€wide alternative splicing profiling in the fungal plant pathogen Sclerotinia sclerotiorum during the colonization of diverse host families. Molecular Plant Pathology, 2021, 22, 31-47.	4.2	25
1324	The p53-induced RNA-binding protein ZMAT3 is a splicing regulator that inhibits the splicing of oncogenic CD44 variants in colorectal carcinoma. Genes and Development, 2021, 35, 102-116.	5.9	29
1325	Using RNA-seq to Assess Off-Target Effects of Antisense Oligonucleotides in Human Cell Lines. Molecular Diagnosis and Therapy, 2021, 25, 77-85.	3.8	8
1326	Genomic investigations of acute munitions exposures on the health and skin microbiome composition of leopard frog (Rana pipiens) tadpoles. Environmental Research, 2021, 192, 110245.	7.5	8

#	Article	IF	Citations
1327	Effects of transcriptional noise on estimates of gene and transcript expression in RNA sequencing experiments. Genome Research, 2021, 31, 301-308.	5.5	13
1328	Transcriptomic response of brain tissue to focused <scp>ultrasoundâ€mediated bloodâ€“brain</scp> barrier disruption depends strongly on anesthesia. Bioengineering and Translational Medicine, 2021, 6, e10198.	7.1	12
1329	Data structures based on k-mers for querying large collections of sequencing data sets. Genome Research, 2021, 31, 1-12.	5.5	67
1330	Two biâ€functional cytochrome P450 CYP72 enzymes from olive (Olea europaea) catalyze the oxidative Câ€C bond cleavage in the biosynthesis of secoxyâ€iridoids â€“ flavor and quality determinants in olive oil. New Phytologist, 2021, 229, 2288-2301.	7.3	17
1331	CIA2 and CIA2â€LIKE are required for optimal photosynthesis and stress responses in Arabidopsis thaliana. Plant Journal, 2021, 105, 619-638.	5.7	20
1332	Detection of severe fever with thrombocytopenia syndrome virus and other viruses in cats via unbiased next-generation sequencing. Journal of Veterinary Diagnostic Investigation, 2021, 33, 279-282.	1.1	7
1333	Determination of isoform-specific RNA structure with nanopore long reads. Nature Biotechnology, 2021, 39, 336-346.	17.5	72
1334	Differential nucleosome occupancy modulates alternative splicing in Arabidopsis thaliana. New Phytologist, 2021, 229, 1937-1945.	7.3	19
1335	Performance and microbial communities of a novel integrated industrial-scale pulp and paper wastewater treatment plant. Journal of Cleaner Production, 2021, 278, 123896.	9.3	40
1336	Mating type specific transcriptomic response to sex inducing pheromone in the pennate diatom Seminavis robusta. ISME Journal, 2021, 15, 562-576.	9.8	17
1337	A MXI1-NUTM1 fusion protein with MYC-like activity suggests a novel oncogenic mechanism in a subset of NUTM1-rearranged tumors. Laboratory Investigation, 2021, 101, 26-37.	3.7	12
1338	Extensive germline genome engineering in pigs. Nature Biomedical Engineering, 2021, 5, 134-143.	22.5	117
1339	Diffusible Signaling Factor, a Quorum-Sensing Molecule, Interferes with and Is Toxic Towards Bdellovibrio bacteriovorus 109J. Microbial Ecology, 2021, 81, 347-356.	2.8	12
1340	Dream: powerful differential expression analysis for repeated measures designs. Bioinformatics, 2021, 37, 192-201.	4.1	138
1341	SCDC: bulk gene expression deconvolution by multiple single-cell RNA sequencing references. Briefings in Bioinformatics, 2021, 22, 416-427.	6.5	156
1342	Novel role for mineralocorticoid receptors in control of a neuronal phenotype. Molecular Psychiatry, 2021, 26, 350-364.	7.9	40
1344	The Transcriptomic and Phenotypic Response of the Melanized Yeast Exophiala dermatitidis to Ionizing Particle Exposure. Frontiers in Microbiology, 2020, 11, 609996.	3.5	3
1345	Pathways involved in pony body size development. BMC Genomics, 2021, 22, 58.	2.8	4

#	Article	IF	Citations
1346	Dynamic RNA Regulation in the Brain Underlies Physiological Plasticity in a Hibernating Mammal. Frontiers in Physiology, 2020, 11, 624677.	2.8	10
1347	The pleiotropic effects of prebiotic galacto-oligosaccharides on the aging gut. Microbiome, 2021, 9, 31.	11.1	43
1351	Nebula: ultra-efficient mapping-free structural variant genotyper. Nucleic Acids Research, 2021, 49, e47-e47.	14.5	14
1352	Locus-specific expression analysis of transposable elements. Briefings in Bioinformatics, 2022, 23, .	6.5	7
1353	Type 2 immunity is maintained during cancer-associated adipose tissue wasting. Immunotherapy Advances, 2021, 1, ltab011.	3.0	13
1354	A comprehensive enhancer screen identifies TRAM2 as a key and novel mediator of YAP oncogenesis. Genome Biology, 2021, 22, 54.	8.8	16
1355	Two novel venom proteins underlie divergent parasitic strategies between a generalist and a specialist parasite. Nature Communications, 2021, 12, 234.	12.8	25
1356	Transkingdom network analysis provides insight into host-microbiome interactions in Atlantic salmon. Computational and Structural Biotechnology Journal, 2021, 19, 1028-1034.	4.1	4
1358	Transcriptomic and genomic changes associated with radioadaptation in Exophiala dermatitidis. Computational and Structural Biotechnology Journal, 2021, 19, 196-205.	4.1	13
1359	CRISPRi enables isoform-specific loss-of-function screens and identification of gastric cancer-specific isoform dependencies. Genome Biology, 2021, 22, 47.	8.8	12
1360	A novel ACE2 isoform is expressed in human respiratory epithelia and is upregulated in response to interferons and RNA respiratory virus infection. Nature Genetics, 2021, 53, 205-214.	21.4	125
1363	Ion channel profiling of the Lymnaea stagnalis ganglia via transcriptome analysis. BMC Genomics, 2021, 22, 18.	2.8	8
1364	Alternative mRNA Processing of Innate Response Pathways in Respiratory Syncytial Virus (RSV) Infection. Viruses, 2021, 13, 218.	3.3	11
1365	Low-dose Drosera rotundifolia induces gene expression changes in 16HBE human bronchial epithelial cells. Scientific Reports, 2021, 11, 2356.	3.3	5
1370	Repression of a large number of genes requires interplay between homologous recombination and HIRA. Nucleic Acids Research, 2021, 49, 1914-1934.	14.5	2
1371	Quantifying alternative polyadenylation in RNAseq data with LABRAT. Methods in Enzymology, 2021, 655, 245-263.	1.0	1
1373	Relevance of Bioinformatics and Database in Omics Study. , 2021, , 19-39.		0
1376	Deconvolution of expression for nascent RNA-sequencing data (DENR) highlights pre-RNA isoform diversity in human cells. Bioinformatics, 2021, 37, 4727-4736.	4.1	4

#	Article	IF	Citations
1377	Bioinformatics Approaches for Fungal Biotechnology. , 2021, , 536-554.		0
1378	Cigarette Smoke Extract Activates Hypoxia-Inducible Factors in a Reactive Oxygen Species-Dependent Manner in Stroma Cells from Human Endometrium. Antioxidants, 2021, 10, 48.	5.1	11
1380	Five multicopy gene family genes expressed during the maternal-to-zygotic transition are not essential for mouse development. Biochemical and Biophysical Research Communications, 2021, 534, 752-757.	2.1	4
1381	Genome-wide identification, evolution and expression analysis of the aspartic protease gene family during rapid growth of moso bamboo (Phyllostachys edulis) shoots. BMC Genomics, 2021, 22, 45.	2.8	9
1382	Somatostatin receptor 2 expression in nasopharyngeal cancer is induced by Epstein Barr virus infection: impact on prognosis, imaging and therapy. Nature Communications, 2021, 12, 117.	12.8	34
1384	Therapeutic Assessment of Targeting ASNS Combined with <scp>l</scp>-Asparaginase Treatment in Solid Tumors and Investigation of Resistance Mechanisms. ACS Pharmacology and Translational Science, 2021, 4, 327-337.	4.9	13
1385	Using RNentropy to Detect Significant Variation in Gene Expression Across Multiple RNA-Seq or Single-Cell RNA-Seq Samples. Methods in Molecular Biology, 2021, 2284, 77-96.	0.9	0
1386	Exploring Translational Control of Maternal in Zebrafish. Methods in Molecular Biology, 2021, 2218, 367-380.	0.9	2
1387	Ribosome profiling analysis of human skeletal muscle identifies reduced translation of mitochondrial proteins with age. RNA Biology, 2021, 18, 1555-1559.	3.1	9
1389	Nrf2 overexpression rescues the RPE in mouse models of retinitis pigmentosa. JCI Insight, 2021, 6, .	5.0	33
1391	Mechanobiological conditioning of mesenchymal stem cells for enhanced vascular regeneration. Nature Biomedical Engineering, 2021, 5, 89-102.	22.5	35
1392	WIND (Workflow for pIRNAs aNd beyonD): a strategy for in-depth analysis of small RNA-seq data. F1000Research, 2021, 10, 1.	1.6	5
1393	Streamlining data-intensive biology with workflow systems. GigaScience, 2021, 10, .	6.4	32
1394	Modulation of microglial activation states by spinal cord stimulation in an animal model of neuropathic pain: Comparing high rate, low rate, and differential target multiplexed programming. Molecular Pain, 2021, 17, 174480692199901.	2.1	24
1395	Characterization and comparison of innate and adaptive immune responses at vaccine sites in melanoma vaccine clinical trials. Cancer Immunology, Immunotherapy, 2021, 70, 2151-2164.	4.2	6
1396	Apobec1 complementation factor overexpression promotes hepatic steatosis, fibrosis, and hepatocellular cancer. Journal of Clinical Investigation, 2021, 131, .	8.2	21
1397	A Tale of Optimizing the Space Taken by de Bruijn Graphs. Lecture Notes in Computer Science, 2021, , 120-134.	1.3	1
1398	Probabilistic Models of k-mer Frequencies (Extended Abstract). Lecture Notes in Computer Science, 2021, , 227-236.	1.3	0

#	Article	IF	Citations
1399	Analysis of ovarian transcriptomes reveals thousands of novel genes in the insect vector Rhodnius prolixus. Scientific Reports, 2021, 11, 1918.	3.3	18
1400	Identification of cancer related genes using feature selection and association rule mining. Informatics in Medicine Unlocked, 2021, 24, 100595.	3.4	15
1401	Optogenetic Stimulation of Prelimbic Pyramidal Neurons Maintains Fear Memories and Modulates Amygdala Pyramidal Neuron Transcriptome. International Journal of Molecular Sciences, 2021, 22, 810.	4.1	8
1402	Sex-specific differences in peripheral blood leukocyte transcriptional response to LPS are enriched for HLA region and X chromosome genes. Scientific Reports, 2021, 11, 1107.	3.3	11
1404	RNA-Sequencing Analysis of Differentially Expressed Genes in Human iPSC-Derived Cardiomyocytes. Methods in Molecular Biology, 2021, 2320, 193-217.	0.9	3
1405	Omics Analysis of Blood-Responsive Regulon in Bordetella pertussis Identifies a Novel Essential T3SS Substrate. International Journal of Molecular Sciences, 2021, 22, 736.	4.1	2
1409	Conserved paradoxical relationships among the evolutionary, structural and expressional features of KRAB zinc-finger proteins reveal their special functional characteristics. BMC Molecular and Cell Biology, 2021, 22, 7.	2.0	7
1412	Reduction of alternative electron acceptors drives biofilm formation in Shewanella algae. Npj Biofilms and Microbiomes, 2021, 7, 9.	6.4	15
1413	Genomic and transcriptomic resources for candidate gene discovery in the Ranunculids. Applications in Plant Sciences, 2021, 9, e11407.	2.1	4
1414	Bioinformatic Pipelines to Analyze lncRNAs RNAseq Data. Methods in Molecular Biology, 2021, 2348, 55-69.	0.9	0
1415	The Global Protein-Rna Interaction Map of Epithelial Splicing Regulatory Protein 1 Defines a Post-Transcriptional Program that is Essential for Epithelial Cell Function. SSRN Electronic Journal, 0, , .	0.4	0
1416	Plasma IL-8 and ICOSLG as prognostic biomarkers in glioblastoma. Neuro-Oncology Advances, 2021, 3, vdab072.	0.7	4
1417	Evolutionary conservation and divergence of the human brain transcriptome. Genome Biology, 2021, 22, 52.	8.8	28
1418	Statistical Modeling of High Dimensional Counts. Methods in Molecular Biology, 2021, 2284, 97-134.	0.9	1
1419	Gene expression signatures of target tissues in type 1 diabetes, lupus erythematosus, multiple sclerosis, and rheumatoid arthritis. Science Advances, 2021, 7, .	10.3	42
1420	Rituximab versus tocilizumab in anti-TNF inadequate responder patients with rheumatoid arthritis (R4RA): 16-week outcomes of a stratified, biopsy-driven, multicentre, open-label, phase 4 randomised controlled trial. Lancet, The, 2021, 397, 305-317.	13.7	145
1421	A mixed community of skin microbiome representatives influences cutaneous processes more than individual members. Microbiome, 2021, 9, 22.	11.1	27
1422	Machine Learning Analysis of Longevity-Associated Gene Expression Landscapes in Mammals. International Journal of Molecular Sciences, 2021, 22, 1073.	4.1	6

#	Article	IF	Citations
1423	Alternative splicing: Human disease and quantitative analysis from high-throughput sequencing. Computational and Structural Biotechnology Journal, 2021, 19, 183-195.	4.1	57
1424	Chromatin regulatory dynamics of early human small intestinal development using a directed differentiation model. Nucleic Acids Research, 2021, 49, 726-744.	14.5	14
1425	Human CHR18: â€œStakhanoviteâ€•Genes, Missing and uPE1 Proteins in Liver Tissue and HepG2 Cells. Biomedical Chemistry Research and Methods, 2021, 4, e00144.	0.4	6
1426	Co(<scp>ii</scp>)-based metalâ€“organic framework induces apoptosis through activating the HIF-1Î±/BNIP3 signaling pathway in microglial cells. Environmental Science: Nano, 2021, 8, 2866-2882.	4.3	7
1427	More than a pore: How voltage-gated calcium channels act on different levels of neuronal communication regulation. Channels, 2021, 15, 322-338.	2.8	10
1428	Signalling pathways and mechanistic cues highlighted by transcriptomic analysis of primordial, primary, and secondary ovarian follicles in domestic cat. Scientific Reports, 2021, 11, 2683.	3.3	10
1429	EUKulele: Taxonomic annotation of the unsung eukaryotic microbes. Journal of Open Source Software, 2021, 6, 2817.	4.6	19
1431	Differential Expression Analysis of Long Noncoding RNAs. Methods in Molecular Biology, 2021, 2284, 193-205.	0.9	1
1432	QuickIsoSeq for Isoform Quantification in Large-Scale RNA Sequencing. Methods in Molecular Biology, 2021, 2284, 135-145.	0.9	1
1434	Evolution of Tandem Repeats Is Mirroring Post-polyploid Cladogenesis in Heliophila (Brassicaceae). Frontiers in Plant Science, 2020, 11, 607893.	3.6	13
1435	Shift and Metabolic Potentials of Microbial Eukaryotic Communities Across the Full Depths of the Mariana Trench. Frontiers in Microbiology, 2020, 11, 603692.	3.5	5
1436	Evolution and Expression of the Immune System of a Facultatively Anadromous Salmonid. Frontiers in Immunology, 2021, 12, 568729.	4.8	7
1438	Transcription Profiles Associated with Inducible Adhesion in Candida parapsilosis. MSphere, 2021, 6, .	2.9	5
1441	Root growth responses to mechanical impedance are regulated by a network of ROS, ethylene and auxin signalling in Arabidopsis. New Phytologist, 2021, 231, 225-242.	7.3	36
1442	Metagenomics workflow for hybrid assembly, differential coverage binning, metatranscriptomics and pathway analysis (MUFFIN). PLoS Computational Biology, 2021, 17, e1008716.	3.2	18
1443	The glucocorticoid receptor recruits the COMPASS complex to regulate inflammatory transcription at macrophage enhancers. Cell Reports, 2021, 34, 108742.	6.4	27
1444	Plant roots employ cell-layer-specific programs to respond to pathogenic and beneficial microbes. Cell Host and Microbe, 2021, 29, 299-310.e7.	11.0	48
1445	Expanded catalog of microbial genes and metagenome-assembled genomes from the pig gut microbiome. Nature Communications, 2021, 12, 1106.	12.8	116

#	Article	IF	Citations
1450	EKLF/KLF1 expression defines a unique macrophage subset during mouse erythropoiesis. ELife, 2021, 10, .	6.0	21
1451	Genome-wide analysis of pseudogenes reveals HBBP1â€™s human-specific essentiality in erythropoiesis and implication in Î²-thalassemia. Developmental Cell, 2021, 56, 478-493.e11.	7.0	22
1452	NPMâ€“ALK-Induced Reprogramming of Mature TCR-Stimulated T Cells Results in Dedifferentiation and Malignant Transformation. Cancer Research, 2021, 81, 3241-3254.	0.9	10
1453	Unraveling the features of somatic transposition in the Drosophila intestine. EMBO Journal, 2021, 40, e106388.	7.8	31
1454	Thermal reaction norms of key metabolic enzymes reflect divergent physiological and behavioral adaptations of closely related amphipod species. Scientific Reports, 2021, 11, 4562.	3.3	7
1455	Caught between Two Genes: Accounting for Operonic Gene Structure Improves Prokaryotic RNA Sequencing Quantification. MSystems, 2021, 6, .	3.8	1
1456	The one-carbon pool controls mitochondrial energy metabolism via complex I and iron-sulfur clusters. Science Advances, 2021, 7, .	10.3	23
1457	The innate sensor ZBP1-IRF3 axis regulates cell proliferation in multiple myeloma. Haematologica, 2022, 107, 721-732.	3.5	17
1458	Multi-scale architecture of archaeal chromosomes. Molecular Cell, 2021, 81, 473-487.e6.	9.7	24
1459	The genetic basis of cytoplasmic male sterility and fertility restoration in wheat. Nature Communications, 2021, 12, 1036.	12.8	58
1460	Clinical and Biological Subtypes of B-cell Lymphoma Revealed by Microenvironmental Signatures. Cancer Discovery, 2021, 11, 1468-1489.	9.4	119
1461	Epigenomic characterization of latent HIV infection identifies latency regulating transcription factors. PLoS Pathogens, 2021, 17, e1009346.	4.7	32
1462	ZMYND11-MBTD1 induces leukemogenesis through hijacking NuA4/TIP60 acetyltransferase complex and a PWWP-mediated chromatin association mechanism. Nature Communications, 2021, 12, 1045.	12.8	27
1463	Nonadditive Transcriptomic Signatures of Genotype-by-Genotype Interactions during the Initiation of Plant-Rhizobium Symbiosis. MSystems, 2021, 6, .	3.8	26
1465	Perinatal granulopoiesis and risk of pediatric asthma. ELife, 2021, 10, .	6.0	2
1468	Low responders to endurance training exhibit impaired hypertrophy and divergent biological process responses in rat skeletal muscle. Experimental Physiology, 2021, 106, 714-725.	2.0	4
1469	Fluid shear stress generates a unique signaling response by activating multiple TGFÎ² family type I receptors in osteocytes. FASEB Journal, 2021, 35, e21263.	0.5	18
1470	Molecular parallelisms between pigmentation in the avian iris and the integument of ectothermic vertebrates. PLoS Genetics, 2021, 17, e1009404.	3.5	8

#	Article	IF	Citations
1471	A molecular quantitative trait locus map for osteoarthritis. Nature Communications, 2021, 12, 1309.	12.8	53
1472	Single-cell analysis of human B cell maturation predicts how antibody class switching shapes selection dynamics. Science Immunology, 2021, 6, .	11.9	149
1473	Contact-dependent traits in Pseudomonas syringae B728a. PLoS ONE, 2021, 16, e0241655.	2.5	3
1474	Meta-Analysis of Oxidative Transcriptomes in Insects. Antioxidants, 2021, 10, 345.	5.1	19
1476	FOXO1 mitigates the SMAD3/FOXL2C134W transcriptomic effect in a model of human adult granulosa cell tumor. Journal of Translational Medicine, 2021, 19, 90.	4.4	5
1477	CRTC1/MAML2 directs a PGC-1Î±-IGF-1 circuit that confers vulnerability to PPARÎ³ inhibition. Cell Reports, 2021, 34, 108768.	6.4	6
1478	Response of bitter and sweet Chenopodium quinoa varieties to cucumber mosaic virus: Transcriptome and small RNASeq perspective. PLoS ONE, 2021, 16, e0244364.	2.5	2
1481	Comparative transcriptome analyses between cultivated and wild grapes reveal conservation of expressed genes but extensive rewiring of co-expression networks. Plant Molecular Biology, 2021, 106, 1-20.	3.9	5
1482	Genomic aberrations after short-term exposure to colibactin-producing E. coli transform primary colon epithelial cells. Nature Communications, 2021, 12, 1003.	12.8	84
1483	Genome-Wide Identification and Characterization of Potato Long Non-coding RNAs Associated With Phytophthora infestans Resistance. Frontiers in Plant Science, 2021, 12, 619062.	3.6	9
1484	Linking Penetrance and Transcription in <scp>DYTâ€THAP1</scp>: Insights From a Human <scp>iPSC</scp>â€Derived Cortical Model. Movement Disorders, 2021, 36, 1381-1391.	3.9	14
1485	Transcription activation depends on the length of the RNA polymerase II Câ€terminal domain. EMBO Journal, 2021, 40, e107015.	7.8	11
1486	Molecular insight into somaclonal variation phenomena from transcriptome profiling of cucumber (Cucumis sativus L.) lines. Plant Cell, Tissue and Organ Culture, 2021, 145, 239-259.	2.3	14
1487	Strain heterogeneity, cooccurrence network, taxonomic composition and functional profile of the healthy ocular surface microbiome. Eye and Vision (London, England), 2021, 8, 6.	3.0	13
1488	Light-Dependent Translation Change of Arabidopsis psbA Correlates with RNA Structure Alterations at the Translation Initiation Region. Cells, 2021, 10, 322.	4.1	9
1489	A membrane-bound ankyrin repeat protein confers race-specific leaf rust disease resistance in wheat. Nature Communications, 2021, 12, 956.	12.8	63
1490	AMPKÎ±1 deletion in myofibroblasts exacerbates post-myocardial infarction fibrosis by a connexin 43 mechanism. Basic Research in Cardiology, 2021, 116, 10.	5.9	26
1491	Transcriptome analysis of salt stress responsiveness in the seedlings of wild and cultivated Ricinus communis L. Journal of Biotechnology, 2021, 327, 106-116.	3.8	17

#	Article	IF	Citations
1493	Inhibition of longevity regulator PAPPâ€A modulates tissue homeostasis via restraint of mesenchymal stromal cells. Aging Cell, 2021, 20, e13313.	6.7	6
1494	Freshwater sponge hosts and their green algae symbionts: a tractable model to understand intracellular symbiosis. PeerJ, 2021, 9, e10654.	2.0	11
1496	lncEvo: automated identification and conservation study of long noncoding RNAs. BMC Bioinformatics, 2021, 22, 59.	2.6	8
1497	Erythrina velutina Willd. alkaloids: Piecing biosynthesis together from transcriptome analysis and metabolite profiling of seeds and leaves. Journal of Advanced Research, 2021, 34, 123-136.	9.5	5
1499	A Two-Gene Signature for Tuberculosis Diagnosis in Persons With Advanced HIV. Frontiers in Immunology, 2021, 12, 631165.	4.8	10
1500	Binnacle: Using Scaffolds to Improve the Contiguity and Quality of Metagenomic Bins. Frontiers in Microbiology, 2021, 12, 638561.	3.5	2
1501	SIN3A Regulates Porcine Early Embryonic Development by Modulating CCNB1 Expression. Frontiers in Cell and Developmental Biology, 2021, 9, 604232.	3.7	2
1502	Dataset for transcriptome and physiological response of mature tomato seed tissues to light and heat during fruit ripening. Data in Brief, 2021, 34, 106671.	1.0	2
1503	FADU: a Quantification Tool for Prokaryotic Transcriptomic Analyses. MSystems, 2021, 6, .	3.8	8
1504	Upregulation of human endogenous retrovirus-K (HML-2) mRNAs in hepatoblastoma: Identification of potential new immunotherapeutic targets and biomarkers. Journal of Pediatric Surgery, 2021, 56, 286-292.	1.6	12
1505	â€œAll-In-Oneâ€•Genetic Tool Assessing Endometrial Receptivity for Personalized Screening of Female Sex Steroid Hormones. Frontiers in Cell and Developmental Biology, 2021, 9, 624053.	3.7	7
1506	Innate immune evasion revealed in a colorectal zebrafish xenograft model. Nature Communications, 2021, 12, 1156.	12.8	41
1507	Genome-wide association study identified candidate genes for seed size and seed composition improvement in M. truncatula. Scientific Reports, 2021, 11, 4224.	3.3	11
1510	SARS-CoV-2 infection is effectively treated and prevented by EIDD-2801. Nature, 2021, 591, 451-457.	27.8	320
1511	Chromatin dysregulation associated with NSD1 mutation in head and neck squamous cell carcinoma. Cell Reports, 2021, 34, 108769.	6.4	42
1512	De Novo Transcriptomic Analyses Revealed Some Detoxification Genes and Related Pathways Responsive to Noposion YihaogongÂ® 5% EC (Lambda-Cyhalothrin 5%) Exposure in Spodoptera frugiperda Third-Instar Larvae. Insects, 2021, 12, 132.	2.2	16
1513	Function of the pseudo phosphotransfer proteins has diverged between rice and Arabidopsis. Plant Journal, 2021, 106, 159-173.	5.7	7
1514	Evidence for reduced immune gene diversity and activity during the evolution of termites. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20203168.	2.6	9

#	Article	IF	Citations
1523	Systematic analyses of the MIR172 family members of Arabidopsis define their distinct roles in regulation of APETALA2 during floral transition. PLoS Biology, 2021, 19, e3001043.	5.6	44
1524	Characterizing RNA stability genome-wide through combined analysis of PRO-seq and RNA-seq data. BMC Biology, 2021, 19, 30.	3.8	38
1525	A versatile workflow to integrate RNA-seq genomic and transcriptomic data into mechanistic models of signaling pathways. PLoS Computational Biology, 2021, 17, e1008748.	3.2	6
1526	Bacteria and Metabolic Potential in Karst Caves Revealed by Intensive Bacterial Cultivation and Genome Assembly. Applied and Environmental Microbiology, 2021, 87, .	3.1	12
1528	Macrophage Activation Status Rather than Repolarization Is Associated with Enhanced Checkpoint Activity in Combination with PI3KÎ³ Inhibition. Molecular Cancer Therapeutics, 2021, 20, 1080-1091.	4.1	7
1529	Single-molecule long-read sequencing reveals a conserved intact long RNA profile in sperm. Nature Communications, 2021, 12, 1361.	12.8	43
1531	Large-scale labeling and assessment of sex bias in publicly available expression data. BMC Bioinformatics, 2021, 22, 168.	2.6	12
1532	Deciphering the transcriptomic regulation of heat stress responses in Nothofagus pumilio. PLoS ONE, 2021, 16, e0246615.	2.5	6
1533	Identification of Microbiome Etiology Associated With Drug Resistance in Pleural Empyema. Frontiers in Cellular and Infection Microbiology, 2021, 11, 637018.	3.9	16
1534	Transcriptional networks identify synaptotagmin-like 3 as a regulator of cortical neuronal migration during early neurodevelopment. Cell Reports, 2021, 34, 108802.	6.4	5
1535	Mutanofactin promotes adhesion and biofilm formation of cariogenic Streptococcus mutans. Nature Chemical Biology, 2021, 17, 576-584.	8.0	28
1536	A Point Mutation in IKAROS ZF1 Causes a B Cell Deficiency in Mice. Journal of Immunology, 2021, 206, 1505-1514.	0.8	2
1538	Enhancerâ€mediated reporter gene expression in Arabidopsis thaliana: a forward genetic screen. Plant Journal, 2021, 106, 661-671.	5.7	4
1539	ASpli: integrative analysis of splicing landscapes through RNA-Seq assays. Bioinformatics, 2021, 37, 2609-2616.	4.1	38
1540	Temporal mechanisms of myogenic specification in human induced pluripotent stem cells. Science Advances, 2021, 7, .	10.3	3
1541	The human intermediate prolactin receptor is a mammary proto-oncogene. Npj Breast Cancer, 2021, 7, 37.	5.2	16
1542	Gut microbial taxa elevated by dietary sugar disrupt memory function. Translational Psychiatry, 2021, 11, 194.	4.8	50
1543	Transcriptional profiling reveals potential involvement of microvillous TRPM5-expressing cells in viral infection of the olfactory epithelium. BMC Genomics, 2021, 22, 224.	2.8	15

#	Article	IF	Citations
1544	The Transcription Factor Shox2 Shapes Neuron Firing Properties and Suppresses Seizures by Regulation of Key Ion Channels in Thalamocortical Neurons. Cerebral Cortex, 2021, 31, 3194-3212.	2.9	2
1545	Acquisition of innate odor preference depends on spontaneous and experiential activities during critical period. ELife, 2021, 10, .	6.0	17
1548	Pan-cancer analysis of RNA expression of ANGIOTENSIN-I-CONVERTING ENZYME 2 reveals high variability and possible impact on COVID-19 clinical outcomes. Scientific Reports, 2021, 11, 5639.	3.3	1
1551	Comparative transcriptomic analysis of the different developmental stages of ovary in red swamp crayfish Procambarus clarkii. BMC Genomics, 2021, 22, 199.	2.8	8
1555	Association between the nucleosome footprint of plasma DNA and neoadjuvant chemotherapy response for breast cancer. Npj Breast Cancer, 2021, 7, 35.	5.2	9
1556	Perspective: targeting VEGF-A and YKL-40 in glioblastoma â€“ matter matters. Cell Cycle, 2021, 20, 702-715.	2.6	6
1557	Breast tumours maintain a reservoir of subclonal diversity during expansion. Nature, 2021, 592, 302-308.	27.8	145
1558	Genomics and transcriptomics of the green mussel explain the durability of its byssus. Scientific Reports, 2021, 11, 5992.	3.3	14
1559	Cleavage and Polyadenylation Specific Factor 1 Promotes Tumor Progression via Alternative Polyadenylation and Splicing in Hepatocellular Carcinoma. Frontiers in Cell and Developmental Biology, 2021, 9, 616835.	3.7	17
1565	Differential normal skin transcriptomic response in total body irradiated mice exposed to scattered versus scanned proton beams. Scientific Reports, 2021, 11, 5876.	3.3	4
1566	The oncogene AAMDC links PI3K-AKT-mTOR signaling with metabolic reprograming in estrogen receptor-positive breast cancer. Nature Communications, 2021, 12, 1920.	12.8	19
1567	Structural Variants at theBRCA1/2Loci are a Common Source of Homologous Repair Deficiency in High-grade Serous Ovarian Carcinoma. Clinical Cancer Research, 2021, 27, 3201-3214.	7.0	27
1569	Validation of a multicellular tumor microenvironment system for modeling patient tumor biology and drug response. Scientific Reports, 2021, 11, 5535.	3.3	4
1570	Molecular mechanism of cytokinin-activated cell division in Arabidopsis. Science, 2021, 371, 1350-1355.	12.6	79
1571	Transcriptional mediators of treatment resistance in lethal prostate cancer. Nature Medicine, 2021, 27, 426-433.	30.7	90
1572	Oncohistone mutations enhance chromatin remodeling and alter cell fates. Nature Chemical Biology, 2021, 17, 403-411.	8.0	50
1575	Case Report: Temozolomide Treatment of Refractory Prolactinoma Resistant to Dopamine Agonists. Frontiers in Endocrinology, 2021, 12, 616339.	3.5	9
1576	KLF11 protects against abdominal aortic aneurysm through inhibition of endothelial cell dysfunction. JCI Insight, 2021, 6, .	5.0	17

#	Article	IF	Citations
1577	seqQscorer: automated quality control of next-generation sequencing data using machine learning. Genome Biology, 2021, 22, 75.	8.8	9
1578	Huntingtonâ€™s disease-specific mis-splicing unveils key effector genes and altered splicing factors. Brain, 2021, 144, 2009-2023.	7.6	32
1579	Rice Transcriptome Analysis Reveals Nitrogen Starvation Modulates Differential Alternative Splicing and Transcript Usage in Various Metabolism-Related Genes. Life, 2021, 11, 285.	2.4	6
1580	Corticosterone inhibits GAS6 to govern hair follicle stem-cell quiescence. Nature, 2021, 592, 428-432.	27.8	73
1581	Novel brain gene-expression patterns are associated with a novel predaceous behaviour in tadpoles. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210079.	2.6	5
1584	Exploring Common Therapeutic Targets for Neurodegenerative Disorders Using Transcriptome Study. Frontiers in Genetics, 2021, 12, 639160.	2.3	11
1586	Shifts in morphology, gene expression, and selection underlie web loss in Hawaiian Tetragnatha spiders. Bmc Ecology and Evolution, 2021, 21, 48.	1.6	6
1587	The Bdkrb2 gene family provides a novel view of viviparity adaptation in Sebastes schlegelii. Bmc Ecology and Evolution, 2021, 21, 44.	1.6	1
1589	The right ventricular transcriptome signature in Ossabaw swine with cardiometabolic heart failure: implications for the coronary vasculature. Physiological Genomics, 2021, 53, 99-115.	2.3	4
1590	HDAC6 inhibition restores TDPâ€43 pathology and axonal transport defects in human motor neurons with TARDBP mutations. EMBO Journal, 2021, 40, e106177.	7.8	51
1593	Alternative splicing dynamics and evolutionary divergence during embryogenesis in wheat species. Plant Biotechnology Journal, 2021, 19, 1624-1643.	8.3	23
1595	SVEP1 is a human coronary artery disease locus that promotes atherosclerosis. Science Translational Medicine, 2021, 13, .	12.4	28
1596	Early transcriptome changes induced by the Geminivirus C4 oncoprotein: setting the stage for oncogenesis. BMC Genomics, 2021, 22, 147.	2.8	5
1598	Characterization of Biological Pathways Regulating Acute Cold Resistance of Zebrafish. International Journal of Molecular Sciences, 2021, 22, 3028.	4.1	28
1599	DGCR8 deficiency impairs macrophage growth and unleashes the interferon response to mycobacteria. Life Science Alliance, 2021, 4, e202000810.	2.8	0
1600	Functional long non-coding and circular RNAs in zebrafish. Briefings in Functional Genomics, 2021, , .	2.7	4
1601	Proteogenomics of glioblastoma associates molecular patterns with survival. Cell Reports, 2021, 34, 108787.	6.4	31
1603	Machine learning analysis using 77,044 genomic and transcriptomic profiles to accurately predict tumor type. Translational Oncology, 2021, 14, 101016.	3.7	22

#	Article	IF	Citations
1604	Nuclear localization of p65 reverses therapy-induced senescence. Journal of Cell Science, 2021, 134, .	2.0	9
1606	Expansions of adaptive-like NK cells with a tissue-resident phenotype in human lung and blood. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	43
1607	Bacteria primed by antimicrobial peptides develop tolerance and persist. PLoS Pathogens, 2021, 17, e1009443.	4.7	39
1608	Alzheimer's disease alters oligodendrocytic glycolytic and ketolytic gene expression. Alzheimer's and Dementia, 2021, 17, 1474-1486.	0.8	37
1609	A co-opted steroid synthesis gene, maintained in sorghum but not maize, is associated with a divergence in leaf wax chemistry. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	26
1610	Harnessing the IL-21-BATF Pathway in the CD8+ T Cell Anti-Tumor Response. Cancers, 2021, 13, 1263.	3.7	17
1612	Model-based feature selection and clustering of RNA-seq data for unsupervised subtype discovery. Annals of Applied Statistics, 2021, 15, 481-508.	1.1	6
1617	Gene co-expression analysis of tomato seed maturation reveals tissue-specific regulatory networks and hubs associated with the acquisition of desiccation tolerance and seed vigour. BMC Plant Biology, 2021, 21, 124.	3.6	15
1619	Transcriptional analysis of sodium valproate in a serotonergic cell line reveals gene regulation through both HDAC inhibition-dependent and independent mechanisms. Pharmacogenomics Journal, 2021, 21, 359-375.	2.0	4
1620	A Comparison of Differential Gene Expression in Response to the Onset of Water Stress Between Three Hybrid Brachiaria Genotypes. Frontiers in Plant Science, 2021, 12, 637956.	3.6	9
1622	Regulation of DNA (de)Methylation Positively Impacts Seed Germination during Seed Development under Heat Stress. Genes, 2021, 12, 457.	2.4	18
1623	Gene expression for secondary metabolite biosynthesis in hop (Humulus lupulus L.) leaf lupulin glands exposed to heat and low-water stress. Scientific Reports, 2021, 11, 5138.	3.3	16
1624	EORNA, a barley gene and transcript abundance database. Scientific Data, 2021, 8, 90.	5.3	20
1625	Changes in the physiological characteristics of Panax ginseng embryogenic calli and molecular mechanism of ginsenoside biosynthesis under cold stress. Planta, 2021, 253, 79.	3.2	10
1627	Pseudomonas fluorescens F113 type VI secretion systems mediate bacterial killing and adaption to the rhizosphere microbiome. Scientific Reports, 2021, 11, 5772.	3.3	31
1628	Drosophila Fezf functions as a transcriptional repressor to direct layer-specific synaptic connectivity in the fly visual system. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	14
1634	Colonial bentgrass transcriptâ€expression differences compared with creeping bentgrass in response to waterâ€deficit stress. Crop Science, 2021, 61, 2135-2147.	1.8	2
1635	An NKX2-1/ERK/WNT feedback loop modulates gastric identity and response to targeted therapy in lung adenocarcinoma. ELife, 2021, 10, .	6.0	15

#	Article	IF	Citations
1636	Systematic identification of A-to-I RNA editing in zebrafish development and adult organs. Nucleic Acids Research, 2021, 49, 4325-4337.	14.5	21
1637	Representative Diatom and Coccolithophore Species Exhibit Divergent Responses throughout Simulated Upwelling Cycles. MSystems, 2021, 6, .	3.8	10
1638	Reduced Nucleoprotein Availability Impairs Negative-Sense RNA Virus Replication and Promotes Host Recognition. Journal of Virology, 2021, 95, .	3.4	26
1639	Conserved and unique transcriptional features of pharyngeal arches in the skate (Leucoraja) Tj ETQq1 1 0.784314 rgBT /Overlock 10	8.9	17
1640	Natural mucosal barriers and COVID-19 in children. JCI Insight, 2021, 6, .	5.0	124
1641	Multi-Omics Approaches to Define Calcific Aortic Valve Disease Pathogenesis. Circulation Research, 2021, 128, 1371-1397.	4.5	39
1642	RNA sequencing data for heat stress response in isolated medicago truncatula seed tissues. Data in Brief, 2021, 35, 106726.	1.0	3
1643	Extensive transcription mis-regulation and membrane defects in AdipoR2-deficient cells challenged with saturated fatty acids. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2021, 1866, 158884.	2.4	13
1646	Merged Affinity Network Association Clustering: Joint multi-omic/clinical clustering to identify disease endotypes. Cell Reports, 2021, 35, 108975.	6.4	12
1647	Identification of Na+/K+-ATPase Î±/Î² isoforms in Rhinella marina tissues by RNAseq and a molecular docking approach at the protein level to evaluate Î± isoform affinities for bufadienolides. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2021, 254, 110906.	1.8	4
1648	Healthy versus inflamed lung environments differentially affect mesenchymal stromal cells. European Respiratory Journal, 2021, 58, 2004149.	6.7	20
1650	Zea mays RNA-seq estimated transcript abundances are strongly affected by read mapping bias. BMC Genomics, 2021, 22, 285.	2.8	3
1651	Impact of preoperative antibiotics and other variables on integrated microbiome-host transcriptomic data generated from colorectal cancer resections. World Journal of Gastroenterology, 2021, 27, 1465-1482.	3.3	4
1652	AS-Quant: Detection and Visualization of Alternative Splicing Events with RNA-seq Data. International Journal of Molecular Sciences, 2021, 22, 4468.	4.1	7
1653	A critical assessment of gene catalogs for metagenomic analysis. Bioinformatics, 2021, 37, 2848-2857.	4.1	15
1654	MicroRNA-29 is an essential regulator of brain maturation through regulation of CH methylation. Cell Reports, 2021, 35, 108946.	6.4	25
1655	Single-Cell Transcriptomics: Current Methods and Challenges in Data Acquisition and Analysis. Frontiers in Neuroscience, 2021, 15, 591122.	2.8	53
1656	Activity-regulated synaptic targeting of lncRNA ADEPTR mediates structural plasticity by localizing Sptn1 and AnkB in dendrites. Science Advances, 2021, 7, .	10.3	29

#	Article	IF	Citations
1657	A NOVEL NOX/PHOX-CD38-NAADP-TFEB AXIS IMPORTANT FOR MACROPHAGE ACTIVATION DURING BACTERIAL PHAGOCYTOSIS. Autophagy, 2022, 18, 124-141.	9.1	17
1659	Common virulence gene expression in adult first-time infected malaria patients and severe cases. ELife, 2021, 10, .	6.0	20
1660	PAX8 and MECOM are interaction partners driving ovarian cancer. Nature Communications, 2021, 12, 2442.	12.8	29
1661	Establishing Sustainable Cell Lines of a Coral, Acropora tenuis. Marine Biotechnology, 2021, 23, 373-388.	2.4	23
1663	Establishing a Risk Prediction Model for Atherosclerosis in Systemic Lupus Erythematosus. Frontiers in Immunology, 2021, 12, 622216.	4.8	11
1664	Cistrome analysis of YY1 uncovers a regulatory axis of YY1:BRD2/4-PFKP during tumorigenesis of advanced prostate cancer. Nucleic Acids Research, 2021, 49, 4971-4988.	14.5	22
1665	<tt>pyrpipe</tt>: a Python package for RNA-Seq workflows. NAR Genomics and Bioinformatics, 2021, 3, lqab049.	3.2	14
1666	Divergent Gene Expression Following Duplication of Meiotic Genes in the Stick Insect Clitarchus hookeri. Genome Biology and Evolution, 2021, 13, .	2.5	1
1668	Impaired viral infection and reduced mortality of diatoms in iron-limited oceanic regions. Nature Geoscience, 2021, 14, 231-237.	12.9	17
1670	Streamlining differential exon and 3â€² UTR usage with diffUTR. BMC Bioinformatics, 2021, 22, 189.	2.6	5
1671	Transcriptome prediction performance across machine learning models and diverse ancestries. Human Genetics and Genomics Advances, 2021, 2, 100019.	1.7	14
1673	Meningeal lymphatics affect microglia responses and anti-Aβ immunotherapy. Nature, 2021, 593, 255-260.	27.8	179
1675	The gill transcriptome reveals unique antimicrobial features that protect Nibeaalbiflora from Cryptocaryonirritans infection. Journal of Fish Diseases, 2021, 44, 1215-1227.	1.9	6
1677	TIPS: trajectory inference of pathway significance through pseudotime comparison for functional assessment of single-cell RNAseq data. Briefings in Bioinformatics, 2021, 22, .	6.5	8
1678	Enhancing clinical and immunological effects of anti-PD-1 with belapectin, a galectin-3 inhibitor. , 2021, 9, e002371.		44
1679	Multi-cohort analysis of host immune response identifies conserved protective and detrimental modules associated with severity across viruses. Immunity, 2021, 54, 753-768.e5.	14.3	42
1680	Incorporation of a nucleoside analog maps genome repair sites in postmitotic human neurons. Science, 2021, 372, 91-94.	12.6	68
1681	Oncogenic translation directs spliceosome dynamics revealing an integral role for SF3A3 in breast cancer. Molecular Cell, 2021, 81, 1453-1468.e12.	9.7	31

#	Article	IF	Citations
1684	Cotranscriptional and Posttranscriptional Features of the Transcriptome in Soybean Shoot Apex and Leaf. Frontiers in Plant Science, 2021, 12, 649634.	3.6	6
1685	Integrated Analysis of the Transcriptome and Metabolome Revealed Candidate Genes Involved in GA3-Induced Dormancy Release in Leymus chinensis Seeds. International Journal of Molecular Sciences, 2021, 22, 4161.	4.1	10
1686	Genome-wide association and transcriptome studies identify candidate genes and pathways for feed conversion ratio in pigs. BMC Genomics, 2021, 22, 294.	2.8	11
1687	RNA sequencing describes both population structure and plasticity-selection dynamics in a non-model fish. BMC Genomics, 2021, 22, 273.	2.8	9
1688	Patterns of Microbiome Variation Among Infrapopulations of Permanent Bloodsucking Parasites. Frontiers in Microbiology, 2021, 12, 642543.	3.5	6
1689	The miR-424(322)/503 gene cluster regulates pro- versus anti-inflammatory skin DC subset differentiation by modulating TGF-Î² signaling. Cell Reports, 2021, 35, 109049.	6.4	4
1691	Indole-3-Carbinolâ€“Dependent Aryl Hydrocarbon Receptor Signaling Attenuates the Inflammatory Response in Experimental Necrotizing Enterocolitis. ImmunoHorizons, 2021, 5, 193-209.	1.8	14
1692	Targeting autocrine amphiregulin robustly and reproducibly inhibits ovarian cancer in a syngeneic model: roles for wildtype p53. Oncogene, 2021, 40, 3665-3679.	5.9	8
1693	Quantifying splice-site usage: a simple yet powerful approach to analyze splicing. NAR Genomics and Bioinformatics, 2021, 3, lqab041.	3.2	7
1694	NASA GeneLab RNA-seq consensus pipeline: Standardized processing of short-read RNA-seq data. IScience, 2021, 24, 102361.	4.1	20
1697	An integrated multi-omics analysis identifies prognostic molecular subtypes of non-muscle-invasive bladder cancer. Nature Communications, 2021, 12, 2301.	12.8	159
1698	Multi-omics phenotyping of the gut-liver axis reveals metabolic perturbations from a low-dose pesticide mixture in rats. Communications Biology, 2021, 4, 471.	4.4	30
1699	Independence of chromatin conformation and gene regulation during Drosophila dorsoventral patterning. Nature Genetics, 2021, 53, 487-499.	21.4	108
1700	Proteomic Identification and Meta-Analysis in Salvia hispanica RNA-Seq de novo Assemblies. Plants, 2021, 10, 765.	3.5	2
1704	Sperm acrosome overgrowth and infertility in mice lacking chromosome 18 pachytene piRNA. PLoS Genetics, 2021, 17, e1009485.	3.5	39
1705	Distinct mRNAs in Cancer Extracellular Vesicles Activate Angiogenesis and Alter Transcriptome of Vascular Endothelial Cells. Cancers, 2021, 13, 2009.	3.7	5
1706	CAR directs T cell adaptation to bile acids in the small intestine. Nature, 2021, 593, 147-151.	27.8	36
1707	Erosion of human X chromosome inactivation causes major remodeling of the iPSC proteome. Cell Reports, 2021, 35, 109032.	6.4	23

#	Article	IF	Citations
1708	Genome-wide identification, evolution, and transcriptome-based expression profiling analysis of suppressors of cytokine signaling (SOCS) in grass carp (Ctenopharyngodon idella). Aquaculture, 2021, 536, 736484.	3.5	3
1709	Characterization of Type I Interferon-Associated Chemokines and Cytokines in Lacrimal Glands of Nonobese Diabetic Mice. International Journal of Molecular Sciences, 2021, 22, 3767.	4.1	7
1711	RNA Sequencing Reveals Distinct Immune Responses in the Chorioamniotic Membranes of Women with Preterm Labor and Microbial or Sterile Intra-amniotic Inflammation. Infection and Immunity, 2021, 89, .	2.2	24
1712	STARCH SYNTHASE 4 is required for normal starch granule initiation in amyloplasts of wheat endosperm. New Phytologist, 2021, 230, 2371-2386.	7.3	25
1713	Molecular Analysis of ZNF71 KRAB in Non-Small-Cell Lung Cancer. International Journal of Molecular Sciences, 2021, 22, 3752.	4.1	12
1714	TAZ-CAMTA1 and YAP-TFE3 alter the TAZ/YAP transcriptome by recruiting the ATAC histone acetyltransferase complex. ELife, 2021, 10, .	6.0	27
1715	The mode of expression divergence in Drosophila fat body is infection-specific. Genome Research, 2021, 31, 1024-1034.	5.5	7
1716	Best practices on the differential expression analysis of multi-species RNA-seq. Genome Biology, 2021, 22, 121.	8.8	51
1718	Functional roles of the chromatin remodeler SMARCA5 in mouse and bovine preimplantation embryosâ€. Biology of Reproduction, 2021, 105, 359-370.	2.7	9
1719	Studying Tumor Angiogenesis and Cancer Invasion in a Threeâ€Dimensional Vascularized Breast Cancer Microâ€Environment. Advanced Biology, 2021, 5, e2100090.	2.5	27
1722	A signaling pathway-driven bioinformatics pipeline for predicting therapeutics against emerging infectious diseases. F1000Research, 2021, 10, 330.	1.6	4
1723	Linking chondrocyte and synovial transcriptional profile to clinical phenotype in osteoarthritis. Annals of the Rheumatic Diseases, 2021, 80, 1070-1074.	0.9	25
1724	Developmental partitioning of SYK and ZAP70 prevents autoimmunity and cancer. Molecular Cell, 2021, 81, 2094-2111.e9.	9.7	17
1725	MDMX acts as a pervasive preleukemic-to-acute myeloid leukemia transition mechanism. Cancer Cell, 2021, 39, 529-547.e7.	16.8	17
1726	The 7SK/P-TEFb snRNP controls ultraviolet radiation-induced transcriptional reprogramming. Cell Reports, 2021, 35, 108965.	6.4	28
1727	Deconvoluting global cytokine signaling networks in natural killer cells. Nature Immunology, 2021, 22, 627-638.	14.5	31
1729	CF monocyte-derived macrophages have an attenuated response to extracellular vesicles secreted by airway epithelial cells. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2021, 320, L530-L544.	2.9	10
1730	Transcriptomic Responses of Deep-Sea Corals Experimentally Exposed to Crude Oil and Dispersant. Frontiers in Marine Science, 2021, 8, .	2.5	9

#	Article	IF	Citations
1731	The long and the short of it: unlocking nanopore long-read RNA sequencing data with short-read differential expression analysis tools. NAR Genomics and Bioinformatics, 2021, 3, lqab028.	3.2	26
1732	Nanopore Sequencing and Hi-C Based De Novo Assembly of Trachidermus fasciatus Genome. Genes, 2021, 12, 692.	2.4	2
1733	Cholesterol-Induced M4-Like Macrophages Recruit Neutrophils and Induce NETosis. Frontiers in Immunology, 2021, 12, 671073.	4.8	11
1734	Induction of OCT2 contributes to regulate the gene expression program in human neutrophils activated via TLR8. Cell Reports, 2021, 35, 109143.	6.4	14
1736	Sex-specific nicotine sensitization and imprinting of self-administration in rats inform GWAS findings on human addiction phenotypes. Neuropsychopharmacology, 2021, 46, 1746-1756.	5.4	4
1738	HDAC1 SUMOylation promotes Argonaute-directed transcriptional silencing in C. elegans. ELife, 2021, 10, .	6.0	18
1739	Potential Role and Clinical Value of PPP2CA in Hepatocellular Carcinoma. Journal of Clinical and Translational Hepatology, 2021, 000, 000-000.	1.4	6
1740	Platelets orchestrate the resolution of pulmonary inflammation in mice by T reg cell repositioning and macrophage education. Journal of Experimental Medicine, 2021, 218, .	8.5	30
1741	Anti-bias training for (sc)RNA-seq: experimental and computational approaches to improve precision. Briefings in Bioinformatics, 2021, 22, .	6.5	8
1742	TimiRGeN: R/Bioconductor package for time series microRNAâ€“mRNA integration and analysis. Bioinformatics, 2021, 37, 3604-3609.	4.1	5
1743	Multiple integrated metabolic strategies allow foraminiferan protists to thrive in anoxic marine sediments. Science Advances, 2021, 7, .	10.3	20
1744	Dynamic transcriptome and histomorphology analysis of developmental traits of hindlimb thigh muscle from Odorrana tormota and its adaptability to different life history stages. BMC Genomics, 2021, 22, 369.	2.8	1
1745	NHR-49/PPAR-Î± and HLH-30/TFEB cooperate for C. elegans host defense via a flavin-containing monooxygenase. ELife, 2021, 10, .	6.0	37
1746	Adaptive Proteome Diversification by Nonsynonymous A-to-I RNA Editing in Coleoid Cephalopods. Molecular Biology and Evolution, 2021, 38, 3775-3788.	8.9	22
1748	Experimental and natural evidence of SARS-CoV-2-infection-induced activation of type I interferon responses. IScience, 2021, 24, 102477.	4.1	49
1749	The multiple myeloma microenvironment is defined by an inflammatory stromal cell landscape. Nature Immunology, 2021, 22, 769-780.	14.5	107
1750	Pharmacological activation of STING blocks SARS-CoV-2 infection. Science Immunology, 2021, 6, .	11.9	123
1751	Smelling in the dark: Phylogenomic insights into the chemosensory system of a subterranean beetle. Molecular Ecology, 2021, 30, 2573-2590.	3.9	9

#	Article	IF	Citations
1752	Setd1a Plays Pivotal Roles for the Survival and Proliferation of Retinal Progenitors via Histone Modifications of Uhrf1. , 2021, 62, 1.		4
1753	Exact transcript quantification over splice graphs. Algorithms for Molecular Biology, 2021, 16, 5.	1.2	4
1755	Tumor and immune reprogramming during immunotherapy in advanced renal cell carcinoma. Cancer Cell, 2021, 39, 649-661.e5.	16.8	263
1756	Pluripotent stem cell-derived endometrial stromal fibroblasts in a cyclic, hormone-responsive, coculture model of human decidua. Cell Reports, 2021, 35, 109138.	6.4	30
1757	Comprehensive Transcriptome Analysis of Rare Carpinus putoensis Plants under NO2 stress. Genes, 2021, 12, 754.	2.4	7
1758	PIE-1 SUMOylation promotes germline fates and piRNA-dependent silencing in C. elegans. ELife, 2021, 10, .	6.0	13
1759	Liver Transcriptome Dynamics During Hibernation Are Shaped by a Shifting Balance Between Transcription and RNA Stability. Frontiers in Physiology, 2021, 12, 662132.	2.8	11
1760	Mutant three-repeat tau expression initiates retinal ganglion cell death through Caspase-2. Neurobiology of Disease, 2021, 152, 105277.	4.4	3
1761	Androgen signaling uses a writer and a reader of ADP-ribosylation to regulate protein complex assembly. Nature Communications, 2021, 12, 2705.	12.8	15
1762	Distributed-Memory k-mer Counting on GPUs. , 2021, , .		3
1764	Differential gene expression in Drosophila melanogaster and D. nigrosparsa infected with the same Wolbachia strain. Scientific Reports, 2021, 11, 11336.	3.3	7
1765	IsoSplitter: identification and characterization of alternative splicing sites without a reference genome. Rna, 2021, 27, 868-875.	3.5	4
1766	Efficient RNA polymerase II pause release requires U2 snRNP function. Molecular Cell, 2021, 81, 1920-1934.e9.	9.7	45
1767	The bundle sheath of rice is conditioned to play an active role in water transport as well as sulfur assimilation and jasmonic acid synthesis. Plant Journal, 2021, 107, 268-286.	5.7	21
1768	Diurnal transcript profiling of the diatom Seminavis robusta reveals adaptations to a benthic lifestyle. Plant Journal, 2021, 107, 315-336.	5.7	15
1769	Conserved, divergent and heterochronic gene expression during Brachypodium and Arabidopsis embryo development. Plant Reproduction, 2021, 34, 207-224.	2.2	22
1770	The RNA landscape of the human placenta in health and disease. Nature Communications, 2021, 12, 2639.	12.8	75
1771	A synthetic RNA editing factor edits its target site in chloroplasts and bacteria. Communications Biology, 2021, 4, 545.	4.4	28

#	Article	IF	Citations
1773	Facultative symbiosis with a saprotrophic soil fungus promotes potassium uptake in American sweetgum trees. Plant, Cell and Environment, 2021, 44, 2793-2809.	5.7	23
1774	The holobiont transcriptome of teneral tsetse fly species of varying vector competence. BMC Genomics, 2021, 22, 400.	2.8	4
1775	SIRT7 regulates lipogenesis in adipocytes through deacetylation of PPARÎ³2. Journal of Diabetes Investigation, 2021, 12, 1765-1774.	2.4	9
1776	Adaptive evolution of Moniliophthora PR-1 proteins towards its pathogenic lifestyle. Bmc Ecology and Evolution, 2021, 21, 84.	1.6	1
1778	Dynamics of SAS-I mediated H4 K16 acetylation during DNA replication in yeast. PLoS ONE, 2021, 16, e0251660.	2.5	1
1780	Cerebrovascular insufficiency and amyloidogenic signaling in Ossabaw swine with cardiometabolic heart failure. JCI Insight, 2021, 6, .	5.0	8
1782	Species and population specific gene expression in blood transcriptomes of marine turtles. BMC Genomics, 2021, 22, 346.	2.8	9
1783	DIOXYGENASE FOR AUXIN OXIDATION 1 catalyzes the oxidation of IAA amino acid conjugates. Plant Physiology, 2021, 187, 103-115.	4.8	22
1785	Metatranscriptomic outlook on green and brown food webs in acid mine drainage. Environmental Microbiology Reports, 2021, 13, 606-615.	2.4	4
1786	ULK1 inhibition overcomes compromised antigen presentation and restores antitumor immunity in LKB1-mutant lung cancer. Nature Cancer, 2021, 2, 503-514.	13.2	72
1787	Bisphenol A biodegradation differs between mudflat and mangrove forest sediments. Chemosphere, 2021, 270, 128664.	8.2	14
1788	Crohn's disease-associated ATG16L1 T300A genotype is associated with improved survival in gastric cancer. EBioMedicine, 2021, 67, 103347.	6.1	10
1790	Abnormal neonatal sodium handling in skin precedes hypertension in the SAME rat. Pflugers Archiv European Journal of Physiology, 2021, 473, 897-910.	2.8	3
1791	Multi-Omic Meta-Analysis of Transcriptomes and the Bibliome Uncovers Novel Hypoxia-Inducible Genes. Biomedicines, 2021, 9, 582.	3.2	18
1792	Diverse Molecular Mechanisms Contribute to Differential Expression of Human Duplicated Genes. Molecular Biology and Evolution, 2021, 38, 3060-3077.	8.9	11
1793	Evaluation of morphological traits, hormonal metabolism, and transcriptional abundance in bitter gourd (Momordica charantia L.) plants in response to ethephon inducement. Scientia Horticulturae, 2021, 282, 110033.	3.6	3
1794	Integrated genomic analysis reveals key features of long undecoded transcript isoform-based gene repression. Molecular Cell, 2021, 81, 2231-2245.e11.	9.7	20
1795	Divergent clonal differentiation trajectories establish CD8+ memory TÂcell heterogeneity during acute viral infections in humans. Cell Reports, 2021, 35, 109174.	6.4	9

#	Article	IF	Citations
1796	Transcriptomic Analysis of Resistant and Susceptible Responses in a New Model Root-Knot Nematode Infection System Using Solanum torvum and Meloidogyne arenaria. Frontiers in Plant Science, 2021, 12, 680151.	3.6	16
1797	Multi-Omics Model Applied to Cancer Genetics. International Journal of Molecular Sciences, 2021, 22, 5751.	4.1	19
1798	satuRn:ÂScalable analysis of differential transcript usageÂfor bulk and single-cell RNA-sequencing applications. F1000Research, 0, 10, 374.	1.6	17
1799	Transcriptomic Analysis of Skin Color in Anole Lizards. Genome Biology and Evolution, 2021, 13, .	2.5	6
1800	As above, so below: Whole transcriptome profiling demonstrates strong molecular similarities between avian dorsal and ventral pallial subdivisions. Journal of Comparative Neurology, 2021, 529, 3222-3246.	1.6	15
1801	Matrix stiffening induces a pathogenic QKI-miR-7-SRSF1 signaling axis in pulmonary arterial endothelial cells. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2021, 320, L726-L738.	2.9	13
1802	SPEAQeasy: a scalable pipeline for expression analysis and quantification for R/bioconductor-powered RNA-seq analyses. BMC Bioinformatics, 2021, 22, 224.	2.6	14
1803	DNMT3A haploinsufficiency causes dichotomous DNA methylation defects at enhancers in mature human immune cells. Journal of Experimental Medicine, 2021, 218, .	8.5	16
1804	TIGIT and PD-1 Immune Checkpoint Pathways Are Associated With Patient Outcome and Anti-Tumor Immunity in Glioblastoma. Frontiers in Immunology, 2021, 12, 637146.	4.8	32
1805	Multi-omic profiling of lung and liver tumor microenvironments of metastatic pancreatic cancer reveals site-specific immune regulatory pathways. Genome Biology, 2021, 22, 154.	8.8	30
1806	Genome-wide CRISPRi/a screens in human neurons link lysosomal failure to ferroptosis. Nature Neuroscience, 2021, 24, 1020-1034.	14.8	170
1807	Acetylation of PAX7 controls muscle stem cell self-renewal and differentiation potential in mice. Nature Communications, 2021, 12, 3253.	12.8	31
1809	Nuclear isoform of FGF13 regulates post-natal neurogenesis in the hippocampus through an epigenomic mechanism. Cell Reports, 2021, 35, 109127.	6.4	5
1813	Developmental bifurcation of human T follicular regulatory cells. Science Immunology, 2021, 6, .	11.9	22
1814	Transcriptomic Signature Differences BetweenÂSARS-CoV-2 and Influenza Virus Infected Patients. Frontiers in Immunology, 2021, 12, 666163.	4.8	27
1817	The reference genome of Miscanthus floridulus illuminates the evolution of Saccharinae. Nature Plants, 2021, 7, 608-618.	9.3	23
1818	Changes in Cell Wall Structure During Rhizoid Formation of Silvetia babingtonii (Fucales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 Td (	2.3	3
1819	High-throughput full-length single-cell RNA-seq automation. Nature Protocols, 2021, 16, 2886-2915.	12.0	13

#	Article	IF	Citations
1820	Mapping Rora expression in resting and activated CD4+ T cells. PLoS ONE, 2021, 16, e0251233.	2.5	29
1825	PP1 regulatory subunit NIPP1 regulates transcription of E2F1 target genes following DNA damage. Cancer Science, 2021, 112, 2739-2752.	3.9	3
1826	Machine Intelligence in Single-Cell Data Analysis: Advances and New Challenges. Frontiers in Genetics, 2021, 12, 655536.	2.3	33
1827	Gene Expression Correlation Analysis Reveals MYC-NAC Regulatory Network in Cotton Pigment Gland Development. International Journal of Molecular Sciences, 2021, 22, 5007.	4.1	3
1828	Selective Requirement of MYB for Oncogenic Hyperactivation of a Translocated Enhancer in Leukemia. Cancer Discovery, 2021, 11, 2868-2883.	9.4	25
1829	Functionally distinct POMC-expressing neuron subpopulations in hypothalamus revealed by intersectional targeting. Nature Neuroscience, 2021, 24, 913-929.	14.8	64
1830	Genomic Imprinting at the Porcine DIRAS3 Locus. Animals, 2021, 11, 1315.	2.3	4
1832	Comparative transcriptome analysis reveals key epigenetic targets in SARS-CoV-2 infection. Npj Systems Biology and Applications, 2021, 7, 21.	3.0	32
1833	ACTOR: a latent Dirichlet model to compare expressed isoform proportions to a reference panel. Biostatistics, 2023, 24, 388-405.	1.5	0
1834	Comparative evaluation of full-length isoform quantification from RNA-Seq. BMC Bioinformatics, 2021, 22, 266.	2.6	15
1835	Transcriptional and epi-transcriptional dynamics of SARS-CoV-2 during cellular infection. Cell Reports, 2021, 35, 109108.	6.4	25
1836	Altered lipid metabolism marks glioblastoma stem and non-stem cells in separate tumor niches. Acta Neuropathologica Communications, 2021, 9, 101.	5.2	60
1837	Combining QTL Mapping and Transcriptomics to Decipher the Genetic Architecture of Phenolic Compounds Metabolism in the Conifer White Spruce. Frontiers in Plant Science, 2021, 12, 675108.	3.6	7
1840	Inflammasome Activation in Ankylosing Spondylitis Is Associated With Gut Dysbiosis. Arthritis and Rheumatology, 2021, 73, 1189-1199.	5.6	32
1843	Metagenome and analysis of metabolic potential of the microbial community in pit mud used for Chinese strong-flavor liquor production. Food Research International, 2021, 143, 110294.	6.2	33
1844	Patient Derived Colonoids as Drug Testing Platformsâ€“Critical Importance of Oxygen Concentration. Frontiers in Pharmacology, 2021, 12, 679741.	3.5	8
1848	Dysregulation of COVID-19 related gene expression in the COPD lung. Respiratory Research, 2021, 22, 164.	3.6	22
1850	Natural CO₂ seeps reveal adaptive potential to ocean acidification in fish. Evolutionary Applications, 2021, 14, 1794-1806.	3.1	9

#	Article	IF	Citations
1851	Characteristics of RNA alternative splicing and its potential roles in ginsenoside biosynthesis in a single plant of ginseng, Panax ginseng C.A. Meyer. Molecular Genetics and Genomics, 2021, 296, 971-983.	2.1	5
1852	Bacterial Quorum-Sensing Signal Arrests Phytoplankton Cell Division and Impacts Virus-Induced Mortality. MSphere, 2021, 6, .	2.9	16
1853	Synaptic FUS accumulation triggers early misregulation of synaptic RNAs in a mouse model of ALS. Nature Communications, 2021, 12, 3027.	12.8	39
1854	Mitofusin-2 boosts innate immunity through the maintenance of aerobic glycolysis and activation of xenophagy in mice. Communications Biology, 2021, 4, 548.	4.4	16
1855	FOXA1 and adaptive response determinants to HER2 targeted therapy in TBCRC 036. Npj Breast Cancer, 2021, 7, 51.	5.2	11
1857	Increased whiB7 expression and antibiotic resistance in Mycobacterium chelonae carrying two prophages. BMC Microbiology, 2021, 21, 176.	3.3	7
1858	High-fat diet-activated fatty acid oxidation mediates intestinal stemness and tumorigenicity. Cell Reports, 2021, 35, 109212.	6.4	85
1859	Computational comparison of common event-based differential splicing tools: practical considerations for laboratory researchers. BMC Bioinformatics, 2021, 22, 347.	2.6	12
1862	Adherent and suspension baby hamster kidney cells have a different cytoskeleton and surface receptor repertoire. PLoS ONE, 2021, 16, e0246610.	2.5	2
1863	Alternative migratory tactics in brown trout (Salmo trutta) are underpinned by divergent regulation of metabolic but not neurological genes. Ecology and Evolution, 2021, 11, 8347-8362.	1.9	3
1864	Endothelial SOCS3 maintains homeostasis and promotes survival in endotoxemic mice. JCI Insight, 2021, 6, .	5.0	20
1866	Successful ATAC-Seq From Snap-Frozen Equine Tissues. Frontiers in Genetics, 2021, 12, 641788.	2.3	8
1868	Deletion of Lats1/2 in adult kidney epithelia leads to renal cell carcinoma. Journal of Clinical Investigation, 2021, 131, .	8.2	12
1869	De novo Transcriptome Sequencing Coupled With Co-expression Analysis Reveal the Transcriptional Regulation of Key Genes Involved in the Formation of Active Ingredients in Peucedanum praeruptorum Dunn Under Bolting Period. Frontiers in Genetics, 2021, 12, 683037.	2.3	10
1870	Analysis of the transcriptome of bovine endometrial cells isolated by laser micro-dissection (2): impacts of post-partum negative energy balance on stromal, glandular and luminal epithelial cells. BMC Genomics, 2021, 22, 450.	2.8	7
1871	Analysis workflow of publicly available RNA-sequencing datasets. STAR Protocols, 2021, 2, 100478.	1.2	9
1873	Increased colonic expression of ACE2 associates with poor prognosis in Crohnâ€™s disease. Scientific Reports, 2021, 11, 13533.	3.3	14
1874	Reconstruction of the full-length transcriptome of cigar tobacco without a reference genome and characterization of anion channel/transporter transcripts. BMC Plant Biology, 2021, 21, 299.	3.6	3

#	Article	IF	Citations
1875	RNA-binding proteins regulate aldosterone homeostasis in human steroidogenic cells. Rna, 2021, 27, 933-945.	3.5	5
1876	Rootstock effects on scion gene expression in maritime pine. Scientific Reports, 2021, 11, 11582.	3.3	12
1877	Transcriptomic analyses of gastrulation-stage mouse embryos with differential susceptibility to alcohol. DMM Disease Models and Mechanisms, 2021, 14, .	2.4	19
1878	Degradation of biological macromolecules supports uncultured microbial populations in Guaymas Basin hydrothermal sediments. ISME Journal, 2021, 15, 3480-3497.	9.8	22
1880	PuffAligner: a fast, efficient and accurate aligner based on the Pufferfish index. Bioinformatics, 2021, 37, 4048-4055.	4.1	19
1881	A Case Series of Metastatic Metaplastic Breast Carcinoma Treated With Anti-PD-1 Therapy. Frontiers in Oncology, 2021, 11, 635237.	2.8	17
1882	Invasion of the body snatchers: the role of parasite introduction in host distribution and response to salinity in invaded estuaries. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20210703.	2.6	9
1883	Proteogenomics Reveals Orthologous Alternatively Spliced Proteoforms in the Same Human and Mouse Brain Regions with Differential Abundance in an Alzheimerâ€™s Disease Mouse Model. Cells, 2021, 10, 1583.	4.1	4
1884	Photosynthesis-independent production of reactive oxygen species in the rice bundle sheath during high light is mediated by NADPH oxidase. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	32
1885	Transcriptional Profiles Reveal Deregulation of Lipid Metabolism and Inflammatory Pathways in Neurons Exposed to Palmitic Acid. Molecular Neurobiology, 2021, 58, 4639-4651.	4.0	3
1888	Balancing precision versus cohort transcriptomic analysis of acute and recovery phase of viral bronchiolitis. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2021, 320, L1147-L1157.	2.9	9
1892	Replicate sequencing libraries are important for quantification of allelic imbalance. Nature Communications, 2021, 12, 3370.	12.8	13
1894	Computational search of hybrid human/SARS-CoV-2 dsRNA reveals unique viral sequences that diverge from those of other coronavirus strains. Heliyon, 2021, 7, e07284.	3.2	10
1895	Pathomechanisms and biomarkers in facioscapulohumeral muscular dystrophy: roles of DUX4 and PAX7. EMBO Molecular Medicine, 2021, 13, e13695.	6.9	39
1900	Analysis of the transcriptome of bovine endometrial cells isolated by laser micro-dissection (1): specific signatures of stromal, glandular and luminal epithelial cells. BMC Genomics, 2021, 22, 451.	2.8	10
1901	Isolating the Role of Corticosterone in the Hypothalamic-Pituitary-Gonadal Transcriptomic Stress Response. Frontiers in Endocrinology, 2021, 12, 632060.	3.5	11
1902	Transcriptional Profiling Identifies Upregulation of Neuroprotective Pathways in Retinitis Pigmentosa. International Journal of Molecular Sciences, 2021, 22, 6307.	4.1	4
1903	Splice site m6A methylation prevents binding of U2AF35 to inhibit RNA splicing. Cell, 2021, 184, 3125-3142.e25.	28.9	103

#	Article	IF	Citations
1906	Dynamics of alternative splicing during somatic cell reprogramming reveals functions for RNA-binding proteins CPSF3, hnRNP UL1, and TIA1. Genome Biology, 2021, 22, 171.	8.8	12
1907	The transcriptome of anal papillae of Aedes aegypti reveals their importance in xenobiotic detoxification and adds significant knowledge on ion, water and ammonia transport mechanisms. Journal of Insect Physiology, 2021, 132, 104269.	2.0	14
1908	MOCCASIN: a method for correcting for known and unknown confounders in RNA splicing analysis. Nature Communications, 2021, 12, 3353.	12.8	12
1909	Type II alveolar cell MHCII improves respiratory viral disease outcomes while exhibiting limited antigen presentation. Nature Communications, 2021, 12, 3993.	12.8	25
1910	Sickle-trait hemoglobin reduces adhesion to both CD36 and EPCR by Plasmodium falciparum-infected erythrocytes. PLoS Pathogens, 2021, 17, e1009659.	4.7	8
1912	Widespread formation of double-stranded RNAs in testis. Genome Research, 2021, 31, 1174-1186.	5.5	6
1915	PGE2 Supplementation of Oocyte Culture Media Improves the Developmental and Cryotolerance Performance of Bovine Blastocysts Derived From a Serum-Free in vitro Production System, Mirroring the Inner Cell Mass Transcriptome. Frontiers in Cell and Developmental Biology, 2021, 9, 672948.	3.7	3
1917	Flower induction and development in saffron: Timing and hormone signalling pathways. Industrial Crops and Products, 2021, 164, 113370.	5.2	18
1918	Granzyme B prevents aberrant IL-17 production and intestinal pathogenicity in CD4+ T cells. Mucosal Immunology, 2021, 14, 1088-1099.	6.0	13
1919	Genomic insights into the sessile life and biofouling of barnacles (Crustacea: Cirripedia). Heliyon, 2021, 7, e07291.	3.2	7
1920	Virusâ€“Host Interaction Gets Curiouser and Curiouser. PART II: Functional Transcriptomics of the E. coli DksA-Deficient Cell upon Phage P1vir Infection. International Journal of Molecular Sciences, 2021, 22, 6159.	4.1	4
1921	PRLâ€3 induces a positive signaling circuit between glycolysis and activation of STAT1/2. FEBS Journal, 2021, 288, 6700-6715.	4.7	9
1924	Frataxin deficiency promotes endothelial senescence in pulmonary hypertension. Journal of Clinical Investigation, 2021, 131, .	8.2	38
1925	RNAdetector: a free user-friendly stand-alone and cloud-based system for RNA-Seq data analysis. BMC Bioinformatics, 2021, 22, 298.	2.6	7
1928	HCV poly U/UC sequenceâ€“induced inflammation leads to metabolic disorders in vulvar lichen sclerosis. Life Science Alliance, 2021, 4, e202000906.	2.8	4
1929	NANOS2 is a sequence-specific mRNA-binding protein that promotes transcript degradation in spermatogonial stem cells. IScience, 2021, 24, 102762.	4.1	11
1931	First de novo transcriptome analysis of the Antarctic springtail Cryptopygus terranovus (Collembola:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.9	2
1932	Gene expression analysis in EBV-infected ataxia-telangiectasia cell lines by RNA-sequencing reveals protein synthesis defect and immune abnormalities. Orphanet Journal of Rare Diseases, 2021, 16, 288.	2.7	1

#	Article	IF	Citations
1933	Human Chr18 transcriptome dataset combined from the Illumina HiSeq, ONT MinION, and qPCR data. Data in Brief, 2021, 36, 107130.	1.0	3
1935	Serine residues 726 and 780 have nonredundant roles regulating STAT5a activity in luminal breast cancer. Scientific Reports, 2021, 11, 13506.	3.3	6
1936	Co-expression analysis identifies neuro-inflammation as a driver of sensory neuron aging in Aplysia californica. PLoS ONE, 2021, 16, e0252647.	2.5	4
1937	Homeotic transformation from stamen to petal in Lilium is associated with MADS-box genes and hormone signal transduction. Plant Growth Regulation, 2021, 95, 49-64.	3.4	8
1938	LIQA: long-read isoform quantification and analysis. Genome Biology, 2021, 22, 182.	8.8	49
1940	Kmerator Suite: design of specific k-mer signatures and automatic metadata discovery in large RNA-seq datasets. NAR Genomics and Bioinformatics, 2021, 3, lqab058.	3.2	2
1943	Gene Dosage- and Age-Dependent Differential Transcriptomic Changes in the Prefrontal Cortex of Shank2-Mutant Mice. Frontiers in Molecular Neuroscience, 2021, 14, 683196.	2.9	5
1946	LABRAT reveals association of alternative polyadenylation with transcript localization, RNA binding protein expression, transcription speed, and cancer survival. BMC Genomics, 2021, 22, 476.	2.8	29
1947	Gene expression changes and DNA damage after ex vivo exposure of peripheral blood cells to various CT photon spectra. Scientific Reports, 2021, 11, 12060.	3.3	7
1948	miR-24 controls the regenerative competence of hair follicle progenitors by targeting Plk3. Cell Reports, 2021, 35, 109225.	6.4	7
1949	Comparative transcriptome analysis reveals genes and pathways associated with anthocyanins in strawberry. Journal of Berry Research, 2021, 11, 317-332.	1.4	7
1950	Unique integrated stress response sensors regulate cancer cell susceptibility when Hsp70 activity is compromised. ELife, 2021, 10, .	6.0	12
1951	AQUARIUM: accurate quantification of circular isoforms using model-based strategy. Bioinformatics, 2021, 37, 4879-4881.	4.1	2
1952	T cells, particularly activated CD4+ cells, maintain anti-CD20-mediated NK cell viability and antibody dependent cellular cytotoxicity. Cancer Immunology, Immunotherapy, 2022, 71, 237-249.	4.2	7
1954	Modeling transcriptomic age using knowledge-primed artificial neural networks. Npj Aging and Mechanisms of Disease, 2021, 7, 15.	4.5	27
1955	Mobile element insertions and associated structural variants in longitudinal breast cancer samples. Scientific Reports, 2021, 11, 13020.	3.3	3
1956	Gene set enrichment analysis for genome-wide DNA methylation data. Genome Biology, 2021, 22, 173.	8.8	68
1957	Immune checkpoint blockade reprograms systemic immune landscape and tumor microenvironment in obesity-associated breast cancer. Cell Reports, 2021, 35, 109285.	6.4	38

#	Article	IF	Citations
1958	SMG5-SMG7 authorize nonsense-mediated mRNA decay by enabling SMG6 endonucleolytic activity. Nature Communications, 2021, 12, 3965.	12.8	54
1960	DNA-RNA Hybrid (R-Loop): From a Unified Picture of the Mammalian Telomere to the Genome-Wide Profile. Cells, 2021, 10, 1556.	4.1	6
1962	Differences in the genome, methylome, and transcriptome do not differentiate isolates of Streptococcus equi subsp. equi from horses with acute clinical signs from isolates of inapparent carriers. PLoS ONE, 2021, 16, e0252804.	2.5	4
1963	Integrating longitudinal clinical laboratory tests with targeted proteomic and transcriptomic analyses reveal the landscape of host responses in COVID-19. Cell Discovery, 2021, 7, 42.	6.7	23
1964	Vocal Fold Fibroblasts in Reinkeâ€™s Edema Show Alterations Involved in Extracellular Matrix Production, Cytokine Response and Cell Cycle Control. Biomedicines, 2021, 9, 735.	3.2	5
1965	Metabolome subtyping of severe bronchiolitis in infancy and risk of childhood asthma. Journal of Allergy and Clinical Immunology, 2022, 149, 102-112.	2.9	25
1966	Lactate dehydrogenase A-dependent aerobic glycolysis promotes natural killer cell anti-viral and anti-tumor function. Cell Reports, 2021, 35, 109210.	6.4	50
1967	A Chinese hamster transcription start site atlas that enables targeted editing of CHO cells. NAR Genomics and Bioinformatics, 2021, 3, lqab061.	3.2	7
1968	Genetic and gene expression analysis of flowering time regulation by light quality in lentil. Annals of Botany, 2021, 128, 481-496.	2.9	12
1969	TPM, FPKM, or Normalized Counts? A Comparative Study of Quantification Measures for the Analysis of RNA-seq Data from the NCI Patient-Derived Models Repository. Journal of Translational Medicine, 2021, 19, 269.	4.4	151
1970	Lung Epithelial Cell Transcriptional Regulation as a Factor in COVID-19â€“associated Coagulopathies. American Journal of Respiratory Cell and Molecular Biology, 2021, 64, 687-697.	2.9	26
1971	The Evolutionary History of Wild, Domesticated, and FeralBrassica oleracea(Brassicaceae). Molecular Biology and Evolution, 2021, 38, 4419-4434.	8.9	49
1972	Integrated omics endotyping of infants with respiratory syncytial virus bronchiolitis and risk of childhood asthma. Nature Communications, 2021, 12, 3601.	12.8	65
1973	Transcriptomics differentiate two novel bioactive strains of Paenibacillus sp. isolated from the perennial ryegrass seed microbiome. Scientific Reports, 2021, 11, 15545.	3.3	6
1974	Accurate transcriptome assembly by Nanopore RNA sequencing reveals novel functional transcripts in hepatocellular carcinoma. Cancer Science, 2021, 112, 3555-3568.	3.9	6
1977	A defect in the NOG gene increases susceptibility to spontaneous superficial chronic corneal epithelial defects (SCCED) in boxer dogs. BMC Veterinary Research, 2021, 17, 254.	1.9	5
1979	Towards omics-based predictions of planktonic functional composition from environmental data. Nature Communications, 2021, 12, 4361.	12.8	16
1981	Traumatic brain injury results in unique microglial and astrocyte transcriptomes enriched for type I interferon response. Journal of Neuroinflammation, 2021, 18, 151.	7.2	40

#	Article	IF	Citations
1982	In silico-driven analysis of the Glossina morsitans morsitans antennae transcriptome in response to repellent or attractant compounds. PeerJ, 2021, 9, e11691.	2.0	2
1983	Development of an Androgen Receptor Inhibitor Targeting the N-Terminal Domain of Androgen Receptor for Treatment of Castration Resistant Prostate Cancer. Cancers, 2021, 13, 3488.	3.7	16
1984	The small Cajal body-specific RNA 15 (SCARNA15) directs p53 and redox homeostasis via selective splicing in cancer cells. NAR Cancer, 2021, 3, zcab026.	3.1	17
1988	The Diversity, Composition, and Metabolic Pathways of Archaea in Pigs. Animals, 2021, 11, 2139.	2.3	8
1989	CD8+ tissue-resident memory T cells promote liver fibrosis resolution by inducing apoptosis of hepatic stellate cells. Nature Communications, 2021, 12, 4474.	12.8	86
1990	Single-molecule, full-length transcript isoform sequencing reveals disease-associated RNA isoforms in cardiomyocytes. Nature Communications, 2021, 12, 4203.	12.8	24
1991	Genome-wide identification of miRNAs and target regulatory network in the invasive ectoparasitic mite Varroa destructor. Genomics, 2021, 113, 2290-2303.	2.9	2
1992	Cell competition acts as a purifying selection to eliminate cells with mitochondrial defects during early mouse development. Nature Metabolism, 2021, 3, 1091-1108.	11.9	33
1993	Comparative Analysis of Host-Associated Variation in Phytophthora cactorum. Frontiers in Microbiology, 2021, 12, 679936.	3.5	10
1995	Transcriptome and metabolome analysis of crGART, a novel cell model of de novo purine synthesis deficiency: Alterations in CD36 expression and activity. PLoS ONE, 2021, 16, e0247227.	2.5	2
1996	Rapid Genomic Evolution Drives the Diversification of Male Reproductive Genes in Dung Beetles. Genome Biology and Evolution, 2021, 13, .	2.5	1
1998	Targeted Lipidomic Analysis of Aqueous Humor Reveals Signaling Lipid-Mediated Pathways in Primary Open-Angle Glaucoma. Biology, 2021, 10, 658.	2.8	11
1999	Polysulfide inhibits hypoxia-elicited hypoxia-inducible factor activation in a mitochondria-dependent manner. Mitochondrion, 2021, 59, 255-266.	3.4	8
2000	A conserved role for arrow in posterior axis patterning across Arthropoda. Developmental Biology, 2021, 475, 91-105.	2.0	14
2001	ANANSE: an enhancer network-based computational approach for predicting key transcription factors in cell fate determination. Nucleic Acids Research, 2021, 49, 7966-7985.	14.5	39
2002	Assessing the effect of treated erythromycin fermentation residue on antibiotic resistome in soybean planting soil: In situ field study. Science of the Total Environment, 2021, 779, 146329.	8.0	10
2006	Direct Molecular Evidence for an Ancient, Conserved Developmental Toolkit Controlling Posttranscriptional Gene Regulation in Land Plants. Molecular Biology and Evolution, 2021, 38, 4765-4777.	8.9	1
2007	RNAâ€sequencing highlights differential regulated pathways involved in cell cycle and inflammation in orbitofacial neurofibromas. Brain Pathology, 2022, 32, e13007.	4.1	2

#	Article	IF	Citations
2010	Genomics accelerated isolation of a new stem rust avirulence geneâ€“wheat resistance gene pair. Nature Plants, 2021, 7, 1220-1228.	9.3	67
2012	Srsf3 mediates alternative RNA splicing downstream of PDGFRÎ± signaling in the facial mesenchyme. Development (Cambridge), 2021, 148, .	2.5	10
2013	Transcriptome Response to Cadmium Exposure in Barley (Hordeum vulgare L.). Frontiers in Plant Science, 2021, 12, 629089.	3.6	17
2014	A Fusion Protein Complex that Combines IL-12, IL-15, and IL-18 Signaling to Induce Memory-Like NK Cells for Cancer Immunotherapy. Cancer Immunology Research, 2021, 9, 1071-1087.	3.4	36
2015	Weakened growth, cell division, and energy metabolism, but enhanced resistance, signaling, and anabolism: responses of Ulva prolifera to copper elucidated by omics. Journal of Applied Phycology, 2021, 33, 3449-3465.	2.8	10
2016	Diet-dependent sex differences in the response to vertical sleeve gastrectomy. American Journal of Physiology - Endocrinology and Metabolism, 2021, 321, E11-E23.	3.5	7
2017	Chia (Salvia hispanica) Gene Expression Atlas Elucidates Dynamic Spatio-Temporal Changes Associated With Plant Growth and Development. Frontiers in Plant Science, 2021, 12, 667678.	3.6	11
2019	Endogenous retrovirus envelope as a tumor-associated immunotherapeutic target in murine osteosarcoma. IScience, 2021, 24, 102759.	4.1	1
2020	Transcriptional response in the whiteleg shrimp (Penaeus vannamei) to short-term microplastic exposure. Aquaculture Reports, 2021, 20, 100713.	1.7	3
2021	Cross-platform transcriptional profiling identifies common and distinct molecular pathologies in Lewy body diseases. Acta Neuropathologica, 2021, 142, 449-474.	7.7	27
2022	WIND (Workflow for pIRNAs aNd beyonD): a strategy for in-depth analysis of small RNA-seq data. F1000Research, 2021, 10, 1.	1.6	22
2023	SPLICE-q: a Python tool for genome-wide quantification of splicing efficiency. BMC Bioinformatics, 2021, 22, 368.	2.6	7
2024	Seasonal Variation in Transcriptomic Profiling of Tetrastigma hemsleyanum Fully Developed Tuberous Roots Enriches Candidate Genes in Essential Metabolic Pathways and Phytohormone Signaling. Frontiers in Plant Science, 2021, 12, 659645.	3.6	12
2025	RyÅ«tÅ: improved multi-sample transcript assembly for differential transcript expression analysis and more. Bioinformatics, 2021, 37, 4307-4313.	4.1	3
2026	Post-transcriptional gene silencing of CYP76AD controls betalain biosynthesis in bracts of bougainvillea. Journal of Experimental Botany, 2021, 72, 6949-6962.	4.8	8
2027	CD177, a specific marker of neutrophil activation, is associated with coronavirus disease 2019 severity and death. IScience, 2021, 24, 102711.	4.1	79
2028	Molecular Mechanisms of Coral Persistence Within Highly Urbanized Locations in the Port of Miami, Florida. Frontiers in Marine Science, 2021, 8, .	2.5	14
2030	iTARGEX analysis of yeast deletome reveals novel regulators of transcriptional buffering in S phase and protein turnover. Nucleic Acids Research, 2021, 49, 7318-7329.	14.5	2

#	Article	IF	Citations
2034	Use of Oxidative Stress Responses to Determine the Efficacy of Inactivation Treatments on Cryptosporidium Oocysts. Microorganisms, 2021, 9, 1463.	3.6	5
2035	Microenvironmental innate immune signaling and cell mechanical responses promote tumor growth. Developmental Cell, 2021, 56, 1884-1899.e5.	7.0	20
2037	Novel Antarctic yeast adapts to cold by switching energy metabolism and increasing small RNA synthesis. ISME Journal, 2022, 16, 221-232.	9.8	21
2038	Venn diagram analysis overestimates the extent of circadian rhythm reprogramming. FEBS Journal, 2022, 289, 6605-6621.	4.7	40
2039	HIV Modifies the m6A and m5C Epitranscriptomic Landscape of the Host Cell. Frontiers in Virology, 2021, 1, .	1.4	6
2041	Systematic dissection of transcriptional regulatory networks by genome-scale and single-cell CRISPR screens. Science Advances, 2021, 7, .	10.3	19
2042	Establishment, maintenance, and recall of inflammatory memory. Cell Stem Cell, 2021, 28, 1758-1774.e8.	11.1	98
2043	Neuronal VCP loss of function recapitulates FTLD-TDP pathology. Cell Reports, 2021, 36, 109399.	6.4	25
2044	Reprogramming of the wheat transcriptome in response to infection with Claviceps purpurea, the causal agent of ergot. BMC Plant Biology, 2021, 21, 316.	3.6	6
2046	Genome-wide transcriptomic analysis of the forebrain of postnatal Slc13a4+/â^' mice. BMC Research Notes, 2021, 14, 269.	1.4	1
2047	Maize DNA Methylation in Response to Drought Stress Is Involved in Target Gene Expression and Alternative Splicing. International Journal of Molecular Sciences, 2021, 22, 8285.	4.1	18
2048	Differences in the Platelet mRNA Landscape Portend Racial Disparities in Platelet Function and Suggest Novel Therapeutic Targets. Clinical Pharmacology and Therapeutics, 2021, 110, 702-713.	4.7	5
2049	Wnt/Î²-Catenin Inhibition Disrupts Carboplatin Resistance in Isogenic Models of Triple-Negative Breast Cancer. Frontiers in Oncology, 2021, 11, 705384.	2.8	17
2051	Characterisation of Neurospheres-Derived Cells from Human Olfactory Epithelium. Cells, 2021, 10, 1690.	4.1	1
2052	The Arabidopsis Iron-Sulfur (Fe-S) Cluster Gene MFDX1 Plays a Role in Host and Nonhost Disease Resistance by Accumulation of Defense-Related Metabolites. International Journal of Molecular Sciences, 2021, 22, 7147.	4.1	5
2053	Sublethal doxorubicin promotes migration and invasion of breast cancer cells: role of Src Family non-receptor tyrosine kinases. Breast Cancer Research, 2021, 23, 76.	5.0	15
2056	Tunable phenotypic variability through an autoregulatory alternative sigma factor circuit. Molecular Systems Biology, 2021, 17, e9832.	7.2	9
2058	A functional genomic approach to identify reference genes for human pancreatic beta cell real-time quantitative RT-PCR analysis. Islets, 2021, 13, 51-65.	1.8	5

#	Article	IF	Citations
2059	Multiomic analysis of Schistosoma mansoni reveals unique expression profiles in cercarial heads and tails. Communications Biology, 2021, 4, 860.	4.4	2
2060	Seizure-mediated iron accumulation and dysregulated iron metabolism after status epilepticus and in temporal lobe epilepsy. Acta Neuropathologica, 2021, 142, 729-759.	7.7	31
2062	Embryonic development in the acoelHofstenia miamia. Development (Cambridge), 2021, 148, .	2.5	10
2063	Transcriptomic Profile Reveals Deregulation of Hearing-Loss Related Genes in Vestibular Schwannoma Cells Following Electromagnetic Field Exposure. Cells, 2021, 10, 1840.	4.1	3
2064	Gene Expression Profile of Human Mesenchymal Stromal Cells Exposed to Hypoxic and Pseudohypoxic Preconditioningâ€"An Analysis by RNA Sequencing. International Journal of Molecular Sciences, 2021, 22, 8160.	4.1	4
2065	The mitochondrial single-stranded DNA binding protein is essential for initiation of mtDNA replication. Science Advances, 2021, 7, .	10.3	36
2066	Cytosolic aggregation of mitochondrial proteins disrupts cellular homeostasis by stimulating the aggregation of other proteins. ELife, 2021, 10, .	6.0	49
2067	An Agrobacteriumâ€mediated stable transformation technique for the hornwort model Anthoceros agrestis. New Phytologist, 2021, 232, 1488-1505.	7.3	18
2068	Vertical Stratification of Dissolved Organic Matter Linked to Distinct Microbial Communities in Subtropic Estuarine Sediments. Frontiers in Microbiology, 2021, 12, 697860.	3.5	12
2070	Transcriptome Dynamics of Epidermal Reprogramming during Direct Shoot Regeneration in Torenia fournieri. Plant and Cell Physiology, 2021, 62, 1335-1354.	3.1	7
2071	Does intervention with GLP-1 receptor agonist semaglutide modulate perception of sweet taste in women with obesity: study protocol of a randomized, single-blinded, placebo-controlled clinical trial. Trials, 2021, 22, 464.	1.6	4
2072	High-Density Blood Transcriptomics Reveals Precision Immune Signatures of SARS-CoV-2 Infection in Hospitalized Individuals. Frontiers in Immunology, 2021, 12, 694243.	4.8	26
2074	Combining multiomics and drug perturbation profiles to identify muscle-specific treatments for spinal muscular atrophy. JCI Insight, 2021, 6, .	5.0	8
2075	Invasion history shapes host transcriptomic response to a bodyâ€snatching parasite. Molecular Ecology, 2021, 30, 4321-4337.	3.9	2
2076	A piRNA-lncRNA regulatory network initiates responder and trailer piRNA formation during mosquito embryonic development. Rna, 2021, 27, 1155-1172.	3.5	12
2077	Bract suppression regulated by the miR156/529-SPLs-NL1-PLA1 module is required for the transition from vegetative to reproductive branching in rice. Molecular Plant, 2021, 14, 1168-1184.	8.3	35
2078	The phase separation-dependent FUS interactome reveals nuclear and cytoplasmic function of liquidâ€"liquid phase separation. Nucleic Acids Research, 2021, 49, 7713-7731.	14.5	53
2079	Evidence of Immune Modulators in the Secretome of the Equine Tapeworm Anoplocephala perfoliata. Pathogens, 2021, 10, 912.	2.8	8

#	Article	IF	Citations
2080	The Dynamic Change of Gene-Regulated Networks in Cashmere Goat Skin with Seasonal Variation. Biochemical Genetics, 2021, , 1.	1.7	2
2081	Multi-omics analysis of glucose-mediated signaling by a moonlighting GÎ² protein Asc1/RACK1. PLoS Genetics, 2021, 17, e1009640.	3.5	13
2082	Preprocessing of Public RNA-Sequencing Datasets to Facilitate Downstream Analyses of Human Diseases. Data, 2021, 6, 75.	2.3	1
2084	Comparing the Predictivity of Human Placental Gene, microRNA, and CpG Methylation Signatures in Relation to Perinatal Outcomes. Toxicological Sciences, 2021, 183, 269-284.	3.1	9
2085	A duplicated amh is the master sex-determining gene for Sebastes rockfish in the Northwest Pacific. Open Biology, 2021, 11, 210063.	3.6	40
2086	Systematic analysis of SARS-CoV-2 infection of an ACE2-negative human airway cell. Cell Reports, 2021, 36, 109364.	6.4	109
2087	De novo transcriptome assembly of the Southern Ocean copepod Rhincalanus gigas sheds light on developmental changes in gene expression. Marine Genomics, 2021, 58, 100835.	1.1	8
2088	iRGvalid: A Robust in silico Method for Optimal Reference Gene Validation. Frontiers in Genetics, 2021, 12, 716653.	2.3	0
2089	Sex-Biased Gene Expression of Mesobuthus martensii Collected from Gansu Province, China, Reveals Their Different Therapeutic Potentials. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-15.	1.2	3
2090	A signaling pathway-driven bioinformatics pipeline for predicting therapeutics against emerging infectious diseases. F1000Research, 0, 10, 330.	1.6	8
2091	Single-Cell Transcriptomics Reveals Core Regulatory Programs That Determine the Heterogeneity of Circulating and Tissue-Resident Memory CD8+ T Cells. Cells, 2021, 10, 2143.	4.1	18
2092	Microbiota Perturbation or Elimination Can Inhibit Normal Development and Elicit a Starvation-Like Response in an Omnivorous Model Invertebrate. MSystems, 2021, 6, e0080221.	3.8	11
2093	Catching SARS-CoV-2 by Sequence Hybridization: a Comparative Analysis. MSystems, 2021, 6, e0039221.	3.8	11
2094	Genetic and Epigenetic Characteristics of Inflammatory Bowel Diseaseâ€“Associated Colorectal Cancer. Gastroenterology, 2021, 161, 592-607.	1.3	81
2096	Technology dictates algorithms: recent developments in read alignment. Genome Biology, 2021, 22, 249.	8.8	51
2097	Glatiramer acetate enhances tumor retention and innate activation of immunostimulants. International Journal of Pharmaceutics, 2021, 605, 120812.	5.2	6
2098	ACE2 protein expression within isogenic cell lines is heterogeneous and associated with distinct transcriptomes. Scientific Reports, 2021, 11, 15900.	3.3	24
2099	Transcriptional reprogramming by oxidative stress occurs within a predefined chromatin accessibility landscape. Free Radical Biology and Medicine, 2021, 171, 319-331.	2.9	6

#	Article	IF	Citations
2100	Red and blue light treatments of ripening bilberry fruits reveal differences in signalling through abscisic acidâ€regulated anthocyanin biosynthesis. Plant, Cell and Environment, 2021, 44, 3227-3245.	5.7	51
2101	Development of the genomic inflammatory index (GII) to assess key maternal antecedents associated with placental inflammation. Placenta, 2021, 111, 82-90.	1.5	1
2102	PPARÎ³-induced upregulation of subcutaneous fat adiponectin secretion, glyceroneogenesis and BCAA oxidation requires mTORC1 activity. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2021, 1866, 158967.	2.4	10
2103	The exon-junction complex helicase eIF4A3 controls cell fate via coordinated regulation of ribosome biogenesis and translational output. Science Advances, 2021, 7, .	10.3	25
2104	qTeller: a tool for comparative multi-genomic gene expression analysis. Bioinformatics, 2021, 38, 236-242.	4.1	15
2106	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. Cell Systems, 2021, 12, 827-838.e5.	6.2	15
2107	Coordination between growth and stress responses by DELLA in the liverwort Marchantia polymorpha. Current Biology, 2021, 31, 3678-3686.e11.	3.9	28
2111	GM-CSF drives myelopoiesis, recruitment and polarisation of tumour-associated macrophages in cholangiocarcinoma and systemic blockade facilitates antitumour immunity. Gut, 2022, 71, 1386-1398.	12.1	28
2112	Medicago ABI3 Splicing Isoforms Regulate the Expression of Different Gene Clusters to Orchestrate Seed Maturation. Plants, 2021, 10, 1710.	3.5	8
2113	Inhibiting SARS-CoV-2 infection in vitro by suppressing its receptor, angiotensin-converting enzyme 2, via aryl-hydrocarbon receptor signal. Scientific Reports, 2021, 11, 16629.	3.3	21
2114	Leveraging the Mendelian disorders of the epigenetic machinery to systematically map functional epigenetic variation. ELife, 2021, 10, .	6.0	10
2115	Altered chromatin states drive cryptic transcription in aging mammalian stem cells. Nature Aging, 2021, 1, 684-697.	11.6	26
2116	Transcriptome Analysis Identifies GATA3-AS1 as a Long Noncoding RNA Associated with Resistance to Neoadjuvant Chemotherapy in Locally Advanced Breast Cancer Patients. Journal of Molecular Diagnostics, 2021, 23, 1306-1323.	2.8	10
2117	Transcriptomics of different tissues of blueberry and diversity analysis of rhizosphere fungi under cadmium stress. BMC Plant Biology, 2021, 21, 389.	3.6	8
2118	Predicting and characterizing a cancer dependency map of tumors with deep learning. Science Advances, 2021, 7, .	10.3	29
2119	SC-JNMF: single-cell clustering integrating multiple quantification methods based on joint non-negative matrix factorization. PeerJ, 2021, 9, e12087.	2.0	6
2120	Nucleo-cytoplasmic shuttling of splicing factor SRSF1 is required for development and cilia function. ELife, 2021, 10, .	6.0	25
2121	Transovarial transmission of a core virome in the Chagas disease vector Rhodnius prolixus. PLoS Pathogens, 2021, 17, e1009780.	4.7	7

#	Article	IF	Citations
2122	A cAMP-Related Gene Network in Microglia Is Inversely Regulated by Morphine Tolerance and Withdrawal. Biological Psychiatry Global Open Science, 2022, 2, 180-189.	2.2	14
2123	Deep learning detects cardiotoxicity in a high-content screen with induced pluripotent stem cell-derived cardiomyocytes. ELife, 2021, 10, .	6.0	25
2124	Atlas of tissue-specific and tissue-preferential gene expression in ecologically and economically significant conifer Pinus sylvestris. PeerJ, 2021, 9, e11781.	2.0	5
2125	Genomic comparison of non-photosynthetic plants from the family Balanophoraceae with their photosynthetic relatives. PeerJ, 2021, 9, e12106.	2.0	7
2127	The transcriptomic blueprint of molt in rooster using various tissues from Ginkkoridak (Korean) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 58	2.8	1
2128	Utilization of Transcriptome, Small RNA, and Degradome Sequencing to Provide Insights Into Drought Stress and Rewatering Treatment in Medicago ruthenica. Frontiers in Plant Science, 2021, 12, 675903.	3.6	9
2129	A stress-induced miR-31â€“CLOCKâ€“ERK pathway is a key driver and therapeutic target for skin aging. Nature Aging, 2021, 1, 795-809.	11.6	15
2130	Metagenomic insights into the effects of submerged plants on functional potential of microbial communities in wetland sediments. Marine Life Science and Technology, 2021, 3, 405-415.	4.6	19
2132	MtExpress, a Comprehensive and Curated RNAseq-based Gene Expression Atlas for the Model Legume Medicago truncatula. Plant and Cell Physiology, 2021, 62, 1494-1500.	3.1	48
2133	A Gut-Specific LITAF-Like Gene in Antheraea pernyi (Lepidoptera: Saturniidae) Involved in the Immune Response to Three Pathogens. Journal of Economic Entomology, 2021, 114, 1975-1982.	1.8	4
2135	Lytic Polysaccharide Monooxygenases as Chitin-Specific Virulence Factors in Crayfish Plague. Biomolecules, 2021, 11, 1180.	4.0	13
2136	The RNA binding protein Quaking represses splicing of the Fibronectin EDA exon and downregulates the interferon response. Nucleic Acids Research, 2021, 49, 10034-10045.	14.5	6
2137	Xyloglucan Remodeling Defines Auxin-Dependent Differential Tissue Expansion in Plants. International Journal of Molecular Sciences, 2021, 22, 9222.	4.1	9
2138	Viable but Nonculturable State of Yeast Candida sp. Strain LN1 Induced by High Phenol Concentrations. Applied and Environmental Microbiology, 2021, 87, e0111021.	3.1	45
2139	Captive Common Marmosets (Callithrix jacchus) Are Colonized throughout Their Lives by a Community of Bifidobacterium Species with Species-Specific Genomic Content That Can Support Adaptation to Distinct Metabolic Niches. MBio, 2021, 12, e0115321.	4.1	8
2141	Transcriptome Analyses of Barley Roots Inoculated with Novel Paenibacillus sp. and Erwinia gerundensis Strains Reveal Beneficial Early-Stage Plantâ€“Bacteria Interactions. Plants, 2021, 10, 1802.	3.5	10
2143	Oral vitamin D supplementation induces transcriptomic changes in rectal mucosa that are linked to anti-tumour effects. BMC Medicine, 2021, 19, 174.	5.5	7
2144	Chemical control of receptor kinase signaling by rapamycin-induced dimerization. Molecular Plant, 2021, 14, 1379-1390.	8.3	12

#	Article	IF	Citations
2146	Nanopore sequencing reveals endogenous NMD-targeted isoforms in human cells. Genome Biology, 2021, 22, 223.	8.8	25
2147	Meta-Analysis of Brain Gene Expression Data from Mouse Model Studies of Maternal Immune Activation Using Poly(I:C). Genes, 2021, 12, 1363.	2.4	4
2148	RNA sequencing reveals niche gene expression effects of beta-hydroxybutyrate in primary myotubes. Life Science Alliance, 2021, 4, e202101037.	2.8	4
2150	H3K4 Trimethylation Is Required for Postnatal Pancreatic Endocrine Cell Functional Maturation. Diabetes, 2021, 70, 2568-2579.	0.6	5
2151	PD-L1+ and XCR1+ dendritic cells are region-specific regulators of gut homeostasis. Nature Communications, 2021, 12, 4907.	12.8	18
2152	Reading between the Lines: RNA-seq Data Mining Reveals the Alternative Message of the Rice Leaf Transcriptome in Response to Heat Stress. Plants, 2021, 10, 1647.	3.5	12
2155	Comprehensive molecular profiling of UV-induced metastatic melanoma in Nme1/Nme2-deficient mice reveals novel markers of survival in human patients. Oncogene, 2021, 40, 6329-6342.	5.9	8
2156	Genome sequencing guide: An introductory toolbox to wholeâ€genome analysis methods. Biochemistry and Molecular Biology Education, 2021, 49, 815-825.	1.2	8
2157	Microbial signatures in the lower airways of mechanically ventilated COVID-19 patients associated with poor clinical outcome. Nature Microbiology, 2021, 6, 1245-1258.	13.3	101
2158	Traces of SARS-CoV-2 RNA in Peripheral Blood Cells of Patients with COVID-19. OMICS A Journal of Integrative Biology, 2021, 25, 475-483.	2.0	10
2159	Histone crotonylation regulates neural stem cell fate decisions by activating bivalent promoters. EMBO Reports, 2021, 22, e52023.	4.5	21
2161	DHX30 Coordinates Cytoplasmic Translation and Mitochondrial Function Contributing to Cancer Cell Survival. Cancers, 2021, 13, 4412.	3.7	9
2162	Immune cell analyses of the tumor microenvironment in prostate cancer highlight infiltrating regulatory <scp>T</scp> cells and macrophages as adverse prognostic factors. Journal of Pathology, 2021, 255, 155-165.	4.5	36
2163	Early white matter pathology in the fornix of the limbic system in Huntington disease. Acta Neuropathologica, 2021, 142, 791-806.	7.7	13
2164	RANKL-Induced Btn2a2 â€“ A T Cell Immunomodulatory Molecule â€“ During Osteoclast Differentiation Fine-Tunes Bone Resorption. Frontiers in Endocrinology, 2021, 12, 685060.	3.5	3
2166	Chromatin accessibility landscapes activated by cell-surface and intracellular immune receptors. Journal of Experimental Botany, 2021, 72, 7927-7941.	4.8	14
2167	TET2 as a tumor suppressor and therapeutic target in T-cell acute lymphoblastic leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	29
2168	CRISPR-Cas9 Technology as a Tool to Target Gene Drivers in Cancer: Proof of Concept and New Opportunities to Treat Chronic Myeloid Leukemia. CRISPR Journal, 2021, 4, 519-535.	2.9	3

#	Article	IF	Citations
2172	Genome-wide detection and classification of terpene synthase genes in Aquilaria agallochum. Physiology and Molecular Biology of Plants, 2021, 27, 1711-1729.	3.1	10
2175	Acquisition of aneuploidy drives mutant p53-associated gain-of-function phenotypes. Nature Communications, 2021, 12, 5184.	12.8	30
2176	Conditional stomatal closure in a fern shares molecular features with flowering plant active stomatal responses. Current Biology, 2021, 31, 4560-4570.e5.	3.9	12
2177	The Most Common VHL Point Mutation R167Q in Hereditary VHL Disease Interferes with Cell Plasticity Regulation. Cancers, 2021, 13, 3897.	3.7	4
2178	Generation of hiPSC-Derived Functional Dopaminergic Neurons in Alginate-Based 3D Culture. Frontiers in Cell and Developmental Biology, 2021, 9, 708389.	3.7	13
2179	Interferon drives HCV scarring of the epigenome and creates targetable vulnerabilities following viral clearance. Hepatology, 2022, 75, 983-996.	7.3	15
2183	RAC1 plays an essential role in estrogen receptor alpha function in breast cancer cells. Oncogene, 2021, 40, 5950-5962.	5.9	8
2184	OTX2 Homeoprotein Functions in Adult Choroid Plexus. International Journal of Molecular Sciences, 2021, 22, 8951.	4.1	4
2186	Aryl Hydrocarbon Receptor Deficiency in Intestinal Epithelial Cells Aggravates Alcohol-Related Liver Disease. Cellular and Molecular Gastroenterology and Hepatology, 2022, 13, 233-256.	4.5	26
2187	Haplotype-Specific Expression Analysis of MHC Class II Genes in Healthy Individuals and Rheumatoid Arthritis Patients. Frontiers in Immunology, 2021, 12, 707217.	4.8	10
2188	Pre-pregnancy BMI-associated miRNA and mRNA expression signatures in the placenta highlight a sexually-dimorphic response to maternal underweight status. Scientific Reports, 2021, 11, 15743.	3.3	9
2189	Increase in carbohydrate content and variation in microbiome are related to the drought tolerance of Codonopsis pilosula. Plant Physiology and Biochemistry, 2021, 165, 19-35.	5.8	12
2190	CTCF is a barrier for 2C-like reprogramming. Nature Communications, 2021, 12, 4856.	12.8	38
2191	Engineering chloroplast development in rice through cellâ€specific control of endogenous genetic circuits. Plant Biotechnology Journal, 2021, 19, 2291-2303.	8.3	15
2192	Iron insufficiency in floral buds impairs pollen development by disrupting tapetum function. Plant Journal, 2021, 108, 244-267.	5.7	6
2193	Gene therapy with AR isoform 2 rescues spinal and bulbar muscular atrophy phenotype by modulating AR transcriptional activity. Science Advances, 2021, 7, .	10.3	20
2194	Amino acids activate mTORC1 to release roe deer embryos from decelerated proliferation during diapause. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	10
2195	The impacts of past, present and future ocean chemistry on predatory planktonic snails. Royal Society Open Science, 2021, 8, 202265.	2.4	4

#	Article	IF	Citations
2198	Multi-omics of the esophageal microenvironment identifies signatures associated with progression of Barrettâ€™s esophagus. Genome Medicine, 2021, 13, 133.	8.2	11
2200	Comparative Analysis of Genomic and Transcriptome Sequences Reveals Divergent Patterns of Codon Bias in Wheat and Its Ancestor Species. Frontiers in Genetics, 2021, 12, 732432.	2.3	9
2202	Determination of variable region sequences from hybridoma immunoglobulins that target Mycobacterium tuberculosis virulence factors. PLoS ONE, 2021, 16, e0256079.	2.5	1
2203	An Open-Source Toolkit To Expand Bioinformatics Training in Infectious Diseases. MBio, 2021, 12, e0121421.	4.1	17
2204	Selection and Evaluation of a Thornless and HLB-Tolerant Bud-Sport of Pummelo Citrus With an Emphasis on Molecular Mechanisms. Frontiers in Plant Science, 2021, 12, 739108.	3.6	8
2205	Pan-transcriptome identifying master genes and regulation network in response to drought and salt stresses in Alfalfa (Medicago sativa L.). Scientific Reports, 2021, 11, 17203.	3.3	16
2206	Aged skeletal stem cells generate an inflammatory degenerative niche. Nature, 2021, 597, 256-262.	27.8	143
2207	The grapevine (Vitis vinifera L.) floral transcriptome in Pinot noir variety: identification of tissue-related gene networks and whorl-specific markers in pre- and post-anthesis phases. Horticulture Research, 2021, 8, 200.	6.3	5
2208	Spatio-Temporal Multiscale Analysis of Western Diet-Fed Mice Reveals a Translationally Relevant Sequence of Events during NAFLD Progression. Cells, 2021, 10, 2516.	4.1	24
2209	MyD88 is an essential regulator of NK cell-mediated clearance of MCMV infection. Molecular Immunology, 2021, 137, 94-104.	2.2	4
2210	CRIS: complete reconstruction of immunoglobulin V-D-J sequences from RNA-seq data. Bioinformatics Advances, 2021, 1, vbab021.	2.4	4
2211	Chromosome-scale assembly of the Dendrobium chrysotoxum genome enhances the understanding of orchid evolution. Horticulture Research, 2021, 8, 183.	6.3	41
2212	Balanced polymorphism fuels rapid selection in an invasive crab despite high gene flow and low genetic diversity. Molecular Ecology, 2022, 31, 55-69.	3.9	14
2213	Comparative Immunogenomics of Canine Natural Killer Cells as Immunotherapy Target. Frontiers in Immunology, 2021, 12, 670309.	4.8	11
2215	Multi-Omics Approach to Dissect the Mechanisms of Rexinoid Signaling in Myoblast Differentiation. Frontiers in Pharmacology, 2021, 12, 746513.	3.5	3
2217	Intestinal Transcriptomic and Histologic Profiling Reveals Tissue Repair Mechanisms Underlying Resistance to the Parasite Ceratonova shasta. Pathogens, 2021, 10, 1179.	2.8	8
2218	DdaSTE12 is involved in trap formation, ring inflation, conidiation, and vegetative growth in the nematode-trapping fungus Drechslerella dactyloides. Applied Microbiology and Biotechnology, 2021, 105, 7379-7393.	3.6	14
2219	ISOTOPE: ISOform-guided prediction of epiTOPEs in cancer. PLoS Computational Biology, 2021, 17, e1009411.	3.2	5

#	Article	IF	Citations
2221	Role of miR-2392 in driving SARS-CoV-2 infection. Cell Reports, 2021, 37, 109839.	6.4	52
2222	OCT2 pre-positioning facilitates cell fate transition and chromatin architecture changes in humoral immunity. Nature Immunology, 2021, 22, 1327-1340.	14.5	11
2223	Temporal Transcriptome Analysis Reveals Dynamic Expression Profiles of Gametes and Embryonic Development in Japanese Flounder (Paralichthys olivaceus). Genes, 2021, 12, 1561.	2.4	2
2224	Alveolar macrophages from persons living with HIV show impaired epigenetic response to Mycobacterium tuberculosis. Journal of Clinical Investigation, 2021, 131, .	8.2	19
2225	Selenoprotein T Protects Endothelial Cells against Lipopolysaccharide-Induced Activation and Apoptosis. Antioxidants, 2021, 10, 1427.	5.1	4
2226	An inferred functional impact map of genetic variants in rice. Molecular Plant, 2021, 14, 1584-1599.	8.3	48
2228	Mechanisms of responsiveness to and resistance against trabectedin in murine models of human myxoid liposarcoma. Genomics, 2021, 113, 3439-3448.	2.9	2
2229	The leukemic oncogene EVI1 hijacks a MYC super-enhancer by CTCF-facilitated loops. Nature Communications, 2021, 12, 5679.	12.8	31
2230	Noncanonical mono(ADP-ribosyl)ation of zinc finger SZF proteins counteracts ubiquitination for protein homeostasis in plant immunity. Molecular Cell, 2021, 81, 4591-4604.e8.	9.7	17
2231	Telomere dysfunction is associated with darkâ€induced bleaching in the reef coral Stylophora pistillata. Molecular Ecology, 2022, 31, 6087-6099.	3.9	8
2235	Microorganisms of Two Thermal Pools on Kunashir Island, Russia. Biology, 2021, 10, 924.	2.8	3
2236	Dietary Supplementation with Transgenic Camelina sativa Oil Containing 20:5n-3 and 22:6n-3 or Fish Oil Induces Differential Changes in the Transcriptome of CD3+ T Lymphocytes. Nutrients, 2021, 13, 3116.	4.1	1
2237	Dysregulation of ribosome-related genes in ankylosing spondylitis: a systems biology approach and experimental method. BMC Musculoskeletal Disorders, 2021, 22, 789.	1.9	3
2238	Chromatin-based, in cis and in trans regulatory rewiring underpins distinct oncogenic transcriptomes in multiple myeloma. Nature Communications, 2021, 12, 5450.	12.8	19
2240	Differential transcript usage analysis of bulk and single-cell RNA-seq data with DTUrtle. Bioinformatics, 2021, 37, 3781-3787.	4.1	10
2241	WRKY Transcription Factors in Cassava Contribute to Regulation of Tolerance and Susceptibility to Cassava Mosaic Disease through Stress Responses. Viruses, 2021, 13, 1820.	3.3	11
2242	Computational workflow for functional characterization of COVID-19 through secondary data analysis. STAR Protocols, 2021, 2, 100873.	1.2	2
2244	Discovery of a first-in-class reversible DNMT1-selective inhibitor with improved tolerability and efficacy in acute myeloid leukemia. Nature Cancer, 2021, 2, 1002-1017.	13.2	99

#	Article	IF	Citations
2245	Differential Regulation of Interferon Signaling Pathways in CD4+ T Cells of the Low Type-2 Obesity-Associated Asthma Phenotype. International Journal of Molecular Sciences, 2021, 22, 10144.	4.1	13
2246	Intratumoral injection of TLR9 agonist promotes an immunopermissive microenvironment transition and causes cooperative antitumor activity in combination with anti-PD1 in pancreatic cancer. , 2021, 9, e002876.		25
2247	Principles of mRNA targeting via the Arabidopsis m6A-binding protein ECT2. ELife, 2021, 10, .	6.0	41
2248	The YTHDF proteins ECT2 and ECT3 bind largely overlapping target sets and influence target mRNA abundance, not alternative polyadenylation. ELife, 2021, 10, .	6.0	33
2249	Molecular adaptations to heat stress in the thermophilic ant genus Cataglyphis. Molecular Ecology, 2021, 30, 5503-5516.	3.9	14
2250	A compendium of uniformly processed human gene expression and splicing quantitative trait loci. Nature Genetics, 2021, 53, 1290-1299.	21.4	193
2251	An ADAR1-dependent RNA editing event in the cyclin-dependent kinase CDK13 promotes thyroid cancer hallmarks. Molecular Cancer, 2021, 20, 115.	19.2	22
2252	Intron retention-induced neoantigen load correlates with unfavorable prognosis in multiple myeloma. Oncogene, 2021, 40, 6130-6138.	5.9	21
2255	CD146 Delineates an Interfascicular Cell Sub-Population in Tendon That Is Recruited during Injury through Its Ligand Laminin-Î±4. International Journal of Molecular Sciences, 2021, 22, 9729.	4.1	12
2256	A single-cell and spatially resolved atlas of human breast cancers. Nature Genetics, 2021, 53, 1334-1347.	21.4	535
2257	Cross-Sectional Study on the Gut Microbiome of Parkinsonâ€™s Disease Patients in Central China. Frontiers in Microbiology, 2021, 12, 728479.	3.5	13
2258	Inhibition of chylomicron assembly leads to dissociation of hepatic steatosis from inflammation and fibrosis. Journal of Lipid Research, 2021, 62, 100123.	4.2	3
2259	Therapeutic radiation exposure of the abdomen during childhood induces chronic adipose tissue dysfunction. JCI Insight, 2021, 6, .	5.0	2
2260	Light intensity and spectral composition drive reproductive success in the marine benthic diatom Seminavis robusta. Scientific Reports, 2021, 11, 17560.	3.3	4
2261	Neofunctionalization of an ancient domain allows parasites to avoid intraspecific competition by manipulating host behaviour. Nature Communications, 2021, 12, 5489.	12.8	15
2262	Genomeâ€•and transcriptomeâ€wide association studies reveal the genetic basis and the breeding history of seed glucosinolate content in Brassica napus. Plant Biotechnology Journal, 2022, 20, 211-225.	8.3	43
2264	Transcriptomics reveal different metabolic strategies for acid resistance and gamma-aminobutyric acid (GABA) production in select Levilactobacillus brevis strains. Microbial Cell Factories, 2021, 20, 173.	4.0	10
2265	Transcriptome profiling reveal key hub genes in co-expression networks involved in Iridoid glycosides biosynthetic machinery in Picrorhiza kurroa. Genomics, 2021, 113, 3381-3394.	2.9	5

#	Article	IF	Citations
2266	Transmission of mushroom virus X and the impact of virus infection on the transcriptomes and proteomes of different strains of Agaricus bisporus. Fungal Biology, 2021, 125, 704-717.	2.5	11
2267	InÂvivo CRISPR screens identify the E3 ligase Cop1 as a modulator of macrophage infiltration and cancer immunotherapy target. Cell, 2021, 184, 5357-5374.e22.	28.9	79
2268	TISMO: syngeneic mouse tumor database to model tumor immunity and immunotherapy response. Nucleic Acids Research, 2022, 50, D1391-D1397.	14.5	41
2269	Altered microbial CAZyme families indicated dead biomass decomposition following afforestation. Soil Biology and Biochemistry, 2021, 160, 108362.	8.8	17
2270	Chronic mineral oil administration increases hepatic inflammation in wild type mice compared to lipocalin 2 null mice. Laboratory Investigation, 2021, 101, 1528-1539.	3.7	2
2271	Different ways to play it cool: Transcriptomic analysis sheds light on different activity patterns of three amphipod species under longâ€term cold exposure. Molecular Ecology, 2021, 30, 5735-5751.	3.9	11
2272	Integrated Analysis of Liver Transcriptome, miRNA, and Proteome of Chinese Indigenous Breed Ningxiang Pig in Three Developmental Stages Uncovers Significant miRNAâ€“mRNAâ€“Protein Networks in Lipid Metabolism. Frontiers in Genetics, 2021, 12, 709521.	2.3	3
2273	Comparative Transcriptome Analysis of Wheat Lines in the Field Reveals Multiple Essential Biochemical Pathways Suppressed by Obligate Pathogens. Frontiers in Plant Science, 2021, 12, 720462.	3.6	14
2275	Marine Synechococcus picocyanobacteria: Light utilization across latitudes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	18
2276	Two promoters integrate multiple enhancer inputs to drive wild-type knirps expression in the Drosophila melanogaster embryo. Genetics, 2021, 219, .	2.9	4
2277	Identification of the gliogenic state of human neural stem cells to optimize in vitro astrocyte differentiation. Journal of Neuroscience Methods, 2021, 361, 109284.	2.5	5
2278	Light regulates alternative splicing outcomes via the TOR kinase pathway. Cell Reports, 2021, 36, 109676.	6.4	34
2279	High contiguity de novo genome assembly and DNA modification analyses for the fungus fly, Sciara coprophila, using single-molecule sequencing. BMC Genomics, 2021, 22, 643.	2.8	17
2281	The Distinct Immune Nature of the Fetal Inflammatory Response Syndrome Type I and Type II. ImmunoHorizons, 2021, 5, 735-751.	1.8	10
2283	Characteristics of steroidogenesis-related factors in the musk gland of Chinese forest musk deer (Moschus berezovskii). Journal of Steroid Biochemistry and Molecular Biology, 2021, 212, 105916.	2.5	8
2285	TDP-43 condensation properties specify its RNA-binding and regulatory repertoire. Cell, 2021, 184, 4680-4696.e22.	28.9	121
2286	A ROR2 coding variant is associated with craniofacial variation in domestic pigeons. Current Biology, 2021, 31, 5069-5076.e5.	3.9	14
2287	Convergent Usage of Amino Acids in Human Cancers as A Reversed Process of Tissue Development. Genomics, Proteomics and Bioinformatics, 2022, 20, 147-162.	6.9	1

#	Article	IF	Citations
2289	Genomic and physiological analyses of the zebrafish atrioventricular canal reveal molecular building blocks of the secondary pacemaker region. Cellular and Molecular Life Sciences, 2021, 78, 6669-6687.	5.4	6
2290	Human cytomegalovirus expands a CD8 ⁺ T cell population with loss of BCL11B expression and gain of NK cell identity. Science Immunology, 2021, 6, eabe6968.	11.9	25
2291	The Expression of IbMYB1 Is Essential to Maintain the Purple Color of Leaf and Storage Root in Sweet Potato [Ipomoea batatas (L.) Lam]. Frontiers in Plant Science, 2021, 12, 688707.	3.6	7
2292	Single-cell RNA-seq unravels alterations of the human spermatogonial stem cell compartment in patients with impaired spermatogenesis. Cell Reports Medicine, 2021, 2, 100395.	6.5	33
2293	AKT signaling is associated with epigenetic reprogramming via the upregulation of TET and its cofactor, alpha-ketoglutarate during iPSC generation. Stem Cell Research and Therapy, 2021, 12, 510.	5.5	7
2294	The role of pollination in controlling Ginkgo biloba ovule development. New Phytologist, 2021, 232, 2353-2368.	7.3	8
2295	tiRNA signaling via stress-regulated vesicle transfer in the hematopoietic niche. Cell Stem Cell, 2021, 28, 2090-2103.e9.	11.1	20
2296	Loss of TDP-43 in male germ cells causes meiotic failure and impairs fertility in mice. Journal of Biological Chemistry, 2021, 297, 101231.	3.4	8
2298	PARP7 negatively regulates the type I interferon response in cancer cells and its inhibition triggers antitumor immunity. Cancer Cell, 2021, 39, 1214-1226.e10.	16.8	72
2299	Orexin receptors 1 and 2 in serotonergic neurons differentially regulate peripheral glucose metabolism in obesity. Nature Communications, 2021, 12, 5249.	12.8	17
2300	NOT-Gated CD93 CAR T Cells Effectively Target AML with Minimized Endothelial Cross-Reactivity. Blood Cancer Discovery, 2021, 2, 648-665.	5.0	37
2301	FTO Suppresses STAT3 Activation and Modulates Proinflammatory Interferon-Stimulated Gene Expression. Journal of Molecular Biology, 2022, 434, 167247.	4.2	11
2302	Activation of TIR signalling boosts pattern-triggered immunity. Nature, 2021, 598, 500-503.	27.8	176
2305	Analysis of mitochondrial regulatory transcripts in publicly available datasets with validation in placentae from pre-term, post-term and fetal growth restriction pregnancies. Placenta, 2021, 112, 162-171.	1.5	9
2306	Choice of pre-processing pipeline influences clustering quality of scRNA-seq datasets. BMC Genomics, 2021, 22, 661.	2.8	5
2307	Early Chronic Memantine Treatment-Induced Transcriptomic Changes in Wild-Type and Shank2-Mutant Mice. Frontiers in Molecular Neuroscience, 2021, 14, 712576.	2.9	6
2308	Baseline Gut Metagenomic Functional Gene Signature Associated with Variable Weight Loss Responses following a Healthy Lifestyle Intervention in Humans. MSystems, 2021, 6, e0096421.	3.8	19
2309	Arms race in a cell: genomic, transcriptomic, and proteomic insights into intracellular phageâ€“bacteria interplay in deep-sea snail holobionts. Microbiome, 2021, 9, 182.	11.1	7

#	Article	IF	Citations
2310	Th1 polarization defines the synovial fluid T cell compartment in oligoarticular juvenile idiopathic arthritis. JCI Insight, 2021, 6, .	5.0	21
2312	Genomic impact of stress-induced transposable element mobility in Arabidopsis. Nucleic Acids Research, 2021, 49, 10431-10447.	14.5	60
2313	Predicted Immunogenicity of CDK12 Biallelic Loss-of-Function Tumors Varies across Cancer Types. Journal of Molecular Diagnostics, 2021, 23, 1761-1773.	2.8	2
2314	Transposition and duplication of MADS-domain transcription factor genes in annual and perennial Arabis species modulates flowering. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	6
2315	Activation of mitochondrial unfolded protein response protects against multiple exogenous stressors. Life Science Alliance, 2021, 4, e202101182.	2.8	15
2316	Prospects and challenges of cancer systems medicine: from genes to disease networks. Briefings in Bioinformatics, 2022, 23, .	6.5	7
2318	Nucleotide variants in hepatitis B virus preS region predict the recurrence of hepatocellular carcinoma. Aging, 2021, 13, 22256-22275.	3.1	2
2320	Raspberry ketone diet supplement reduces attraction of sterile male Queensland fruit fly to cuelure by altering expression of chemoreceptor genes. Scientific Reports, 2021, 11, 17632.	3.3	2
2321	The time course of molecular acclimation to seawater in a euryhaline fish. Scientific Reports, 2021, 11, 18127.	3.3	9
2322	Production of functional oocytes requires maternally expressed PIWI genes and piRNAs in golden hamsters. Nature Cell Biology, 2021, 23, 1002-1012.	10.3	30
2324	Nanopore Assay Reveals Cell-Type-Dependent Gene Expression of Vesicular Stomatitis Indiana Virus and Differential Host Cell Response. Pathogens, 2021, 10, 1196.	2.8	2
2325	Transcriptomic Response Dynamics of Human Primary and Immortalized Adrenocortical Cells to Steroidogenic Stimuli. Cells, 2021, 10, 2376.	4.1	6
2326	Molecular characterization and cell type composition deconvolution of fibrosis in NAFLD. Scientific Reports, 2021, 11, 18045.	3.3	36
2328	Global approaches for profiling transcription initiation. Cell Reports Methods, 2021, 1, 100081.	2.9	11
2329	Engineered SARS-CoV-2 receptor binding domain improves manufacturability in yeast and immunogenicity in mice. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	68
2331	The role of glutathione-mediated triacylglycerol synthesis in the response to ultra-high cadmium stress in Auxenochlorella protothecoides. Journal of Environmental Sciences, 2021, 108, 58-69.	6.1	12
2332	Dysregulation of cholesterol homeostasis in human lung cancer tissue and tumour-associated macrophages. EBioMedicine, 2021, 72, 103578.	6.1	43
2333	Establishment of human induced trophoblast stem-like cells from term villous cytotrophoblasts. Stem Cell Research, 2021, 56, 102507.	0.7	18

#	Article	IF	Citations
2334	The ETS transcription factor ERF controls the exit from the naÃ¨ve pluripotent state in a MAPK-dependent manner. Science Advances, 2021, 7, eabg8306.	10.3	6
2335	MCPIP1 is a novel link between diabetogenic conditions and impaired insulin secretory capacity. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2021, 1867, 166199.	3.8	4
2336	Transcriptomics reveal triphenyltin-induced molecular toxicity in the marine mussel Perna viridis. Science of the Total Environment, 2021, 790, 148040.	8.0	7
2337	Metagenomic analysis of microbial communities continuously exposed to Bisphenol A in mangrove rhizosphere and non-rhizosphere soils. Science of the Total Environment, 2021, 792, 148486.	8.0	13
2338	Transcriptomic study of the night break in Chenopodium rubrum reveals possible upstream regulators of the floral activator CrFTL1. Journal of Plant Physiology, 2021, 265, 153492.	3.5	0
2339	Effects of fish farm activities on the sponge Weberella bursa, and its associated microbiota. Ecological Indicators, 2021, 129, 107879.	6.3	10
2340	Concentration-dependent transcriptome of zebrafish larvae for environmental bisphenol S assessment. Ecotoxicology and Environmental Safety, 2021, 223, 112574.	6.0	3
2341	A metatranscriptomic analysis of changing dynamics in the plankton communities adjacent to aquaculture leases in southern Tasmania, Australia. Marine Genomics, 2021, 59, 100858.	1.1	1
2342	Selective Suppression of Cellular Immunity and Increased Cytotoxicity in Skin Lesions of Disseminated Leishmaniasis Uncovered by Transcriptome-Wide Analysis. Journal of Investigative Dermatology, 2021, 141, 2542-2546.e5.	0.7	0
2343	B-cells are abnormal in psychosocial stress and regulate meningeal myeloid cell activation. Brain, Behavior, and Immunity, 2021, 97, 226-238.	4.1	13
2345	Establishment of myoblast cell line and identification of key genes regulating myoblast differentiation in a marine teleost, Sebastes schlegelii. Gene, 2021, 802, 145869.	2.2	17
2346	Epigenetic differences in an identical genetic background modulate alternative splicing in A. thaliana. Genomics, 2021, 113, 3476-3486.	2.9	5
2347	Conformational Changes of RORÎ³ During Response Element Recognition and Coregulator Engagement. Journal of Molecular Biology, 2021, 433, 167258.	4.2	4
2348	A quantitative metabolic analysis reveals Acetobacterium woodii as a flexible and robust host for formate-based bioproduction. Metabolic Engineering, 2021, 68, 68-85.	7.0	18
2349	Non-coding Natural Antisense Transcripts: Analysis and Application. Journal of Biotechnology, 2021, 340, 75-101.	3.8	12
2350	Large within, and between, species differences in marine cellular responses: Unpredictability in a changing environment. Science of the Total Environment, 2021, 794, 148594.	8.0	10
2351	Early adaptive chromatin remodeling events precede pathologic phenotypes and are reinforced in the failing heart. Journal of Molecular and Cellular Cardiology, 2021, 160, 73-86.	1.9	17
2352	A haploid diamondback moth (Plutella xylostella L.) genome assembly resolves 31 chromosomes and identifies a diamide resistance mutation. Insect Biochemistry and Molecular Biology, 2021, 138, 103622.	2.7	19

#	Article	IF	Citations
2353	Hepatic mTORC1 signaling activates ATF4 as part of its metabolic response to feeding and insulin. Molecular Metabolism, 2021, 53, 101309.	6.5	16
2354	Comparative transcriptome analysis reveals changes in gene expression in sea cucumber (Holothuria) Tj ETQq1 1 0.784314 rgBT /Ove D: Genomics and Proteomics, 2021, 40, 100883.	1.0	12
2355	Genes involved in the Type I pheromone biosynthesis pathway and chemoreception from the sex pheromone gland transcriptome of Dioryctria abietella. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 40, 100892.	1.0	1
2356	Interferon stimulated binding of ISRE is cell type specific and is predicted by homeostatic chromatin state. Cytokine: X, 2021, 3, 100056.	1.4	3
2357	A putative long noncoding RNA-encoded micropeptide maintains cellular homeostasis in pancreatic Î² cells. Molecular Therapy - Nucleic Acids, 2021, 26, 307-320.	5.1	19
2358	CreA-mediated repression of gene expression occurs at low monosaccharide levels during fungal plant biomass conversion in a time and substrate dependent manner. Cell Surface, 2021, 7, 100050.	3.0	16
2359	Transcriptome analysis of growth variation in early juvenile stage sandfish Holothuria scabra. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 40, 100904.	1.0	2
2360	Triiodothyronine and dexamethasone alter potassium channel expression and promote electrophysiological maturation of human-induced pluripotent stem cell-derived cardiomyocytes. Journal of Molecular and Cellular Cardiology, 2021, 161, 130-138.	1.9	12
2361	Survival strategy of comammox bacteria in a wastewater nutrient removal system with sludge fermentation liquid as additional carbon source. Science of the Total Environment, 2022, 802, 149862.	8.0	13
2362	Functional filtering and random processes affect the assembly of microbial communities of snow algae blooms at Maritime Antarctic. Science of the Total Environment, 2022, 805, 150305.	8.0	11
2363	From surviving to thriving, the assembly processes of microbial communities in stone biodeterioration: A case study of the West Lake UNESCO World Heritage area in China. Science of the Total Environment, 2022, 805, 150395.	8.0	25
2364	Response of soil protozoa to acid mine drainage in a contaminated terrace. Journal of Hazardous Materials, 2022, 421, 126790.	12.4	33
2365	Freshwater mussels (Unionidae) brought into captivity exhibit up-regulation of genes involved in stress and energy metabolism. Scientific Reports, 2021, 11, 2241.	3.3	8
2366	Sept8/SEPTIN8 involvement in cellular structure and kidney damage is identified by genetic mapping and a novel human tubule hypoxic model. Scientific Reports, 2021, 11, 2071.	3.3	13
2367	Coxsackievirus B3 Infection Early in Pregnancy Induces Congenital Heart Defects Through Suppression of Fetal Cardiomyocyte Proliferation. Journal of the American Heart Association, 2021, 10, e017995.	3.7	13
2368	Multiple freeze-thaw cycles lead to a loss of consistency in poly(A)-enriched RNA sequencing. BMC Genomics, 2021, 22, 69.	2.8	12
2369	Genome-wide association study reveals the genetic complexity of fructan accumulation patterns in barley grain. Journal of Experimental Botany, 2021, 72, 2383-2402.	4.8	17
2370	RORÎ± is a critical checkpoint for T cell and ILC2 commitment in the embryonic thymus. Nature Immunology, 2021, 22, 166-178.	14.5	51

#	Article	IF	Citations
2372	Sox9EGFP Defines Biliary Epithelial Heterogeneity Downstream of Yap Activity. Cellular and Molecular Gastroenterology and Hepatology, 2021, 11, 1437-1462.	4.5	9
2373	Fly-over phylogeny across invertebrate to vertebrate: The giant panda and insects share a highly similar gut microbiota. Computational and Structural Biotechnology Journal, 2021, 19, 4676-4683.	4.1	7
2374	Acquired mutations and transcriptional remodeling in long-term estrogen-deprived locoregional breast cancer recurrences. Breast Cancer Research, 2021, 23, 1.	5.0	43
2375	Accelerating functional gene discovery in osteoarthritis. Nature Communications, 2021, 12, 467.	12.8	33
2376	Comprehensive analysis of epigenetic signatures of human transcription control. Molecular Omics, 2021, 17, 692-705.	2.8	1
2377	Dll1+ quiescent tumor stem cells drive chemoresistance in breast cancer through NF-Î²B survival pathway. Nature Communications, 2021, 12, 432.	12.8	38
2378	Spectral Prediction Features as a Solution for the Search Space Size Problem in Proteogenomics. Molecular and Cellular Proteomics, 2021, 20, 100076.	3.8	31
2379	Differential contribution of transcriptomic regulatory layers in the definition of neuronal identity. Nature Communications, 2021, 12, 335.	12.8	20
2380	Human ex vivo lung perfusion: a novel model to study human lung diseases. Scientific Reports, 2021, 11, 490.	3.3	15
2381	Heat stress destabilizes symbiotic nutrient cycling in corals. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	179
2382	Cysteine: an overlooked energy and carbon source. Scientific Reports, 2021, 11, 2139.	3.3	22
2383	Comprehensive genomic resources related to domestication and crop improvement traits in Lima bean. Nature Communications, 2021, 12, 702.	12.8	39
2384	Barley Anther and Meiocyte Transcriptome Dynamics in Meiotic Prophase I. Frontiers in Plant Science, 2020, 11, 619404.	3.6	19
2386	A <i>ROR2</i> Coding Variant is Associated with Craniofacial Variation in Domestic Pigeons. SSRN Electronic Journal, 0, , .	0.4	0
2387	Compression of quantification uncertainty for scRNA-seq counts. Bioinformatics, 2021, 37, 1699-1707.	4.1	4
2390	Aedes aegypti post-emergence transcriptome: Unveiling the molecular basis for the hematophagic and gonotrophic capacitation. PLoS Neglected Tropical Diseases, 2021, 15, e0008915.	3.0	3
2392	Cell-Intrinsic Tumorigenic Functions of PPARÎ³ in Bladder Urothelial Carcinoma. Molecular Cancer Research, 2021, 19, 598-611.	3.4	7
2394	HIV Protein Tat Induces Macrophage Dysfunction and Atherosclerosis Development in Low-Density Lipoprotein Receptorâ€“Deficient Mice. Cardiovascular Drugs and Therapy, 2022, 36, 201-215.	2.6	7

#	Article	IF	Citations
2395	Discovery of a Functional Covalent Ligand Targeting an Intrinsically Disordered Cysteine within MYC. Cell Chemical Biology, 2021, 28, 4-13.e17.	5.2	70
2396	Preprocessing choices affect RNA velocity results for droplet scRNA-seq data. PLoS Computational Biology, 2021, 17, e1008585.	3.2	46
2397	Algorithms meet sequencing technologies â€“ 10th edition of the RECOMB-Seq workshop. IScience, 2021, 24, 101956.	4.1	0
2398	Optimized RNA-targeting CRISPR/Cas13d technology outperforms shRNA in identifying functional circRNAs. Genome Biology, 2021, 22, 41.	8.8	75
2399	Gut-licensed IFNÎ³+ NK cells drive LAMP1+TRAIL+ anti-inflammatory astrocytes. Nature, 2021, 590, 473-479.	27.8	178
2400	Durvalumab, Tremelimumab Alone or in Combination With Low-Dose or Hypofractionated Targeted Radiotherapy in Metastatic Non-Small Cell Lung Cancer Refractory to Prior PD-1 Therapy: A Multicentre, Open-Label, Randomized, Phase 2 Trial. SSRN Electronic Journal, 0, , .	0.4	0
2401	Trace gas oxidizers are widespread and active members of soil microbial communities. Nature Microbiology, 2021, 6, 246-256.	13.3	97
2402	Mesenchymal stromal cells reprogram monocytes and macrophages with processing bodies. Stem Cells, 2021, 39, 115-128.	3.2	22
2403	HLApers: HLA Typing and Quantification of Expression with Personalized Index. Methods in Molecular Biology, 2020, 2120, 101-112.	0.9	12
2404	Methodologies for Following EMT In Vivo at Single Cell Resolution. Methods in Molecular Biology, 2021, 2179, 303-314.	0.9	7
2405	Single-Cell Transcriptome Analysis of T Cells. Methods in Molecular Biology, 2019, 2048, 155-205.	0.9	3
2406	Using RNA Sequencing to Characterize the Tumor Microenvironment. Methods in Molecular Biology, 2020, 2055, 245-272.	0.9	3
2407	The Penium margaritaceum Genome: Hallmarks of the Origins of Land Plants. Cell, 2020, 181, 1097-1111.e12.	28.9	153
2408	Single-Cell RNA Sequencing Reveals a Dynamic Stromal Niche That Supports Tumor Growth. Cell Reports, 2020, 31, 107628.	6.4	186
2409	Pressure-Driven Mitochondrial Transfer Pipeline Generates Mammalian Cells of Desired Genetic Combinations and Fates. Cell Reports, 2020, 33, 108562.	6.4	21
2410	De novo assembly and functional annotation of the heartÂ+Âhemolymph transcriptome in the Caribbean spiny lobster Panulirus argus. Marine Genomics, 2020, 54, 100783.	1.1	6
2411	The Alazami Syndrome-Associated Protein LARP7 Guides U6 Small Nuclear RNA Modification and Contributes to Splicing Robustness. Molecular Cell, 2020, 77, 1014-1031.e13.	9.7	45
2412	Will a Non-antibiotic Metalloid Enhance the Spread of Antibiotic Resistance Genes: The Selenate Story. Environmental Science & Technology, 2021, 55, 1004-1014.	10.0	42

#	Article	IF	Citations
2413	Single-cell transcriptomics identifies CD44 as a marker and regulator of endothelial to haematopoietic transition. Nature Communications, 2020, 11, 586.	12.8	69
2414	Ribosomes guide pachytene piRNA formation on long intergenic piRNA precursors. Nature Cell Biology, 2020, 22, 200-212.	10.3	29
2415	Decoding myofibroblast origins in human kidney fibrosis. Nature, 2021, 589, 281-286.	27.8	380
2416	Interleukin-23 engineering improves CAR T cell function in solid tumors. Nature Biotechnology, 2020, 38, 448-459.	17.5	145
2417	Three-dimensional genome restructuring across timescales of activity-induced neuronal gene expression. Nature Neuroscience, 2020, 23, 707-717.	14.8	99
2418	Insights into gene expression changes under conditions that facilitate horizontal gene transfer (mating) of a model archaeon. Scientific Reports, 2020, 10, 22297.	3.3	8
2419	Transcriptomic profiling for prolonged drought in Dendrobium catenatum. Scientific Data, 2018, 5, 180233.	5.3	22
2420	RNA-seq transcriptomic profiling of crassulacean acid metabolism pathway in Dendrobium catenatum. Scientific Data, 2018, 5, 180252.	5.3	21
2421	Sex diversity in proximal tubule and endothelial gene expression in mice with ischemic acute kidney injury. Clinical Science, 2020, 134, 1887-1909.	4.3	21
2422	Seasonal and diel patterns of abundance and activity of viruses in the Red Sea. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29738-29747.	7.1	27
2423	Mycobacteria excise DNA damage in 12- or 13-nucleotide-long oligomers by prokaryotic-type dual incisions and performs transcription-coupled repair. Journal of Biological Chemistry, 2020, 295, 17374-17380.	3.4	9
2424	Longevity, clonal relationship, and transcriptional program of celiac diseaseâ€“specific plasma cells. Journal of Experimental Medicine, 2021, 218, .	8.5	25
2425	NGPINT: a next-generation proteinâ€“protein interaction software. Briefings in Bioinformatics, 2021, 22, .	6.5	12
2426	The Iron-Responsive Genome of the Chiton Acanthopleura granulata. Genome Biology and Evolution, 2021, 13, .	2.5	42
2427	Prey sensing and response in a nematode-trapping fungus is governed by the MAPK pheromone response pathway. Genetics, 2021, 217, .	2.9	30
2428	Photoreceptor Diversification Accompanies the Evolution of Anthozoa. Molecular Biology and Evolution, 2021, 38, 1744-1760.	8.9	20
2429	dearseq: a variance component score test for RNA-seq differential analysis that effectively controls the false discovery rate. NAR Genomics and Bioinformatics, 2020, 2, lqaa093.	3.2	18
2430	Distinct signaling routes mediate intercellular and intracellular rhizobial infection inLotus japonicus. Plant Physiology, 2021, 185, 1131-1147.	4.8	26

#	Article	IF	Citations
2431	Alternative splicing creates a pseudo-strictosidine Î²-<scp>d</scp>-glucosidase modulating alkaloid synthesis in Catharanthus roseus. Plant Physiology, 2021, 185, 836-856.	4.8	19
2432	Aryl Hydrocarbon Receptor Mediates Larval Zebrafish Fin Duplication Following Exposure to Benzofluoranthenes. Toxicological Sciences, 2020, 176, 46-64.	3.1	5
2433	YAP1-FAM118B Fusion Defines a Rare Subset of Childhood and Young Adulthood Meningiomas. American Journal of Surgical Pathology, 2021, 45, 329-340.	3.7	14
2434	Fatty acid bioconversion in harpacticoid copepods in a changing environment: a transcriptomic approach. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190645.	4.0	26
2681	Identification of Smad3â€related transcriptomes in typeâ€2 diabetic nephropathy by whole transcriptome RNA sequencing. Journal of Cellular and Molecular Medicine, 2021, 25, 2052-2068.	3.6	5
2682	An Autochthonous Mouse Model ofMyd88- andBCL2-Driven Diffuse Large B-cell Lymphoma Reveals Actionable Molecular Vulnerabilities. Blood Cancer Discovery, 2021, 2, 70-91.	5.0	21
2683	The Route of Infection Influences the Contribution of Key Immunity Genes to Antibacterial Defense in <i>Anopheles gambiae</i>. Journal of Innate Immunity, 2021, 13, 107-126.	3.8	14
2684	Integrated RNA Sequencing Reveals Epigenetic Impacts of Diesel Particulate Matter Exposure in Human Cerebral Organoids. Developmental Neuroscience, 2020, 42, 195-207.	2.0	12
2685	Colonic epithelial miR-31 associates with the development of Crohnâ€™s phenotypes. JCI Insight, 2018, 3, .	5.0	20
2686	Antisense oligonucleotide treatment ameliorates IFN-Î³â€“induced proteinuria in APOL1-transgenic mice. JCI Insight, 2019, 4, .	5.0	64
2687	Precocious neuronal differentiation and disrupted oxygen responses in Kabuki syndrome. JCI Insight, 2019, 4, .	5.0	41
2688	Precocious chondrocyte differentiation disrupts skeletal growth in Kabuki syndrome mice. JCI Insight, 2019, 4, .	5.0	29
2689	Irreversible JNK1-JUN inhibition by JNK-IN-8 sensitizes pancreatic cancer to 5-FU/FOLFOX chemotherapy. JCI Insight, 2020, 5, .	5.0	25
2690	Th17 reprogramming of T cells in systemic juvenile idiopathic arthritis. JCI Insight, 2020, 5, .	5.0	43
2691	Neoadjuvant pazopanib and molecular analysis of tissue response in renal cell carcinoma. JCI Insight, 2020, 5, .	5.0	11
2692	Effects of tesamorelin on hepatic transcriptomic signatures in HIV-associated NAFLD. JCI Insight, 2020, 5, .	5.0	13
2693	ETV6 germline mutations cause HDAC3/NCOR2 mislocalization and upregulation of interferon response genes. JCI Insight, 2020, 5, .	5.0	15
2694	Exome-capture RNA sequencing of decade-old breast cancers and matched decalcified bone metastases. JCI Insight, 2017, 2, .	5.0	111

#	Article	IF	Citations
2695	Endogenous retroviral signatures predict immunotherapy response in clear cell renal cell carcinoma. Journal of Clinical Investigation, 2018, 128, 4804-4820.	8.2	210
2696	Tumor cellâ€“intrinsic EPHA2 suppresses antitumor immunity by regulating PTGS2 (COX-2). Journal of Clinical Investigation, 2019, 129, 3594-3609.	8.2	115
2697	Transcriptional and cytopathological hallmarks of FSHD in chronic DUX4-expressing mice. Journal of Clinical Investigation, 2020, 130, 2465-2477.	8.2	44
2698	DCAF1 regulates Treg senescence via the ROS axis during immunological aging. Journal of Clinical Investigation, 2020, 130, 5893-5908.	8.2	71
2699	Salt generates antiinflammatory Th17 cells but amplifies pathogenicity in proinflammatory cytokine microenvironments. Journal of Clinical Investigation, 2020, 130, 4587-4600.	8.2	42
2700	PMP22 antisense oligonucleotides reverse Charcot-Marie-Tooth disease type 1A features in rodent models. Journal of Clinical Investigation, 2017, 128, 359-368.	8.2	117
2701	intePareto: an R package for integrative analyses of RNA-Seq and ChIP-Seq data. BMC Genomics, 2020, 21, 802.	2.8	11
2702	Tuberomics: a molecular profiling for the adaption of edible fungi (Tuber magnatum Pico) to different natural environments. BMC Genomics, 2020, 21, 90.	2.8	15
2703	Gene expression of functionally-related genes coevolves across fungal species: detecting coevolution of gene expression using phylogenetic comparative methods. BMC Genomics, 2020, 21, 370.	2.8	10
2704	Physiologic RNA targets and refined sequence specificity of coronavirus EndoU. Rna, 2020, 26, 1976-1999.	3.5	24
2705	bcbioRNASeq: R package for bcbio RNA-seq analysis. F1000Research, 0, 6, 1976.	1.6	6
2706	bcbioRNASeq: R package for bcbio RNA-seq analysis. F1000Research, 0, 6, 1976.	1.6	21
2707	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. F1000Research, 2018, 7, 952.	1.6	63
2708	Correction of gene model annotations improves isoform abundance estimates: the example of ketohexokinase (Khk). F1000Research, 2018, 7, 1956.	1.6	5
2709	Correction of gene model annotations improves isoform abundance estimates: the example of ketohexokinase (Khk). F1000Research, 2018, 7, 1956.	1.6	7
2710	Large-scale sequence comparisons with sourmash. F1000Research, 2019, 8, 1006.	1.6	130
2711	Fast analysis of scATAC-seq data using a predefined set of genomic regions. F1000Research, 2020, 9, 199.	1.6	11
2712	PVDF Nanofiber Scaffold Coated with a Vitronectin Peptide Facilitates the Neural Differentiation of Human Embryonic Stem Cells. Development & Reproduction, 2020, 24, 135-147.	0.4	8

#	Article	IF	Citations
2713	Discovery and Functional Prediction of Long Non-Coding RNAs Common to Ischemic Stroke and Myocardial Infarction. Journal of Lipid and Atherosclerosis, 2020, 9, 449.	3.5	10
2714	Argonaute2 and LaminB modulate gene expression by controlling chromatin topology. PLoS Genetics, 2018, 14, e1007276.	3.5	20
2715	A nonsense variant in Rap Guanine Nucleotide Exchange Factor 5 (RAPGEF5) is associated with equine familial isolated hypoparathyroidism in Thoroughbred foals. PLoS Genetics, 2020, 16, e1009028.	3.5	6
2716	Comparison of alternative approaches for analysing multi-level RNA-seq data. PLoS ONE, 2017, 12, e0182694.	2.5	25
2717	Innate immune gene expression in Acropora palmata is consistent despite variance in yearly disease events. PLoS ONE, 2020, 15, e0228514.	2.5	12
2718	ZBTB38 is dispensable for antibody responses. PLoS ONE, 2020, 15, e0235183.	2.5	4
2719	Transcriptomic signatures of cold adaptation and heat stress in the winter ant (Prenolepis imparis). PLoS ONE, 2020, 15, e0239558.	2.5	6
2720	The latency-associated transcript locus of herpes simplex virus 1 is a virulence determinant in human skin. PLoS Pathogens, 2020, 16, e1009166.	4.7	11
2722	Microglia promote glioblastoma via mTORâ€mediated immunosuppression of the tumour microenvironment. EMBO Journal, 2020, 39, e103790.	7.8	77
2723	Involvement of circulating factors in the transmission of paternal experiences through the germline. EMBO Journal, 2020, 39, e104579.	7.8	28
2724	Alternative splicing coupled mRNA decay shapes the temperatureâ€dependent transcriptome. EMBO Reports, 2020, 21, e51369.	4.5	28
2725	Mild mitochondrial impairment enhances innate immunity and longevity through ATFSâ€1 and p38 signaling. EMBO Reports, 2021, 22, e52964.	4.5	28
2726	Phosphoproteomics identifies microglial Siglecâ€F inflammatory response during neurodegeneration. Molecular Systems Biology, 2020, 16, e9819.	7.2	20
2727	Generation of a Transcriptional Radiation Exposure Signature in Human Blood Using Long-Read Nanopore Sequencing. Radiation Research, 2019, 193, 143.	1.5	29
2728	SNCA overexpression disturbs hippocampal gene expression trajectories in midlife. Aging, 2018, 10, 4024-4041.	3.1	10
2729	Multi-omics network analysis reveals distinct stages in the human aging progression in epidermal tissue. Aging, 2020, 12, 12393-12409.	3.1	21
2730	Genetic variation between long-lived versus short-lived bats illuminates the molecular signatures of longevity. Aging, 2020, 12, 15962-15977.	3.1	10
2731	Patient-derived glioblastoma cultures as a tool for small-molecule drug discovery. Oncotarget, 2020, 11, 443-451.	1.8	16

#	Article	IF	Citations
2732	Entinostat augments NK cell functions via epigenetic upregulation of IFIT1-STING-STAT4 pathway. Oncotarget, 2020, 11, 1799-1815.	1.8	22
2734	Origin and Differentiation Trajectories of Fibroblastic Reticular Cells in the Splenic White Pulp. SSRN Electronic Journal, 0, , .	0.4	1
2735	Analysis of the Skeletal Muscle Proteome Uncovers Alteration in Splicing, Mitochondria, and Immune Factors with Aging. SSRN Electronic Journal, 0, , .	0.4	1
2736	Pathogenic Tau Causes a Toxic Depletion of Nuclear Calcium Mediated by BK Channels. SSRN Electronic Journal, 0, , .	0.4	1
2737	A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs. Life Science Alliance, 2019, 2, e201800175.	2.8	19
2738	Identification of Novel Genes and Biological Pathways That Overlap in Infectious and Nonallergic Diseases of the Upper and Lower Airways Using Network Analyses. Frontiers in Genetics, 2019, 10, 1352.	2.3	9
2739	The Effect of Drought on Transcriptome and Hormonal Profiles in Barley Genotypes With Contrasting Drought Tolerance. Frontiers in Plant Science, 2020, 11, 618491.	3.6	33
2740	The Developmental Transcriptome of Bagworm, Metisa plana (Lepidoptera: Psychidae) and Insights into Chitin Biosynthesis Genes. Genes, 2021, 12, 7.	2.4	4
2741	Novel Allergen Discovery through Comprehensive De Novo Transcriptomic Analyses of Five Shrimp Species. International Journal of Molecular Sciences, 2021, 22, 32.	4.1	15
2742	Adaptation to Endoplasmic Reticulum Stress Enhances Resistance of Oral Cancer Cells to Cisplatin by Up-Regulating Polymerase Î· and Increasing DNA Repair Efficiency. International Journal of Molecular Sciences, 2021, 22, 355.	4.1	11
2743	The first Antechinus reference genome provides a resource for investigating the genetic basis of semelparity and age-related neuropathologies. GigaByte, 0, 2020, 1-22.	0.0	18
2744	Bioinformatics as a Tool for the Structural and Evolutionary Analysis of Proteins. , 0, , .		7
2745	Robust manipulation of the behavior of Drosophila melanogaster by a fungal pathogen in the laboratory. ELife, 2018, 7, .	6.0	58
2746	BRG1 governs glucocorticoid receptor interactions with chromatin and pioneer factors across the genome. ELife, 2018, 7, .	6.0	59
2747	An intrinsic cell cycle timer terminates limb bud outgrowth. ELife, 2018, 7, .	6.0	24
2748	Control of RNA viruses in mosquito cells through the acquisition of vDNA and endogenous viral elements. ELife, 2019, 8, .	6.0	104
2749	Genetic effects on promoter usage are highly context-specific and contribute to complex traits. ELife, 2019, 8, .	6.0	53
2750	Beta-catenin signaling regulates barrier-specific gene expression in circumventricular organ and ocular vasculatures. ELife, 2019, 8, .	6.0	74

#	Article	IF	Citations
2751	Gene-centric functional dissection of human genetic variation uncovers regulators of hematopoiesis. ELife, 2019, 8, .	6.0	14
2752	PI3K-Yap activity drives cortical gyrification and hydrocephalus in mice. ELife, 2019, 8, .	6.0	28
2753	Mucosal infection rewires TNFÉ‘ signaling dynamics to skew susceptibility to recurrence. ELife, 2019, 8, .	6.0	24
2754	An evolutionary recent IFN/IL-6/CEBP axis is linked to monocyte expansion and tuberculosis severity in humans. ELife, 2019, 8, .	6.0	27
2755	Systematic identification of cancer cell vulnerabilities to natural killer cell-mediated immune surveillance. ELife, 2019, 8, .	6.0	69
2756	Androgen-regulated transcription of ESRP2 drives alternative splicing patterns in prostate cancer. ELife, 2019, 8, .	6.0	56
2757	Neuronal TORC1 modulates longevity via AMPK and cell nonautonomous regulation of mitochondrial dynamics in C. elegans. ELife, 2019, 8, .	6.0	75
2758	Nanopore direct RNA sequencing maps the complexity of Arabidopsis mRNA processing and m6A modification. ELife, 2020, 9, .	6.0	312
2759	A unicellular relative of animals generates a layer of polarized cells by actomyosin-dependent cellularization. ELife, 2019, 8, .	6.0	41
2760	Discovery proteomics in aging human skeletal muscle finds change in spliceosome, immunity, proteostasis and mitochondria. ELife, 2019, 8, .	6.0	132
2761	An RNAi screen unravels the complexities of Rho GTPase networks in skin morphogenesis. ELife, 2019, 8, .	6.0	9
2762	Soluble PD-L1 generated by endogenous retroelement exaptation is a receptor antagonist. ELife, 2019, 8, .	6.0	44
2763	Myofibril diameter is set by a finely tuned mechanism of protein oligomerization in Drosophila. ELife, 2019, 8, .	6.0	27
2764	Diversification of the Caenorhabditis heat shock response by Helitron transposable elements. ELife, 2019, 8, .	6.0	21
2765	A genome-wide view of the de-differentiation of central nervous system endothelial cells in culture. ELife, 2020, 9, .	6.0	41
2766	Single-cell transcriptome reveals the novel role of T-bet in suppressing the immature NK gene signature. ELife, 2020, 9, .	6.0	19
2767	FMRP promotes RNA localization to neuronal projections through interactions between its RGG domain and G-quadruplex RNA sequences. ELife, 2020, 9, .	6.0	89
2768	Selective egg cell polyspermy bypasses the triploid block. ELife, 2020, 9, .	6.0	24

#	Article	IF	Citations
2769	Dissecting the phenotypic and functional heterogeneity of mouse inflammatory osteoclasts by the expression of Cx3cr1. ELife, 2020, 9, .	6.0	38
2770	A new genetic strategy for targeting microglia in development and disease. ELife, 2020, 9, .	6.0	99
2771	Osterix-Cre marks distinct subsets of CD45- and CD45+ stromal populations in extra-skeletal tumors with pro-tumorigenic characteristics. ELife, 2020, 9, .	6.0	11
2772	Srsf10 and the minor spliceosome control tissue-specific and dynamic SR protein expression. ELife, 2020, 9, .	6.0	18
2773	A tudor domain protein, SIMR-1, promotes siRNA production at piRNA-targeted mRNAs in C. elegans. ELife, 2020, 9, .	6.0	45
2774	Population-scale proteome variation in human induced pluripotent stem cells. ELife, 2020, 9, .	6.0	40
2775	Isolation and transcriptomic analysis of Anopheles gambiae oenocytes enables the delineation of hydrocarbon biosynthesis. ELife, 2020, 9, .	6.0	20
2776	EDF1 coordinates cellular responses to ribosome collisions. ELife, 2020, 9, .	6.0	96
2777	Single molecule poly(A) tail-seq shows LARP4 opposes deadenylation throughout mRNA lifespan with most impact on short tails. ELife, 2020, 9, .	6.0	24
2778	Evidence for widespread dysregulation of circadian clock progression in human cancer. PeerJ, 2018, 6, e4327.	2.0	75
2779	The Oyster River Protocol: a multi-assembler and kmer approach for de novo transcriptome assembly. PeerJ, 2018, 6, e5428.	2.0	85
2780	LiBiNorm: an htseq-count analogue with improved normalisation of Smart-seq2 data and library preparation diagnostics. PeerJ, 2019, 7, e6222.	2.0	21
2781	Simphony: simulating large-scale, rhythmic data. PeerJ, 2019, 7, e6985.	2.0	8
2782	Transcriptome sequencing and analysis reveals the molecular response to selenium stimuli in Pueraria lobata (willd.) Ohwi. PeerJ, 2020, 8, e8768.	2.0	8
2783	The level of putative carotenoid-binding proteins determines the body color in two species of endemic Lake Baikal amphipods. PeerJ, 2020, 8, e9387.	2.0	5
2785	Cardiac radiotherapy induces electrical conduction reprogramming in the absence of transmural fibrosis. Nature Communications, 2021, 12, 5558.	12.8	75
2788	Differential expression profile of gluten-specific T cells identified by single-cell RNA-seq. PLoS ONE, 2021, 16, e0258029.	2.5	4
2789	IL-1-driven stromalâ€“neutrophil interactions define a subset of patients with inflammatory bowel disease that does not respond to therapies. Nature Medicine, 2021, 27, 1970-1981.	30.7	117

#	Article	IF	Citations
2790	Genomeâ€wide transcriptome signatures of antâ€farmed Squamellaria epiphytes reveal key functions in a unique symbiosis. Ecology and Evolution, 2021, 11, 15882-15895.	1.9	3
2791	P75 neurotrophin receptor controls subventricular zone neural stem cell migration after stroke. Cell and Tissue Research, 2021, 387, 415.	2.9	9
2792	Modulation of Global Gene Expression by Aneuploidy and CNV of Dosage Sensitive Regulatory Genes. Genes, 2021, 12, 1606.	2.4	5
2793	Potential Diagnostic Value of the Differential Expression of Histone H3 Variants between Low- and High-Grade Gliomas. Cancers, 2021, 13, 5261.	3.7	4
2795	Heading towards a dead end: The role of DND1 in germ line differentiation of human iPSCs. PLoS ONE, 2021, 16, e0258427.	2.5	2
2796	Novel and Annotated Long Noncoding RNAs Associated with Ischemia in the Human Heart. International Journal of Molecular Sciences, 2021, 22, 11324.	4.1	4
2797	Nuclear-localized human respiratory syncytial virus NS1 protein modulates host gene transcription. Cell Reports, 2021, 37, 109803.	6.4	18
2800	Bromodomain Containing Protein 4 (BRD4) Regulates Expression of its Interacting Coactivators in the Innate Response to Respiratory Syncytial Virus. Frontiers in Molecular Biosciences, 2021, 8, 728661.	3.5	12
2801	A chromosome-level genome sequence of Chrysanthemum seticuspe, a model species for hexaploid cultivated chrysanthemum. Communications Biology, 2021, 4, 1167.	4.4	32
2802	Impact of human gene annotations on RNA-seq differential expression analysis. BMC Genomics, 2021, 22, 730.	2.8	6
2804	MINTIE: identifying novel structural and splice variants in transcriptomes using RNA-seq data. Genome Biology, 2021, 22, 296.	8.8	16
2807	Transcriptomic Profile and Probiotic Properties of Lactiplantibacillus pentosus Pre-adapted to Edible Oils. Frontiers in Microbiology, 2021, 12, 747043.	3.5	6
2808	Benchmarking sequencing methods and tools that facilitate the study of alternative polyadenylation. Genome Biology, 2021, 22, 291.	8.8	23
2809	Computational repurposing of therapeutic small molecules from cancer to pulmonary hypertension. Science Advances, 2021, 7, eabh3794.	10.3	16
2810	Translational repression of NMD targets by GIGYF2 and EIF4E2. PLoS Genetics, 2021, 17, e1009813.	3.5	25
2811	KDM5B promotes immune evasion by recruiting SETDB1 to silence retroelements. Nature, 2021, 598, 682-687.	27.8	117
2812	Aberrant RNA methylation triggers recruitment of an alkylation repair complex. Molecular Cell, 2021, 81, 4228-4242.e8.	9.7	18
2813	Multi-tumor analysis of cancer-stroma interactomes of patient-derived xenografts unveils the unique homeostatic process in renal cell carcinomas. IScience, 2021, 24, 103322.	4.1	5

#	Article	IF	Citations
2814	A new paradigm for leprosy diagnosis based on host gene expression. PLoS Pathogens, 2021, 17, e1009972.	4.7	11
2816	Histone Variant H2A.J Is Enriched in Luminal Epithelial Gland Cells. Genes, 2021, 12, 1665.	2.4	6
2817	Chromatin accessibility and gene expression during adipocyte differentiation identify context-dependent effects at cardiometabolic GWAS loci. PLoS Genetics, 2021, 17, e1009865.	3.5	9
2818	Complex Age- and Cancer-Related Changes in Human Blood Transcriptomeâ€"Implications for Pan-Cancer Diagnostics. Frontiers in Genetics, 2021, 12, 746879.	2.3	7
2819	Comparative epigenetic analysis of tumour initiating cells and syngeneic EPSC-derived neural stem cells in glioblastoma. Nature Communications, 2021, 12, 6130.	12.8	14
2820	CRISPR activation of endogenous genes reprograms fibroblasts into cardiovascular progenitor cells for myocardial infarction therapy. Molecular Therapy, 2022, 30, 54-74.	8.2	22
2821	Comparative transcriptomic analysis of races 1, 2, 5 and 6 of Fusarium oxysporum f.sp. pisi in a susceptible pea host identifies differential pathogenicity profiles. BMC Genomics, 2021, 22, 734.	2.8	7
2822	Molecular characterization of biphenotypic epithelioid and plexiform melanoma with deep penetrating nevusâ€like features. Pigment Cell and Melanoma Research, 2021, , .	3.3	3
2823	Nlrp3 Increases the Hostâ€™s Susceptibility to Tularemia. Frontiers in Microbiology, 2021, 12, 725572.	3.5	4
2824	Transcriptome Analysis of Potato Infected with the Necrotrophic Pathogen Alternaria solani. Plants, 2021, 10, 2212.	3.5	7
2825	Transcriptome and de novo analysis of Rosa xanthina f. spontanea in response to cold stress. BMC Plant Biology, 2021, 21, 472.	3.6	7
2826	Annotation depth confounds direct comparison of gene expression across species. BMC Bioinformatics, 2021, 22, 499.	2.6	3
2827	Global quantification exposes abundant low-level off-target activity by base editors. Genome Research, 2021, 31, 2354-2361.	5.5	14
2828	MetaMLP: A Fast Word Embedding Based Classifier to Profile Target Gene Databases in Metagenomic Samples. Journal of Computational Biology, 2021, 28, 1063-1074.	1.6	2
2829	scAAVengr, a transcriptome-based pipeline for quantitative ranking of engineered AAVs with single-cell resolution. ELife, 2021, 10, .	6.0	33
2830	Splicing machinery is impaired in rheumatoid arthritis, associated with disease activity and modulated by anti-TNF therapy. Annals of the Rheumatic Diseases, 2022, 81, 56-67.	0.9	18
2832	Decreased Activated CD4⁺T Cell Repertoire Diversity After Antiretroviral Therapy in HIV-1/HCV Coinfection Correlates with CD4⁺T Cell Recovery. Viral Immunology, 2021, 34, 622-631.	1.3	2
2833	Transcriptome profiling of Arabidopsis thaliana roots in response to allelopathic effects of Conyza canadensis. Ecotoxicology, 2022, 31, 53-63.	2.4	5

#	Article	IF	Citations
2835	Transcriptome profile of the sinoatrial ring reveals conserved and novel genetic programs of the zebrafish pacemaker. BMC Genomics, 2021, 22, 715.	2.8	14
2836	CHD1 controls H3.3 incorporation in adult brain chromatin to maintain metabolic homeostasis and normal lifespan. Cell Reports, 2021, 37, 109769.	6.4	10
2838	Genome-wide RNA structure changes during human neurogenesis modulate gene regulatory networks. Molecular Cell, 2021, 81, 4942-4953.e8.	9.7	15
2839	Transcriptomic and Coexpression Network Analyses Revealed Pine Chalcone Synthase Genes Associated with Pine Wood Nematode Infection. International Journal of Molecular Sciences, 2021, 22, 11195.	4.1	11
2840	Experimental Design for Time-Series RNA-Seq Analysis of Gene Expression and Alternative Splicing. Methods in Molecular Biology, 2022, 2398, 173-188.	0.9	2
2843	Impact of Sickle Cell Trait Hemoglobin on the Intraerythrocytic Transcriptional Program of Plasmodium falciparum. MSphere, 2021, 6, e0075521.	2.9	7
2844	Trends in biological data integration for the selection of enzymes and transcription factors related to cellulose and hemicellulose degradation in fungi. 3 Biotech, 2021, 11, 475.	2.2	3
2845	Hallmarks of Retroelement Expression in T-Cells Treated With HDAC Inhibitors. Frontiers in Virology, 2021, 1, .	1.4	5
2846	Placental Gene Co-expression Network for Maternal Plasma Lipids Revealed Enrichment of Inflammatory Response Pathways. Frontiers in Genetics, 2021, 12, 681095.	2.3	1
2847	Mucin Expression and Splicing Determine Novel Subtypes and Patient Mortality in Pancreatic Ductal Adenocarcinoma. Clinical Cancer Research, 2021, 27, 6787-6799.	7.0	9
2848	Microbial ecology of sulfur cycling near the sulfateâ€“methane transition of deepâ€sea cold seep sediments. Environmental Microbiology, 2021, 23, 6844-6858.	3.8	31
2849	Transcriptional signatures in iPSC-derived neurons are reproducible across labs when differentiation protocols are closely matched. Stem Cell Research, 2021, 56, 102558.	0.7	2
2850	Loss of Resf1 reduces the efficiency of embryonic stem cell self-renewal and germline entry. Life Science Alliance, 2021, 4, e202101190.	2.8	2
2852	RBFOX splicing factors contribute to a broad but selective recapitulation of peripheral tissue splicing patterns in the thymus. Genome Research, 2021, 31, 2022-2034.	5.5	2
2853	Lactitol Supplementation Modulates Intestinal Microbiome in Liver Cirrhotic Patients. Frontiers in Medicine, 2021, 8, 762930.	2.6	9
2854	High expression of SARS-CoV2 viral entry-related proteins in human limbal stem cells. Ocular Surface, 2022, 23, 197-200.	4.4	6
2855	Circall: fast and accurate methodology for discovery of circular RNAs from paired-end RNA-sequencing data. BMC Bioinformatics, 2021, 22, 495.	2.6	8
2856	Coupled protein synthesis and ribosome-guided piRNA processing on mRNAs. Nature Communications, 2021, 12, 5970.	12.8	13

#	Article	IF	Citations
2857	Assessing Host-Pathogen Interaction Networks via RNA-Seq Profiling: A Systems Biology Approach. , 0, , .		1
2859	Ferroptosis-dependent extracellular vesicles from macrophage contribute to asbestos-induced mesothelial carcinogenesis through loading ferritin. Redox Biology, 2021, 47, 102174.	9.0	50
2860	Transcriptomics of the depressed and PTSD brain. Neurobiology of Stress, 2021, 15, 100408.	4.0	8
2861	Comprehensive analysis of hub mRNA, lncRNA and miRNA, and associated ceRNA networks implicated in grass carp (Ctenopharyngodon idella) growth traits. Genomics, 2021, 113, 4004-4014.	2.9	9
2862	Epinephrine affects gene expression levels and has a complex effect on biofilm formation in Micrococcus luteus strain C01 isolated from human skin. Biofilm, 2021, 3, 100058.	3.8	8
2863	Photo-driven heterogeneous microbial consortium reducing CO2 to hydrocarbons fuel. Journal of Cleaner Production, 2021, 326, 129397.	9.3	4
2887	MicroRNA-7 Specifically Marks the Gut Endocrine Lineage and Controls Progenitor Cell Proliferation Through <i>Egfr</i>. SSRN Electronic Journal, 0, , .	0.4	0
2893	Identification of Novel mRNA Transcripts in the Sympathetic Stellate Ganglia using RNA Sequencing. FASEB Journal, 2018, 32, 596.4.	0.5	0
2914	Transcriptome of Xenopus andrei, an octoploid frog, during embryonic development. Data in Brief, 2018, 19, 501-505.	1.0	1
2935	Big Data Technologies for DNA Sequencing. , 2019, , 330-336.		1
2949	Fast and accurate differential transcript usage by testing equivalence class counts. F1000Research, 2019, 8, 265.	1.6	3
2952	Using equivalence class counts for fast and accurate testing of differential transcript usage. F1000Research, 2019, 8, 265.	1.6	8
2965	Compare Expression Profiles for Pre-defined Gene Groups with C-REx. Journal of Open Source Software, 2019, 4, 1255.	4.6	0
2994	GUESSmyLT: Software to guess the RNA-Seq library type of paired and single end read files. Journal of Open Source Software, 2019, 4, 1344.	4.6	0
3008	Discovery of a Robust Gene Regulatory Network with a Complex Transcription Factor Network on Organ Cancer Cell-line RNA Sequence Data. Chem-Bio Informatics Journal, 2019, 19, 32-55.	0.3	0
3042	Bioinformatic Methods for the Analysis of High-Throughput RNA Sequencing in Arbuscular Mycorrhizal Fungi. Methods in Molecular Biology, 2020, 2146, 137-153.	0.9	1
3043	Tools for the assessment of epigenetic regulation. , 2020, , 33-64.		2
3044	Fluent genomics withÂplyrangesÂandÂtximeta. F1000Research, 2020, 9, 109.	1.6	2

#	Article	IF	Citations
3099	Functional profiling of the endometrium transcriptome during preimplantation development in Finnsheep, Texel and their F1 crosses. Agricultural and Food Science, 2020, 29, .	0.9	1
3100	Multi-species transcriptomics reveals evolutionary diversity in the mechanisms regulating shrimp tail muscle excitation-contraction coupling. Gene, 2020, 752, 144765.	2.2	4
3108	EffectorP 3.0: Prediction of Apoplastic and CytoplasmicÂEffectors in Fungi and Oomycetes. Molecular Plant-Microbe Interactions, 2022, 35, 146-156.	2.6	179
3110	Plasma Gradient of Soluble Urokinase-Type Plasminogen Activator Receptor Is Linked to Pathogenic Plasma Proteome and Immune Transcriptome and Stratifies Outcomes in Severe COVID-19. Frontiers in Immunology, 2021, 12, 738093.	4.8	11
3111	Accurate Quantification of Overlapping Herpesvirus Transcripts from RNA Sequencing Data. Journal of Virology, 2022, 96, JVI0163521.	3.4	6
3112	Application of third-generation sequencing in cancer research. Medical Review, 2021, 1, 150-171.	1.2	6
3113	Depth-dependent variability of biological nitrogen fixation and diazotrophic communities in mangrove sediments. Microbiome, 2021, 9, 212.	11.1	24
3115	Maternal Benzophenone Exposure Impairs Hippocampus Development and Cognitive Function in Mouse Offspring. Advanced Science, 2021, 8, e2102686.	11.2	3
3116	Transcriptomic and Metabolomic Differences Between Two Saposhnikovia divaricata (Turcz.) Schischk Phenotypes With Single- and Double-Headed Roots. Frontiers in Bioengineering and Biotechnology, 2021, 9, 764093.	4.1	3
3117	Genomeâ€scale metabolic modeling reveals SARSâ€CoVâ€2â€induced metabolic changes and antiviral targets. Molecular Systems Biology, 2021, 17, e10260.	7.2	26
3118	Overlapping functions of RBBP4 and RBBP7 in regulating cell proliferation and histone H3.3 deposition during mouse preimplantation development. Epigenetics, 2022, 17, 1205-1218.	2.7	10
3119	Calcineurin regulates the stability and activity of estrogen receptor Î±. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	13
3120	Alternative splicing during fruit development among fleshy fruits. BMC Genomics, 2021, 22, 762.	2.8	9
3121	Genome-wide screening of novel RT-qPCR reference genes for study of GLRaV-3 infection in wine grapes and refinement of an RNA isolation protocol for grape berries. Plant Methods, 2021, 17, 110.	4.3	7
3125	Organ-specific, integrated omics data-based study on the metabolic pathways of the medicinal plant Bletilla striata (Orchidaceae). BMC Plant Biology, 2021, 21, 504.	3.6	8
3126	Isolation of multipotent progenitor cells from pleura and pericardium for tracheal tissue engineering purposes. Journal of Cellular and Molecular Medicine, 2021, 25, 10869-10878.	3.6	5
3127	Characterisation of the enzyme transport path between shipworms and their bacterial symbionts. BMC Biology, 2021, 19, 233.	3.8	8
3128	Histology and transcriptomic analyses of barnacles with different base materials and habitats shed lights on the duplication and chemical diversification of barnacle cement proteins. BMC Genomics, 2021, 22, 783.	2.8	12

#	Article	IF	Citations
3129	Safety, pharmacokinetic, pharmacodynamic and clinical activity of molibresib for the treatment of nuclear protein of the testis carcinoma and other cancers: Results of a Phase <scp>I</scp>/<scp>II</scp> openâ€label, dose escalation study. International Journal of Cancer, 2022, 150, 993-1006.	5.1	28
3130	Analyzing Immunity in Non-model Insects Using De Novo Transcriptomics. Springer Protocols, 2020, , 35-51.	0.3	1
3133	Alteration of the Premature tRNA Landscape by Gammaherpesvirus Infection. MBio, 2020, 11, .	4.1	10
3138	Run or Die in the Evolution of New MicroRNAsâ€"Testing the Red Queen Hypothesis on De Novo New Genes. Molecular Biology and Evolution, 2021, 38, 1544-1553.	8.9	11
3139	Transcriptome analysis of Caenorhabditis elegans lacking heme peroxidase SKPO-1 reveals an altered response to Enterococcus faecalis. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	4
3140	RNA-Seq transcriptome data of human cells infected with influenza A/Puerto Rico/8/1934 (H1N1) virus. Data in Brief, 2020, 33, 106604.	1.0	7
3142	Regulation of hostâ€infection ability in the grassâ€symbiotic fungus EpichloÃ« festucae by histone <scp>H3K9</scp> and <scp>H3K36</scp> methyltransferases. Environmental Microbiology, 2021, 23, 2116-2131.	3.8	9
3146	Probably Correct: Rescuing Repeats with Short and Long Reads. Genes, 2021, 12, 48.	2.4	5
3147	Automated Isoform Diversity Detector (AIDD): a pipeline for investigating transcriptome diversity of RNA-seq data. BMC Bioinformatics, 2020, 21, 578.	2.6	3
3151	IKZF3 deficiency potentiates chimeric antigen receptor T cells targeting solid tumors. Cancer Letters, 2022, 524, 121-130.	7.2	20
3160	Toward uncharted territory of cellular heterogeneity: advances and applications of single-cell RNA-seq. , 2021, 5, 1-21.		2
3162	Gene Expression Analysis of Litter-Associated Fungi Using RNA-Seq. , 2020, , 355-367.		0
3163	Processing Oxford Nanopore Long Reads Using Amazon Web Services. Biomedical Chemistry Research and Methods, 2020, 3, e00131.	0.4	4
3166	Nuclear Isoform of FGF13 Regulates Postnatal Neurogenesis in Hippocampus Through Epigenetic Mechanism. SSRN Electronic Journal, 0, , .	0.4	0
3167	Anti-CD3 Stimulated T Cell Transcriptome Reveals Novel ncRNAs and Correlates with a Suppressive Profile. Lecture Notes in Computer Science, 2020, , 180-191.	1.3	0
3184	Fast analysis of scATAC-seq data using a predefined set of genomic regions. F1000Research, 2020, 9, 199.	1.6	6
3186	Methods for analyzing next-generation sequencing data XV. RNA-seq analysis (Part 3). Japanese Journal of Lactic Acid Bacteria, 2020, 31, 25-34.	0.1	0
3197	RNA sequencing of whole blood reveals early alterations in immune cells and gene expression in Parkinsonâ€™s disease. Nature Aging, 2021, 1, 734-747.	11.6	18

#	Article	IF	Citations
3198	The Capacity to Produce Hydrogen Sulfide (H2S) via Cysteine Degradation Is Ubiquitous in the Human Gut Microbiome. Frontiers in Microbiology, 2021, 12, 705583.	3.5	37
3199	Computational screening of miRNAs and their targets in saffron (Crocus sativus L.) by transcriptome mining. Planta, 2021, 254, 117.	3.2	12
3201	Joint transcriptomic and metabolomic analysis reveals the mechanism of low-temperature tolerance in Hosta ventricosa. PLoS ONE, 2021, 16, e0259455.	2.5	11
3202	Circular RNAs exhibit limited evidence for translation, or translation regulation of the mRNA counterpart in terminal hematopoiesis. Rna, 2022, 28, 194-209.	3.5	3
3203	Targeting glioblastoma signaling and metabolism with a re-purposed brain-penetrant drug. Cell Reports, 2021, 37, 109957.	6.4	38
3204	Unveiling the occurrence, hosts and mobility potential of antibiotic resistance genes in the deep ocean. Science of the Total Environment, 2022, 816, 151539.	8.0	14
3205	Modeling population size independent tissue epigenomes by ChILâ€seq with single thin sections. Molecular Systems Biology, 2021, 17, e10323.	7.2	1
3206	Long reads and Hiâ€C sequencing illuminate the twoâ€compartment genome of the model arbuscular mycorrhizal symbiont Rhizophagus irregularis. New Phytologist, 2022, 233, 1097-1107.	7.3	36
3207	Composition and functional profiles of microbial communities in two geochemically and mineralogically different caves. Applied Microbiology and Biotechnology, 2021, 105, 8921-8936.	3.6	7
3209	Transcriptional response of the calcification and stress response toolkits in an octocoral under heat and pH stress. Molecular Ecology, 2022, 31, 798-810.	3.9	7
3210	Chromatin-accessibility estimation from single-cell ATAC-seq data with scOpen. Nature Communications, 2021, 12, 6386.	12.8	57
3211	Cross-species transcriptomic signatures predict response to MK2 inhibition in mouse models of chronic inflammation. IScience, 2021, 24, 103406.	4.1	3
3212	Cross-platform transcriptomic profiling of the response to recombinant human erythropoietin. Scientific Reports, 2021, 11, 21705.	3.3	5
3213	Rare t(X;14)(q28;q32) translocation reveals link between MTCP1 and chronic lymphocytic leukemia. Nature Communications, 2021, 12, 6338.	12.8	3
3214	Untangling the molecular basis of coral response to sedimentation. Molecular Ecology, 2022, 31, 884-901.	3.9	5
3215	High rates of evolution preceded shifts to sex-biased gene expression in Leucadendron, the most sexually dimorphic angiosperms. ELife, 2021, 10, .	6.0	15
3216	Cigarette smoking-associated isoform switching and 3â€² UTR lengthening via alternative polyadenylation. Genomics, 2021, 113, 4184-4195.	2.9	3
3217	Identification of the sex-determining factor in the liverwort Marchantia polymorpha reveals unique evolution of sex chromosomes in a haploid system. Current Biology, 2021, 31, 5522-5532.e7.	3.9	36

#	Article	IF	Citations
3219	Doxycycline Changes the Transcriptome Profile of mIMCD3 Renal Epithelial Cells. Frontiers in Physiology, 2021, 12, 771691.	2.8	4
3223	Effects of JAK1-Preferential Inhibitor Filgotinib on Circulating Biomarkers and Whole Blood Genes/Pathways of Patients With Moderately to Severely Active Crohnâ€™s Disease. Inflammatory Bowel Diseases, 2022, 28, 1207-1218.	1.9	6
3224	Oxford Nanopore MinION Direct RNA-Seq for Systems Biology. Biology, 2021, 10, 1131.	2.8	15
3225	The FASTK family proteins fine-tune mitochondrial RNA processing. PLoS Genetics, 2021, 17, e1009873.	3.5	16
3226	Establishment of Human-Induced Pluripotent Stem Cell-Derived Neuronsâ€”A Promising In Vitro Model for a Molecular Study of Rabies Virus and Host Interaction. International Journal of Molecular Sciences, 2021, 22, 11986.	4.1	8
3227	Is rice-crayfish co-culture a better aquaculture model: From the perspective of antibiotic resistome profiles. Environmental Pollution, 2022, 292, 118450.	7.5	21
3228	Evidence for Long-Term Anthropogenic Pollution: The Hadal Trench as a Depository and Indicator for Dissemination of Antibiotic Resistance Genes. Environmental Science & Technology, 2021, 55, 15136-15148.	10.0	41
3230	PIM-Quantifier: A Processing-in-Memory Platform for mRNA Quantification. , 2021, , .		5
3267	<scp>MLLT</scp>6 maintains <scp>PD</scp>â€Ł1 expression and mediates tumor immune resistance. EMBO Reports, 2020, 21, e50155.	4.5	13
3277	RNA sequencing of whole blood in dogs with primary immune-mediated hemolytic anemia (IMHA) reveals novel insights into disease pathogenesis. PLoS ONE, 2020, 15, e0240975.	2.5	5
3278	Specific ablation of the NCoR corepressor Î´ splice variant reveals alternative RNA splicing as a key regulator of hepatic metabolism. PLoS ONE, 2020, 15, e0241238.	2.5	2
3290	Monocytic Ontogeny of Regenerated Macrophages Characterizes the Mesotheliomagenic Responses to Carbon Nanotubes. Frontiers in Immunology, 2021, 12, 666107.	4.8	5
3291	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. Clinical Cancer Research, 2021, 27, 5049-5061.	7.0	0
3292	The Molecular Basis of Ocean Acidification Sensitivity and Adaptation in Mytilus galloprovincialis. SSRN Electronic Journal, 0, , .	0.4	0
3293	Investigation of the expression of P-element-induced wimpy testis-interacting RNAs in human acute myeloid leukemia. Meta Gene, 2022, 31, 100998.	0.6	2
3294	Tyrosine phosphatases regulate resistance to ALK inhibitors in ALK+ anaplastic large cell lymphoma. Blood, 2022, 139, 717-731.	1.4	22
3296	Intracellular and Intercellular Gene Regulatory Network Inference From Time-Course Individual RNA-Seq. Frontiers in Bioinformatics, 2021, 1, .	2.1	3
3297	Xylan alleviates dietary fiber deprivation-induced dysbiosis by selectively promoting Bifidobacterium pseudocatenulatum in pigs. Microbiome, 2021, 9, 227.	11.1	28

#	Article	IF	Citations
3298	Comprehensive Analysis of Large-Scale Transcriptomes from Multiple Cancer Types. Genes, 2021, 12, 1865.	2.4	3
3300	Modulation of the Tomato Rhizosphere Microbiome via Changes in Root Exudation Mediated by the Ethylene Receptor NR. Microorganisms, 2021, 9, 2456.	3.6	12
3301	Highly flexible metabolism of the marine euglenozoan protist Diplonema papillatum. BMC Biology, 2021, 19, 251.	3.8	19
3303	RNA-Seq Data Analysis Pipeline for Plants: Transcriptome Assembly, Alignment, and Differential Expression Analysis. Methods in Molecular Biology, 2022, 2396, 47-60.	0.9	2
3304	Novel Mechanisms of Tumor Promotion by the Insulin Receptor Isoform A in Triple-Negative Breast Cancer Cells. Cells, 2021, 10, 3145.	4.1	14
3306	The Laccase Gene Family Mediate Multi-Perspective Trade-Offs during Tea Plant (Camellia sinensis) Development and Defense Processes. International Journal of Molecular Sciences, 2021, 22, 12554.	4.1	8
3307	Transcriptomics of tapping and healing process in frankincense tree during resin production. Genomics, 2021, 113, 4337-4351.	2.9	2
3308	Multiple stages of evolutionary change in anthrax toxin receptor expression in humans. Nature Communications, 2021, 12, 6590.	12.8	2
3310	A Câ€tterm truncated <scp>EIF2BÎ³</scp> protein encoded by an intronically polyadenylated isoform introduces unfavorable <scp>EIF2BÎ³â€“EIF2Î³</scp> interactions. Proteins: Structure, Function and Bioinformatics, 2022, 90, 889-897.	2.6	1
3311	Modulation of JA signalling reveals the influence of StJAZ1â€like on tuber initiation and tuber bulking in potato. Plant Journal, 2022, 109, 952-964.	5.7	15
3313	ZHX2 promotes HIF1Î± oncogenic signaling in triple-negative breast cancer. ELife, 2021, 10, .	6.0	21
3314	Temporal and sequential order of nonoverlapping gene networks unraveled in mated female Drosophila. Life Science Alliance, 2022, 5, e202101119.	2.8	4
3315	Jumper enables discontinuous transcript assembly in coronaviruses. Nature Communications, 2021, 12, 6728.	12.8	4
3316	p38 Mediates Resistance to FGFR Inhibition in Non-Small Cell Lung Cancer. Cells, 2021, 10, 3363.	4.1	6
3317	A growth factorâ€“expressing macrophage subpopulation orchestrates regenerative inflammation via GDF-15. Journal of Experimental Medicine, 2022, 219, .	8.5	31
3318	Sinomenine Hydrochloride Ameliorates Fish Foodborne Enteritis via Î±7nAchR-Mediated Anti-Inflammatory Effect Whilst Altering Microbiota Composition. Frontiers in Immunology, 2021, 12, 766845.	4.8	14
3319	CHK1 protects oncogenic KRAS-expressing cells from DNA damage and is a target for pancreatic cancer treatment. Cell Reports, 2021, 37, 110060.	6.4	14
3321	Nitrate restricts nodule organogenesis through inhibition of cytokinin biosynthesis in Lotus japonicus. Nature Communications, 2021, 12, 6544.	12.8	28

#	Article	IF	Citations
3322	Altered temporal sequence of transcriptional regulators in the generation of human cerebellar granule cells. ELife, 2021, 10, .	6.0	12
3323	Comparative Toxicogenomics of Glyphosate and Roundup Herbicides by Mammalian Stem Cell-Based Genotoxicity Assays and Molecular Profiling in Sprague-Dawley Rats. Toxicological Sciences, 2022, 186, 83-101.	3.1	27
3324	Single-nucleus transcriptomes reveal evolutionary and functional properties of cell types in the Drosophila accessory gland. Genetics, 2022, 220, .	2.9	10
3326	RNA-Binding Protein Expression Alters Upon Differentiation of Human B Cells and T Cells. Frontiers in Immunology, 2021, 12, 717324.	4.8	13
3327	Csp1, a Cold Shock Protein Homolog in Xylella fastidiosa Influences Cell Attachment, Pili Formation, and Gene Expression. Microbiology Spectrum, 2021, 9, e0159121.	3.0	9
3328	Deletion of pancreas-specific miR-216a reduces beta-cell mass and inhibits pancreatic cancer progression in mice. Cell Reports Medicine, 2021, 2, 100434.	6.5	10
3329	Inhibition of the renin-angiotensin system causes concentric hypertrophy of renal arterioles in mice and humans. JCI Insight, 2021, 6, .	5.0	16
3330	Genomeâ€wide identification and characterization of long noncoding RNAs in maize under rice black streaked dwarf virus infection. Plant Pathology, 0, , .	2.4	1
3336	Human Islet MicroRNA-200c Is Elevated in Type 2 Diabetes and Targets the Transcription Factor ETV5 to Reduce Insulin Secretion. Diabetes, 2022, 71, 275-284.	0.6	14
3337	recount3: summaries and queries for large-scale RNA-seq expression and splicing. Genome Biology, 2021, 22, 323.	8.8	103
3338	Scalable, methanolâ€free manufacturing of the SARSâ€CoVâ€2 receptorâ€binding domain in engineered Komagataella phaffii. Biotechnology and Bioengineering, 2022, 119, 657-662.	3.3	17
3339	Symbiotic responses of Lotus japonicus to two isogenic lines of a mycorrhizal fungus differing in the presence/absence of an endobacterium. Plant Journal, 2021, 108, 1547-1564.	5.7	15
3341	Psychological stress impairs IL22-driven protective gut mucosal immunity against colonising pathobionts. Nature Communications, 2021, 12, 6664.	12.8	26
3342	TRIB1 regulates LDL metabolism through CEBPÎ±-mediated effects on the LDL receptor in hepatocytes. Journal of Clinical Investigation, 2021, 131, .	8.2	9
3343	Protective Role of Spermidine in Colitis and Colon Carcinogenesis. Gastroenterology, 2022, 162, 813-827.e8.	1.3	40
3344	Locus-specific expression of transposable elements in single cells with CELLO-seq. Nature Biotechnology, 2022, 40, 546-554.	17.5	38
3345	A Computational Analysis in a Cohort of Parkinsonâ€™s Disease Patients and Clock-Modified Colorectal Cancer Cells Reveals Common Expression Alterations in Clock-Regulated Genes. Cancers, 2021, 13, 5978.	3.7	14
3346	Inositol 1,4,5â€trisphosphate receptor typeÂ3 is involved in resistance to apoptosis and maintenance of human hepatocellular carcinoma. Oncology Letters, 2021, 23, 32.	1.8	1

#	Article	IF	Citations
3348	Accurate expression quantification from nanopore direct RNA sequencing with NanoCount. Nucleic Acids Research, 2022, 50, e19-e19.	14.5	44
3349	Transcript-targeted analysis reveals isoform alterations and double-hop fusions in breast cancer. Communications Biology, 2021, 4, 1320.	4.4	13
3350	The Antifungal Effects of Citral on Magnaporthe oryzae Occur via Modulation of Chitin Content as Revealed by RNA-Seq Analysis. Journal of Fungi (Basel, Switzerland), 2021, 7, 1023.	3.5	8
3351	Multi-omic characterization of the thermal stress phenome in the stony coral Montipora capitata. PeerJ, 2021, 9, e12335.	2.0	16
3353	Stem cells expand potency and alter tissue fitness by accumulating diverse epigenetic memories. Science, 2021, 374, eabh2444.	12.6	56
3354	Transcriptome analysis in Alcea rosea L. and identification of critical genes involved in stamen petaloid. Scientia Horticulturae, 2022, 293, 110732.	3.6	2
3357	Telomere-to-telomere genome assembly of asparaginase-producing Trichoderma simmonsii. BMC Genomics, 2021, 22, 830.	2.8	9
3358	Reprogramming NK cells and macrophages via combined antibody and cytokine therapy primes tumors for elimination by checkpoint blockade. Cell Reports, 2021, 37, 110021.	6.4	21
3359	Long-term selective stimulation of transplanted neural stem/progenitor cells for spinal cord injury improves locomotor function. Cell Reports, 2021, 37, 110019.	6.4	34
3360	An NR2F1-specific agonist suppresses metastasis by inducing cancer cell dormancy. Journal of Experimental Medicine, 2022, 219, .	8.5	42
3361	Single-cell transcriptomic characterization of a gastrulating human embryo. Nature, 2021, 600, 285-289.	27.8	202
3362	Loss of PRC2 subunits primes lineage choice during exit of pluripotency. Nature Communications, 2021, 12, 6985.	12.8	23
3363	Effects of the noncoding subgenomic RNA of red clover necrotic mosaic virus in virus infection. Journal of Virology, 2021, , JVI0181521.	3.4	5
3364	CCR5 and Biological Complexity: The Need for Data Integration and Educational Materials to Address Genetic/Biological Reductionism at the Interface of Ethical, Legal, and Social Implications. Frontiers in Immunology, 2021, 12, 790041.	4.8	5
3368	Multiomics Analysis of Spatially Distinct Stromal Cells Reveals Tumor-Induced O-Glycosylation of the CDK4â€“pRB Axis in Fibroblasts at the Invasive Tumor Edge. Cancer Research, 2022, 82, 648-664.	0.9	9
3369	Evolution of the Parvalbumin Genes in Teleost Fishes after the Whole-Genome Duplication. Fishes, 2021, 6, 70.	1.7	9
3370	Pharmacological targeting of Sam68 functions in colorectal cancer stem cells. IScience, 2021, 24, 103442.	4.1	8
3371	Plant circadian clock control of Medicago truncatula nodulation via regulation of nodule cysteine-rich peptides. Journal of Experimental Botany, 2022, 73, 2142-2156.	4.8	9

#	Article	IF	Citations
3372	KSHV transactivator-derived small peptide traps coactivators to attenuate MYC and inhibits leukemia and lymphoma cell growth. Communications Biology, 2021, 4, 1330.	4.4	7
3374	A Novel Vitronectin Peptide Facilitates Differentiation of Oligodendrocytes from Human Pluripotent Stem Cells (Synthetic ECM for Oligodendrocyte Differentiation). Biology, 2021, 10, 1254.	2.8	4
3375	Naive and memory CD4+ T cell subsets can contribute to the generation of human Tfh cells. IScience, 2021, 25, 103566.	4.1	3
3376	Secretory MPP3 Reinforce Myeloid Differentiation Trajectory and Amplify Myeloid Cell Production. SSRN Electronic Journal, 0, , .	0.4	0
3377	CTCF Expression and Dynamic Motif Accessibility Modulates Epithelialâ€“Mesenchymal Gene Expression. Cancers, 2022, 14, 209.	3.7	15
3378	Transcriptome analyses of the Chinese white pine beetle-fungal symbiont Leptographium qinlingensis under terpene stress or growth on host pine sawdust. Symbiosis, 2022, 86, 17-31.	2.3	10
3380	Transcriptomic analysis of Pseudomonas ogarae F113 reveals the antagonistic roles of AmrZ and FleQ during rhizosphere adaption. Microbial Genomics, 2022, 8, .	2.0	6
3381	Integrated Application of Multiomics Strategies Provides Insights Into the Environmental Hypoxia Response in Pelteobagrus vachelliÂMuscle. Molecular and Cellular Proteomics, 2022, 21, 100196.	3.8	10
3382	Subcutaneous adipose tissue splice quantitative trait loci reveal differences in isoform usage associated with cardiometabolic traits. American Journal of Human Genetics, 2022, 109, 66-80.	6.2	13
3383	A simple guide to de novo transcriptome assembly and annotation. Briefings in Bioinformatics, 2022, 23, .	6.5	42
3384	Unique structure and positive selection promote the rapid divergence of Drosophila Y chromosomes. ELife, 2022, 11, .	6.0	22
3385	Structure and Function of Rhizosphere Soil and Root Endophytic Microbial Communities Associated With Root Rot of Panax notoginseng. Frontiers in Plant Science, 2021, 12, 752683.	3.6	13
3386	Conditional immortalization of human atrial myocytes for the generation of in vitro models of atrial fibrillation. Nature Biomedical Engineering, 2022, 6, 389-402.	22.5	16
3387	A test of the pioneer factor hypothesis using ectopic liver gene activation. ELife, 2022, 11, .	6.0	35
3388	Cortical diurnal rhythms remain intact with microglial depletion. Scientific Reports, 2022, 12, 114.	3.3	18
3391	Gene Co-Expression Network Analysis Identifies Vitamin D-Associated Gene Modules in Adult Normal Rectal Epithelium Following Supplementation. Frontiers in Genetics, 2021, 12, 783970.	2.3	3
3392	First Draft Genome of a Mud Loach (Misgurnus mizolepis) in the Family Cobitidae. Frontiers in Marine Science, 2022, 8, .	2.5	0
3393	Cross-species prediction of essential genes in insects. Bioinformatics, 2022, 38, 1504-1513.	4.1	4

#	Article	IF	Citations
3394	Comparative Studies of Renin-Null Zebrafish and Mice Provide New Functional Insights. Hypertension, 2022, 79, HYPERTENSIONAHA12118600.	2.7	4
3395	A comprehensive study on the exposure of nanoplastics to constructed wetland ecological systems: Macrophyte physiology and microbial enzymology, community composition and metabolic functions. Chemical Engineering Journal, 2022, 434, 134592.	12.7	28
3396	Proteogenomic characterization identifies clinically relevant subgroups of intrahepatic cholangiocarcinoma. Cancer Cell, 2022, 40, 70-87.e15.	16.8	120
3397	APOE4 confers transcriptomic and functional alterations to primary mouse microglia. Neurobiology of Disease, 2022, 164, 105615.	4.4	22
3398	The bud dormancy disconnect: latent buds of grapevine are dormant during summer despite a high metabolic rate. Journal of Experimental Botany, 2022, 73, 2061-2076.	4.8	10
3399	Transcriptomic analysis of brine shrimp Artemia franciscana across a wide range of salinities. Marine Genomics, 2022, 61, 100919.	1.1	10
3400	Gene expression patterns of sea urchins (Strongylocentrotus intermedius) exposed to different combinations of temperature and hypoxia. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2022, 41, 100953.	1.0	3
3401	Metagenomic analysis reveals the response of microbial community in river sediment to accidental antimony contamination. Science of the Total Environment, 2022, 813, 152484.	8.0	12
3404	The High Concentrations of Abscisic, Jasmonic, and Salicylic Acids Produced Under Long Days Do Not Accelerate Flowering in Chenopodium Ficifolium 459. SSRN Electronic Journal, 0, , .	0.4	0
3406	Transcription Elongation Machinery Is a Druggable Dependency and Potentiates Immunotherapy in Glioblastoma Stem Cells. Cancer Discovery, 2022, 12, 502-521.	9.4	29
3407	RNA-Scoop: interactive visualization of transcripts in single-cell transcriptomes. NAR Genomics and Bioinformatics, 2021, 3, lqab105.	3.2	0
3408	Diversity and Function of Wolf Spider Gut Microbiota Revealed by Shotgun Metagenomics. Frontiers in Microbiology, 2021, 12, 758794.	3.5	7
3409	Iodoacetic acid exposure alters the transcriptome in mouse ovarian antral follicles. Journal of Environmental Sciences, 2022, 117, 46-57.	6.1	5
3410	BRD2 inhibition blocks SARS-CoV-2 infection by reducing transcription of the host cell receptor ACE2. Nature Cell Biology, 2022, 24, 24-34.	10.3	47
3411	Multi-time scale transcriptomic analysis on the dynamic process of tamoxifen resistance development in breast cancer cell lines. Breast Cancer, 2022, 29, 458-467.	2.9	2
3412	Histamine H4 Receptor Agonism Induces Antitumor Effects in Human T-Cell Lymphoma. International Journal of Molecular Sciences, 2022, 23, 1378.	4.1	5
3413	Comparative analysis of common alignment tools for single-cell RNA sequencing. GigaScience, 2022, 11, .	6.4	17
3414	Sirt6 regulates lifespan in Drosophila melanogaster. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	29

#	Article	IF	Citations
3415	Epigenomic and transcriptomic analyses reveal differences between low-grade inflammation and severe exhaustion in LPS-challenged murine monocytes. Communications Biology, 2022, 5, 102.	4.4	20
3419	Microbiomes of air dust collected during the ground-based closed bioregenerative life support experiment "Lunar Palace 365". Environmental Microbiomes, 2022, 17, 4.	5.0	4
3420	Potential Mechanisms of Quercetin Influence the ClfB Protein During Biofilm Formation of Staphylococcus aureus. Frontiers in Pharmacology, 2022, 13, 825489.	3.5	8
3421	Multi-omics analyses of the ulcerative colitis gut microbiome link Bacteroides vulgatus proteases with disease severity. Nature Microbiology, 2022, 7, 262-276.	13.3	110
3422	AGAMEMNON: an Accurate metaGenomics And MEtatranscriptoMics quaNtificatiON analysis suite. Genome Biology, 2022, 23, 39.	8.8	3
3423	Wholistic approach: Transcriptomic analysis and beyond using archival material for molecular diagnosis. Genes Chromosomes and Cancer, 2022, 61, 382-393.	2.8	18
3424	Maternal-fetal immune responses in pregnant women infected with SARS-CoV-2. Nature Communications, 2022, 13, 320.	12.8	117
3425	Assembly of 97 Novel Bacterial Genomes in the Microbial Community Affiliated with Polyvinyl Alcohol in Soil of Northern China. BioMed Research International, 2022, 2022, 1-14.	1.9	1
3426	Effects of activated sludge and UV disinfection processes on the bacterial community and antibiotic resistance profile in a municipal wastewater treatment plant. Environmental Science and Pollution Research, 2022, 29, 36088-36099.	5.3	4
3427	Exploring the Possible Link between the Gut Microbiome and Fat Deposition in Pigs. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-13.	4.0	16
3428	Effects of IFIH1 rs1990760 variants on systemic inflammation and outcome in critically ill COVID-19 patients in an observational translational study. ELife, 2022, 11, .	6.0	16
3429	Effect of short-term hindlimb immobilization on skeletal muscle atrophy and the transcriptome in a low compared with high responder to endurance training model. PLoS ONE, 2022, 17, e0261723.	2.5	1
3430	Morphological, physiological, biochemical, and transcriptome studies reveal the importance of transporters and stress signaling pathways during salinity stress in Prunus. Scientific Reports, 2022, 12, 1274.	3.3	15
3431	Mechanical Compression of Human Airway Epithelial Cells Induces Release of Extracellular Vesicles Containing Tenascin C. Cells, 2022, 11, 256.	4.1	6
3432	Revisiting hematopoiesis: applications of the bulk and single-cell transcriptomics dissecting transcriptional heterogeneity in hematopoietic stem cells. Briefings in Functional Genomics, 2022, 21, 159-176.	2.7	15
3433	RNA sequencing identifies genes reliant upon Ser26 in early growth response-1 in vascular endothelial cells exposed to fibroblast growth factor-2. Vascular Pharmacology, 2022, , 106952.	2.1	2
3434	Improved Genomic Identification, Clustering, and Serotyping of Shiga Toxin-Producing Escherichia coli Using Cluster/Serotype-Specific Gene Markers. Frontiers in Cellular and Infection Microbiology, 2021, 11, 772574.	3.9	9
3435	The embryonic transcriptome of Parhyale hawaiensis reveals different dynamics of microRNAs and mRNAs during the maternal-zygotic transition. Scientific Reports, 2022, 12, 174.	3.3	3

#	Article	IF	Citations
3437	Identification of an integrated stress and growth response signaling switch that directs vertebrate intestinal regeneration. BMC Genomics, 2022, 23, 6.	2.8	1
3438	Deriving Ranges of Optimal Estimated Transcript Expression due to Nonidentifiability. Journal of Computational Biology, 2022, 29, 121-139.	1.6	8
3439	ZFP207 sustains pluripotency by coordinating OCT4 stability, alternative splicing and RNA export. EMBO Reports, 2022, 23, e53191.	4.5	5
3440	Evaluation of CRISPR gene-editing tools in zebrafish. BMC Genomics, 2022, 23, 12.	2.8	12
3441	MGcount: a total RNA-seq quantification tool to address multi-mapping and multi-overlapping alignments ambiguity in non-coding transcripts. BMC Bioinformatics, 2022, 23, 39.	2.6	6
3442	NuA4 and H2A.Z control environmental responses and autotrophic growth in Arabidopsis. Nature Communications, 2022, 13, 277.	12.8	32
3443	LncRNAs Are Differentially Expressed between Wildtype and Cell Line Strains of African Trypanosomes. Non-coding RNA, 2022, 8, 7.	2.6	1
3444	Rapid idiosyncratic mechanisms of clinical resistance to KRAS G12C inhibition. Journal of Clinical Investigation, 2022, 132, .	8.2	43
3445	Analysis of the transcriptome of the needles and bark of Pinus radiata induced by bark stripping and methyl jasmonate. BMC Genomics, 2022, 23, 52.	2.8	2
3446	Transcriptome Analysis of an Aedes albopictus Cell Line Single- and Dual-Infected with Lammi Virus and WNV. International Journal of Molecular Sciences, 2022, 23, 875.	4.1	2
3447	Single-cell architecture and functional requirement of alternative splicing during hematopoietic stem cell formation. Science Advances, 2022, 8, eabg5369.	10.3	12
3448	Down-regulation of the brain-specific cell-adhesion molecule contactin-3 in tuberous sclerosis complex during the early postnatal period. Journal of Neurodevelopmental Disorders, 2022, 14, 8.	3.1	4
3449	Cytosolic adaptation to mitochondria-induced proteostatic stress causes progressive muscle wasting. IScience, 2022, 25, 103715.	4.1	6
3450	Patient-specific MDS-RS iPSCs define the mis-spliced transcript repertoire and chromatin landscape of SF3B1-mutant HSPCs. Blood Advances, 2022, 6, 2992-3005.	5.2	7
3451	DNA methylation aging and transcriptomic studies in horses. Nature Communications, 2022, 13, 40.	12.8	34
3452	Brain transcriptome analysis reveals gene expression differences associated with dispersal behaviour between rangeâ€front and rangeâ€core populations of invasive cane toads in Australia. Molecular Ecology, 2022, 31, 1700-1715.	3.9	9
3454	PSD3 downregulation confers protection against fatty liver disease. Nature Metabolism, 2022, 4, 60-75.	11.9	15
3456	Comparative metagenomics analysis reveals how the diet shapes the gut microbiota in several small mammals. Ecology and Evolution, 2022, 12, e8470.	1.9	8

#	Article	IF	Citations
3457	Modulation of Host Immune Response during Leishmania infantum Natural Infection: A Whole-Transcriptome Analysis of the Popliteal Lymph Nodes in Dogs. Frontiers in Immunology, 2021, 12, 794627.	4.8	8
3458	Androgens increase excitatory neurogenic potential in human brain organoids. Nature, 2022, 602, 112-116.	27.8	47
3459	A single-cell atlas of the normal and malformed human brain vasculature. Science, 2022, 375, eabi7377.	12.6	129
3460	Inhalable antibiotic resistomes emitted from hospitals: metagenomic insights into bacterial hosts, clinical relevance, and environmental risks. Microbiome, 2022, 10, 19.	11.1	39
3461	PIEZO1 mediates a mechanothrombotic pathway in diabetes. Science Translational Medicine, 2022, 14, eabk1707.	12.4	28
3462	The Drosophila functional Smad suppressing element fuss, a homologue of the human Skor genes, retains pro-oncogenic properties of the Ski/Sno family. PLoS ONE, 2022, 17, e0262360.	2.5	1
3464	TcTI, a Kunitz-type trypsin inhibitor from cocoa associated with defense against pathogens. Scientific Reports, 2022, 12, 698.	3.3	10
3465	Restoration of DNA repair mitigates genome instability and increases productivity of Chinese hamster ovary cells. Biotechnology and Bioengineering, 2022, 119, 963-982.	3.3	11
3466	Metagenomic analysis reveals wide distribution of phototrophic bacteria in hydrothermal vents on the ultraslow-spreading Southwest Indian Ridge. Marine Life Science and Technology, 2022, 4, 255-267.	4.6	4
3467	SCP4-STK35/PDIK1L complex is a dual phospho-catalytic signaling dependency in acute myeloid leukemia. Cell Reports, 2022, 38, 110233.	6.4	1
3470	Two phylogenetically unrelated peptideâ€receptor modules jointly regulate lateral root initiation via a partially shared signaling pathway in Arabidopsis thaliana. New Phytologist, 2022, 233, 1780-1796.	7.3	10
3471	Seasonal shift of the gut microbiome synchronizes host peripheral circadian rhythm for physiological adaptation to a low-fat diet in the giant panda. Cell Reports, 2022, 38, 110203.	6.4	49
3472	Integration of Aspergillus niger transcriptomic profile with metabolic model identifies potential targets to optimise citric acid production from lignocellulosic hydrolysate. , 2022, 15, 4.		3
3474	Regulation of Tomato Specialised Metabolism after Establishment of Symbiosis with the Endophytic Fungus Serendipita indica. Microorganisms, 2022, 10, 194.	3.6	8
3475	Differential Expression of CREM/ICER Isoforms Is Associated with the Spontaneous Control of HIV Infection. MBio, 2022, 13, e0197921.	4.1	3
3476	Treatment of Acute Kidney Injury Using a Dual Enzyme Embedded Zeolitic Imidazolate Frameworks Cascade That Catalyzes In Vivo Reactive Oxygen Species Scavenging. Frontiers in Bioengineering and Biotechnology, 2021, 9, 800428.	4.1	7
3477	Generation of cDC-like cells from human induced pluripotent stem cells via Notch signaling. , 2022, 10, e003827.		14
3478	Metagenomic and metatranscriptomic analyses reveal minor-yet-crucial roles of gut microbiome in deep-sea hydrothermal vent snail. Animal Microbiome, 2022, 4, 3.	3.8	7

#	Article	IF	Citations
3479	Glioblastoma stem cells reprogram chromatin in vivo to generate selective therapeutic dependencies on DPY30 and phosphodiesterases. Science Translational Medicine, 2022, 14, eabf3917.	12.4	13
3480	Improved 93-11 Genome and Time-Course Transcriptome Expand Resources for Rice Genomics. Frontiers in Plant Science, 2021, 12, 769700.	3.6	4
3482	p53 Promotes Cytokine Expression in Melanoma to Regulate Drug Resistance and Migration. Cells, 2022, 11, 405.	4.1	3
3483	Gene and metabolite expression dependence on body mass index in human myocardium. Scientific Reports, 2022, 12, 1425.	3.3	3
3486	NetSeekR: a network analysis pipeline for RNA-Seq time series data. BMC Bioinformatics, 2022, 23, 54.	2.6	4
3487	The contribution of uncharted RNA sequences to tumor identity in lung adenocarcinoma. NAR Cancer, 2022, 4, zcac001.	3.1	2
3489	Inhibition of Viral Replication Reduces Transcriptionally Active Distinct Hepatitis B Virus Integrations With Implications on Host Gene Dysregulation. Gastroenterology, 2022, 162, 1160-1170.e1.	1.3	31
3490	Stem-like breast cancer cells in the activated state resist genetic stress via TGFBI-ZEB1. Npj Breast Cancer, 2022, 8, 5.	5.2	8
3491	Transcriptomic and genomic studies classify NKL54 as a histone deacetylase inhibitor with indirect influence on MEF2-dependent transcription. Nucleic Acids Research, 2022, 50, 2566-2586.	14.5	12
3493	Differences in Gene Expression Profiles of Botrytis Cinerea During Noble and Gray Rot Development in Grapevine. SSRN Electronic Journal, 0, , .	0.4	0
3496	Genetic alterations of the SUMO isopeptidase SENP6 drive lymphomagenesis and genetic instability in diffuse large B-cell lymphoma. Nature Communications, 2022, 13, 281.	12.8	18
3497	Proteomics and Transcriptomics Uncover Key Processes for Elasnin Tolerance in Methicillin-Resistant Staphylococcus aureus. MSystems, 2022, 7, e0139321.	3.8	4
3499	Targeting the Meningeal Compartment to Resolve Chemobrain and Neuropathy via Nasal Delivery of Functionalized Mitochondria. Advanced Healthcare Materials, 2022, 11, e2102153.	7.6	8
3500	Stereotyped Bâ€cell responses are linked to IgG constant region polymorphisms in multiple sclerosis. European Journal of Immunology, 2022, 52, 550-565.	2.9	10
3501	A comparative genomics examination of desiccation tolerance and sensitivity in two sister grass species. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	8
3502	Progesterone differentially affects the transcriptomic profiles of cow endometrial cell types. BMC Genomics, 2022, 23, 82.	2.8	5
3503	Myeloid-Biased HSC Require Semaphorin 4A From the Bone Marrow Niche for Self-Renewal Under Stress and Life-Long Persistence. SSRN Electronic Journal, 0, , .	0.4	0
3504	Long read sequencing reveals novel isoforms and insights into splicing regulation during cell state changes. BMC Genomics, 2022, 23, 42.	2.8	11

#	Article	IF	Citations
3505	Impaired function of rDNA transcription initiation machinery leads to derepression of ribosomal genes with insertions of R2 retrotransposon. Nucleic Acids Research, 2022, 50, 867-884.	14.5	9
3506	Multi-Omics Analysis of Multiple Glucose-Sensing Receptor Systems in Yeast. Biomolecules, 2022, 12, 175.	4.0	9
3507	Epigenomic priming of immune genes implicates oligodendroglia in multiple sclerosis susceptibility. Neuron, 2022, 110, 1193-1210.e13.	8.1	36
3509	Spindle pole body component 24 homolog potentiates tumor progression via regulation of SRYâ€box transcription factor 2 in clear cell renal cell carcinoma. FASEB Journal, 2022, 36, e22086.	0.5	0
3511	A molecular map of long non-coding RNA expression, isoform switching and alternative splicing in osteoarthritis. Human Molecular Genetics, 2022, 31, 2090-2105.	2.9	15
3512	Identification of shared tumor epitopes from endogenous retroviruses inducing high-avidity cytotoxic T cells for cancer immunotherapy. Science Advances, 2022, 8, eabj3671.	10.3	38
3513	New Insights of Transcriptional Regulator AflR in Aspergillus flavus Physiology. Microbiology Spectrum, 2022, 10, e0079121.	3.0	14
3514	Amlodipine, an antiâ€hypertensive drug, alleviates nonâ€alcoholic fatty liver disease by modulating gut microbiota. British Journal of Pharmacology, 2022, 179, 2054-2077.	5.4	19
3515	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. Cell Reports Medicine, 2022, 3, 100522.	6.5	24
3516	PHOSPHATE STARVATION RESPONSE transcription factors enable arbuscular mycorrhiza symbiosis. Nature Communications, 2022, 13, 477.	12.8	81
3517	Metagenomic Views of Microbial Communities in Sand Sediments Associated with Coral Reefs. Microbial Ecology, 2023, 85, 465-477.	2.8	10
3518	Diel Patterns in Marine Microbial Metatranscriptomes Reflect Differences in Community Metabolic Activity Over Depth on the Continental Shelf of the North Atlantic. Frontiers in Marine Science, 2022, 9, .	2.5	2
3519	Adipocyte-Specific Ablation of PU.1 Promotes Energy Expenditure and Ameliorates Metabolic Syndrome in Aging Mice. Frontiers in Aging, 2022, 2, .	2.6	3
3520	Mechanical phenotyping reveals unique biomechanical responses in retinoic acid-resistant acute promyelocytic leukemia. IScience, 2022, 25, 103772.	4.1	4
3521	Manipulation of RNA polymerase III by Herpes Simplex Virus-1. Nature Communications, 2022, 13, 623.	12.8	15
3522	Whole transcriptome profiling of prospective endomyocardial biopsies reveals prognostic and diagnostic signatures of cardiac allograft rejection. Journal of Heart and Lung Transplantation, 2022, 41, 840-848.	0.6	9
3523	Transcriptomic analysis of interactions between Lymantria dispar larvae and carvacrol. Pesticide Biochemistry and Physiology, 2022, 181, 105012.	3.6	2
3524	Translational profile of developing phellem cells in Arabidopsis thaliana roots. Plant Journal, 2022, 110, 899-915.	5.7	9

#	Article	IF	Citations
3525	Lima1 mediates the pluripotency control of membrane dynamics and cellular metabolism. Nature Communications, 2022, 13, 610.	12.8	8
3526	Immune Activity and Response Differences of Oncolytic Viral Therapy in Recurrent Glioblastoma: Gene Expression Analyses of a Phase IB Study. Clinical Cancer Research, 2022, 28, 498-506.	7.0	12
3527	Transcriptome Profiling During Muscadine Berry Development Reveals the Dynamic of Polyphenols Metabolism. Frontiers in Plant Science, 2021, 12, 818071.	3.6	8
3528	The spatial self-organization within pluripotent stem cell colonies is continued in detaching aggregates. Biomaterials, 2022, 282, 121389.	11.4	15
3529	RNA-Seq Experiment and Data Analysis. Methods in Molecular Biology, 2022, 2418, 405-424.	0.9	6
3530	OUP accepted manuscript. Nucleic Acids Research, 2022, , .	14.5	6
3531	Genetic Perturbation of the Starch Biosynthesis in Maize Endosperm Reveals Sugar-Responsive Gene Networks. Frontiers in Plant Science, 2021, 12, 800326.	3.6	8
3532	Placental genomics mediates genetic associations with complex health traits and disease. Nature Communications, 2022, 13, 706.	12.8	20
3534	The dynamic trophic architecture of open-ocean protist communities revealed through machine-guided metatranscriptomics. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	27
3536	Chlamydomonas CHT7 is involved in repressing DNA replication and mitotic genes during synchronous growth. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	3
3537	Degradation of the Escherichia coli Essential Proteins DapB and Dxr Results in Oxidative Stress, which Contributes to Lethality through Incomplete Base Excision Repair. MBio, 2022, 13, e0375621.	4.1	8
3539	Short Term Changes in Dietary Fat Content and Metformin Treatment During Lactation Impact Milk Composition and Mammary Gland Morphology. Journal of Mammary Gland Biology and Neoplasia, 2022, 27, 1-18.	2.7	2
3540	Transcriptome-Wide Identification of Coding and Noncoding RNA-Binding Proteins Defines the Comprehensive RNA Interactome of Leishmania mexicana. Microbiology Spectrum, 2022, 10, e0242221.	3.0	8
3541	Mass cytometric and transcriptomic profiling of epithelial-mesenchymal transitions in human mammary cell lines. Scientific Data, 2022, 9, 44.	5.3	5
3542	The Lipid Droplet Knowledge Portal: A resource for systematic analyses of lipid droplet biology. Developmental Cell, 2022, 57, 387-397.e4.	7.0	22
3543	Partial Monosomy 21 Mirrors Gene Expression of Trisomy 21 in a Patient-Derived Neuroepithelial Stem Cell Model. Frontiers in Genetics, 2021, 12, 803683.	2.3	1
3547	Blood mRNA Expression in Alzheimer's Disease and Dementia With Lewy Bodies. American Journal of Geriatric Psychiatry, 2022, 30, 964-975.	1.2	9
3551	Evaluation of methods to detect circular RNAs from single-end RNA-sequencing data. BMC Genomics, 2022, 23, 106.	2.8	4

#	Article	IF	Citations
3552	Novel insights from a multiomics dissection of the Hayflick limit. ELife, 2022, 11, .	6.0	38
3554	DAISM-DNNXMBD: Highly accurate cell type proportion estimation with in silico data augmentation and deep neural networks. Patterns, 2022, 3, 100440.	5.9	10
3555	Differential expression of long non-coding RNAs under Peste des petits ruminants virus (PPRV) infection in goats. Virulence, 2022, 13, 310-322.	4.4	2
3556	Suppression of premature transcription termination leads to reduced mRNA isoform diversity and neurodegeneration. Neuron, 2022, 110, 1340-1357.e7.	8.1	12
3557	The gut microbiome and antibiotic resistome of chronic diarrhea rhesus macaques (Macaca mulatta) and its similarity to the human gut microbiome. Microbiome, 2022, 10, 29.	11.1	24
3558	DNA-Dependent Binding of Nargenicin to DnaE1 Inhibits Replication in Mycobacterium tuberculosis. ACS Infectious Diseases, 2022, 8, 612-625.	3.8	11
3560	Comparison of Transcriptome Responses between Sogatella furcifera Females That Acquired Southern Rice Black-Streaked Dwarf Virus and Not. Insects, 2022, 13, 182.	2.2	1
3561	Intron-Retention Neoantigen Load Predicts Favorable Prognosis in Pancreatic Cancer. JCO Clinical Cancer Informatics, 2022, 6, e2100124.	2.1	6
3562	RNACache: A scalable approach to rapid transcriptomic read mapping using locality sensitive hashing. Journal of Computational Science, 2022, 60, 101572.	2.9	1
3563	An In Vivo CRISPR Screen Identifies Stepwise Genetic Dependencies of Metastatic Progression. Cancer Research, 2022, 82, 681-694.	0.9	14
3564	Bradyrhizobium japonicum IRAT FA3 Alters Arabidopsis thaliana Root Architecture via Regulation of Auxin Efflux Transporters PIN2, PIN3, PIN7, and ABCB19. Molecular Plant-Microbe Interactions, 2022, 35, 215-229.	2.6	6
3565	The long non-coding RNA landscape of Candida yeast pathogens. Nature Communications, 2021, 12, 7317.	12.8	10
3566	GCN2 kinase activation by ATP-competitive kinase inhibitors. Nature Chemical Biology, 2022, 18, 207-215.	8.0	19
3567	Analysis of subcellular transcriptomes by RNA proximity labeling with Halo-seq. Nucleic Acids Research, 2022, 50, e24-e24.	14.5	25
3568	Cluster-specific gene markers enhance Shigella and enteroinvasive Escherichia coli in silico serotyping. Microbial Genomics, 2021, 7, .	2.0	9
3570	Benchmarking UMI-based single-cell RNA-seq preprocessing workflows. Genome Biology, 2021, 22, 339.	8.8	25
3571	Gene Expression and Mutational Profile in BAP-1 Inactivated Melanocytic Lesions of Progressive Malignancy from a Patient with Multiple Lesions. Genes, 2022, 13, 10.	2.4	6
3572	FMRP regulates mRNAs encoding distinct functions in the cell body and dendrites of CA1 pyramidal neurons. ELife, 2021, 10, .	6.0	28

#	Article	IF	Citations
3573	Discovery of a first-in-class reversible DNMT1-selective inhibitor with improved tolerability and efficacy in acute myeloid leukemia. Nature Cancer, 2021, 2, 1002-1017.	13.2	23
3574	Modern Approaches for Transcriptome Analyses in Plants. Advances in Experimental Medicine and Biology, 2021, 1346, 11-50.	1.6	0
3575	Neuronal Differentiation Pathways and Compound-Induced Developmental Neurotoxicity in the Human Neural Progenitor Cell Test (Hnpt) Revealed by Rna-Seq. SSRN Electronic Journal, 0, , .	0.4	0
3576	An engineered nano-liposome-human ACE2 decoy neutralizes SARS-CoV-2 Spike protein-induced inflammation in both murine and human macrophages. Theranostics, 2022, 12, 2639-2657.	10.0	19
3577	The Architecture of a Precision Oncology Platform. Advances in Experimental Medicine and Biology, 2022, 1361, 1-22.	1.6	1
3578	Halotolerant Bacteria are Key Antibiotic Resistant Players in Saline Soils Revealed by Metagenomic Analysis: Exploration of the Underlying Co-Selection Mechanisms. SSRN Electronic Journal, 0, , .	0.4	0
3579	Analysis of Liver Responses to Non-alcoholic Steatohepatitis by mRNA-Sequencing. Methods in Molecular Biology, 2022, 2455, 163-179.	0.9	1
3580	LncRNA Biomarkers of Inflammation and Cancer. Advances in Experimental Medicine and Biology, 2022, 1363, 121-145.	1.6	15
3581	Functional Genes Highlight Contrasting Elevational Pattern of Bacteria- and Fungi-Derived Compound Decompositions in Forest Soils. SSRN Electronic Journal, 0, , .	0.4	0
3582	Identification of differential mRNA and lncRNA expression in AcMNPV-infected Sf9 cells. Biocell, 2022, 46, 1675-1686.	0.7	0
3583	Tumor Heterogeneity and Molecular Characteristics of Glioblastoma Revealed by Single-Cell RNA-Seq Data Analysis. Genes, 2022, 13, 428.	2.4	2
3584	Integrative molecular and clinical profiling of acral melanoma links focal amplification of 22q11.21 to metastasis. Nature Communications, 2022, 13, 898.	12.8	19
3588	Reactive Oxygen Species Differentially Modulate the Metabolic and Transcriptomic Response of Endothelial Cells. Antioxidants, 2022, 11, 434.	5.1	9
3590	EZH2 noncanonically binds cMyc and p300 through a cryptic transactivation domain to mediate gene activation and promote oncogenesis. Nature Cell Biology, 2022, 24, 384-399.	10.3	88
3592	Full Issue PDF. Molecular Plant-Microbe Interactions, 2022, 35, 97-176.	2.6	0
3593	Screening and Identification of Human Endogenous Retrovirus-K mRNAs for Breast Cancer Through Integrative Analysis of Multiple Datasets. Frontiers in Oncology, 2022, 12, 820883.	2.8	6
3596	Transcription Factors Evolve Faster Than Their Structural Gene Targets in the Flavonoid Pigment Pathway. Molecular Biology and Evolution, 2022, 39, .	8.9	23
3599	The Polarity and Specificity of Antiviral T Lymphocyte Responses Determine Susceptibility to SARS-CoV-2 Infection in Patients with Cancer and Healthy Individuals. Cancer Discovery, 2022, 12, 958-983.	9.4	10

#	Article	IF	Citations
3600	TDP-43 loss and ALS-risk SNPs drive mis-splicing and depletion of UNC13A. Nature, 2022, 603, 131-137.	27.8	188
3601	Early Transcriptional Changes in the Midgut of Ornithodoros moubata after Feeding and Infection with Borrelia duttonii. Microorganisms, 2022, 10, 525.	3.6	3
3602	A gut-derived metabolite alters brain activity and anxiety behaviour in mice. Nature, 2022, 602, 647-653.	27.8	179
3603	Populus SVL Acts in Leaves to Modulate the Timing of Growth Cessation and Bud Set. Frontiers in Plant Science, 2022, 13, 823019.	3.6	8
3605	ATF-4 and hydrogen sulfide signalling mediate longevity in response to inhibition of translation or mTORC1. Nature Communications, 2022, 13, 967.	12.8	40
3606	Larval transcriptomic responses of a stony coral, Acropora tenuis, during initial contact with the native symbiont, Symbiodinium microadriaticum. Scientific Reports, 2022, 12, 2854.	3.3	7
3608	Mosaic cis-regulatory evolution drives transcriptional partitioning of HERVH endogenous retrovirus in the human embryo. ELife, 2022, 11, .	6.0	31
3612	Annual transcriptome of a key zooplankton species, the copepod Calanus finmarchicus. Ecology and Evolution, 2022, 12, e8605.	1.9	6
3614	Two wrongs make a right: heat stress reversion of a  male-sterile Brassica napus line. Journal of Experimental Botany, 2022, , .	4.8	0
3615	Infection by Moniliophthora perniciosa reprograms tomato Micro-Tom physiology, establishes a sink, and increases secondary cell wall synthesis. Journal of Experimental Botany, 2022, 73, 3651-3670.	4.8	2
3617	Chemerin Impact on Alternative mRNA Transcription in the Porcine Luteal Cells. Cells, 2022, 11, 715.	4.1	7
3618	Modeling iPSC-derived human neurofibroma-like tumors in mice uncovers the heterogeneity of Schwann cells within plexiform neurofibromas. Cell Reports, 2022, 38, 110385.	6.4	19
3619	DNAJB1-PRKACA in HEK293T cells induces LINC00473 overexpression that depends on PKA signaling. PLoS ONE, 2022, 17, e0263829.	2.5	6
3620	The Medaka Inbred Kiyosu-Karlsruhe (MIKK) panel. Genome Biology, 2022, 23, 59.	8.8	6
3623	Transcriptome changes in the developing sugarcane culm associated with high yield and early-season high sugar content. Theoretical and Applied Genetics, 2022, 135, 1619-1636.	3.6	1
3624	A hemimetabolous wing development suggests the wing origin from lateral tergum of a wingless ancestor. Nature Communications, 2022, 13, 979.	12.8	13
3625	Cross-species transcriptomics identifies core regulatory changes differentiating the asymptomatic asexual and virulent sexual life cycles of grass-symbioticEpichloÃ«fungi. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	4
3626	DJExpress: An Integrated Application for Differential Splicing Analysis and Visualization. Frontiers in Bioinformatics, 2022, 2, .	2.1	5

#	Article	IF	Citations
3627	Ischemiaâ€“Reperfusion Injury and Immunosuppressants Promote Polyomavirus Replication Through Common Molecular Mechanisms. Frontiers in Immunology, 2022, 13, 835584.	4.8	1
3628	Long Noncoding RNAs Regulate Hyperammonemia-Induced Neuronal Damage in Hepatic Encephalopathy. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-13.	4.0	6
3631	The NADPARK study: A randomized phase I trial of nicotinamide riboside supplementation in Parkinsonâ€™s disease. Cell Metabolism, 2022, 34, 396-407.e6.	16.2	111
3632	Full Issue PDF. Molecular Plant-Microbe Interactions, 2022, 35, 177-299.	2.6	0
3633	Strong parallel differential gene expression induced by hatchery rearing weakly associated with methylation signals in adult Coho Salmon (O. kisutch). Genome Biology and Evolution, 2022, , .	2.5	4
3635	Transcriptional Regulation of Pine Male and Female Cone Initiation and Development: Key Players Identified Through Comparative Transcriptomics. Frontiers in Genetics, 2022, 13, 815093.	2.3	1
3636	Circular RNA detection identifies circPSEN1 alterations in brain specific to autosomal dominant Alzheimer's disease. Acta Neuropathologica Communications, 2022, 10, 29.	5.2	11
3637	Transcriptome-wide analysis of glioma stem cell specific m6A modifications in long-non-coding RNAs. Scientific Reports, 2022, 12, 5431.	3.3	6
3639	The Ovarian Transcriptome at the Early Stage of Testis Removal-Induced Male-To-Female Sex Change in the Protandrous Black Porgy Acanthopagrus schlegelii. Frontiers in Genetics, 2022, 13, 816955.	2.3	4
3640	Size-dependent resistance to amoebic gill disease in naÃ¯ve Atlantic salmon (Salmo salar). Fish and Shellfish Immunology, 2022, 122, 437-445.	3.6	3
3641	Merkel Cell Carcinoma Sensitivity to EZH2 Inhibition Is Mediated by SIX1 Derepression. Journal of Investigative Dermatology, 2022, 142, 2783-2792.e15.	0.7	10
3642	A single-cell atlas of human and mouse white adipose tissue. Nature, 2022, 603, 926-933.	27.8	277
3645	Slc6a20a Heterozygous and Homozygous Mutant Mice Display Differential Behavioral and Transcriptomic Changes. Frontiers in Molecular Neuroscience, 2022, 15, 857820.	2.9	1
3647	RNA sequencing analysis of hepatocellular carcinoma identified oxidative phosphorylation as a major pathologic feature. Hepatology Communications, 2022, 6, 2170-2181.	4.3	9
3648	Database search engines and target database features impinge upon the identification of postâ€translationally cisâ€spliced peptides in HLA class I immunopeptidomes. Proteomics, 2022, 22, e2100226.	2.2	7
3649	Loss of transcriptional plasticity but sustained adaptive capacity after adaptation to global change conditions in a marine copepod. Nature Communications, 2022, 13, 1147.	12.8	27
3650	Generation and Gene Expression Profiles of Grevy's Zebra Induced Pluripotent Stem Cells. Stem Cells and Development, 2022, 31, 250-257.	2.1	3
3651	CREBBP/EP300 acetyltransferase inhibition disrupts FOXA1-bound enhancers to inhibit the proliferation of ER+ breast cancer cells. PLoS ONE, 2022, 17, e0262378.	2.5	5

#	Article	IF	Citations
3652	Transcriptomic Analysis Reveals Potential Candidate Pathways and Genes Involved in Toxin Biosynthesis in True Toads. Journal of Heredity, 2022, 113, 311-324.	2.4	3
3653	Analysis of mRNA Decay Intermediates in Bacillus subtilis 3â€² Exoribonuclease and RNA Helicase Mutant Strains. MBio, 2022, 13, e0040022.	4.1	3
3655	Apoplastic class III peroxidases PRX62 and PRX69 promote Arabidopsis root hair growth at low temperature. Nature Communications, 2022, 13, 1310.	12.8	25
3656	Starvation causes changes in the intestinal transcriptome and microbiome that are reversed upon refeeding. BMC Genomics, 2022, 23, 225.	2.8	10
3658	Evolutionary divergence of Firre localization and expression. Rna, 2022, , rna.079070.121.	3.5	8
3659	Adaptive divergence generates distinct plasticÂresponses in two closely relatedÂSenecioÂspecies. Evolution; International Journal of Organic Evolution, 2022, 76, 1229-1245.	2.3	13
3660	Alevin-fry unlocks rapid, accurate and memory-frugal quantification of single-cell RNA-seq data. Nature Methods, 2022, 19, 316-322.	19.0	31
3661	Single-cell transcriptomics identifies potential cells of origin of MYC rhabdoid tumors. Nature Communications, 2022, 13, 1544.	12.8	9
3662	Summarizing internal dynamics boosts differential analysis and functional interpretation of super enhancers. Nucleic Acids Research, 2022, 50, 3115-3127.	14.5	4
3663	A conserved superlocus regulates above- and belowground root initiation. Science, 2022, 375, eabf4368.	12.6	57
3664	A Drosophila toolkit for HA-tagged proteins unveils a block in autophagy flux in the last instar larval fat body. Development (Cambridge), 2022, 149, .	2.5	2
3667	The cation channel TRPM8 influences the differentiation and function of human monocytes. Journal of Leukocyte Biology, 2022, 112, 365-381.	3.3	11
3668	Function Analysis of the ERF and DREB Subfamilies in Tomato Fruit Development and Ripening. Frontiers in Plant Science, 2022, 13, 849048.	3.6	10
3669	Systematic mapping of nuclear domain-associated transcripts reveals speckles and lamina as hubs of functionally distinct retained introns. Molecular Cell, 2022, 82, 1035-1052.e9.	9.7	31
3670	Integration of mRNA and miRNA Profiling Reveals Heterosis in Oreochromis niloticus Ã— O. aureus Hybrid Tilapia. Animals, 2022, 12, 640.	2.3	6
3671	NeoScore Integrates Characteristics of the Neoantigen:MHC Class I Interaction and Expression to Accurately Prioritize Immunogenic Neoantigens. Journal of Immunology, 2022, 208, 1813-1827.	0.8	4
3673	GXP: Analyze and Plot Plant Omics Data in Web Browsers. Plants, 2022, 11, 745.	3.5	1
3675	Transcriptome Analysis of Immune Responses and Metabolic Regulations of Chinese Soft-Shelled Turtle (Pelodiscus sinensis) against Edwardsiella tarda Infection. Fishes, 2022, 7, 79.	1.7	3

#	Article	IF	Citations
3677	Mouse Paternal RNAs Initiate a Pattern of Metabolic Disorders in a Line-Dependent Manner. Frontiers in Genetics, 2022, 13, 839841.	2.3	2
3678	The XRN1-regulated RNA helicase activity of YTHDC2 ensures mouse fertility independently of m6A recognition. Molecular Cell, 2022, 82, 1678-1690.e12.	9.7	31
3679	Evolution Increases Primates Brain Complexity Extending RbFOX1 Splicing Activity to LSD1 Modulation. Journal of Neuroscience, 2022, 42, 3689-3703.	3.6	1
3680	Functional Enrichment Analysis of Regulatory Elements. Biomedicines, 2022, 10, 590.	3.2	53
3681	Whole-transcriptome sequencingâ€“based concomitant detection of viral and human genetic determinants of cutaneous lesions. JCI Insight, 2022, 7, .	5.0	6
3682	The genetic basis of variation in sexual aggression: Evolution versus social plasticity. Molecular Ecology, 2022, , .	3.9	0
3683	Enhanced Bioremediation Potential of Shewanella decolorationis RNA Polymerase Mutants and Evidence for Novel Azo Dye Biodegradation Pathways. Frontiers in Microbiology, 2022, 13, 843807.	3.5	0
3684	Transcriptome-Wide Effects of NusA on RNA Polymerase Pausing in Bacillus subtilis. Journal of Bacteriology, 2022, 204, e0053421.	2.2	9
3685	Auxin boosts energy generation pathways to fuel pollen maturation in barley. Current Biology, 2022, 32, 1798-1811.e8.	3.9	16
3686	Increased Butyrate Production in Clostridium saccharoperbutylacetonicum from Lignocellulose-Derived Sugars. Applied and Environmental Microbiology, 2022, , e0241921.	3.1	3
3687	Pharmacologic Activation of STING in the Bladder Induces Potent Antitumor Immunity in Nonâ€“Muscle Invasive Murine Bladder Cancer. Molecular Cancer Therapeutics, 2022, 21, 914-924.	4.1	9
3688	The Neoantigen Landscape of the Coding and Noncoding Cancer Genome Space. Journal of Molecular Diagnostics, 2022, , .	2.8	0
3689	Comparative analysis of the daily brain transcriptomes of Asian particolored bat. Scientific Reports, 2022, 12, 3876.	3.3	2
3690	Transcriptome Sequencing Highlights the Regulatory Role of DNA Methylation in Immune-Related Genesâ€™ Expression of Chinese Oak Silkworm, Antheraea pernyi. Insects, 2022, 13, 296.	2.2	2
3692	The Effect of Anti-browning Agent Activated Carbon and Polyvinyl Pyrrolidone on the Rooting of Embryo Seedlings of â€œFengDanâ€•and Its Transcriptome Analysis. Frontiers in Plant Science, 2022, 13, 832619.	3.6	2
3693	Weaning Time Affects the Archaeal Community Structure and Functional Potential in Pigs. Frontiers in Microbiology, 2022, 13, 845621.	3.5	5
3694	The Enzymatic Core of Scorpion Venoms. Toxins, 2022, 14, 248.	3.4	11
3695	Osteogenic Commitment of Human Periodontal Ligament Cells Is Predetermined by Methylation, Chromatin Accessibility and Expression of Key Transcription Factors. Cells, 2022, 11, 1126.	4.1	7

#	Article	IF	Citations
3696	Novel genetic basis of resistance to Bt toxin Cry1Ac inHelicoverpa zea. Genetics, 2022, 221, .	2.9	14
3697	Primary cilia on muscle stem cells are critical to maintain regenerative capacity and are lost during aging. Nature Communications, 2022, 13, 1439.	12.8	35
3698	Nuclear hormone receptor NHR-49 acts in parallel with HIF-1 to promote hypoxia adaptation in Caenorhabditis elegans. ELife, 2022, 11, .	6.0	14
3700	Energyâ€conserving dimethyl sulfoxide reduction in the acetogenic bacterium Moorella thermoacetica. Environmental Microbiology, 2022, 24, 2000-2012.	3.8	7
3703	Chromosome-Scale Assembly of the Dendrobium nobile Genome Provides Insights Into the Molecular Mechanism of the Biosynthesis of the Medicinal Active Ingredient of Dendrobium. Frontiers in Genetics, 2022, 13, 844622.	2.3	21
3704	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways. Nature Neuroscience, 2022, 25, 381-389.	14.8	27
3708	Epstein-Barr virus BNRF1 destabilizes SMC5/6 cohesin complexes to evade its restriction of replication compartments. Cell Reports, 2022, 38, 110411.	6.4	31
3709	Genome assembly of the roundjaw bonefish (Albula glossodonta), aÂvulnerable circumtropical sportfish. GigaByte, 0, 2022, 1-29.	0.0	1
3710	Cerebral Intraparenchymal Hemorrhage Changes Patientsâ€™ Gut Bacteria Composition and Function. Frontiers in Cellular and Infection Microbiology, 2022, 12, 829491.	3.9	13
3711	Recalcitrant Cutaneous Warts in a Family with Inherited ICOS Deficiency. Journal of Investigative Dermatology, 2022, 142, 2435-2445.	0.7	4
3712	KIR ⁺ CD8 ⁺ T cells suppress pathogenic T cells and are active in autoimmune diseases and COVID-19. Science, 2022, 376, eabi9591.	12.6	113
3713	Broad domains of histone marks in the highly compact Paramecium macronuclear genome. Genome Research, 2022, 32, 710-725.	5.5	7
3714	Candidate master microRNA regulator of arsenic-induced pancreatic beta cell impairment revealed by multi-omics analysis. Archives of Toxicology, 2022, 96, 1685-1699.	4.2	6
3716	Convergence of case-specific epigenetic alterations identify a confluence of genetic vulnerabilities tied to opioid overdose. Molecular Psychiatry, 2022, 27, 2158-2170.	7.9	9
3718	Transcriptional neighborhoods regulate transcript isoform lengths and expression levels. Science, 2022, 375, 1000-1005.	12.6	23
3719	Genome assembly of the numbat (Myrmecobius fasciatus), the only termitivorous marsupial. GigaByte, 0, 2022, 1-17.	0.0	7
3720	Characterization of the Ocular Surface Microbiome in Keratitis Patients after Repeated Ophthalmic Antibiotic Exposure. Microbiology Spectrum, 2022, 10, e0216221.	3.0	5
3721	Analysis of transcribed sequences from young and mature zebrafish thrombocytes. PLoS ONE, 2022, 17, e0264776.	2.5	4

#	Article	IF	Citations
3722	Abundant and persistent sulfurâ€oxidizing microbial populations are responsive to hypoxia in the Chesapeake Bay. Environmental Microbiology, 2022, 24, 2315-2332.	3.8	10
3723	Sex differences in the early life stages of the salmon louse Lepeophtheirus salmonis (Copepoda:) Tj ETQq1 1 0.784314 rgBT /Overlock	2.5	2
3724	Transcriptomic characterization of the molecular mechanisms induced by RGMa during skeletal muscle nuclei accretion and hypertrophy. BMC Genomics, 2022, 23, 188.	2.8	2
3725	Transcriptional Profiling of Malignant Melanoma Reveals Novel and Potentially Targetable Gene Fusions. Cancers, 2022, 14, 1505.	3.7	1
3726	Human gut bacteria produce ÎÎ—17-modulating bileÂacid metabolites. Nature, 2022, 603, 907-912.	27.8	210
3727	B lymphocyte-derived acetylcholine limits steady-state and emergency hematopoiesis. Nature Immunology, 2022, 23, 605-618.	14.5	33
3728	Chikungunya virus time course infection of human macrophages reveals intracellular signaling pathways relevant to repurposed therapeutics. PeerJ, 2022, 10, e13090.	2.0	5
3729	Adaptive variation in homologue number within transcript families promotes expression divergence in reefâ€building coral. Molecular Ecology, 2022, 31, 2594-2610.	3.9	4
3730	A comparison of transcriptome analysis methods with reference genome. BMC Genomics, 2022, 23, 232.	2.8	18
3733	Perplexity: evaluating transcript abundance estimation in the absence of ground truth. Algorithms for Molecular Biology, 2022, 17, 6.	1.2	0
3734	Btla signaling in conventional and regulatory lymphocytes coordinately tempers humoral immunity in the intestinal mucosa. Cell Reports, 2022, 38, 110553.	6.4	9
3738	Exploration of the Potential Relationship Between Gut Microbiota Remodeling Under the Influence of High-Protein Diet and Crohnâ€™s Disease. Frontiers in Microbiology, 2022, 13, 831176.	3.5	6
3739	Single-cell transcriptomics reveals a distinct developmental state of KMT2A-rearranged infant B-cell acute lymphoblastic leukemia. Nature Medicine, 2022, 28, 743-751.	30.7	35
3740	Nematostella vectensis exhibits an enhanced molecular stress response upon co-exposure to highly weathered oil and surface UV radiation. Marine Environmental Research, 2022, 175, 105569.	2.5	2
3741	Longitudinal intronic RNA-Seq analysis of Parkinsonâ€™s disease patients reveals disease-specific nascent transcription. Experimental Biology and Medicine, 2022, 247, 945-957.	2.4	5
3742	Glutathione S-transferase: a candidate gene for berry color in muscadine grapes (<i>Vitis) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.8	5
3744	Glutamine-dependent signaling controls pluripotent stem cell fate. Developmental Cell, 2022, 57, 610-623.e8.	7.0	9
3745	Multi-Omic Epigenetic-Based Model Reveals Key Molecular Mechanisms Associated with Palmitic Acid Lipotoxicity in Human Astrocyte. , 0, , .		0

#	Article	IF	Citations
3746	Sustained Downregulation of Vascular Smooth Muscle Acta2 After Transient Angiotensin II Infusion: A New Model of â€œVascular Memoryâ€• Frontiers in Cardiovascular Medicine, 2022, 9, 854361.	2.4	1
3747	Inferring gene expression from cell-free DNA fragmentation profiles. Nature Biotechnology, 2022, 40, 585-597.	17.5	63
3749	Long noncoding RNA ELDR promotes cell cycle progression in normal oral keratinocytes through induction of a CTCF-FOXM1-AURKA signaling axis. Journal of Biological Chemistry, 2022, 298, 101895.	3.4	5
3750	Transcriptome datasets of neural progenitors and neurons differentiated from induced pluripotent stem cells of healthy donors and Parkinson's disease patients with mutations in the PARK2 gene. Data in Brief, 2022, 41, 107958.	1.0	5
3751	Complete genomic and epigenetic maps of human centromeres. Science, 2022, 376, eabl4178.	12.6	204
3752	Different Genes are Recruited During Convergent Evolution of Pregnancy and the Placenta. Molecular Biology and Evolution, 2022, 39, .	8.9	9
3754	The medusa of Aurelia coerulea is similar to its polyp in molecular composition and different from the medusa of Stomolophus meleagris in toxicity. Toxicon, 2022, 210, 89-99.	1.6	1
3755	Cytotoxic granzyme Câ€“expressing ILC1s contribute to antitumor immunity and neonatal autoimmunity. Science Immunology, 2022, 7, eabi8642.	11.9	47
3756	The adjustment of life history strategies drives the ecological adaptations of soil microbiota to aridity. Molecular Ecology, 2022, 31, 2920-2934.	3.9	18
3757	Long-Read RNA Sequencing Identifies Polyadenylation Elongation and Differential Transcript Usage of Host Transcripts During SARS-CoV-2 In Vitro Infection. Frontiers in Immunology, 2022, 13, 832223.	4.8	9
3760	Transcriptome and Small RNA Sequencing Reveal the Mechanisms Regulating Harvest Index in Brassica napus. Frontiers in Plant Science, 2022, 13, 855486.	3.6	2
3763	The phyllosphere microbiome shifts toward combating melanose pathogen. Microbiome, 2022, 10, 56.	11.1	54
3764	Developmental pyrethroid exposure and age influence phenotypes in a Chd8 haploinsufficient autism mouse model. Scientific Reports, 2022, 12, 5555.	3.3	9
3765	Elastic dosage compensation by X-chromosome upregulation. Nature Communications, 2022, 13, 1854.	12.8	18
3766	Comparative transcriptome profiling of virulent and avirulent isolates of Neoparamoeba perurans. Scientific Reports, 2022, 12, 5860.	3.3	0
3767	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
3769	Comparative transcriptomic analysis of in situ and onboard fixed deep-sea limpets reveals sample preparation-related differences. IScience, 2022, 25, 104092.	4.1	6
3771	SARS-CoV-2 and human retroelements: a case for molecular mimicry?. BMC Genomic Data, 2022, 23, 27.	1.7	4

#	Article	IF	Citations
3772	Metatranscriptomic Analyses Reveal the Functional Role of Botrytis cinerea in Biochemical and Textural Changes during Noble Rot of Grapevines. Journal of Fungi (Basel, Switzerland), 2022, 8, 378.	3.5	3
3773	Transcriptomeâ€based drug repositioning identifies TPCAâ€1 as a potential selective inhibitor of esophagus squamous carcinoma cell viability. International Journal of Molecular Medicine, 2022, 49, .	4.0	7
3774	Recovering metagenome-assembled genomes from shotgun metagenomic sequencing data: Methods, applications, challenges, and opportunities. Microbiological Research, 2022, 260, 127023.	5.3	17
3775	The proâ€apoptotic Bax gene modifies susceptibility to craniofacial dysmorphology following gastrulationâ€stage alcohol exposure. Birth Defects Research, 2022, 114, 1229-1243.	1.5	3
3776	Discordant prognosis of mismatch repair deficiency in colorectal and endometrial cancer reflects variation in antitumour immune response and immune escape. Journal of Pathology, 2022, 257, 340-351.	4.5	11
3777	Porcine gut microbiota in mediating host metabolic adaptation to cold stress. Npj Biofilms and Microbiomes, 2022, 8, 18.	6.4	17
3778	The chromosome-level genome assembly of Gentiana dahurica (Gentianaceae) provides insights into gentiopicroside biosynthesis. DNA Research, 2022, 29, .	3.4	12
3779	Combined metabolomic and transcriptomic profiling approaches reveal the cardiac response to high-fat diet. IScience, 2022, 25, 104184.	4.1	1
3780	Differential expression profiling of heat stressed tardigrades reveals major shift in the transcriptome. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2022, 267, 111169.	1.8	11
3781	Dioxin-like polychlorinated biphenyl 126 (PCB126) disrupts gut microbiota-host metabolic dysfunction in mice via aryl hydrocarbon receptor activation. Ecotoxicology and Environmental Safety, 2022, 236, 113448.	6.0	6
3782	Linkage and driving mechanisms of antibiotic resistome in surface and ground water: Their responses to land use and seasonal variation. Water Research, 2022, 215, 118279.	11.3	28
3783	Expression of BRCA1, BRCA2, RAD51, and other DSB repair factors is regulated by CRL4WDR70. DNA Repair, 2022, 113, 103320.	2.8	2
3784	De novo transcriptome analysis identifies key genes involved in dehydration stress response in kodo millet (Paspalum scrobiculatum L.). Genomics, 2022, 114, 110347.	2.9	8
3785	VEGFA-targeting miR-agshRNAs combine efficacy with specificity and safety for retinal gene therapy. Molecular Therapy - Nucleic Acids, 2022, 28, 58-76.	5.1	6
3786	Silicon mitigates potassium deficiency by enhanced remobilization and modulated potassium transporter regulation. Environmental and Experimental Botany, 2022, 198, 104849.	4.2	11
3787	Metagenomic and physicochemical analyses reveal microbial community and functional differences between three types of low-temperature Daqu. Food Research International, 2022, 156, 111167.	6.2	32
3788	Notch3 signaling between myeloma cells and osteocytes in the tumor niche promotes tumor growth and bone destruction. Neoplasia, 2022, 28, 100785.	5.3	5
3789	Abnormal mitochondria in Down syndrome iPSC-derived GABAergic interneurons and organoids. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2022, 1868, 166388.	3.8	6

#	Article	IF	Citations
3790	Metagenomic evidence for the microbial transformation of carboxyl-rich alicyclic molecules: A long-term macrocosm experiment. Water Research, 2022, 216, 118281.	11.3	11
3791	The high concentrations of abscisic, jasmonic, and salicylic acids produced under long days do not accelerate flowering in Chenopodium ficifolium 459. Plant Science, 2022, 320, 111279.	3.6	5
3792	Harnessing secretory pathway differences between HEK293 and CHO to rescue production of difficult to express proteins. Metabolic Engineering, 2022, 72, 171-187.	7.0	13
3793	Freezeâ€“thaw cycles characterize varietal aroma of Vidal blanc grape during late harvest by shaping self-assembled microeukaryotic communities. Food Chemistry, 2022, 384, 132553.	8.2	5
3794	Complex genetic architecture of threeâ€dimensional craniofacial shape variation in domestic pigeons. Evolution & Development, 2021, 23, 477-495.	2.0	4
3795	Interactions of Both Pathogenic and Nonpathogenic CUG Clade Candida Species with Macrophages Share a Conserved Transcriptional Landscape. MBio, 2021, 12, e0331721.	4.1	11
3798	Prognostic Significance of NLR About NETosis and Lymphocytes Perturbations in Localized Renal Cell Carcinoma With Tumor Thrombus. Frontiers in Oncology, 2021, 11, 771545.	2.8	10
3799	A reference genome for the critically endangered woylie, Bettongia penicillata ogilbyi. GigaByte, 0, 2021, 1-15.	0.0	8
3800	Predicting patient response with models trained on cell lines and patient-derived xenografts by nonlinear transfer learning. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	19
3801	Transcriptomic and Proteomic Characterizations of the Molecular Response to Blue Light and Salicylic Acid in Haematococcus pluvialis. Marine Drugs, 2022, 20, 1.	4.6	20
3803	Meta-analysis of human and mouse ALS astrocytes reveals multi-omic signatures of inflammatory reactive states. Genome Research, 2022, 32, 71-84.	5.5	46
3804	Sexual Dimorphism of Early Transcriptional Reprogramming in Dorsal Root Ganglia After Peripheral Nerve Injury. Frontiers in Molecular Neuroscience, 2021, 14, 779024.	2.9	10
3805	YTHDC2 is essential for pachytene progression and prevents aberrant microtubule-driven telomere clustering in male meiosis. Cell Reports, 2021, 37, 110110.	6.4	24
3806	Enhancer RNA Expression in Response to Glucocorticoid Treatment in Murine Macrophages. Cells, 2022, 11, 28.	4.1	7
3808	A Multi-Omics Network of a Seven-Gene Prognostic Signature for Non-Small Cell Lung Cancer. International Journal of Molecular Sciences, 2022, 23, 219.	4.1	8
3809	Lineage-specific energy and carbon metabolism of sponge symbionts and contributions to the host carbon pool. ISME Journal, 2022, 16, 1163-1175.	9.8	13
3811	Insulin signalling in tanycytes gates hypothalamic insulin uptake and regulation of AgRP neuron activity. Nature Metabolism, 2021, 3, 1662-1679.	11.9	32
3813	A microRNA Cluster Controls Fat Cell Differentiation and Adipose Tissue Expansion By Regulating SNCG. Advanced Science, 2022, 9, 2104759.	11.2	9

#	Article	IF	Citations
3814	Shared Gene Expression and Immune Pathway Changes Associated with Progression from Nevi to Melanoma. Cancers, 2022, 14, 3.	3.7	13
3815	Epigenomic translocation of H3K4me3 broad domains over oncogenes following hijacking of super-enhancers. Genome Research, 2022, 32, 1343-1354.	5.5	8
3817	Catulin Based Reporter System to Track and Characterize the Population of Invasive Cancer Cells in the Head and Neck Squamous Cell Carcinoma. International Journal of Molecular Sciences, 2022, 23, 140.	4.1	3
3820	Diverse tumorigenic consequences of human papillomavirus integration in primary oropharyngeal cancers. Genome Research, 2022, 32, 55-70.	5.5	18
3821	Low Transcriptomic Plasticity of Antarctic Giant Isopod Glyptonotus antarcticus Juveniles Exposed to Acute Thermal Stress. Frontiers in Marine Science, 2021, 8, .	2.5	5
3824	Molecular mechanisms of embryonic tail development in the self-fertilizing mangrove killifish Kryptolebias marmoratus. Development (Cambridge), 2021, 148, .	2.5	2
3826	Constitutional chromothripsis of the APC locus as a cause of genetic predisposition to colon cancer. Journal of Medical Genetics, 2021, , jmedgenet-2021-108147.	3.2	6
3828	GeneTonic: an R/Bioconductor package for streamlining the interpretation of RNA-seq data. BMC Bioinformatics, 2021, 22, 610.	2.6	21
3829	A Review of Prostate Organogenesis and a Role for iPSC-Derived Prostate Organoids to Study Prostate Development and Disease. International Journal of Molecular Sciences, 2021, 22, 13097.	4.1	5
3830	Patient-derived gene and protein expression signatures of NGLY1 deficiency. Journal of Biochemistry, 2022, 171, 187-199.	1.7	9
3831	Isoform-level quantification for single-cell RNA sequencing. Bioinformatics, 2022, 38, 1287-1294.	4.1	6
3833	Sex- and Mutation-Specific p53 Gain-of-Function Activity in Gliomagenesis. Cancer Research Communications, 2021, 1, 148-163.	1.7	6
3835	Transcriptomics of single dose and repeated carbon black and ozone inhalation co-exposure highlight progressive pulmonary mitochondrial dysfunction. Particle and Fibre Toxicology, 2021, 18, 44.	6.2	8
3836	Complex Genetic Interactions between Piwi and HP1a in the Repression of Transposable Elements and Tissue-Specific Genes in the Ovarian Germline. International Journal of Molecular Sciences, 2021, 22, 13430.	4.1	3
3837	The cnidarian parasite Ceratonova shasta utilizes inherited and recruited venom-like compounds during infection. PeerJ, 2021, 9, e12606.	2.0	4
3838	Evaluation of Factors Affecting In Planta Gene Editing Efficiency in Wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Overlock 1	2.3	3
3839	Characteristics of Intestinal Flora in Pregnant Women with Mild Thalassemia Revealed by Metagenomics. Jundishapur Journal of Microbiology, 2021, 14, .	0.5	0
3840	Lyl-1 regulates primitive macrophages and microglia development. Communications Biology, 2021, 4, 1382.	4.4	8

#	Article	IF	Citations
3841	GCH1 Deficiency Activates Brain Innate Immune Response and Impairs Tyrosine Hydroxylase Homeostasis. Journal of Neuroscience, 2022, 42, 702-716.	3.6	10
3843	5-Hydroxymethylcytosine-mediated active demethylation is required for mammalian neuronal differentiation and function. ELife, 2021, 10, .	6.0	21
3844	Comparison of Oxidative and Hypoxic Stress Responsive Genes from Meta-Analysis of Public Transcriptomes. Biomedicines, 2021, 9, 1830.	3.2	10
3845	Randomized, open-label, phase 2 study of andecaliximab plus nivolumab versus nivolumab alone in advanced gastric cancer identifies biomarkers associated with survival. , 2021, 9, e003580.		20
3846	Epithelial phenotype restoring drugs suppress macular degeneration phenotypes in an iPSC model. Nature Communications, 2021, 12, 7293.	12.8	32
3847	Discovering microbe functionality in human disease with a gene-ontology-aware model. , 2021, , .		0
3849	Foster thy young: enhanced prediction of orphan genes in assembled genomes. Nucleic Acids Research, 2022, 50, e37-e37.	14.5	13
3850	Comparative transcriptomic analysis of apple and peach fruits: insights into fruit type specification. Plant Journal, 2022, 109, 1614-1629.	5.7	4
3851	Trophoblast glycoprotein is a new candidate gene for Parkinsonâ€™s disease. Npj Parkinson's Disease, 2021, 7, 110.	5.3	2
3852	Vitamin D treatment induces in vitro and ex vivo transcriptomic changes indicating antiâ€tumor effects. FASEB Journal, 2022, 36, e22082.	0.5	6
3853	Interactions between mitochondrial and nuclear genomes and co-regulation of mitochondrial and nuclear gene expression in reciprocal intergeneric hybrids between Carassius auratus red var. Ã— Cyprinus carpio L.. Reproduction and Breeding, 2021, 1, 213-220.	1.6	1
3857	Natural rodent model of viral transmission reveals biological features of virus population dynamics. Journal of Experimental Medicine, 2022, 219, .	8.5	18
3859	Salivary and Intestinal Transcriptomes Reveal Differential Gene Expression in Starving, Fed and Trypanosoma cruzi-Infected Rhodnius neglectus. Frontiers in Cellular and Infection Microbiology, 2021, 11, 773357.	3.9	1
3860	TMEM176B Regulates AKT/mTOR Signaling and Tumor Growth in Triple-Negative Breast Cancer. Cells, 2021, 10, 3430.	4.1	3
3861	Temporal Gene Expression in Apical Culms Shows Early Changes in Cell Wall Biosynthesis Genes in Sugarcane. Frontiers in Plant Science, 2021, 12, 736797.	3.6	1
3862	Nanopore sequencing of RNA and cDNA molecules in Escherichia coli. Rna, 2022, 28, 400-417.	3.5	38
3864	Selection for seed size has uneven effects on specialized metabolite abundance in oat (Avena) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.8	9
3865	Lipid droplet availability affects neural stem/progenitor cell metabolism and proliferation. Nature Communications, 2021, 12, 7362.	12.8	51

#	Article	IF	Citations
3866	A blood drop through the pore: nanopore sequencing in hematology. Trends in Genetics, 2022, 38, 572-586.	6.7	2
3867	Singleâ€Cell Sequencing to Unveil the Mystery of Embryonic Development. Advanced Biology, 2022, 6, e2101151.	2.5	2
3868	Dysregulated splicing factor SF3B1 unveils a dual therapeutic vulnerability to target pancreatic cancer cells and cancer stem cells with an anti-splicing drug. Journal of Experimental and Clinical Cancer Research, 2021, 40, 382.	8.6	25
3871	Improved High-Quality Genome Assembly and Annotation of Pineapple (Ananas comosus) Cultivar MD2 Revealed Extensive Haplotype Diversity and Diversified FRS/FRF Gene Family. Genes, 2022, 13, 52.	2.4	6
3872	Reduced NCOR2 expression accelerates androgen deprivation therapy failure in prostate cancer. Cell Reports, 2021, 37, 110109.	6.4	19
3875	Risk and protection strategies of Amolops wuyiensis intestine against gastrointestinal nematode (Cosmocercoides wuyiensis n. sp.) infection. Environmental Microbiology, 2022, 24, 1454-1466.	3.8	2
3876	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. Clinical Cancer Research, 2021, 27, 5049-5061.	7.0	6
3877	Identification and comparative analysis of long non-coding RNAs in the brain of fire ant queens in two different reproductive states. BMC Genomics, 2021, 22, 917.	2.8	2
3879	Transcriptome Analysis and Identification of the Cholesterol Side Chain Cleavage Enzyme BbgCYP11A1 From Bufo bufo gargarizans. Frontiers in Genetics, 2022, 13, 828877.	2.3	2
3880	Linnemannia elongata (Mortierellaceae) stimulates Arabidopsis thaliana aerial growth and responses to auxin, ethylene, and reactive oxygen species. PLoS ONE, 2022, 17, e0261908.	2.5	10
3883	Population-scale long-read sequencing uncovers transposable elements associated with gene expression variation and adaptive signatures in Drosophila. Nature Communications, 2022, 13, 1948.	12.8	53
3884	A phase 1b study of <scp>OXIRI</scp> in pancreatic adenocarcinoma patients and its immunomodulatory effects. International Journal of Cancer, 2022, , .	5.1	0
3885	Stochastic Variation in DNA Methylation Modulates Nucleosome Occupancy and Alternative Splicing in Arabidopsis thaliana. Plants, 2022, 11, 1105.	3.5	2
3886	Alternative Splicing of Neuropeptide Prohormone and Receptor Genes Associated with Pain Sensitivity Was Detected with Zero-Inflated Models. Biomedicines, 2022, 10, 877.	3.2	4
3887	DSMZCellDive: Diving into high-throughput cell line data. F1000Research, 0, 11, 420.	1.6	3
3888	ESR1 mutant breast cancers show elevated basal cytokeratins and immune activation. Nature Communications, 2022, 13, 2011.	12.8	29
3889	CCNE1 amplification is synthetic lethal with PKMYT1 kinase inhibition. Nature, 2022, 604, 749-756.	27.8	60
3891	Placental Transcription Profiling in 6â€“23 Weeksâ€™ Gestation Reveals Differential Transcript Usage in Early Development. International Journal of Molecular Sciences, 2022, 23, 4506.	4.1	3

#	Article	IF	Citations
3892	Airway Aging and Methylation Disruptions in HIV-associated Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2022, 206, 150-160.	5.6	13
3893	An interolog-based barley interactome as an integration framework for immune signaling. Genetics, 2022, 221, .	2.9	3
3894	The nuclear receptor ERR cooperates with the cardiogenic factor GATA4 to orchestrate cardiomyocyte maturation. Nature Communications, 2022, 13, 1991.	12.8	20
3897	Bronchial epithelium epithelial-mesenchymal plasticity forms aberrant basaloid-like cells in vitro. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2022, 322, L822-L841.	2.9	4
3899	PAMP-triggered genetic reprogramming involves widespread alternative transcription initiation and an immediate transcription factor wave. Plant Cell, 2022, 34, 2615-2637.	6.6	12
3900	CavÎ²1 regulates T cell expansion and apoptosis independently of voltage-gated Ca2+ channel function. Nature Communications, 2022, 13, 2033.	12.8	18
3901	Allele-specific analysis reveals exon- and cell-type-specific regulatory effects of Alzheimerâ€™s disease-associated genetic variants. Translational Psychiatry, 2022, 12, 163.	4.8	10
3902	Pathogen exposure leads to a transcriptional downregulation of core cellular functions that may dampen the immune response in a macroalga. Molecular Ecology, 2022, 31, 3468-3480.	3.9	3
3903	A pair of non-Mendelian genes at the Ga2 locus confer unilateral cross-incompatibility in maize. Nature Communications, 2022, 13, 1993.	12.8	10
3905	A Survey on the Distribution of Ovothiol and ovoA Gene Expression in Different Tissues and Cells: A Comparative Analysis in Sea Urchins and Mussels. Marine Drugs, 2022, 20, 268.	4.6	4
3906	Repurposing ibudilast to mitigate Alzheimerâ€™s disease by targeting inflammation. Brain, 2023, 146, 898-911.	7.6	13
3907	Loss of PBRM1 Alters Promoter Histone Modifications and Activates ALDH1A1 to Drive Renal Cell Carcinoma. Molecular Cancer Research, 2022, 20, 1193-1207.	3.4	7
3909	Multi-Cohort Transcriptomic Subtyping of B-Cell Acute Lymphoblastic Leukemia. International Journal of Molecular Sciences, 2022, 23, 4574.	4.1	9
3910	Coral holobiont cues prime Endozoicomonas for a symbiotic lifestyle. ISME Journal, 2022, 16, 1883-1895.	9.8	36
3911	Activation of transcription factor HIF inhibits IL-1Î²-induced NO production in primary cultured rat hepatocytes. Nitric Oxide - Biology and Chemistry, 2022, 124, 1-14.	2.7	5
3912	Botrytis cinerea expression profile and metabolism differs between noble and grey rot of grapes. Food Microbiology, 2022, 106, 104037.	4.2	5
3913	Integrative Transcriptomics and Proteomics Elucidate the Regulatory Mechanism of Hydrangea macrophylla Flower-Color Changes Induced by Exogenous Aluminum. Agronomy, 2022, 12, 969.	3.0	3
3914	Genomeâ€wide loss of <scp>CHH</scp> methylation with limited transcriptome changes in Setaria viridis DOMAINS REARRANGED METHYLTRANSFERASE (<scp>DRM</scp>) mutants. Plant Journal, 2022, 111, 103-116.	5.7	2

#	Article	IF	Citations
3915	Tidal flat aquaculture pollution governs sedimentary antibiotic resistance gene profiles but not bacterial community based on metagenomic data. Science of the Total Environment, 2022, 833, 155206.	8.0	13
4229	Barley (Hordeum Vulgare) Anther and Meiocyte RNA Sequencing: Mapping Sequencing Reads and Downstream Data Analyses. Methods in Molecular Biology, 2022, 2484, 291-311.	0.9	2
4230	Identifying small RNAs and Analyzing Their Association with Gene Expression Using IsolatedÂÂrabidopsis Male Meiocytes. Methods in Molecular Biology, 2022, 2484, 23-41.	0.9	0
4231	Cumulus cell antioxidant system is modulated by patientsâ€™ clinical characteristics and correlates with embryo development. Journal of Assisted Reproduction and Genetics, 2022, , 1.	2.5	1
4232	Transcriptome profiling of plerocercoid and adult developmental stages of the neglected medical tapeworm Spirometra erinaceieuropaei. Acta Tropica, 2022, 232, 106483.	2.0	10
4233	Nanoparticle Properties Influence Transendothelial Migration of Monocytes. Langmuir, 2022, 38, 5603-5616.	3.5	5
4234	Landscape and regulation of alternative splicing and alternative polyadenylation in a plant pathogenic fungus. New Phytologist, 2022, 235, 674-689.	7.3	21
4235	Molecular Insight into Gene Response of Diorcinol- and Rubrolide-Treated Biofilms of the Emerging Pathogen Stenotrophomonas maltophilia. Microbiology Spectrum, 2022, , e0258221.	3.0	2
4236	Bacillus Calmette-GuÃ©rinâ€“induced trained immunity protects against SARS-CoV-2 challenge in K18-hACE2 mice. JCI Insight, 2022, 7, .	5.0	29
4237	Synthetic amyloid beta does not induce a robust transcriptional response in innate immune cell culture systems. Journal of Neuroinflammation, 2022, 19, 99.	7.2	6
4238	Metal content and kinetic properties of yeast RNA lariat debranching enzyme Dbr1. Rna, 2022, 28, 927-936.	3.5	3
4239	Human UPF3A and UPF3B enable faultâ€tolerant activation of nonsenseâ€mediated mRNA decay. EMBO Journal, 2022, 41, e109191.	7.8	21
4240	A human coronavirus OC43â€derived polypeptide causes neuropathic pain. EMBO Reports, 2022, , e54069.	4.5	1
4241	The value of genotype-specific reference for transcriptome analyses in barley. Life Science Alliance, 2022, 5, e202101255.	2.8	2
4242	Effects of Cryopreservation on Sperm with Cryodiluent in Viviparous Black Rockfish (Sebastes) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	4.1	16
4243	Exploiting induced vulnerability to overcome PARPi resistance and clonal heterogeneity in BRCA mutant triple-negative inflammatory breast cancer.. American Journal of Cancer Research, 2022, 12, 337-354.	1.4	0
4244	Identification of Taxonomically Restricted Transcripts from Illumina RNA Sequencing Data. Methods in Molecular Biology, 2022, 2477, 91-103.	0.9	0
4245	Exon junction complex-associated multi-adapter RNPS1 nucleates splicing regulatory complexes to maintain transcriptome surveillance. Nucleic Acids Research, 2022, 50, 5899-5918.	14.5	9

#	Article	IF	Citations
4249	Bioluminescent Zebrafish Transplantation Model for Drug Discovery. Frontiers in Pharmacology, 2022, 13, 893655.	3.5	5
4250	An organâ€specific transcriptomic atlas of the medicinal plant Bletilla striata: Proteinâ€coding genes, microRNAs, and regulatory networks. Plant Genome, 2022, 15, e20210.	2.8	5
4252	Glucose-Dependent miR-125b Is a Negative Regulator of Î²-Cell Function. Diabetes, 2022, 71, 1525-1545.	0.6	10
4253	Homozygous iMycCÎ± transgenic mice as a model of plasma B-cell lymphomas. Leukemia and Lymphoma, 2022, , 1-12.	1.3	0
4254	The Arabidopsis gene coâ€expression network. Plant Direct, 2022, 6, e396.	1.9	4
4255	Mechanisms of Isothiocyanate Detoxification in Larvae of Two Belowground Herbivores, Delia radicum and D. floralis (Diptera: Anthomyiidae). Frontiers in Physiology, 2022, 13, 874527.	2.8	3
4256	Quantitative single-cell transcriptome-based ranking of engineered AAVs in human retinal explants. Molecular Therapy - Methods and Clinical Development, 2022, 25, 476-489.	4.1	5
4257	Low Complexity Regions in Mammalian Proteins are Associated with Low Protein Abundance and High Transcript Abundance. Molecular Biology and Evolution, 2022, 39, .	8.9	5
4258	Chronic psychological stress alters gene expression in rat colon epithelial cells promoting chromatin remodeling, barrier dysfunction and inflammation. PeerJ, 2022, 10, e13287.	2.0	5
4259	NMDA Receptor Antagonists Increase the Release of GLP-1 From Gut Endocrine Cells. Frontiers in Pharmacology, 2022, 13, 861311.	3.5	0
4260	Fast, Ungapped Reads Mapping Using Squid. International Journal of Environmental Research and Public Health, 2022, 19, 5442.	2.6	1
4261	Formation of Blood Neutrophil Extracellular Traps Increases the Mastitis Risk of Dairy Cows During the Transition Period. Frontiers in Immunology, 2022, 13, 880578.	4.8	6
4262	Silencing alanine transaminase 2 in diabetic liver attenuates hyperglycemia by reducing gluconeogenesis from amino acids. Cell Reports, 2022, 39, 110733.	6.4	18
4263	Transcriptome analysis from muscle biopsy tissues in late-onset myopathies identifies potential biomarkers correlating to muscle pathology. Neuromuscular Disorders, 2022, , .	0.6	0
4266	The X-linked splicing regulator MBNL3 has been co-opted to restrict placental growth in eutherians. PLoS Biology, 2022, 20, e3001615.	5.6	4
4269	Nasopharyngeal airway dual-transcriptome of infants with severe bronchiolitis and risk of childhood asthma: A multicenter prospective study. Journal of Allergy and Clinical Immunology, 2022, 150, 806-816.	2.9	19
4270	Activated SUMOylation restricts MHC class I antigen presentation to confer immune evasion in cancer. Journal of Clinical Investigation, 2022, 132, .	8.2	22
4271	A chromosomal inversion may facilitate adaptation despite periodic gene flow in a freshwater fish. Ecology and Evolution, 2022, 12, e8898.	1.9	6

#	Article	IF	Citations
4272	Bioinformatic analyses to uncover genes involved in trehalose metabolism in the polyploid sugarcane. Scientific Reports, 2022, 12, 7516.	3.3	2
4273	Ivermectin-induced gene expression changes in adult Parascaris univalens and Caenorhabditis elegans: a comparative approach to study anthelminthic metabolism and resistance in vitro. Parasites and Vectors, 2022, 15, 158.	2.5	7
4275	Single-cell analysis reveals the Comma-1D cell line as a unique model for mammary gland development and breast cancer. Journal of Cell Science, 2022, 135, .	2.0	2
4276	Transcriptome analysis of clock disrupted cancer cells reveals differential alternative splicing of cancer hallmarks genes. Npj Systems Biology and Applications, 2022, 8, 17.	3.0	4
4277	Inhaled Corticosteroids Selectively Alter the Microbiome and Host Transcriptome in the Small Airways of Patients with Chronic Obstructive Pulmonary Disease. Biomedicines, 2022, 10, 1110.	3.2	8
4278	Development of a double shmiR lentivirus effectively targeting both BCL11A and ZNF410 for enhanced induction of fetal hemoglobin to treat Î²-hemoglobinopathies. Molecular Therapy, 2022, 30, 2693-2708.	8.2	11
4279	GEMmaker: process massive RNA-seq datasets on heterogeneous computational infrastructure. BMC Bioinformatics, 2022, 23, 156.	2.6	2
4280	Reactive Astrocytes Derived From Human Induced Pluripotent Stem Cells Suppress Oligodendrocyte Precursor Cell Differentiation. Frontiers in Molecular Neuroscience, 2022, 15, .	2.9	6
4282	Transcriptome Analysis Using RNA Sequencing for Finding Genes Related to Fiber in Cotton: A Review. , 0, , .		0
4283	CDK12 promotes tumorigenesis but induces vulnerability to therapies inhibiting folate one-carbon metabolism in breast cancer. Nature Communications, 2022, 13, 2642.	12.8	15
4284	Comparative transcriptome analysis of two maize genotypes with different tolerance to salt stress. Cereal Research Communications, 0, , 1.	1.6	0
4285	Unravelling the physiological roles of mazEF toxinâ€“antitoxin system on clinical MRSA strain by CRISPR RNA-guided cytidine deaminase. Journal of Biomedical Science, 2022, 29, 28.	7.0	4
4286	Transcription Factor 4 loss-of-function is associated with deficits in progenitor proliferation and cortical neuron content. Nature Communications, 2022, 13, 2387.	12.8	26
4287	A Case Study to Dissect Immunity to SARS-CoV-2 in a Neonate Nonhuman Primate Model. Frontiers in Immunology, 2022, 13, .	4.8	3
4288	Extent and complexity of RNA processing in honey bee queen and worker caste development. IScience, 2022, 25, 104301.	4.1	9
4289	Vertical sleeve gastrectomy induces enteroendocrine cell differentiation of intestinal stem cells through bile acid signaling. JCI Insight, 2022, 7, .	5.0	4
4290	Identification of functional features underlying heat stress response in Sprague–Dawley rats using mixed linear models. Scientific Reports, 2022, 12, 7671.	3.3	0
4291	Comprehensive Transcriptional Profiling and Mouse Phenotyping Reveals Dispensable Role for Adipose Tissue Selective Long Noncoding RNA Gm15551. Non-coding RNA, 2022, 8, 32.	2.6	1

#	Article	IF	Citations
4292	Haloâ€seq: An RNA Proximity Labeling Method for the Isolation and Analysis of Subcellular RNA Populations. Current Protocols, 2022, 2, e424.	2.9	1
4293	Genotoxic effects of chlorinated disinfection by-products of 1,3-diphenylguanidine (DPG): Cell-based in-vitro testing and formation potential during water disinfection. Journal of Hazardous Materials, 2022, 436, 129114.	12.4	14
4294	miR-486 is essential for muscle function and suppresses a dystrophic transcriptome. Life Science Alliance, 2022, 5, e202101215.	2.8	10
4295	Lymph node colonization induces tumor-immune tolerance to promote distant metastasis. Cell, 2022, 185, 1924-1942.e23.	28.9	111
4296	Proteomic Alterations and Novel Markers of Neurotoxic Reactive Astrocytes in Human Induced Pluripotent Stem Cell Models. Frontiers in Molecular Neuroscience, 2022, 15, 870085.	2.9	15
4297	Straw waste promotes microbial functional diversity and lignocellulose degradation during the aerobic process of pig manure in an ectopic fermentation system via metagenomic analysis. Science of the Total Environment, 2022, 838, 155637.	8.0	6
4298	Robust transcriptional indicators of immune cell death revealed by spatiotemporal transcriptome analyses. Molecular Plant, 2022, 15, 1059-1075.	8.3	17
4301	Intraovarian, Isoform-Specific Transcriptional Roles of Progesterone Receptor in Ovulation. Cells, 2022, 11, 1563.	4.1	5
4302	PTBP1 promotes hematopoietic stem cell maintenance and red blood cell development by ensuring sufficient availability of ribosomal constituents. Cell Reports, 2022, 39, 110793.	6.4	3
4303	Mutual exclusivity of ESR1 and TP53 mutations in endocrine resistant metastatic breast cancer. Npj Breast Cancer, 2022, 8, 62.	5.2	10
4304	Topical therapy for regression and melanoma prevention of congenital giant nevi. Cell, 2022, 185, 2071-2085.e12.	28.9	13
4305	MTG16 regulates colonic epithelial differentiation, colitis, and tumorigenesis by repressing E protein transcription factors. JCI Insight, 2022, 7, .	5.0	9
4306	Decoding the dynamic H3K9cr landscapes during neural commitment of P19 embryonal carcinoma cells. Biochemical and Biophysical Research Communications, 2022, 613, 187-192.	2.1	1
4308	Zika virus impacts extracellular vesicle composition and cellular gene expression in macaque early gestation trophoblasts. Scientific Reports, 2022, 12, 7348.	3.3	5
4309	Metagenomic exploration of antibiotic resistance genes and their hosts in aquaculture waters of the semi-closed Dongshan Bay (China). Science of the Total Environment, 2022, 838, 155784.	8.0	12
4310	Enhanced safety and efficacy of protease-regulated CAR-T cell receptors. Cell, 2022, 185, 1745-1763.e22.	28.9	88
4311	Interleukin-6 inhibition in ST-elevation myocardial infarction: Immune cell profile in the randomised ASSAIL-MI trial. EBioMedicine, 2022, 80, 104013.	6.1	22
4312	Metagenomic assembly reveals the circadian oscillations of the microbiome and antibiotic resistance genes in a model of laying hens. Science of the Total Environment, 2022, 836, 155692.	8.0	4

#	Article	IF	Citations
4313	Oviductal epithelial cells transcriptome and extracellular vesicles characterization during thermoneutral and heat stress conditions in dairy cows. Theriogenology, 2022, 187, 152-163.	2.1	4
4314	Microbially mediated arsenic mobilization in the clay layer and underlying aquifer in the Hetao Basin, Inner Mongolia, China. Science of the Total Environment, 2022, 836, 155597.	8.0	5
4315	Whole exome sequencing reveals the genetic heterogeneity and evolutionary history of primary gliomas and matched recurrences. Computational and Structural Biotechnology Journal, 2022, 20, 2235-2246.	4.1	11
4316	High GILT Expression Is Associated with Improved Survival in Metastatic Melanoma Patients Treated with Immune Checkpoint Inhibition. Cancers, 2022, 14, 2200.	3.7	1
4317	Loss of METTL3 attenuates blastic plasmacytoid dendritic cell neoplasm response to PRMT5 inhibition via IFN signaling. Blood Advances, 2022, 6, 5330-5344.	5.2	2
4318	Characterisation of the testicular transcriptome in stallions with ageâ€related testicular degeneration. Equine Veterinary Journal, 2023, 55, 239-252.	1.7	1
4319	Alpha-synuclein overexpression induces epigenomic dysregulation of glutamate signaling and locomotor pathways. Human Molecular Genetics, 2022, 31, 3694-3714.	2.9	5
4320	Insights into the fates of plasmids and antimicrobial resistance genes during swine manure treatment and related factors based on plasmidome and metagenome analyses. Environmental Science and Pollution Research, 2022, 29, 69037-69047.	5.3	5
4321	GSK3 inhibition rescues growth and telomere dysfunction in dyskeratosis congenita iPSC-derived type II alveolar epithelial cells. ELife, 2022, 11, .	6.0	6
4322	A chemoproteoinformatics approach demonstrates that aspirin increases sensitivity to MEK inhibition by directly binding to RPS5. , 0, , .		1
4323	Placental Gene Transcript Proportions are Altered in the Presence of In Utero Arsenic and Cadmium Exposures, Genetic Variants, and Birth Weight Differences. Frontiers in Genetics, 2022, 13, .	2.3	0
4324	White tea alleviates non-alcoholic fatty liver disease by regulating energy expenditure and lipid metabolism. Gene, 2022, 833, 146553.	2.2	5
4325	Recent Bioinformatic Progress to Identify Epigenetic Changes Associated to Transposable Elements. Frontiers in Genetics, 2022, 13, .	2.3	7
4326	Pervasive sequence-level variation in the transcriptome of Plasmodium falciparum. NAR Genomics and Bioinformatics, 2022, 4, lqac036.	3.2	3
4327	A conserved YAP/Notch/REST network controls the neuroendocrine cell fate in the lungs. Nature Communications, 2022, 13, 2690.	12.8	19
4328	Meta-Analysis of Two Human RNA-seq Datasets to Determine Periodontitis Diagnostic Biomarkers and Drug Target Candidates. International Journal of Molecular Sciences, 2022, 23, 5580.	4.1	6
4329	WEE1 inhibition enhances the antitumor immune response to PD-L1 blockade by the concomitant activation of STING and STAT1 pathways in SCLC. Cell Reports, 2022, 39, 110814.	6.4	43
4330	Transcriptomic Responses of Adult Versus Juvenile Atlantids to Ocean Acidification. Frontiers in Marine Science, 2022, 9, .	2.5	2

#	Article	IF	Citations
4331	Comparative Transcriptomics Unveil the Crucial Genes Involved in Coumarin Biosynthesis in Peucedanum praeruptorum Dunn. Frontiers in Plant Science, 2022, 13, .	3.6	4
4332	Comparative transcriptomics reveals circadian and pluripotency networks as two pillars of longevity regulation. Cell Metabolism, 2022, 34, 836-856.e5.	16.2	33
4333	Arginine-mediated gut microbiome remodeling promotes host pulmonary immune defense against nontuberculous mycobacterial infection. Gut Microbes, 2022, 14, 2073132.	9.8	21
4334	Identifying common transcriptome signatures of cancer by interpreting deep learning models. Genome Biology, 2022, 23, 117.	8.8	11
4335	OCA-T1 and OCA-T2 are coactivators of POU2F3 in the tuft cell lineage. Nature, 2022, 607, 169-175.	27.8	35
4336	Fibrotic Signaling in Cardiac Fibroblasts and Vascular Smooth Muscle Cells: The Dual Roles of Fibrosis in HFpEF and CAD. Cells, 2022, 11, 1657.	4.1	7
4337	Enhancers regulate 3â€² end processing activity to control expression of alternative 3â€²UTR isoforms. Nature Communications, 2022, 13, 2709.	12.8	22
4338	Consuming fresh macroalgae induces specific catabolic pathways, stress reactions and Type IX secretion in marine flavobacterial pioneer degraders. ISME Journal, 2022, 16, 2027-2039.	9.8	10
4339	RNA splicing is a key mediator of tumour cell plasticity and a therapeutic vulnerability in colorectal cancer. Nature Communications, 2022, 13, 2791.	12.8	11
4340	Rituximab versus tocilizumab in rheumatoid arthritis: synovial biopsy-based biomarker analysis of the phase 4 R4RA randomized trial. Nature Medicine, 2022, 28, 1256-1268.	30.7	105
4341	Genome-wide DNA methylation and gene expression patterns of androgenetic haploid tiger pufferfish (Takifugu rubripes) provide insights into haploid syndrome. Scientific Reports, 2022, 12, 8252.	3.3	1
4342	A male pheromone that improves the quality of the oogenic germline. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2015576119.	7.1	15
4343	Acquisition of a complex root microbiome reshapes the transcriptomes of rice plants. New Phytologist, 2022, 235, 2008-2021.	7.3	8
4344	Genome-wide identification and characterization of superoxide dismutases in four oyster species reveals functional differentiation in response to biotic and abiotic stress. BMC Genomics, 2022, 23, 378.	2.8	3
4345	Snrpb is required in murine neural crest cells for proper splicing and craniofacial morphogenesis. DMM Disease Models and Mechanisms, 2022, 15, .	2.4	9
4346	Myeloid cellâ€specific topoisomerase 1 inhibition using DNA origami mitigates neuroinflammation. EMBO Reports, 2022, 23, e54499.	4.5	14
4347	Dietary Cholesterol Causes Inflammatory Imbalance and Exacerbates Morbidity in Mice Infected with Influenza A Virus. Journal of Immunology, 2022, 208, 2523-2539.	0.8	9
4348	Omics sciences. , 2022, , 105-118.		0

#	Article	IF	Citations
4350	Single-Cell Analysis of the Transcriptome and Epigenome. Methods in Molecular Biology, 2022, , 21-60.	0.9	5
4351	Characterization of Auxin Metabolism in the Ovaries of the Lychee (<i>Litchi chinensis</i>) â€˜Salathielâ€™. Horticulture Journal, 2022, 91, 302-311.	0.8	1
4355	From head to rootlet: comparative transcriptomic analysis of a rhizocephalan barnacle Peltogaster reticulata (Crustacea: Rhizocephala). F1000Research, 0, 11, 583.	1.6	4
4357	Genome-wide identification and association analysis for virus-responsive lncRNAs in rice (Oryza sativa) Tj ETQq1 1 0.784314 rgBT /Ov	3.4	2
4360	Viral communities in the parasite Varroa destructor and in colonies of their honey bee host (Apis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	3.3	12
4361	Transcriptome sequencing of 3,3â€²,4,4â€²,5-Pentachlorobiphenyl (PCB126)-treated human preadipocytes demonstrates progressive changes in pathways associated with inflammation and diabetes.. Toxicology in Vitro, 2022, 83, 105396.	2.4	8
4362	Alanine-specific appetite in slow growing chickens is associated with impaired glucose transport and TCA cycle. BMC Genomics, 2022, 23, .	2.8	5
4363	The effect of the probiotic consortia on SARS-CoV-2 infection in ferrets and on human immune cell response in vitro. IScience, 2022, 25, 104445.	4.1	3
4365	Generation of a mouse model of the neurodevelopmental disorder with dysmorphic facies and distal limb anomalies syndrome. Human Molecular Genetics, 2022, 31, 3405-3421.	2.9	2
4367	SingleCAnalyzer: Interactive Analysis of Single Cell RNA-Seq Data on the Cloud. Frontiers in Bioinformatics, 2022, 2, .	2.1	14
4369	Short-term lingonberry feeding is associated with decreased insulin levels and altered adipose tissue function in high-fat diet fed C57BL/6J mice. Journal of Functional Foods, 2022, 94, 105125.	3.4	0
4371	Transcriptomics in Plant. , 2022, , 99-127.		1
4372	Transactive Response DNA-Binding Protein (TARDBP/TDP-43) Regulates Cell Permissivity to HIV-1 Infection by Acting on HDAC6. International Journal of Molecular Sciences, 2022, 23, 6180.	4.1	6
4375	Hypoxia classifier for transcriptome datasets. BMC Bioinformatics, 2022, 23, .	2.6	1
4376	NF-ÎºB over-activation portends improved outcomes in HPV-associated head and neck cancer. Oncotarget, 2022, 13, 707-722.	1.8	5
4378	Mapping cis-regulatory elements in human neurons links psychiatric disease heritability and activity-regulated transcriptional programs. Cell Reports, 2022, 39, 110877.	6.4	12
4379	Sticking Together an Updated Model for Temporary Adhesion. Marine Drugs, 2022, 20, 359.	4.6	2
4382	Host hepatic metabolism is modulated by gut microbiota-derived sphingolipids. Cell Host and Microbe, 2022, 30, 798-808.e7.	11.0	25

#	Article	IF	Citations
4383	De novo transcriptome assembly of the cotyledon of Camellia oleifera for discovery of genes regulating seed germination. BMC Plant Biology, 2022, 22, .	3.6	6
4385	KIL1 terminates fertility in maize by controlling silk senescence. Plant Cell, 2022, 34, 2852-2870.	6.6	9
4387	Comparative genomics highlight the importance of lineage-specific gene families in evolutionary divergence of the coral genus, Montipora. Bmc Ecology and Evolution, 2022, 22, .	1.6	7
4388	Transcriptomic Points of Departure Calculated from Rainbow Trout Gill, Liver, and Gut Cell Lines Exposed to Methylmercury and Fluoxetine. Environmental Toxicology and Chemistry, 2022, 41, 1982-1992.	4.3	9
4389	Structural variants shape the genomic landscape and clinical outcome of multiple myeloma. Blood Cancer Journal, 2022, 12, .	6.2	7
4390	Transcriptional profiling of human VÎ´1 TÂcells reveals a pathogen-driven adaptive differentiation program. Cell Reports, 2022, 39, 110858.	6.4	13
4391	The peptide SCOOP12 acts on reactive oxygen species homeostasis to modulate cell division and elongation in Arabidopsis primary root. Journal of Experimental Botany, 2022, 73, 6115-6132.	4.8	12
4392	Subclinical endometritis differentially affects the transcriptomic profiles of endometrial glandular, luminal, and stromal cells of postpartum dairy cows. Journal of Dairy Science, 2022, 105, 6125-6143.	3.4	5
4394	Transcriptomics and metagenomics of common cutworm (Spodoptera litura) and fall armyworm (Spodoptera frugiperda) demonstrate differences in detoxification and development. BMC Genomics, 2022, 23, .	2.8	5
4395	Epithelioid Pleural Mesothelioma Is Characterized by Tertiary Lymphoid Structures in Long Survivors: Results from the MATCH Study. International Journal of Molecular Sciences, 2022, 23, 5786.	4.1	9
4396	Inventory of ATP-binding cassette proteins in Lithospermum erythrorhizon as a model plant producing divergent secondary metabolites. DNA Research, 0, , .	3.4	2
4398	Ketamine exerts its sustained antidepressant effects via cell-type-specific regulation of Kcnq2. Neuron, 2022, 110, 2283-2298.e9.	8.1	40
4399	ADAR1 masks the cancer immunotherapeutic promise of ZBP1-driven necroptosis. Nature, 2022, 606, 594-602.	27.8	149
4403	ExplorATE: a new pipeline to explore active transposable elements from RNA-seq data. Bioinformatics, 2022, 38, 3361-3366.	4.1	0
4404	Evolutionary targets of gene expression divergence in a complex of closely related pine species. Journal of Systematics and Evolution, 2023, 61, 198-212.	3.1	1
4406	Transcriptional Regulation of Quinoa Seed Quality: Identification of Novel Candidate Genetic Markers for Increased Protein Content. Frontiers in Plant Science, 2022, 13, .	3.6	5
4407	The carnitine degradation pathway ofAcinetobacter baumanniiand its role in virulence. Environmental Microbiology, 2022, 24, 4437-4448.	3.8	5
4408	Essential role of CK2Î± for the interaction and stability of replication fork factors during DNA synthesis and activation of the S-phase checkpoint. Cellular and Molecular Life Sciences, 2022, 79, .	5.4	2

#	Article	IF	Citations
4409	BRAFâ€V600E utilizes posttranscriptional mechanisms to amplify LPSâ€induced TNFÎ± production in dendritic cells in a mouse model of Langerhans cell histiocytosis. Journal of Leukocyte Biology, 0, , .	3.3	0
4411	FLOWERING LOCUS T paralogs control the annual growth cycle in Populus trees. Current Biology, 2022, 32, 2988-2996.e4.	3.9	24
4412	Nuclear RIPK1 promotes chromatin remodeling to mediate inflammatory response. Cell Research, 2022, 32, 621-637.	12.0	18
4413	Comparative analysis of nitrogen removals and microbial communities in air and pure oxygen aeration systems during treatment of municipal solid waste incineration (MSWI) leachate. Journal of Water Process Engineering, 2022, 48, 102900.	5.6	0
4414	The transcriptomic (RNA-Sequencing) datasets collected in the course of floral induction in Chenopodium ficifolium 459. Data in Brief, 2022, 43, 108333.	1.0	3
4415	Extreme freeze-tolerance in cryophilic tardigrades relies on controlled ice formation but does not involve significant change in transcription. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2022, 271, 111245.	1.8	8
4416	Comparative transcriptome analysis reveals the molecular mechanism underlying lily double flowering. Scientia Horticulturae, 2022, 303, 111221.	3.6	1
4419	Metagenomic and Metabolomic Insights Into the Mechanism Underlying the Disparity in Milk Yield of Holstein Cows. Frontiers in Microbiology, 0, 13, .	3.5	3
4420	Pathogenic Mutation of TDP-43 Impairs RNA Processing in a Cell Type-Specific Manner: Implications for the Pathogenesis of ALS/FTLD. ENeuro, 2022, 9, ENEURO.0061-22.2022.	1.9	12
4421	The Gut Microbiota Composition of Cnaphalocrocis medinalis and Their Predicted Contribution to Larval Nutrition. Frontiers in Microbiology, 0, 13, .	3.5	3
4422	Lymphatics act as a signaling hub to regulate intestinal stem cell activity. Cell Stem Cell, 2022, 29, 1067-1082.e18.	11.1	53
4423	Reference nodule transcriptomes for <scp>Melilotus officinalis</scp> and <scp>Medicago sativa</scp> cv. Algonquin. Plant Direct, 2022, 6, .	1.9	4
4426	Single-nucleus profiling of human dilated and hypertrophic cardiomyopathy. Nature, 2022, 608, 174-180.	27.8	115
4427	Remote ischemic preconditioning causes transient cell cycle arrest and renal protection by a NF-ÎºBâ€“dependent Sema5B pathway. JCI Insight, 2022, 7, .	5.0	6
4428	Seasonal and sex-dependent gene expression in emu (Dromaius novaehollandiae) fat tissues. Scientific Reports, 2022, 12, .	3.3	2
4429	High sorbic acid resistance of Penicillium roqueforti is mediated by the SORBUS gene cluster. PLoS Genetics, 2022, 18, e1010086.	3.5	4
4431	Seasonal and Form-Specific Gene Expression Signatures Uncover Different Generational Strategies of the Pelagic Tunicate Salpa thompsoni During the Southern Ocean Winter. Frontiers in Marine Science, 0, 9, .	2.5	3
4432	Anaerobic sulfamethoxazoleâ€degrading bacterial consortia in antibioticâ€contaminated wetland sediments identified by <scp>DNA</scp>â€stable isotope probing and metagenomics analysis. Environmental Microbiology, 2022, 24, 3751-3763.	3.8	8

#	Article	IF	Citations
4433	Identification of diverse viruses associated with grasshoppers unveils the parallel relationship between host phylogeny and virome composition. Virus Evolution, 2022, 8, .	4.9	5
4434	Endosymbiont population genomics sheds light on transmission mode, partner specificity, and stability of the scaly-foot snail holobiont. ISME Journal, 2022, 16, 2132-2143.	9.8	6
4435	Rapid, scalable assessment of SARS-CoV-2 cellular immunity by whole-blood PCR. Nature Biotechnology, 2022, 40, 1680-1689.	17.5	29
4436	Immature Brain Cortical Neurons Have Low Transcriptional Competence to Activate Antiviral Defences and Control RNA Virus Infections. Journal of Innate Immunity, 2023, 15, 50-66.	3.8	1
4437	Transcriptional Profiling of Leishmania infantum Infected Dendritic Cells: Insights into the Role of Immunometabolism in Host-Parasite Interaction. Microorganisms, 2022, 10, 1271.	3.6	6
4438	A single <scp>promoterâ€TALE</scp> system for tissueâ€specific and tuneable expression of multiple genes in rice. Plant Biotechnology Journal, 2022, 20, 1786-1806.	8.3	6
4439	Three-Year Consecutive Field Application of Erythromycin Fermentation Residue Following Hydrothermal Treatment: Cumulative Effect on Soil Antibiotic Resistance Genes. Engineering, 2022, 15, 78-88.	6.7	12
4440	RNA-Seq and Gene Ontology Analysis Reveal Differences Associated With Low R/FR-Induced Shade Responses in Cultivated Lentil and a Wild Relative. Frontiers in Genetics, 0, 13, .	2.3	0
4442	<scp>BaRTv2</scp>: a highly resolved barley reference transcriptome for accurate transcriptâ€specific <scp>RNA</scp>â€seq quantification. Plant Journal, 2022, 111, 1183-1202.	5.7	17
4443	High throughput SARS-CoV-2 variant analysis using molecular barcodes coupled with next generation sequencing. PLoS ONE, 2022, 17, e0253404.	2.5	3
4444	The roles of growth regulation and appendage patterning genes in the morphogenesis of treehopper pronota. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, .	2.6	5
4445	Functional and phylogenetic analyses of camel rumen microbiota associated with different lignocellulosic substrates. Npj Biofilms and Microbiomes, 2022, 8, .	6.4	15
4446	Ontology Specific Alternative Splicing Changes in Alzheimerâ€™s Disease. Frontiers in Genetics, 0, 13, .	2.3	5
4447	Acute thermal stress elicits interactions between gene expression and alternative splicing in a fish of conservation concern. Journal of Experimental Biology, 2022, 225, .	1.7	6
4448	A gene deriving from the ancestral sex chromosomes was lost from the X and retained on the Y chromosome in eutherian mammals. BMC Biology, 2022, 20, .	3.8	2
4449	The <scp>GENOMES UNCOUPLED1</scp> protein has an ancient, highly conserved role but not in retrograde signalling. New Phytologist, 2022, 236, 99-113.	7.3	11
4450	A macaque clonal hematopoiesis model demonstrates expansion of TET2-disrupted clones and utility forÂtesting interventions. Blood, 2022, 140, 1774-1789.	1.4	13
4451	Inhibition of citral nanoemulsion to growth, spoilage ability and AI-2/luxS quorum sensing system of Shewanella putrefaciens CN-32: a study on bacteriostasis from in vitro culture and gene expression analysis. Food Quality and Safety, 2022, 6, .	1.8	3

#	Article	IF	Citations
4453	Identifying plant genes shaping microbiota composition in the barley rhizosphere. Nature Communications, 2022, 13, .	12.8	44
4454	Haplotype-resolved powdery mildew resistance loci reveal the impact of heterozygous structural variation on NLR genes inMuscadinia rotundifolia. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	7
4455	Strain Specific Variations in Acinetobacter baumannii Complement Sensitivity. Frontiers in Immunology, 0, 13, .	4.8	3
4456	Characterization of the Intra-tumoral B Cell Immunoglobulin Repertoire Is of Prognostic Value for Esophageal Squamous Cell Carcinoma. Frontiers in Immunology, 0, 13, .	4.8	5
4457	riboCleaner: a pipeline to identify and quantify rRNA read contamination from RNA-seq data in plants. Bioinformatics, 2022, 38, 3840-3843.	4.1	0
4458	Identifying ribosome heterogeneity using ribosome profiling. Nucleic Acids Research, 2022, 50, e95-e95.	14.5	7
4459	Genome-wide analysis of the inÂvivo tRNA structurome reveals RNA structural and modification dynamics under heat stress. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	20
4461	Comparative analysis of wildâ€type accessions reveals novel determinants of Arabidopsis seed longevity. Plant, Cell and Environment, 2022, 45, 2708-2728.	5.7	9
4463	Identification and functional annotation of long intergenic non-coding RNAs in Brassicaceae. Plant Cell, 2022, 34, 3233-3260.	6.6	22
4464	Development of <scp>DNA</scp> markers that distinguish male and female haploid germlings of the brown alga, <scp>Cladosiphon okamuranus</scp>. Phycological Research, 2022, 70, 160-166.	1.6	2
4465	500 metagenome-assembled microbial genomes from 30 subtropical estuaries in South China. Scientific Data, 2022, 9, .	5.3	9
4466	Functional genomics screening identifies aspartylâ€<scp>tRNA</scp> synthetase as a novel prognostic marker and a therapeutic target for gastric cancers. Journal of Pathology, 2022, 258, 106-120.	4.5	2
4467	Lipocalin-2 negatively regulates epithelialâ€“mesenchymal transition through matrix metalloprotease-2 downregulation in gastric cancer. Gastric Cancer, 2022, 25, 850-861.	5.3	3
4468	3-oxo-C12:2-HSL, quorum sensing molecule from human intestinal microbiota, inhibits pro-inflammatory pathways in immune cells via bitter taste receptors. Scientific Reports, 2022, 12, .	3.3	9
4469	Accumulation of endosymbiont genomes in an insect autosome followed by endosymbiont replacement. Current Biology, 2022, 32, 2786-2795.e5.	3.9	8
4470	FAM111A is dispensable for electrolyte homeostasis in mice. Scientific Reports, 2022, 12, .	3.3	3
4471	<scp>SET</scp> domain containing 2 (<scp>SETD2</scp>) influences metabolism and alternative splicing during myogenesis. FEBS Journal, 2022, 289, 6799-6816.	4.7	2
4472	Single-cell RNA-seq of a soft-tissue sarcoma model reveals the critical role of tumor-expressed MIF in shaping macrophage heterogeneity. Cell Reports, 2022, 39, 110977.	6.4	17

#	Article	IF	Citations
4474	Metatranscriptomics captures dynamic shifts in mycorrhizal coordination in boreal forests. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	12
4476	CF-Seq, an accessible web application for rapid re-analysis of cystic fibrosis pathogen RNA sequencing studies. Scientific Data, 2022, 9, .	5.3	7
4477	Metabolic-scale gene activation screens identify SLCO2B1 as a heme transporter that enhances cellular iron availability. Molecular Cell, 2022, 82, 2832-2843.e7.	9.7	13
4480	Staphylococcal saoABC Operon Codes for a DNA-Binding Protein SaoC Implicated in the Response to Nutrient Deficit. International Journal of Molecular Sciences, 2022, 23, 6443.	4.1	1
4481	Estimating intraclonal heterogeneity and subpopulation changes from bulk expression profiles in CMap. Life Science Alliance, 2022, 5, e202101299.	2.8	2
4482	Comprehensive Viral Genotyping Reveals Prognostic Viral Phylogenetic Groups in HPV16-Associated Squamous Cell Carcinoma of the Oropharynx. Molecular Cancer Research, 2022, 20, 1489-1501.	3.4	5
4483	MacroH2As regulate enhancer-promoter contacts affecting enhancer activity and sensitivity to inflammatory cytokines. Cell Reports, 2022, 39, 110988.	6.4	5
4484	Transcriptome analysis provides new insights into the tolerance and aerobic reduction of Shewanella decolorationis Ni1-3 to bromate. Applied Microbiology and Biotechnology, 2022, 106, 4749-4761.	3.6	2
4485	Comparative transcriptomics reveals the molecular toolkit used by an algivorous protist for cell wall perforation. Current Biology, 2022, 32, 3374-3384.e5.	3.9	4
4486	The embryonic zebrafish brain is seeded by a lymphatic-dependent population of mrc1+ microglia precursors. Nature Neuroscience, 2022, 25, 849-864.	14.8	10
4488	SARS-CoV-2 infection in hamsters and humans results in lasting and unique systemic perturbations after recovery. Science Translational Medicine, 2022, 14, .	12.4	129
4489	Unexpected Effect of IL-1Î² on the Function of GABAA Receptors in Pediatric Focal Cortical Dysplasia. Brain Sciences, 2022, 12, 807.	2.3	5
4490	A Transcriptomic Atlas Underlying Developmental Plasticity of Seasonal Forms of Bicyclus anynana Butterflies. Molecular Biology and Evolution, 2022, 39, .	8.9	9
4491	Nucleome programming is required for the foundation of totipotency in mammalian germline development. EMBO Journal, 2022, 41, .	7.8	9
4492	The digenean complex life cycle: phylostratigraphy analysis of the molecular signatures. Biological Communications, 2022, 67, .	0.8	0
4494	Syntaxin 18 regulates the DNA damage response and epithelial-to-mesenchymal transition to promote radiation resistance of lung cancer. Cell Death and Disease, 2022, 13, .	6.3	1
4495	Dynamic profiling and functional interpretation of histone lysine crotonylation and lactylation during neural development. Development (Cambridge), 2022, 149, .	2.5	30
4496	Short- and long-read metagenomics expand individualized structural variations in gut microbiomes. Nature Communications, 2022, 13, .	12.8	35

#	Article	IF	Citations
4498	Distinct Roles of NANOS1 and NANOS3 in the Cell Cycle and NANOS3-PUM1-FOXM1 Axis to Control G2/M Phase in a Human Primordial Germ Cell Model. International Journal of Molecular Sciences, 2022, 23, 6592.	4.1	7
4499	TSC22D4 promotes TGFÎ²1-induced activation of hepatic stellate cells. Biochemical and Biophysical Research Communications, 2022, 618, 46-53.	2.1	2
4500	Numeric Lyndon-based feature embedding of sequencing reads for machine learning approaches. Information Sciences, 2022, 607, 458-476.	6.9	2
4501	Neuronal differentiation pathways and compound-induced developmental neurotoxicity in the human neural progenitor cell test (hNPT) revealed by RNA-seq. Chemosphere, 2022, 304, 135298.	8.2	6
4502	Sediment organic matter properties facilitate understanding nitrogen transformation potentials in East African lakes. Science of the Total Environment, 2022, 841, 156607.	8.0	6
4503	Metagenomic Insights into the Influence of Thallium Spill on Sediment Microbial Community. SSRN Electronic Journal, 0, , .	0.4	0
4504	Metagenomic Analysis Reveals Resistome Characteristics of Acidic, Multimetal(Loid) Enriched Coal Source Mine Drainage Environment Under Heavy Metal(Loid)S-Induced Co-Selection. SSRN Electronic Journal, 0, , .	0.4	0
4505	A genome and gene catalog of glacier microbiomes. Nature Biotechnology, 2022, 40, 1341-1348.	17.5	50
4507	Conserved secreted effectors contribute to endophytic growth and multihost plant compatibility in a vascular wilt fungus. Plant Cell, 2022, 34, 3214-3232.	6.6	20
4508	Telomeric 8-oxo-guanine drives rapid premature senescence in the absence of telomere shortening. Nature Structural and Molecular Biology, 2022, 29, 639-652.	8.2	35
4509	JunB Is Critical for Survival of T Helper Cells. Frontiers in Immunology, 0, 13, .	4.8	6
4510	Taxonomically Restricted Genes Are Associated With Responses to Biotic and Abiotic Stresses in Sugarcane (Saccharum spp.). Frontiers in Plant Science, 0, 13, .	3.6	3
4512	Analysis of the Plasmid-Based ts Allele of PA0006 Reveals Its Function in Regulation of Cell Morphology and Biosynthesis of Core Lipopolysaccharide in Pseudomonas aeruginosa. Applied and Environmental Microbiology, 2022, 88, .	3.1	1
4513	Transcriptomic evidence for visual adaptation during the aquatic to terrestrial metamorphosis in leopard frogs. BMC Biology, 2022, 20, .	3.8	7
4514	Transcriptomic modulation in response to an intoxication with deltamethrin in a population of Triatoma infestans with low resistance to pyrethroids. PLoS Neglected Tropical Diseases, 2022, 16, e0010060.	3.0	6
4515	Marine Microeukaryote Metatranscriptomics: Sample Processing and Bioinformatic Workflow Recommendations for Ecological Applications. Frontiers in Marine Science, 0, 9, .	2.5	8
4516	Seed Transmission of Pathogens: Non-Canonical Immune Response in Arabidopsis Germinating Seeds Compared to Early Seedlings against the Necrotrophic Fungus Alternaria brassicicola. Plants, 2022, 11, 1708.	3.5	3
4517	Rescue of a peroxisome proliferator activated receptor gamma gene network in muscle after growth of human breast tumour xenografts. JCSM Rapid Communications, 2022, 5, 239-253.	1.6	0

#	Article	IF	Citations
4519	Systematic Functional Annotation Workflow for Insects. Insects, 2022, 13, 586.	2.2	12
4520	The Î²-TrCP-Mediated Pathway Cooperates with the Keap1-Mediated Pathway in Nrf2 Degradation In Vivo. Molecular and Cellular Biology, 2022, 42, .	2.3	13
4521	A dual role for the RNA helicase DHX34 in NMD and pre-mRNA splicing and its function in hematopoietic differentiation. Rna, 0, , rna.079277.122.	3.5	4
4522	GenomicSuperSignature facilitates interpretation of RNA-seq experiments through robust, efficient comparison to public databases. Nature Communications, 2022, 13, .	12.8	6
4524	Targeting Lysine-Specific Demethylase 1 Rescues Major Histocompatibility Complex Class I Antigen Presentation and Overcomes Programmed Death-Ligand 1 Blockade Resistance in SCLC. Journal of Thoracic Oncology, 2022, 17, 1014-1031.	1.1	31
4525	Recreational physical activity before and during pregnancy and placental DNA methylationâ€"an epigenome-wide association study. American Journal of Clinical Nutrition, 2022, 116, 1168-1183.	4.7	7
4526	Transcriptome Analysis of Fusariumâ€"Tomato Interaction Based on an Updated Genome Annotation of Fusarium oxysporum f. sp. lycopersici Identifies Novel Effector Candidates That Suppress or Induce Cell Death in Nicotiana benthamiana. Journal of Fungi (Basel, Switzerland), 2022, 8, 672.	3.5	8
4528	Regulation of HLA class I expression by non-coding gene variations. PLoS Genetics, 2022, 18, e1010212.	3.5	8
4529	Dynamics of Small Non-coding RNA Profiles and the Intestinal Microbiome of High and Low Weight Chickens. Frontiers in Microbiology, 0, 13, .	3.5	3
4531	Identification and Expression Analysis of Chemosensory Genes in the Antennal Transcriptome of Chrysanthemum Aphid Macrosiphoniella sanborni. Insects, 2022, 13, 597.	2.2	6
4532	Diet triggers specific responses of hypothalamic astrocytes in time and region dependent manner. Glia, 2022, 70, 2062-2078.	4.9	12
4534	TOP2B Is Required to Maintain the Adrenergic Neural Phenotype and for ATRA-Induced Differentiation of SH-SY5Y Neuroblastoma Cells. Molecular Neurobiology, 2022, 59, 5987-6008.	4.0	10
4535	PVT1 is a stress-responsive lncRNA that drives ovarian cancer metastasis and chemoresistance. Life Science Alliance, 2022, 5, e202201370.	2.8	7
4537	Bioinformatics roadmap for therapy selection in cancer genomics. Molecular Oncology, 2022, 16, 3881-3908.	4.6	6
4538	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. Nature Genetics, 2022, 54, 1037-1050.	21.4	26
4540	An atlas of endogenous DNA double-strand breaks arising during human neural cell fate determination. Scientific Data, 2022, 9, .	5.3	3
4541	Dendritic cell-mediated cross presentation of tumor-derived peptides is biased against plasma membrane proteins. , 2022, 10, e004159.		5
4542	Pleiotropic effects of trans-regulatory mutations on fitness and gene expression. Science, 2022, 377, 105-109.	12.6	26

#	Article	IF	Citations
4543	Temporal Dynamic Analysis of Alternative Splicing During Embryonic Development in Zebrafish. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	1
4545	NF-Î²B signaling controls H3K9me3 levels at intronic LINE-1 and hematopoietic stem cell genes in cis. Journal of Experimental Medicine, 2022, 219, .	8.5	4
4546	Multiâ€omics analysis reveals multiple mechanisms causing Praderâ€“Willi like syndrome in a family with a X;15 translocation. Human Mutation, 2022, 43, 1567-1575.	2.5	3
4547	Î²2-Microglobulin Maintains Glioblastoma Stem Cells and Induces M2-like Polarization of Tumor-Associated Macrophages. Cancer Research, 2022, 82, 3321-3334.	0.9	31
4548	RNA Sequencing Reveals Beneficial Effects of Atorvastatin on Endothelial Cells in Acute Kawasaki Disease. Journal of the American Heart Association, 0, , .	3.7	2
4549	Prognostic value of tumor immune biomarkers in biopsies from patients with refractory solid cancers. Cancer Treatment and Research Communications, 2022, 32, 100611.	1.7	0
4550	Mutations in DNA polymerase Î´ subunit 1 co-segregate with CMD2-type resistance to Cassava Mosaic Geminiviruses. Nature Communications, 2022, 13, .	12.8	8
4551	Approaches in Gene Coexpression Analysis in Eukaryotes. Biology, 2022, 11, 1019.	2.8	4
4552	Tumor treating fields affect mesothelioma cell proliferation by exerting histotype-dependent cell cycle checkpoint activations and transcriptional modulations. Cell Death and Disease, 2022, 13, .	6.3	2
4553	A high-resolution single-molecule sequencing-based Arabidopsis transcriptome using novel methods of Iso-seq analysis. Genome Biology, 2022, 23, .	8.8	35
4554	A thorough annotation of the krill transcriptome offers new insights for the study of physiological processes. Scientific Reports, 2022, 12, .	3.3	6
4556	Mechanism of fertilization-induced auxin synthesis in the endosperm for seed and fruit development. Nature Communications, 2022, 13, .	12.8	28
4557	GLI3 regulates muscle stem cell entry into GAlert and self-renewal. Nature Communications, 2022, 13, .	12.8	21
4559	Repeated ketamine anesthesia during neurodevelopment upregulates hippocampal activity and enhances drug reward in male mice. Communications Biology, 2022, 5, .	4.4	1
4560	Needle: a fast and space-efficient prefilter for estimating the quantification of very large collections of expression experiments. Bioinformatics, 2022, 38, 4100-4108.	4.1	3
4561	EBAG9 silencing exerts an immune checkpoint function without aggravating adverse effects. Molecular Therapy, 2022, 30, 3358-3378.	8.2	2
4562	Wheat yield potential can be maximized by increasing red to farâ€red light conditions at critical developmental stages. Plant, Cell and Environment, 2022, 45, 2652-2670.	5.7	8
4563	High-throughput muscle fiber typing from RNA sequencing data. Skeletal Muscle, 2022, 12, .	4.2	5

#	Article	IF	Citations
4564	Combined MEK and JAK/STAT3 pathway inhibition effectively decreases SHH medulloblastoma tumor progression. Communications Biology, 2022, 5, .	4.4	8
4565	H3K27me3 shapes DNA methylome by inhibiting UHRF1-mediated H3 ubiquitination. Science China Life Sciences, 2022, 65, 1685-1700.	4.9	4
4568	ILRUN Promotes Atherosclerosis Through Lipid-Dependent and Lipid-Independent Factors. Arteriosclerosis, Thrombosis, and Vascular Biology, 0, , .	2.4	2
4569	Weight Cycling Impairs Pancreatic Insulin Secretion but Does Not Perturb Whole-Body Insulin Action in Mice With Diet-Induced Obesity. Diabetes, 2022, 71, 2313-2330.	0.6	9
4570	Real age prediction from the transcriptome with RAPToR. Nature Methods, 2022, 19, 969-975.	19.0	12
4571	Reversal of viral and epigenetic HLA class I repression in Merkel cell carcinoma. Journal of Clinical Investigation, 2022, 132, .	8.2	10
4572	Batch effect detection and correction in RNA-seq data using machine-learning-based automated assessment of quality. BMC Bioinformatics, 2022, 23, .	2.6	10
4573	Mining Amphibian and Insect Transcriptomes for Antimicrobial Peptide Sequences with rAMPage. Antibiotics, 2022, 11, 952.	3.7	10
4575	Light-induced asymmetries in embryonic retinal gene expression are mediated by the vascular system and extracellular matrix. Scientific Reports, 2022, 12, .	3.3	4
4577	17q21.31 sub-haplotypes underlying H1-associated risk for Parkinsonâ€™s disease are associated with LRRC37A/2 expression in astrocytes. Molecular Neurodegeneration, 2022, 17, .	10.8	15
4578	Uncover landfilled antimicrobial resistance: a critical review of antibiotics flux, resistome dynamics and risk assessment. , 2022, 1, 20220012.		3
4580	Mechanical checkpoint regulates monocyte differentiation in fibrotic niches. Nature Materials, 2022, 21, 939-950.	27.5	22
4581	Impaired Cell Cycle Progression and Self-Renewal of Fetal Neural Stem and Progenitor Cells in a Murine Model of Intrauterine Growth Restriction. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	1
4582	Quantification of mutantâ€“allele expression at isoform level in cancer from RNA-seq data. NAR Genomics and Bioinformatics, 2022, 4, .	3.2	1
4583	What can coldâ€induced transcriptomes of Arctic Brassicaceae tell us about the evolution of cold tolerance?. Molecular Ecology, 2022, 31, 4271-4285.	3.9	5
4586	Early Transcriptome Differences Between Pre-Infected and NaÃ¯ve Kid Goats Infected With Haemonchus contortus. Frontiers in Veterinary Science, 0, 9, .	2.2	3
4587	Tissue Specificity of Gene Expression Evolves Across Mammal Species. Journal of Computational Biology, 2022, 29, 880-891.	1.6	5
4589	Integrated DNA and RNA Sequencing Reveals Drivers of Endocrine Resistance in Estrogen Receptorâ€“Positive Breast Cancer. Clinical Cancer Research, 2022, 28, 3618-3629.	7.0	12

#	Article	IF	Citations
4590	Triple-Negative Breast Cancer circRNAome Reveals Hsa_circ_0072309 as a Potential Risk Biomarker. Cancers, 2022, 14, 3280.	3.7	3
4591	Demographic, physiological and genetic factors linked to the poleward range expansion of the snail Nerita yoldii along the shoreline of China. Molecular Ecology, 2022, 31, 4510-4526.	3.9	8
4592	iCodon customizes gene expression based on the codon composition. Scientific Reports, 2022, 12, .	3.3	11
4593	Full-Length Transcriptome Reconstruction Reveals the Genetic Mechanisms of Eyestalk Displacement and Its Potential Implications on the Interspecific Hybrid Crab (Scylla serrata â™€ Ã— S. paramamosain â™‚). Biology, 2022, 11, 1026.	2.8	3
4594	Molecular signatures of in situ to invasive progression for basal-like breast cancers: An integrated mouse model and human DCIS study. Npj Breast Cancer, 2022, 8, .	5.2	4
4595	Greater functional diversity and redundancy of coral endolithic microbiomes align with lower coral bleaching susceptibility. ISME Journal, 2022, 16, 2406-2420.	9.8	21
4596	The Lund Molecular Taxonomy Applied to Nonâ€“Muscle-Invasive Urothelial Carcinoma. Journal of Molecular Diagnostics, 2022, 24, 992-1008.	2.8	13
4598	A Path-Based Analysis of Infected Cell Line and COVID-19 Patient Transcriptome Reveals Novel Potential Targets and Drugs Against SARS-CoV-2. Frontiers in Immunology, 0, 13, .	4.8	6
4599	Molecular basis of ocean acidification sensitivity and adaptation in Mytilus galloprovincialis. IScience, 2022, 25, 104677.	4.1	3
4600	Determining the primary sources of groundwater bacterial communities in a large-scale plain area: Microbial source tracking and interpretation for different land use patterns. Agriculture, Ecosystems and Environment, 2022, 338, 108092.	5.3	5
4601	Sex chromosome aneuploidies give rise to changes in the circular RNA profile: A circular transcriptome-wide study of Turner and Klinefelter syndrome across different tissues. Frontiers in Genetics, 0, 13, .	2.3	9
4603	Meta-Analysis of RNA Sequencing Data of Arabidopsis and Rice under Hypoxia. Life, 2022, 12, 1079.	2.4	11
4604	Mutant KRAS regulates transposable element RNA and innate immunity via KRAB zinc-finger genes. Cell Reports, 2022, 40, 111104.	6.4	7
4606	Microglia-derived PDGFB promotes neuronal potassium currents to suppress basal sympathetic tonicity and limit hypertension. Immunity, 2022, 55, 1466-1482.e9.	14.3	20
4607	A Carotenoid- and Nuclease-Producing Bacterium Can Mitigate Enterococcus faecalis Transformation by Antibiotic Resistance Genes. Environmental Science & Technology, 2022, 56, 15167-15178.	10.0	11
4608	Type II alveolar epithelial cell aryl hydrocarbon receptor protects against allergic airway inflammation through controlling cell autophagy. Frontiers in Immunology, 0, 13, .	4.8	7
4609	Comprehensive Analysis of the Immunogenomics of Triple-Negative Breast Cancer Brain Metastases From LCCC1419. Frontiers in Oncology, 0, 12, .	2.8	2
4610	Divergent Specialization of Simple Venom Gene Profiles among Rear-Fanged Snake Genera (Helicops and) Tj ETQq1 1 0.784314 rgBT	3.4	3

#	Article	IF	Citations
4611	Comprehensive Analysis of CRIP1 Expression in Acute Myeloid Leukemia. Frontiers in Genetics, 0, 13, .	2.3	3
4612	Characterization of MET Exon 14 Skipping Alterations (METex14) in Non-Small Cell Lung Cancer (NSCLC) and Identification of Potential Therapeutic Targets using Whole Transcriptome Sequencing (WTS). JTO Clinical and Research Reports, 2022, , 100381.	1.1	3
4613	Variation in TAF1 Expression in Female Carrier-Induced Pluripotent Stem Cells and Human Brain Ontogeny Has Implications for Adult Neostriatum Vulnerability in X-Linked Dystonia Parkinsonism. ENeuro, 2022, 9, ENEURO.0129-22.2022.	1.9	0
4614	DSMZCellDive: Diving into high-throughput cell line data. F1000Research, 0, 11, 420.	1.6	8
4616	An in vivo model of glioblastoma radiation resistance identifies long noncoding RNAs and targetable kinases. JCI Insight, 2022, 7, .	5.0	5
4617	Comparative Transcriptome Analysis Reveals Coordinated Transcriptional Regulation of Central and Secondary Metabolism in the Trichomes of Cannabis Cultivars. International Journal of Molecular Sciences, 2022, 23, 8310.	4.1	1
4618	Global and precise identification of functional <scp>miRNA</scp> targets in <scp>mESCs</scp> by integrative analysis. EMBO Reports, 2022, 23, .	4.5	5
4620	Deterministic assembly process dominates bacterial antibiotic resistome in wastewater effluents receiving river. Environmental Science and Pollution Research, 2022, 29, 90207-90218.	5.3	5
4621	Regulation of alternative polyadenylation by the C2H2-zinc-finger protein Sp1. Molecular Cell, 2022, 82, 3135-3150.e9.	9.7	14
4622	DNA methylation and transcriptomic features are preserved throughout disease recurrence and chemoresistance in high grade serous ovarian cancers. Journal of Experimental and Clinical Cancer Research, 2022, 41, .	8.6	8
4623	Integration of p16/HPV DNA Status with a 24-miRNA-Defined Molecular Phenotype Improves Clinically Relevant Stratification of Head and Neck Cancer Patients. Cancers, 2022, 14, 3745.	3.7	2
4624	Locally adaptive temperature response of vegetative growth in Arabidopsis thaliana. ELife, 0, 11, .	6.0	10
4625	Proteotoxicity caused by perturbed protein complexes underlies hybrid incompatibility in yeast. Nature Communications, 2022, 13, .	12.8	2
4626	HNRNPK alleviates RNA toxicity by counteracting DNA damage in C9orf72 ALS. Acta Neuropathologica, 2022, 144, 465-488.	7.7	8
4627	Transcription factor network analysis identifies REST/NRSF as an intrinsic regulator of CNS regeneration in mice. Nature Communications, 2022, 13, .	12.8	18
4628	Intronic Cis-Element DR8 in hTERT Is Bound by Splicing Factor SF3B4 and Regulates hTERT Splicing in Nonâ€“Small Cell Lung Cancer. Molecular Cancer Research, 2022, 20, 1574-1588.	3.4	4
4629	Full-Length Spatial Transcriptomics Reveals the Unexplored Isoform Diversity of the Myocardium Post-MI. Frontiers in Genetics, 0, 13, .	2.3	15
4630	Loss of Monoallelic Expression of IGF2 in the Adult Liver Via Alternative Promoter Usage and Chromatin Reorganization. Frontiers in Genetics, 0, 13, .	2.3	4

#	Article	IF	Citations
4631	Transcriptome analysis demonstrating the therapeutic effect of <scp> Tenodera angustipennis </scp> (Mantidis Ootheca) extracts on radiationâ€induced gonadal toxicity in mouse testis. Entomological Research, 2022, 52, 319-326.	1.1	2
4634	Nasopharyngeal lipidomic endotypes of infants with bronchiolitis and risk of childhood asthma: a multicentre prospective study. Thorax, 2022, 77, 1059-1069.	5.6	12
4635	BIRC6 modifies risk of invasive bacterial infection in Kenyan children. ELife, 0, 11, .	6.0	6
4636	HOTAIR interacts with PRC2 complex regulating the regional preadipocyte transcriptome and human fat distribution. Cell Reports, 2022, 40, 111136.	6.4	17
4637	Allergic sensitization impairs lung resident memory CD8 T-cell response and virus clearance. Journal of Allergy and Clinical Immunology, 2022, 150, 1415-1426.e9.	2.9	2
4638	ERK5 Is a Major Determinant of Chemical Sarcomagenesis: Implications in Human Pathology. Cancers, 2022, 14, 3509.	3.7	2
4639	Rapid and robust directed differentiation of mouse epiblast stem cells into definitive endoderm and forebrain organoids. Development (Cambridge), 2022, 149, .	2.5	3
4640	Reciprocal SOX2 regulation by SMAD1-SMAD3 is critical for anoikis resistance and metastasis in cancer. Cell Reports, 2022, 40, 111066.	6.4	16
4642	circRAB3IP modulates cell proliferation by reorganizing gene expression and mRNA processing in a paracrine manner. Rna, 0, , rna.079195.122.	3.5	1
4643	TGS1 impacts snRNA 3â€²-end processing, ameliorates survival motor neuron-dependent neurological phenotypes in vivo and prevents neurodegeneration. Nucleic Acids Research, 2022, 50, 12400-12424.	14.5	2
4644	Comparative analysis of the daily liver transcriptomes in wild nocturnal bats. BMC Genomics, 2022, 23, .	2.8	0
4645	Drought Stress Stimulates the Terpenoid Backbone and Triterpenoid Biosynthesis Pathway to Promote the Synthesis of Saikosaponin in Bupleurum chinense DC. Roots. Molecules, 2022, 27, 5470.	3.8	4
4646	Laminin 511 and WNT signalling sustain prolonged expansion of hiPSC-derived hippocampal progenitors. Development (Cambridge), 2022, 149, .	2.5	3
4649	Co-expression network analysis of genes and networks associated with wheat pistillody. PeerJ, 0, 10, e13902.	2.0	1
4650	Transcriptome variation in human tissues revealed by long-read sequencing. Nature, 2022, 608, 353-359.	27.8	103
4651	Transcriptomic effects of propranolol and primidone converge on molecular pathways relevant to essential tremor. Npj Genomic Medicine, 2022, 7, .	3.8	4
4653	PKD1 and PKD2 mRNA cis-inhibition drives polycystic kidney disease progression. Nature Communications, 2022, 13, .	12.8	17
4654	Expression plasticity regulates intraspecific variation in the acclimatization potential of a reef-building coral. Nature Communications, 2022, 13, .	12.8	10

#	Article	IF	Citations
4655	Origination of LTR retroelement-derived NYNRIN coincides with therian placental emergence. Molecular Biology and Evolution, 0, , .	8.9	2
4656	Generation of functional hepatocytes by forward programming with nuclear receptors. ELife, 0, 11, .	6.0	8
4657	Bridging the splicing gap in human genetics with long-read RNA sequencing: finding the protein isoform drivers of disease. Human Molecular Genetics, 2022, 31, R123-R136.	2.9	10
4658	Modulation of sol mRNA expression by the long non-coding RNA Assolrna in Clostridium saccharoperbutylacetonicum affects solvent formation. Frontiers in Genetics, 0, 13, .	2.3	0
4659	aTAP: automated transcriptome analysis platform for processing RNA-seq data by de novo assembly. Heliyon, 2022, 8, e10255.	3.2	0
4660	SOX transcription factors direct TCF-independent WNT/Î²-catenin responsive transcription to govern cell fate in human pluripotent stem cells. Cell Reports, 2022, 40, 111247.	6.4	21
4662	Genetic inhibition of serum glucocorticoid kinase 1 prevents obesity-related atrial fibrillation. JCI Insight, 2022, 7, .	5.0	6
4663	Identification of early quassinoid biosynthesis in the invasive tree of heaven (Ailanthus altissima) confirms evolutionary origin from protolimonoids. Frontiers in Plant Science, 0, 13, .	3.6	12
4665	Novel Method of Full-Length RNA-seq That Expands the Identification of Non-Polyadenylated RNAs Using Nanopore Sequencing. Analytical Chemistry, 2022, 94, 12342-12351.	6.5	2
4666	<scp>CDK9</scp> and <scp>PP2A</scp> regulate <scp>RNA</scp> polymerase <scp>II</scp> transcription termination and coupled <scp>RNA</scp> maturation. EMBO Reports, 2022, 23, .	4.5	15
4667	Repurposing Azacitidine and Carboplatin to Prime Immune Checkpoint Blockadeâ€“resistant Melanoma for Anti-PD-L1 Rechallenge. Cancer Research Communications, 2022, 2, 814-826.	1.7	1
4668	The A to I editing landscape in melanoma and its relation to clinical outcome. RNA Biology, 2022, 19, 996-1006.	3.1	5
4669	Rapid and simple analysis of short and long sequencing reads using DuesselporeTM. Frontiers in Genetics, 0, 13, .	2.3	2
4670	Expanding the environmental virome: Infection profile in a native rainforest tree species. Frontiers in Microbiology, 0, 13, .	3.5	2
4671	Transcriptome analysis of the 2,4-dichlorophenoxyacetic acid (2,4-D)-tolerant cotton chromosome substitution line CS-B15sh and its susceptible parental lines G. hirsutum L. cv. Texas Marker-1 and G. barbadense L. cv. Pima 379. Frontiers in Plant Science, 0, 13, .	3.6	1
4672	Functional Redundancy in Bat Microbial Assemblage in the Presence of the White Nose Pathogen. Microbial Ecology, 0, , .	2.8	0
4673	Ancestral SARS-CoV-2, but not Omicron, replicates less efficiently in primary pediatric nasal epithelial cells. PLoS Biology, 2022, 20, e3001728.	5.6	15
4674	JMJD3 activated hyaluronan synthesis drives muscle regeneration in an inflammatory environment. Science, 2022, 377, 666-669.	12.6	31

#	Article	IF	Citations
4675	Integrated Transcriptomic and Metabolomic Analysis of the Mechanism of Foliar Application of Hormone-Type Growth Regulator in the Improvement of Grape (Vitis vinifera L.) Coloration in Saline-Alkaline Soil. Plants, 2022, 11, 2115.	3.5	2
4677	A diversified and segregated mRNA spliced-leader system in the parasitic Perkinsozoa. Open Biology, 2022, 12, .	3.6	3
4678	Failure of diet-induced transcriptional adaptations in alpha-synuclein transgenic mice. Human Molecular Genetics, 0, , .	2.9	0
4679	Mode of action of elasnin as biofilm formation eradicator of methicillin-resistant Staphylococcus aureus. Frontiers in Microbiology, 0, 13, .	3.5	3
4681	Systematic exploration of dynamic splicing networks reveals conserved multistage regulators of neurogenesis. Molecular Cell, 2022, 82, 2982-2999.e14.	9.7	10
4682	Multi-omics analysis reveals RNA splicing alterations and their biological and clinical implications in lung adenocarcinoma. Signal Transduction and Targeted Therapy, 2022, 7, .	17.1	7
4683	Detection of orthologous exons and isoforms using EGIO. Bioinformatics, 2022, 38, 4474-4480.	4.1	1
4684	Phylogenetically and catabolically diverse diazotrophs reside in deep-sea cold seep sediments. Nature Communications, 2022, 13, .	12.8	29
4685	Rop plays conserved roles in the reproductive and digestive processes of spider mites. Insect Science, 2023, 30, 351-364.	3.0	1
4687	A CRISPRi/a platform in human iPSC-derived microglia uncovers regulators of disease states. Nature Neuroscience, 2022, 25, 1149-1162.	14.8	79
4689	Transcription Factors YAP/TAZ and SRF Cooperate To Specify Renal Myofibroblasts in the Developing Mouse Kidney. Journal of the American Society of Nephrology: JASN, 2022, 33, ASN.2021121559.	6.1	6
4690	Gut microbiota-derived metabolites confer protection against SARS-CoV-2 infection. Gut Microbes, 2022, 14, .	9.8	26
4691	CCR9 axis inhibition enhances hepatic migration of plasmacytoid DCs and protects against liver injury. JCI Insight, 2022, 7, .	5.0	3
4693	Evolutionary Changes in the Chromatin Landscape Contribute to Reorganization of a Developmental Gene Network During Rapid Life History Evolution in Sea Urchins. Molecular Biology and Evolution, 2022, 39, .	8.9	7
4695	Endothelial Loss of ETS1 Impairs Coronary Vascular Development and Leads to Ventricular Non-Compaction. Circulation Research, 2022, 131, 371-387.	4.5	12
4696	Sequencing introduced false positive rare taxa lead to biased microbial community diversity, assembly, and interaction interpretation in amplicon studies. Environmental Microbiomes, 2022, 17, .	5.0	17
4697	Sexually dimorphic transcriptional programs of early-phase response in regenerating peripheral nerves. Frontiers in Molecular Neuroscience, 0, 15, .	2.9	4
4698	Multi-Omic Investigations of a 17â€“19 Translocation Links MINK1 Disruption to Autism, Epilepsy and Osteoporosis. International Journal of Molecular Sciences, 2022, 23, 9392.	4.1	2

#	Article	IF	Citations
4700	CRISPR base editing of cis-regulatory elements enables the perturbation of neurodegeneration-linked genes. Molecular Therapy, 2022, 30, 3619-3631.	8.2	10
4702	Acetate reprograms gut microbiota during alcohol consumption. Nature Communications, 2022, 13, .	12.8	34
4703	PIF4 enhances DNA binding of CDF2 to co-regulate target gene expression and promote Arabidopsis hypocotyl cell elongation. Nature Plants, 2022, 8, 1082-1093.	9.3	16
4704	De Novo Long-Read Whole-Genome Assemblies and the Comparative Pan-Genome Analysis of Ascochyta Blight Pathogens Affecting Field Pea. Journal of Fungi (Basel, Switzerland), 2022, 8, 884.	3.5	0
4706	APAview: A web-based platform for alternative polyadenylation analyses in hematological cancers. Frontiers in Genetics, 0, 13, .	2.3	2
4707	Human dyskerin binds to cytoplasmic H/ACA-box-containing transcripts affecting nuclear hormone receptor dependence. Genome Biology, 2022, 23, .	8.8	5
4709	Captivity induces large and populationâ€dependent brain transcriptomic changes in wildâ€caught cane toads (Rhinella marina). Molecular Ecology, 2022, 31, 4949-4961.	3.9	5
4710	A multiomics disease progression signature of low-risk ccRCC. Scientific Reports, 2022, 12, .	3.3	3
4712	The wound-activated ERF15 transcription factor drives Marchantia polymorpha regeneration by activating an oxylipin biosynthesis feedback loop. Science Advances, 2022, 8, .	10.3	6
4713	Transcriptional response of a target plant to benzoxazinoid and diterpene allelochemicals highlights commonalities in detoxification. BMC Plant Biology, 2022, 22, .	3.6	0
4714	Investigation of Peptide Toxin Diversity in Ribbon Worms (Nemertea) Using a Transcriptomic Approach. Toxins, 2022, 14, 542.	3.4	2
4715	Chimeric GPCRs mimic distinct signaling pathways and modulate microglia responses. Nature Communications, 2022, 13, .	12.8	5
4717	Cascading effects of prey identity on gene expression in a kleptoplastidic ciliate. Journal of Eukaryotic Microbiology, 0, , .	1.7	2
4718	Rituximab versus tocilizumab and B-cell status in TNF-alpha inadequate-responder rheumatoid arthritis patients: the R4-RA RCT. Efficacy and Mechanism Evaluation, 2022, 9, 1-58.	0.7	0
4720	Correlations of expression of nuclear and mitochondrial genes in triploid fish. G3: Genes, Genomes, Genetics, 0, , .	1.8	0
4722	Phylotranscriptomics reveals the reticulate evolutionary history of a widespread diatom species complex. Journal of Phycology, 2022, 58, 643-656.	2.3	8
4723	The transcription factor Cdx2 regulates inflammasome activity through expression of the NLRP3 suppressor TRIM31 to maintain intestinal homeostasis. Journal of Biological Chemistry, 2022, 298, 102386.	3.4	5
4724	White matter damage as a consequence of vascular dysfunction in a spontaneous mouse model of chronic mild chronic hypoperfusion with eNOS deficiency. Molecular Psychiatry, 2022, 27, 4754-4769.	7.9	16

#	Article	IF	Citations
4725	Large-scale multiplexed mosaic CRISPR perturbation in the whole organism. Cell, 2022, 185, 3008-3024.e16.	28.9	15
4726	Integrated analysis of small RNAs, transcriptome and degradome sequencing reveal the drought stress network in Agropyron mongolicum Keng. Frontiers in Plant Science, 0, 13, .	3.6	2
4727	Transcription factorâ€“nucleosome dynamics from plasma cfDNA identifies ER-driven states in breast cancer. Science Advances, 2022, 8, .	10.3	8
4728	Analysis of Thioredoxins and Glutaredoxins in Soybean: Evidence of Translational Regulation under Water Restriction. Antioxidants, 2022, 11, 1622.	5.1	6
4729	Nascent transcriptome reveals orchestration of zygotic genome activation in early embryogenesis. Current Biology, 2022, 32, 4314-4324.e7.	3.9	7
4730	A small RNA-guided PRC2 complex eliminates DNA as an extreme form of transposon silencing. Cell Reports, 2022, 40, 111263.	6.4	23
4731	Effects of Two Distinct Psychoactive Microbes, Lacticaseibacillus rhamnosus JB-1 and Limosilactobacillus reuteri 6475, on Circulating and Hippocampal mRNA in Male Mice. International Journal of Molecular Sciences, 2022, 23, 9653.	4.1	4
4733	Metagenomic assembly reveals hosts and mobility of common antibiotic resistome in animal manure and commercial compost. Environmental Microbiomes, 2022, 17, .	5.0	20
4734	Macrophages take up VLDL-sized emulsion particles through caveolae-mediated endocytosis and excrete part of the internalized triglycerides as fatty acids. PLoS Biology, 2022, 20, e3001516.	5.6	7
4735	satuRn:ÂScalable analysis of differential transcript usageÂfor bulk and single-cell RNA-sequencing applications. F1000Research, 0, 10, 374.	1.6	1
4737	Monoclonal Antibody Sequence Variants Disguised as Fragments: Identification, Characterization, and Their Removal by Purification Process Optimization. Journal of Pharmaceutical Sciences, 2022, 111, 3009-3016.	3.3	4
4738	Alpha-methylacyl-CoA racemase (AMACR) protein is upregulated in early proliferative lesions of the breast irrespective of apocrine differentiation. Human Pathology, 2022, 129, 40-46.	2.0	2
4740	Antibody therapy reverses biological signatures of COVID-19 progression. Cell Reports Medicine, 2022, 3, 100721.	6.5	3
4741	Characterization of Macrophage-Tropic HIV-1 Infection of Central Nervous System Cells and the Influence of Inflammation. Journal of Virology, 2022, 96, .	3.4	9
4743	Loss of key endosymbiont genes may facilitate early host control of the chromatophore in Paulinella. IScience, 2022, 25, 104974.	4.1	7
4745	Transcriptomics and Proteomics Analyses Reveal JAK Signaling and Inflammatory Phenotypes during Cellular Senescence in Blind Mole Rats: The Reflections of Superior Biology. Biology, 2022, 11, 1253.	2.8	2
4746	Distinct microglia alternative splicing in Alzheimer's disease. Aging, 2022, 14, 6554-6566.	3.1	3
4747	scRNA-seq of gastric tumor shows complex intercellular interaction with an alternative T cell exhaustion trajectory. Nature Communications, 2022, 13, .	12.8	32

#	Article	IF	Citations
4748	hiPSC-derived bone marrow milieu identifies a clinically actionable driver of niche-mediated treatment resistance in leukemia. Cell Reports Medicine, 2022, 3, 100717.	6.5	11
4749	Identification of putative enhancer-like elements predicts regulatory networks active in planarian adult stem cells. ELife, 0, 11, .	6.0	9
4754	Ribosome impairment regulates intestinal stem cell identity via ZAKÉ‘ activation. Nature Communications, 2022, 13, .	12.8	8
4755	Endometrial gland-specific progestagen-associated endometrial protein and cilia gene splicing changes in recurrent pregnancy loss. Reproduction and Fertility, 2022, 3, 162-172.	1.8	2
4756	Development of dim-light vision in the nocturnal reef fish family Holocentridae. I: Retinal gene expression. Journal of Experimental Biology, 2022, 225, .	1.7	7
4757	Complement factor B is critical for sub-RPE deposit accumulation in a model of Doyne honeycomb retinal dystrophy with features of age-related macular degeneration. Human Molecular Genetics, 0, , .	2.9	4
4758	Genome-wide identification and expression analysis of carotenoid cleavage oxygenase genes in Litchi (Litchi chinensis Sonn.). BMC Plant Biology, 2022, 22, .	3.6	13
4759	Lymphatics and fibroblasts support intestinal stem cells in homeostasis and injury. Cell Stem Cell, 2022, 29, 1246-1261.e6.	11.1	35
4760	A Long-Read Genome Assembly of a Native Mite in China Pyemotes zhonghuajia Yu, Zhang & He (Prostigmata: Pyemotidae) Reveals Gene Expansion in Toxin-Related Gene Families. Toxins, 2022, 14, 571.	3.4	3
4761	Genetic evidence that uptake of the fluorescent analog 2NBDG occurs independently of known glucose transporters. PLoS ONE, 2022, 17, e0261801.	2.5	9
4762	Differential gene expression in iPSC-derived human intestinal epithelial cell layers following exposure to two concentrations of butyrate, propionate and acetate. Scientific Reports, 2022, 12, .	3.3	8
4763	Post-translational control of beige fat biogenesis by PRDM16 stabilization. Nature, 2022, 609, 151-158.	27.8	31
4765	Protocol to estimate cell type proportions from bulk RNA-seq using DAISM-DNNXMBD. STAR Protocols, 2022, 3, 101587.	1.2	0
4766	Comparative transcriptomics of two coral holobionts collected during the 2017 El NiÃ±o heat wave reveal differential stress response mechanisms. Marine Pollution Bulletin, 2022, 182, 114017.	5.0	8
4767	Dual-transcriptomic datasets evaluating the effect of the necrotrophic fungus Alternaria brassicicola on Arabidopsis germinating seeds. Data in Brief, 2022, 44, 108530.	1.0	2
4768	Microbial community structure and function of activated sludge from a wastewater treatment plant at the Polar Arctic Circle as revealed by metatranscriptomic and next-generation sequencing. Journal of Environmental Chemical Engineering, 2022, 10, 108393.	6.7	6
4769	Sex-dependent differential transcript expression in the placenta of growth restricted infants. Placenta, 2022, 128, 1-8.	1.5	2
4770	Host-pathogen coevolution drives innate immune response to Aphanomyces astaci infection in freshwater crayfish: transcriptomic evidence. BMC Genomics, 2022, 23, .	2.8	6

#	Article	IF	Citations
4776	Insulin and serine metabolism as sex-specific hallmarks of Alzheimerâ€™s disease in the human hippocampus. Cell Reports, 2022, 40, 111271.	6.4	19
4777	Microtubule modification defects underlie cilium degeneration in cell models of retinitis pigmentosa associated with pre-mRNA splicing factor mutations. Frontiers in Genetics, 0, 13, .	2.3	4
4780	Coping with harsh heat environments: molecular adaptation of metabolic depression in the intertidal snail Echinolittorina radiata. Cell Stress and Chaperones, 2023, 28, 477-491.	2.9	8
4781	Spatially resolved whole transcriptome profiling in human and mouse tissue using Digital Spatial Profiling. Genome Research, 0, , .	5.5	9
4782	Human PSCs determine the competency of cerebral organoid differentiation via FGF signaling and epigenetic mechanisms. IScience, 2022, 25, 105140.	4.1	3
4783	Dual assessment of transcriptional and metabolomic responses in the American dog tick following exposure to different pesticides and repellents. Ticks and Tick-borne Diseases, 2022, 13, 102033.	2.7	2
4784	Deciphering discriminative antibiotic resistance genes and pathogens in agricultural soil following chemical and organic fertilizer. Journal of Environmental Management, 2022, 322, 116110.	7.8	5
4785	Two R2R3-MYB transcription factors, CsMYB33 and CsMYB78 are involved in the regulation of anthocyanin biosynthesis in Cannabis sativa L.. Industrial Crops and Products, 2022, 188, 115546.	5.2	10
4786	Exposure to low-dose perfluorooctanoic acid promotes hepatic steatosis and disrupts the hepatic transcriptome in mice. Molecular Metabolism, 2022, 66, 101602.	6.5	21
4787	Land use intensification in a dry-hot valley reduced the constraints of water content on soil microbial diversity and multifunctionality but increased CO2 production. Science of the Total Environment, 2022, 852, 158397.	8.0	6
4788	De novo assembly and annotation of the transcriptome of the endangered seagrass Zostera capensis: Insights from differential gene expression under thermal stress. Marine Genomics, 2022, 66, 100984.	1.1	2
4789	Transcriptomics of a Greenlandic Snailfish Reveals Exceptionally High Expression of Antifreeze Protein Transcripts. Evolutionary Bioinformatics, 2022, 18, 117693432211183.	1.2	2
4790	Genomic Insights into Non-steroidal Nuclear Receptors in Prostate and Breast Cancer. Advances in Experimental Medicine and Biology, 2022, , 227-239.	1.6	2
4791	Early on-treatment transcriptional profiling as a tool for improving pathological response prediction in HER2-positive inflammatory breast cancer. Therapeutic Advances in Medical Oncology, 2022, 14, 175883592211132.	3.2	3
4792	Alpha-Methylacyl-CoA Racemase (AMACR) Protein is Upregulated in Early Proliferative Lesions of the Breast Irrespective of Apocrine Differentiation. SSRN Electronic Journal, 0, , .	0.4	0
4793	Developmental System Drift in One Tooth Facilitates the Adaptation of the Other. SSRN Electronic Journal, 0, , .	0.4	0
4794	Matrin3 Regulates Cell Proliferation and Spindle Dynamics via Alternative Splicing of CDC14B. SSRN Electronic Journal, 0, , .	0.4	0
4795	Comparative transcriptome analysis of different tissues of Rheum tanguticum Maxim. ex Balf. (Polygonaceae) reveals putative genes involved in anthraquinone biosynthesis. Genetics and Molecular Biology, 2022, 45, .	1.3	3

#	Article	IF	Citations
4796	Metagenomics, Microbial Diversity, and Environmental Cleanup. , 2022, , 47-72.		0
4797	Hepatic Glucagon Receptor Signaling Controls Amino Acid Metabolism and Regulates Alpha Cell Mass. SSRN Electronic Journal, 0, , .	0.4	0
4798	Metals Mixtures Modeling Identifies Birth Weight-Associated Gene Networks in the Placentas of Children Born Extremely Preterm. SSRN Electronic Journal, 0, , .	0.4	0
4799	Changes in resistome profile of potential probiotic Lactiplantibacillus pentosus in response to edible oil adaptation. Food Microbiology, 2023, 109, 104148.	4.2	4
4800	EventPointer 3.0: flexible and accurate splicing analysis that includes studying the differential usage of protein-domains. NAR Genomics and Bioinformatics, 2022, 4, .	3.2	2
4801	Integrated relationship of nasopharyngeal airway host response and microbiome associates with bronchiolitis severity. Nature Communications, 2022, 13, .	12.8	12
4802	auts2 Features and Expression Are Highly Conserved during Evolution Despite Different Evolutionary Fates Following Whole Genome Duplication. Cells, 2022, 11, 2694.	4.1	3
4803	Identification of Src Family Kinases as Potential Therapeutic Targets for Chemotherapy-Resistant Triple Negative Breast Cancer. Cancers, 2022, 14, 4220.	3.7	6
4804	Leveraging big data of immune checkpoint blockade response identifies novel potential targets. Annals of Oncology, 2022, 33, 1304-1317.	1.2	20
4805	Arid1a mutation suppresses TGF-Î² signaling and induces cholangiocarcinoma. Cell Reports, 2022, 40, 111253.	6.4	14
4806	Cellular and gene expression patterns associated with root bifurcation in Selaginella. Plant Physiology, 2022, 190, 2398-2416.	4.8	4
4807	Mapping of promoter usage QTL using RNA-seq data reveals their contributions to complex traits. PLoS Computational Biology, 2022, 18, e1010436.	3.2	2
4808	Analysis of Dormancy-Associated Transcriptional Networks Reveals a Shared Quiescence Signature in Lung and Colorectal Cancer. International Journal of Molecular Sciences, 2022, 23, 9869.	4.1	9
4809	Exploration and analysis of R-loop mapping data with RLBase. Nucleic Acids Research, 2023, 51, D1129-D1137.	14.5	1
4810	The placenta epigenomeâ€“brain axis: placental epigenomic and transcriptomic responses that preprogram cognitive impairment. Epigenomics, 2022, 14, 897-911.	2.1	8
4812	TROP2 Represents a Negative Prognostic Factor in Colorectal Adenocarcinoma and Its Expression Is Associated with Features of Epithelialâ€“Mesenchymal Transition and Invasiveness. Cancers, 2022, 14, 4137.	3.7	5
4813	Failure of human rhombic lip differentiation underlies medulloblastoma formation. Nature, 2022, 609, 1021-1028.	27.8	52
4817	Abnormal molecular signatures of inflammation, energy metabolism, and vesicle biology in human Huntington disease peripheral tissues. Genome Biology, 2022, 23, .	8.8	10

#	Article	IF	Citations
4818	Small molecule quercetin binds MALAT1 triplex and modulates its cellular function. Molecular Therapy - Nucleic Acids, 2022, 30, 241-256.	5.1	7
4819	Transcription and splicing regulation by NLRC5 shape the interferon response in human pancreatic Î² cells. Science Advances, 2022, 8, .	10.3	9
4821	Genome-wide analysis identifies Homothorax and Extradenticle as regulators of insulin in Drosophila Insulin-Producing cells. PLoS Genetics, 2022, 18, e1010380.	3.5	0
4822	NUDT21 limits CD19 levels through alternative mRNA polyadenylation in B cell acute lymphoblastic leukemia. Nature Immunology, 2022, 23, 1424-1432.	14.5	14
4823	Virtual screening for small-molecule pathway regulators by image-profile matching. Cell Systems, 2022, 13, 724-736.e9.	6.2	18
4824	Identification of the Thyrotropin-Releasing Hormone (TRH) as a Novel Biomarker in the Prognosis for Acute Myeloid Leukemia. Biomolecules, 2022, 12, 1359.	4.0	3
4825	A recessive mutation in muscadine grapes causes berry color-loss without influencing anthocyanin pathway. Communications Biology, 2022, 5, .	4.4	5
4826	Weakly activated core neuroinflammation pathways were identified as a central signaling mechanism contributing to the chronic neurodegeneration in Alzheimerâ€™s disease. Frontiers in Aging Neuroscience, 0, 14, .	3.4	7
4827	Strain-specific impacts of probiotics are a significant driver of gut microbiome development in very preterm infants. Nature Microbiology, 2022, 7, 1525-1535.	13.3	48
4828	De novo metatranscriptomic exploration of gene function in the millipede holobiont. Scientific Reports, 2022, 12, .	3.3	4
4829	Understanding the Function and Mechanism of Zebrafish Tmem39b in Regulating Cold Resistance. International Journal of Molecular Sciences, 2022, 23, 11442.	4.1	6
4830	HMGN5 Escorts Oncogenic STAT3 Signaling by Regulating the Chromatin Landscape in Breast Cancer Tumorigenesis. Molecular Cancer Research, 2022, 20, 1724-1738.	3.4	1
4831	Cell-type profiling in salamanders identifies innovations in vertebrate forebrain evolution. Science, 2022, 377, .	12.6	38
4833	A glycan-based approach to cell characterization and isolation: Hematopoiesis as a paradigm. Journal of Experimental Medicine, 2022, 219, .	8.5	1
4836	Comparison of Intracellular Transcriptional Response of NHBE Cells to Infection with SARS-CoV-2 Washington and New York Strains. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	2
4837	Comparative transcriptome analysis of leaves of sour jujube seedlings under salt stress. Acta Physiologiae Plantarum, 2022, 44, .	2.1	2
4838	Trace Element Interactions, Inflammatory Signaling, and Male Sex Implicated in Reduced Growth Following Excess Oral Iron Supplementation in Pre-Weanling Rats. Nutrients, 2022, 14, 3913.	4.1	1
4839	Dissecting the role of the human microbiome in COVID-19 via metagenome-assembled genomes. Nature Communications, 2022, 13, .	12.8	24

#	Article	IF	Citations
4840	Role of LGR5-positive mesenchymal cells in craniofacial development. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	2
4842	Detailed Analysis of Dorsal-Ventral Gradients of Gene Expression in the Hippocampus of Adult Rats. International Journal of Molecular Sciences, 2022, 23, 9948.	4.1	3
4843	Time-course RNA-seq analysis provides an improved understanding of genetic regulation in response to cold stress from white clover (Trifolium repens L.). Biotechnology and Biotechnological Equipment, 2022, 36, 745-752.	1.3	6
4845	Metatranscriptomic holobiont analysis of carbohydrate-active enzymes in the millipede Telodeinopus aoutii (Diplopoda, Spirostreptida). Frontiers in Ecology and Evolution, 0, 10, .	2.2	8
4846	Evidence for Assimilatory Nitrate Reduction as a Previously Overlooked Pathway of Reactive Nitrogen Transformation in Estuarine Suspended Particulate Matter. Environmental Science & Technology, 2022, 56, 14852-14866.	10.0	16
4847	Acute frataxin knockdown in induced pluripotent stem cell-derived cardiomyocytes activates a type I interferon response. DMM Disease Models and Mechanisms, 2023, 16, .	2.4	7
4848	Differential Gene Expression Correlates with Behavioural Polymorphism during Collective Behaviour in Cockroaches. Animals, 2022, 12, 2354.	2.3	0
4851	Hepatic Deletion of X-Box Binding Protein 1 in FXR Null Mice Leads to Enhanced Liver Injury. Journal of Lipid Research, 2022, 63, 100289.	4.2	2
4852	A mechanism for oxidative damage repair at gene regulatory elements. Nature, 2022, 609, 1038-1047.	27.8	12
4853	Evaluation of pathways to the C â€glycosyl isoflavone puerarin in roots of kudzu ( ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.9	4
4854	Transcriptomic clustering of critically ill COVID-19 patients. European Respiratory Journal, 2023, 61, 2200592.	6.7	8
4856	Heterologous reporter expression in the planarian Schmidtea mediterranea through somatic mRNA transfection. Cell Reports Methods, 2022, 2, 100298.	2.9	5
4857	Plant mitochondrial RNA editing factors can perform targeted C-to-U editing of nuclear transcripts in human cells. Nucleic Acids Research, 2022, 50, 9966-9983.	14.5	13
4858	De novo transcriptome analysis of Justicia adhatoda reveals candidate genes involved in major biosynthetic pathway. Molecular Biology Reports, 2022, 49, 10307-10314.	2.3	4
4859	MarpolBase Expression: A Web-Based, Comprehensive Platform for Visualization and Analysis of Transcriptomes in the Liverwort Marchantia polymorpha. Plant and Cell Physiology, 2022, 63, 1745-1755.	3.1	17
4861	Larvae of a marine gastropod and a marine bivalve share common gene expression signatures during metamorphic competence. Marine Biology, 2022, 169, .	1.5	1
4862	Antigens Expressed by Breast Cancer Cells Undergoing EMT Stimulate Cytotoxic CD8+ T Cell Immunity. Cancers, 2022, 14, 4397.	3.7	2
4864	Integrated analysis of multi-omics and fine-mapping reveals a candidate gene regulating pericarp color and flavonoids accumulation in wax gourd (Benincasa hispida). Frontiers in Plant Science, 0, 13, .	3.6	4

#	Article	IF	Citations
4865	ER stress transforms random olfactory receptor choice into axon targeting precision. Cell, 2022, 185, 3896-3912.e22.	28.9	15
4866	Interference and co-existence of staphylococci and Cutibacterium acnes within the healthy human skin microbiome. Communications Biology, 2022, 5, .	4.4	14
4867	Formal Meta-Analysis of Hypoxic Gene Expression Profiles Reveals a Universal Gene Signature. Biomedicines, 2022, 10, 2229.	3.2	1
4868	Meta-Analysis of Transcriptomes in Insects Showing Density-Dependent Polyphenism. Insects, 2022, 13, 864.	2.2	3
4870	HTCA: a database with an in-depth characterization of the single-cell human transcriptome. Nucleic Acids Research, 2023, 51, D1019-D1028.	14.5	11
4871	Comprehensive and scalable quantification of splicing differences with MntJULiP. Genome Biology, 2022, 23, .	8.8	1
4872	Sex differences in susceptibility to influenza A virus infection depend on host genotype. PLoS ONE, 2022, 17, e0273050.	2.5	4
4873	Genome-wide analysis of the WRKY gene family unveil evolutionary history and expression characteristics in tomato and its wild relatives. Frontiers in Genetics, 0, 13, .	2.3	5
4875	Balance between immunoregulatory B cells and plasma cells drives pancreatic tumor immunity. Cell Reports Medicine, 2022, 3, 100744.	6.5	20
4876	Bioinformatics in bioscience and bioengineering: Recent advances, applications, and perspectives. Journal of Bioscience and Bioengineering, 2022, 134, 363-373.	2.2	14
4878	CDK11 regulates pre-mRNA splicing by phosphorylation of SF3B1. Nature, 2022, 609, 829-834.	27.8	22
4879	Gut Microbiomeâ€“Wide Search for Bacterial Azoreductases Reveals Potentially Uncharacterized Azoreductases Encoded in the Human Gut Microbiome. Drug Metabolism and Disposition, 2023, 51, 142-153.	3.3	2
4880	Hepatic damage caused by long-term high cholesterol intake induces a dysfunctional restorative macrophage population in experimental NASH. Frontiers in Immunology, 0, 13, .	4.8	6
4881	Identification of candidate MYB transcription factors that influence CslF6 expression in barley grain. Frontiers in Plant Science, 0, 13, .	3.6	5
4882	ACTN2 Mutant Causes Proteopathy in Human iPSC-Derived Cardiomyocytes. Cells, 2022, 11, 2745.	4.1	10
4883	Oncohistone interactome profiling uncovers contrasting oncogenic mechanisms and identifies potential therapeutic targets in high grade glioma. Acta Neuropathologica, 2022, 144, 1027-1048.	7.7	10
4884	BAF60c prevents abdominal aortic aneurysm formation through epigenetic control of vascular smooth muscle cell homeostasis. Journal of Clinical Investigation, 2022, 132, .	8.2	10
4888	Small and long RNA transcriptome of whole human cerebrospinal fluid and serum as compared to their extracellular vesicle fractions reveal profound differences in expression patterns and impacts on biological processes. Journal of Translational Medicine, 2022, 20, .	4.4	0

#	Article	IF	Citations
4889	Genome assembly and chemogenomic profiling of National Flower of Singapore Papilionanthe Miss Joaquim â€˜Agnesâ€™ reveals metabolic pathways regulating floral traits. Communications Biology, 2022, 5, .	4.4	2
4890	Hypoxia inducible factors regulate infectious SARS-CoV-2, epithelial damage and respiratory symptoms in a hamster COVID-19 model. PLoS Pathogens, 2022, 18, e1010807.	4.7	15
4891	Islet primary cilia motility controls insulin secretion. Science Advances, 2022, 8, .	10.3	23
4892	Group 3 innate lymphoid cells require BATF to regulate gut homeostasis in mice. Journal of Experimental Medicine, 2022, 219, .	8.5	12
4893	Siponimod ameliorates metabolic oligodendrocyte injury via the sphingosine-1 phosphate receptor 5. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	9
4895	HLA allele-specific expression: Methods, disease associations, and relevance in hematopoietic stem cell transplantation. Frontiers in Immunology, 0, 13, .	4.8	4
4896	Histone H1 regulates non-coding RNA turnover on chromatin in a m6A-dependent manner. Cell Reports, 2022, 40, 111329.	6.4	5
4897	High-quality reference transcriptome construction improves RNA-seq quantification in Oryza sativa indica. Frontiers in Genetics, 0, 13, .	2.3	0
4898	The roles of divergent and parallel molecular evolution contributing to thermal adaptive strategies in trees. Plant, Cell and Environment, 0, , .	5.7	1
4900	Improved Bladder Tumor RNA Isolation from Archived Tissues Using Methylene Blue for Normalization, Multiplex RNA Hybridization, Sequencing and Subtyping. International Journal of Molecular Sciences, 2022, 23, 10267.	4.1	1
4901	Evidence for evolutionary adaptation of mixotrophic nanoflagellates to warmer temperatures. Global Change Biology, 2022, 28, 7094-7107.	9.5	9
4903	Normalized Workflow to Optimize Hybrid De Novo Transcriptome Assembly for Non-Model Species: A Case Study in Lilium ledebourii (Baker) Boiss. Plants, 2022, 11, 2365.	3.5	3
4905	Postnatal age-differential ASD-like transcriptomic, synaptic, and behavioral deficits in Myt1l-mutant mice. Cell Reports, 2022, 40, 111398.	6.4	9
4906	Molecular characterization of ESR1 variants in breast cancer. Breast Cancer Research and Treatment, 2022, 196, 279-289.	2.5	4
4907	Human Stem Cell-Derived TRPV1-Positive Sensory Neurons: A New Tool to Study Mechanisms of Sensitization. Cells, 2022, 11, 2905.	4.1	4
4909	CTCF acetylation at lysine 20 is required for the early cardiac mesoderm differentiation of embryonic stem cells. Cell Regeneration, 2022, 11, .	2.6	1
4910	Malnourishment affects gene expression along the length of the small intestine. Frontiers in Nutrition, 0, 9, .	3.7	1
4911	Phenotypic impacts and genetic regulation characteristics of the DNA adenine methylase gene (dam) in Salmonella Typhimurium biofilm forms. Research in Microbiology, 2023, 174, 103991.	2.1	1

#	Article	IF	Citations
4912	What Do the Transcriptome and Proteome of Menstrual Blood-Derived Mesenchymal Stem Cells Tell Us about Endometriosis?. International Journal of Molecular Sciences, 2022, 23, 11515.	4.1	5
4913	Targeting dual oncogenic machineries driven by TAL1 and PI3K-AKT pathways in T-cell acute lymphoblastic leukemia. Haematologica, 2023, 108, 367-381.	3.5	1
4914	Tumor suppressor role of RBM22 in prostate cancer acting as a dual-factor regulating alternative splicing and transcription of key oncogenic genes. Translational Research, 2022, , .	5.0	0
4915	Multi-omics analysis reveals the hostâ€“microbe interactions in aged rhesus macaques. Frontiers in Microbiology, 0, 13, .	3.5	4
4916	Differential transcriptomic responses to heat stress in surface and subterranean diving beetles. Scientific Reports, 2022, 12, .	3.3	6
4917	A nuclear cAMP microdomain suppresses tumor growth by Hippo pathway inactivation. Cell Reports, 2022, 40, 111412.	6.4	3
4918	Positive resolution of the wound-healing response in lens epithelial cells by Ti₃C₂T _x MXene coatings for use in accommodative intraocular lens devices. 2D Materials, 0, , .	4.4	2
4919	<scp>MtING2</scp> encodes an <scp>ING</scp> domain <scp>PHD</scp> finger protein which affects Medicago growth, flowering, global patterns of <scp>H3K4me3</scp>, and gene expression. Plant Journal, 2022, 112, 1029-1050.	5.7	3
4921	Functional integration of a semi-synthetic azido-queuosine derivative into translation and a tRNA modification circuit. Nucleic Acids Research, 2022, 50, 10785-10800.	14.5	6
4922	Intestinal microbiome-mediated resistance against vibriosis for Cynoglossus semilaevis. Microbiome, 2022, 10, .	11.1	13
4924	Progeria and Agingâ€”Omics Based Comparative Analysis. Biomedicines, 2022, 10, 2440.	3.2	3
4926	Borrelia burgdorferi, the Lyme disease spirochete, possesses genetically-encoded responses to doxycycline, but not to amoxicillin. PLoS ONE, 2022, 17, e0274125.	2.5	0
4927	The northern corn leaf blight resistance gene Ht1 encodes an nucleotideâ€binding, leucineâ€rich repeat immune receptor. Molecular Plant Pathology, 2023, 24, 758-767.	4.2	4
4928	Dynamic Transcriptional Landscape of Grass Carp (Ctenopharyngodon idella) Reveals Key Transcriptional Features Involved in Fish Development. International Journal of Molecular Sciences, 2022, 23, 11547.	4.1	2
4929	Transmission of the gut microbiome in cohousing goats and pigs. Frontiers in Microbiology, 0, 13, .	3.5	1
4931	Wolbachia manipulates reproduction of spider mites by influencing herbivore salivary proteins. Pest Management Science, 2023, 79, 315-323.	3.4	3
4932	Genome-wide identification, characterization, and functional analysis of lncRNAs in Hevea brasiliensis. Frontiers in Plant Science, 0, 13, .	3.6	2
4933	Genome assembly and annotation of Periplaneta americana reveal a comprehensive cockroach allergen profile. Allergy: European Journal of Allergy and Clinical Immunology, 2023, 78, 1088-1103.	5.7	8

#	Article	IF	Citations
4934	PIDDosome-SCAP crosstalk controls high-fructose-diet-dependent transition from simple steatosis to steatohepatitis. Cell Metabolism, 2022, 34, 1548-1560.e6.	16.2	13
4935	Understanding of mercury and methylmercury transformation in sludge composting by metagenomic analysis. Water Research, 2022, 226, 119204.	11.3	7
4936	iBench: A ground truth approach for advanced validation of mass spectrometry identification method. Proteomics, 2023, 23, .	2.2	6
4937	Characterization of the chicken melanocortin 5 receptor and its potential role in regulating hepatic glucolipid metabolism. Frontiers in Physiology, 0, 13, .	2.8	3
4938	Expanding the Prostate Cancer Cell Line Repertoire with ACRJ-PC28, an AR-negative Neuroendocrine Cell Line Derived From an African-Caribbean Patient. Cancer Research Communications, 2022, 2, 1355-1371.	1.7	1
4939	The global Protein-RNA interaction map of ESRP1 defines a post-transcriptional program that is essential for epithelial cell function. IScience, 2022, 25, 105205.	4.1	3
4940	Deeper insights into transcriptional features of cancer-associated fibroblasts: An integrated meta-analysis of single-cell and bulk RNA-sequencing data. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	1
4941	Species-specific transcriptomic changes upon respiratory syncytial virus infection in cotton rats. Scientific Reports, 2022, 12, .	3.3	2
4943	Differences in stromal component of chordoma are associated with contrast enhancement in MRI and differential gene expression in RNA sequencing. Scientific Reports, 2022, 12, .	3.3	1
4944	To stripe or not to stripe: the origin of a novel foliar pigmentation pattern in monkeyflowers (Mimulus). New Phytologist, 2023, 237, 310-322.	7.3	5
4945	Genome engineering for estrogen receptor mutations reveals differential responses to anti-estrogens and new prognostic gene signatures for breast cancer. Oncogene, 2022, 41, 4905-4915.	5.9	9
4946	Mating strategy predicts gene presence/absence patterns in a genus of simultaneously hermaphroditic flatworms. Evolution; International Journal of Organic Evolution, 0, , .	2.3	1
4948	Opposing effects of chronic glucagon receptor agonism and antagonism on amino acids, hepatic gene expression, and alpha cells. IScience, 2022, 25, 105296.	4.1	10
4950	Single-cell dissection of the obesity-exercise axis in adipose-muscle tissues implies a critical role for mesenchymal stem cells. Cell Metabolism, 2022, 34, 1578-1593.e6.	16.2	35
4951	The contribution of sex chromosome conflict to disrupted spermatogenesis in hybrid house mice. Genetics, 2022, 222, .	2.9	2
4952	Comparative meta-analysis of host transcriptional response during Streptococcus pneumoniae carriage or infection. Microbial Pathogenesis, 2022, 173, 105816.	2.9	1
4953	Activation function 1 of progesterone receptor is required for progesterone antagonism of oestrogen action in the uterus. BMC Biology, 2022, 20, .	3.8	4
4955	Colicins of Escherichia coli Lead to Resistance against the Diarrhea-Causing Pathogen Enterotoxigenic E. coli in Pigs. Microbiology Spectrum, 0, , .	3.0	3

#	Article	IF	Citations
4956	The lncRNA ALPHA specifically targets chikungunya virus to control infection. Molecular Cell, 2022, 82, 3729-3744.e10.	9.7	6
4957	DUX4 expression activates JNK and p38 MAP kinases in myoblasts. DMM Disease Models and Mechanisms, 2022, 15, .	2.4	7
4958	Comparative oncology reveals DNMT3B as a molecular vulnerability in undifferentiated pleomorphic sarcoma. Cellular Oncology (Dordrecht), 2022, 45, 1277-1295.	4.4	1
4959	Identifying the genes impacted by cell proliferation in proteomics and transcriptomics studies. PLoS Computational Biology, 2022, 18, e1010604.	3.2	3
4960	The Vinca minor genome highlights conserved evolutionary traits in monoterpene indole alkaloid synthesis. G3: Genes, Genomes, Genetics, 0, , .	1.8	5
4962	Viruses direct carbon cycling in lake sediments under global change. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	8
4963	Cross-lineage potential of Ascl1 uncovered by comparing diverse reprogramming regulatomes. Cell Stem Cell, 2022, 29, 1491-1504.e9.	11.1	19
4964	SMAD2/3 mediate oncogenic effects of TGF-Î² in the absence of SMAD4. Communications Biology, 2022, 5, .	4.4	13
4966	A novel testis-enriched gene, Samd4a, regulates spermatogenesis as a spermatid-specific factor. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	1
4968	Exposure to 17Î±-Ethinylestradiol Results in Differential Susceptibility of Largemouth Bass (Micropterus salmoides) to Bacterial Infection. Environmental Science & Technology, 2022, 56, 14375-14386.	10.0	3
4969	Transcriptomic analysis of paternal behaviors in prairie voles. BMC Genomics, 2022, 23, .	2.8	2
4970	Short-term transcriptomic changes in the mouse neural tube induced by an acute alcohol exposure. Alcohol, 2023, 106, 1-9.	1.7	1
4972	A MYC-ZNF148-ID1/3 regulatory axis modulating cancer stem cell traits in aggressive breast cancer. Oncogenesis, 2022, 11, .	4.9	5
4973	Transcriptomic and genomic profiling revealed the unique cellular response mechanism involved in arsenite stress in Thermus tengchongensis. International Biodeterioration and Biodegradation, 2022, 175, 105504.	3.9	1
4974	Single-cell transcriptomics of peripheral blood reveals anti-tumor systemic immunity induced by oncolytic virotherapy. Theranostics, 2022, 12, 7371-7389.	10.0	4
4975	Joint Secondary Transcriptomic Analysis of Non-Hodgkinâ€™s B-Cell Lymphomas Predicts Reliance on Pathways Associated with the Extracellular Matrix and Robust Diagnostic Biomarkers. Journal of Bioinformatics and Systems Biology, 2022, 05, .	0.3	4
4976	Med1 Controls Effector CD8+ T Cell Differentiation and Survival through C/EBPÎ²-Mediated Transcriptional Control of T-bet. Journal of Immunology, 2022, 209, 855-863.	0.8	2
4977	Dissecting super-enhancer driven transcriptional dependencies reveals novel therapeutic strategies and targets for group 3 subtype medulloblastoma. Journal of Experimental and Clinical Cancer Research, 2022, 41, .	8.6	5

#	Article	IF	Citations
4978	Up-regulation of the PI3K/AKT and RHO/RAC/PAK signalling pathways in CHK1 inhibitor resistant EÂµ-Myc lymphoma cells. Biochemical Journal, 2022, 479, 2131-2151.	3.7	4
4979	Mutation of the RelA(p65) Thr505 phosphosite disrupts the DNA replication stress response leading to CHK1 inhibitor resistance. Biochemical Journal, 2022, 479, 2087-2113.	3.7	8
4980	MetaGT: A pipeline for de novo assembly of metatranscriptomes with the aid of metagenomic data. Frontiers in Microbiology, 0, 13, .	3.5	1
4982	Differential expression and roles of Huntingtin and Huntingtin-associated protein 1 in the mouse and primate brains. Cellular and Molecular Life Sciences, 2022, 79, .	5.4	3
4984	Cellular shape reinforces niche to stem cell signaling in the small intestine. Science Advances, 2022, 8, .	10.3	12
4985	Symbiont specificity differs among green hydra strains. Royal Society Open Science, 2022, 9, .	2.4	1
4986	The Role of the Environment in Horizontal Gene Transfer. Molecular Biology and Evolution, 2022, 39, .	8.9	7
4987	Long-term effects of early postnatal stress on Sertoli cells. Frontiers in Genetics, 0, 13, .	2.3	2
4988	High-resolution ribosome profiling reveals translational selectivity for transcripts in bovine preimplantation embryo development. Development (Cambridge), 0, , .	2.5	3
4989	Cistanche tubulosa phenylethanoid glycosides suppressed adipogenesis inâ€‚3T3-L1â€‚adipocytesâ€‚and improved obesity and insulin resistance in high-fat diet induced obese mice. BMC Complementary Medicine and Therapies, 2022, 22, .	2.7	5
4992	Genome Assembly of the Medicinal Plant Voacanga thouarsii. Genome Biology and Evolution, 2022, 14, .	2.5	4
4994	Gut microbiome dysbiosis contributes to abdominal aortic aneurysm by promoting neutrophil extracellular trap formation. Cell Host and Microbe, 2022, 30, 1450-1463.e8.	11.0	59
4995	A FOXO1-dependent transcription network is a targetable vulnerability of mantle cell lymphomas. Journal of Clinical Investigation, 2022, 132, .	8.2	8
4996	Sexual dimorphism of early transcriptional reprogramming in degenerating peripheral nerves. Frontiers in Molecular Neuroscience, 0, 15, .	2.9	1
4997	USP7 substrates identified by proteomics analysis reveal the specificity of USP7. Genes and Development, 0, , .	5.9	2
4998	A Molecular Switch between Mammalian MLL Complexes Dictates Response to Meninâ€“MLL Inhibition. Cancer Discovery, 2023, 13, 146-169.	9.4	12
5000	Pre-treatment differential correlation of gene expression and response to topical steroids in eosinophilic esophagitis. Ecological Management and Restoration, 2023, 36, .	0.4	3
5002	Rencofilstat, a cyclophilin inhibitor: A phase 2a, multicenter, singleâ€blind, placeboâ€controlled study in F2/F3 NASH. Hepatology Communications, 2022, 6, 3379-3392.	4.3	9

#	Article	IF	Citations
5003	Age, brain region, and gene dosage-differential transcriptomic changes in Shank3-mutant mice. Frontiers in Molecular Neuroscience, 0, 15, .	2.9	9
5005	Brain region and gene dosage-differential transcriptomic changes in Shank2-mutant mice. Frontiers in Molecular Neuroscience, 0, 15, .	2.9	3
5006	Identifying Candidate Circulating RNA Markers for Coronary Artery Disease by Deep RNA-Sequencing in Human Plasma. Cells, 2022, 11, 3191.	4.1	6
5008	Regulation of CHK1 inhibitor resistance by a c-Rel and USP1 dependent pathway. Biochemical Journal, 2022, 479, 2063-2086.	3.7	7
5012	Establishing Physalis as a Solanaceae model system enables genetic reevaluation of the inflated calyx syndrome. Plant Cell, 2023, 35, 351-368.	6.6	7
5015	Regulatory network of ginsenoside biosynthesis under Ro stress in the hairy roots of Panax ginseng revealed by RNA sequencing. Frontiers in Bioengineering and Biotechnology, 0, 10, .	4.1	4
5016	Host genetic factors related to innate immunity, environmental sensing and cellular functions are associated with human skin microbiota. Nature Communications, 2022, 13, .	12.8	10
5018	Improving RNA Assembly via Safety and Completeness in Flow Decompositions. Journal of Computational Biology, 2022, 29, 1270-1287.	1.6	6
5019	Machine learning on syngeneic mouse tumor profiles to model clinical immunotherapy response. Science Advances, 2022, 8, .	10.3	6
5021	Relevance of Abnormal KCNN1 Expression and Osmotic Hypersensitivity in Ewing Sarcoma. Cancers, 2022, 14, 4819.	3.7	4
5022	<scp>AabHLH113</scp> integrates jasmonic acid and abscisic acid signaling to positively regulate artemisinin biosynthesis in Artemisia annua. New Phytologist, 2023, 237, 885-899.	7.3	10
5023	Recent reconfiguration of an ancient developmental gene regulatory network in Heliocidaris sea urchins. Nature Ecology and Evolution, 2022, 6, 1907-1920.	7.8	12
5024	Microbial diversity and biogeochemical cycling potential in deep-sea sediments associated with seamount, trench, and cold seep ecosystems. Frontiers in Microbiology, 0, 13, .	3.5	1
5025	Analyses of adult transcriptomes from four different populations of the spongy moth, Lymantria dispar L., from China and the USA. Scientific Reports, 2022, 12, .	3.3	2
5026	Metagenomic Analysis of Gut Microbiome in Gout Patients with Different Chinese Traditional Medicine Treatments. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-12.	1.2	1
5027	Metabolic, fibrotic and splicing pathways are all altered in Emery-Dreifuss muscular dystrophy spectrum patients to differing degrees. Human Molecular Genetics, 2023, 32, 1010-1031.	2.9	1
5028	Non-heme iron overload impairs monocyte to macrophage differentiation via mitochondrial oxidative stress. Frontiers in Immunology, 0, 13, .	4.8	3
5029	Metformin Treatment Modulates Long Non-Coding RNA Isoforms Expression in Human Cells. Non-coding RNA, 2022, 8, 68.	2.6	4

#	Article	IF	Citations
5031	Antiviral function and viral antagonism of the rapidly evolving dynein activating adaptor NINL. ELife, 0, 11, .	6.0	6
5032	Two type I topoisomerases maintain DNA topology in human mitochondria. Nucleic Acids Research, 2022, 50, 11154-11174.	14.5	7
5033	Transcriptional responses of hypericin and hyperforin to methyl jasmonate elicitation in Hypericum perforatum. Plant Biotechnology Reports, 0, , .	1.5	0
5034	Identification of the genes at S and Z reveals the molecular basis and evolution of grass self-incompatibility. Frontiers in Plant Science, 0, 13, .	3.6	2
5035	Towards localizing head shots â€“ Forensic sub-differentiation of anatomical brain regions by differential RNA expression. Forensic Science International: Genetics Supplement Series, 2022, , .	0.3	0
5038	Deoxygenation lowers the thermal threshold of coral bleaching. Scientific Reports, 2022, 12, .	3.3	16
5040	Elucidation of Functional Genes Associated with Long Chain-Polyunsaturated Fatty Acids (LC-PUFAs) Metabolism in Oleaginous Diatom Phaeodactylum tricornutum. Hydrobiology, 2022, 1, 451-468.	1.7	2
5041	A local tumor microenvironment acquired super-enhancer induces an oncogenic driver in colorectal carcinoma. Nature Communications, 2022, 13, .	12.8	9
5042	Role of Staphylococcus aureus Formate Metabolism during Prosthetic Joint Infection. Infection and Immunity, 2022, 90, .	2.2	11
5043	A cryptic transactivation domain of EZH2 binds AR and ARâ€™s splice variant, promoting oncogene activation and tumorous transformation. Nucleic Acids Research, 2022, 50, 10929-10946.	14.5	12
5045	Astrocytic Yin Yang 1 is critical for murine brain development and protection against apoptosis, oxidative stress, and inflammation. Glia, 2023, 71, 450-466.	4.9	8
5046	Unpacking COVID-19 Systems Biology in Lung and Whole Blood with Transcriptomics and miRNA Regulators. OMICS A Journal of Integrative Biology, 2022, 26, 608-621.	2.0	1
5048	Fine mapping and identification of candidate genes for the hull-less seed phenotype in Cucurbita pepo. Euphytica, 2022, 218, .	1.2	0
5049	Capacity of deepâ€sea corals to obtain nutrition from cold seeps aligned with microbiome reorganization. Global Change Biology, 2023, 29, 189-205.	9.5	4
5050	ESRP1-regulated isoform switching of LRRFIP2 determines metastasis of gastric cancer. Nature Communications, 2022, 13, .	12.8	13
5051	Profiling subcellular localization of nuclear-encoded mitochondrial gene products in zebrafish. Life Science Alliance, 2023, 6, e202201514.	2.8	2
5052	Human PRPF39 is an alternative splicing factor recruiting U1 snRNP to weak 5â€² splice sites. Rna, 2023, 29, 97-110.	3.5	5
5054	Integrated Metabolite and Transcriptome Profiling-Mediated Gene Mining of Sida cordifolia Reveals Medicinally Important Genes. Genes, 2022, 13, 1909.	2.4	1

#	Article	IF	Citations
5056	Tumor microbiome links cellular programs and immunity in pancreatic cancer. Cancer Cell, 2022, 40, 1240-1253.e5.	16.8	44
5057	The N6-methyladenosine methyltransferase METTL16 enables erythropoiesis through safeguarding genome integrity. Nature Communications, 2022, 13, .	12.8	13
5058	Variation in plant Toll/Interleukin-1 receptor domain protein dependence on ENHANCED DISEASE SUSCEPTIBILITY 1. Plant Physiology, 2023, 191, 626-642.	4.8	19
5059	A universal model of RNA.DNA:DNA triplex formation accurately predicts genome-wide RNAâ€“DNA interactions. Briefings in Bioinformatics, 2022, 23, .	6.5	6
5060	Epstein Barr virus-mediated transformation of B cells from XIAP-deficient patients leads to increased expression of the tumor suppressor CADM1. Cell Death and Disease, 2022, 13, .	6.3	2
5061	Splicing factor BUD31 promotes ovarian cancer progression through sustaining the expression of anti-apoptotic BCL2L12. Nature Communications, 2022, 13, .	12.8	8
5063	Shared Patterns of Gene Expression and Protein Evolution Associated with Adaptation to Desert Environments in Rodents. Genome Biology and Evolution, 2022, 14, .	2.5	3
5065	A Multi-Center Clinical Study to Harvest and Characterize Circulating Tumor Cells from Patients with Metastatic Breast Cancer Using the ParsortixÂ® PC1 System. Cancers, 2022, 14, 5238.	3.7	16
5066	Druggable transcriptomic pathways revealed in Parkinsonâ€™s patient-derived midbrain neurons. Npj Parkinson's Disease, 2022, 8, .	5.3	9
5067	Identifying the Transcriptional Drivers of Metastasis Embedded within Localized Melanoma. Cancer Discovery, 2023, 13, 194-215.	9.4	5
5068	Identification of DAPK1 as an autophagy-related biomarker for myotonic dystrophy type 1. Frontiers in Genetics, 0, 13, .	2.3	0
5069	A Case Series Exploration of Multi-Regional Expression Heterogeneity in Triple-Negative Breast Cancer Patients. International Journal of Molecular Sciences, 2022, 23, 13322.	4.1	2
5071	CRISPR-mediated correction of skeletal muscle Ca2+ handling in a novel DMD patient-derived pluripotent stem cell model. Neuromuscular Disorders, 2022, , .	0.6	1
5073	A chromosome-level phased genome enabling allele-level studies in sweet orange: a case study on citrus Huanglongbing tolerance. Horticulture Research, 2023, 10, .	6.3	6
5074	Temporal analysis suggests a reciprocal relationship between 3D chromatin structure and transcription. Cell Reports, 2022, 41, 111567.	6.4	19
5075	Behavioral and transcriptomic changes in butenolide treated larvae of the cosmopolitan fouling bryozoan Bugulina (Bugula) neritina. Frontiers in Marine Science, 0, 9, .	2.5	0
5076	The epigenetic state of IL-4-polarized macrophages enables inflammatory cistromic expansion and extended synergistic response to TLR ligands. Immunity, 2022, 55, 2006-2026.e6.	14.3	14
5077	iPSCs derived from esophageal atresia patients reveal SOX2 dysregulation at the anterior foregut stage. DMM Disease Models and Mechanisms, 2022, 15, .	2.4	1

#	Article	IF	Citations
5079	Allele-specific expression reveals functional SNPs affecting muscle-related genes in bovine. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, 1865, 194886.	1.9	2
5080	Unraveling potential enzymes and their functional role in fine cocoa beans fermentation using temporal shotgun metagenomics. Frontiers in Microbiology, 0, 13, .	3.5	1
5081	Tumor-intrinsic SIRPA promotes sensitivity to checkpoint inhibition immunotherapy in melanoma. Cancer Cell, 2022, 40, 1324-1340.e8.	16.8	11
5082	MYC promotes immune-suppression in triple-negative breast cancer via inhibition of interferon signaling. Nature Communications, 2022, 13, .	12.8	30
5083	Mining the transcriptome of target tissues of autoimmune and degenerative pancreatic Î²-cell and brain diseases to discover therapies. IScience, 2022, 25, 105376.	4.1	2
5084	Analysis of the caudate nucleus transcriptome in individuals with schizophrenia highlights effects of antipsychotics and new risk genes. Nature Neuroscience, 2022, 25, 1559-1568.	14.8	19
5085	Metatranscriptomics reveals contrasting effects of elevation on the activity of bacteria and bacterial viruses in soil. Molecular Ecology, 2023, 32, 6552-6563.	3.9	5
5086	The snoRNA-like lncRNA LNC-SNO49AB drives leukemia by activating the RNA-editing enzyme ADAR1. Cell Discovery, 2022, 8, .	6.7	11
5087	Variation in immuno-reproductive milieu of testis in Clarias magur from pre-spawning to spawning phase: An indication towards non-canonical role of immune elements in testes. Journal of Reproductive Immunology, 2022, 154, 103757.	1.9	0
5088	Omics insights into spermatozoa activation induced by Fetal bovine serum in viviparous black rockfish (Sebastes schlegelii). Gene, 2023, 851, 147014.	2.2	1
5089	Transcriptomic analysis of genes: expression and regulation. , 2023, , 1-41.		1
5090	Transcriptome responses to salt stress in roots and leaves of Lilium pumilum. Scientia Horticulturae, 2023, 309, 111622.	3.6	5
5091	Metagenomics insights into the effects of lactic acid bacteria inoculation on the biological reduction of antibiotic resistance genes in alfalfa silage. Journal of Hazardous Materials, 2023, 443, 130329.	12.4	6
5092	Type I interferon receptor (IFNAR2) deficiency reveals Zika virus cytopathicity in human macrophages and microglia. Frontiers in Immunology, 0, 13, .	4.8	1
5094	Inflammatory Non-CpG Antisense Oligonucleotides Are Signaling Through TLR9 in Human Burkitt Lymphoma B Bjab Cells. Nucleic Acid Therapeutics, 2022, 32, 473-485.	3.6	4
5095	The seeker R package: simplified fetching and processing of transcriptome data. PeerJ, 0, 10, e14372.	2.0	2
5096	Deficiency for SAMHD1 activates MDA5 in a cGAS/STING-dependent manner. Journal of Experimental Medicine, 2023, 220, .	8.5	11
5097	Lineage abundance estimation for SARS-CoV-2 in wastewater using transcriptome quantification techniques. Genome Biology, 2022, 23, .	8.8	20

#	Article	IF	Citations
5098	Loss of the Nuclear Envelope Protein LAP1B Disrupts the Myogenic Differentiation of Patient-Derived Fibroblasts. International Journal of Molecular Sciences, 2022, 23, 13615.	4.1	3
5099	Clinical characteristics of the host DNA-removed metagenomic next-generation sequencing technology for detecting SARS-CoV-2, revealing host local immune signaling and assisting genomic epidemiology. Frontiers in Immunology, 0, 13, .	4.8	2
5100	Novel RNA viruses in oysters revealed by virome. , 2022, 1, .		6
5102	Avirulent phenotype promotes Bordetella pertussis adaptation to the intramacrophage environment. Emerging Microbes and Infections, 2023, 12, .	6.5	3
5103	Neurotensin Expression, Regulation, and Function during the Ovulatory Period in the Mouse Ovary. Biology of Reproduction, 0, , .	2.7	3
5106	Methylome and transcriptome data integration reveals potential roles of DNA methylation and candidate biomarkers of cow Streptococcus uberis subclinical mastitis. Journal of Animal Science and Biotechnology, 2022, 13, .	5.3	9
5107	Silybum marianum chemotype differentiation is genetically determined by factors involved in silydianin biosynthesis. Journal of Applied Research on Medicinal and Aromatic Plants, 2023, 32, 100442.	1.5	0
5109	Transcriptome analysis of human mammary epithelial cells treated with bisphenol A and bisphenol A analogue mixtures reveals major alterations in multiple cellular pathways. , 2022, 2, 1-10.		2
5111	The complex, dynamic SpliceOme of the small GTPase transcripts altered by technique, sex, genetics, tissue specificity, and RNA base editing. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	2
5114	Dopamine-inhibited POMCDrd2+ neurons in the ARC acutely regulate feeding and body temperature. JCI Insight, 2022, 7, .	5.0	2
5115	Dynamic alterations in yak (Bos grunniens) rumen microbiome in response to seasonal variations in diet. Physiological Genomics, 2022, 54, 514-525.	2.3	4
5116	Histone H3 proline 16 hydroxylation regulates mammalian gene expression. Nature Genetics, 2022, 54, 1721-1735.	21.4	22
5117	In vitro methods to ensure absence of residual undifferentiated human induced pluripotent stem cells intermingled in induced nephron progenitor cells. PLoS ONE, 2022, 17, e0275600.	2.5	4
5119	Engineering Skeletal Muscle Grafts with PAX7::GFP-Sorted Human Pluripotent Stem Cell-Derived Myogenic Progenitors on Fibrin Microfiber Bundles for Tissue Regeneration. Bioengineering, 2022, 9, 693.	3.5	2
5121	Elucidating host cell response pathways and repurposing therapeutics for SARS-CoV-2 and other coronaviruses. Scientific Reports, 2022, 12, .	3.3	2
5123	Integrated next-generation sequencing and comparative transcriptomic analysis of leaves provides novel insights into the ethylene pathway of Chrysanthemum morifolium in response to a Chinese isolate of chrysanthemum virus B. Virology Journal, 2022, 19, .	3.4	6
5125	RBPMS2 Is a Myocardial-Enriched Splicing Regulator Required for Cardiac Function. Circulation Research, 2022, 131, 980-1000.	4.5	9
5126	Evaluation of Protein Kinase cAMP-Activated Catalytic Subunit Alpha as a Therapeutic Target for Fibrolamellar Carcinoma. , 2022, , .		0

#	Article	IF	Citations
5128	Hepatitis C Core Protein Induces a Genotype-Specific Susceptibility of Hepatocytes to TNF-Induced Death In Vitro and In Vivo. Viruses, 2022, 14, 2521.	3.3	1
5133	CXCR1/2 dual-inhibitor ladarixin reduces tumour burden and promotes immunotherapy response in pancreatic cancer. British Journal of Cancer, 2023, 128, 331-341.	6.4	5
5135	Establishment of transgenic pigs overexpressing human PKD2-D511V mutant. Frontiers in Genetics, 0, 13, .	2.3	0
5138	Autotoxin-mediated latecomer killing in yeast communities. PLoS Biology, 2022, 20, e3001844.	5.6	6
5140	Cross-validation of correlation networks using modular structure. Applied Network Science, 2022, 7, .	1.5	1
5141	An organ-on-chip model of pulmonary arterial hypertension identifies a BMPR2-SOX17-prostacyclin signalling axis. Communications Biology, 2022, 5, .	4.4	10
5142	Acetate supplementation restores cognitive deficits caused by <scp>ARID1A</scp> haploinsufficiency in excitatory neurons. EMBO Molecular Medicine, 2022, 14, .	6.9	4
5143	Metagenomics revealing molecular profiles of microbial community structure and metabolic capacity in Bamucuo lake, Tibet. Environmental Research, 2023, 217, 114847.	7.5	2
5144	Metagenomic insights into the changes in the rhizosphere microbial community caused by the root-knot nematode Meloidogyne incognita in tobacco. Environmental Research, 2023, 216, 114848.	7.5	8
5145	RNAseq analysis of olfactory neuroepithelium cytological samples in individuals with Down syndrome compared to euploid controls: a pilot study. Neurological Sciences, 0, , .	1.9	1
5146	Splice Variants of mRNA of Cytochrome P450 Genes: Analysis by the Nanopore Sequencing Method in Human Liver Tissue and HepG2 Cell Line. Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry, 2022, 16, 318-327.	0.4	1
5147	Integrative network analysis interweaves the missing links in cardiomyopathy diseasome. Scientific Reports, 2022, 12, .	3.3	8
5149	Challenges in neoantigen-directed therapeutics. Cancer Cell, 2023, 41, 15-40.	16.8	27
5150	A Computational Pipeline for Predicting Cancer Neoepitopes. Methods in Molecular Biology, 2023, , 475-488.	0.9	1
5151	Collaborative study from the Bladder Cancer Advocacy Network for the genomic analysis of metastatic urothelial cancer. Nature Communications, 2022, 13, .	12.8	14
5152	Identification of a minority population of LMO2 ⁺ breast cancer cells that integrate into the vasculature and initiate metastasis. Science Advances, 2022, 8, .	10.3	1
5153	Early developmental plasticity enables the induction of an intermediate extraembryonic cell state. Science Advances, 2022, 8, .	10.3	4
5154	Perchlorate reduction kinetics and genome-resolved metagenomics identify metabolic interactions in acclimated saline lake perchlorate-reducing consortia. Water Research, 2022, 227, 119343.	11.3	2

#	Article	IF	Citations
5155	Dissection of Besnoitia besnoiti intermediate host life cycle stages: From morphology to gene expression. PLoS Pathogens, 2022, 18, e1010955.	4.7	3
5157	Transcriptomic study reveals lncRNA-mediated downregulation of innate immune and inflammatory response in the SARS-CoV-2 vaccination breakthrough infections. Frontiers in Immunology, 0, 13, .	4.8	6
5158	Global analysis of alternative splicing events based on long- and short-read RNA sequencing during grape berry development. Gene, 2023, 852, 147056.	2.2	1
5159	<scp>CRISPR</scp>/Cas9 genomeâ€editing applied to <scp>MdPGT1</scp> in apple results in reduced foliar phloridzin without impacting plant growth. Plant Journal, 2023, 113, 92-105.	5.7	9
5161	Hyaluronan nanoscale clustering and Hyaluronan synthase 2 expression are linked to the invasion of child fibroblasts and infantile fibrosarcoma in vitro and in vivo. Scientific Reports, 2022, 12, .	3.3	1
5162	Tissue-Specific Human Extracellular Matrix Scaffolds Promote Pancreatic Tumour Progression and Chemotherapy Resistance. Cells, 2022, 11, 3652.	4.1	3
5163	An ancestral Wntâ€“Brachyury feedback loop in axial patterning and recruitment of mesoderm-determining target genes. Nature Ecology and Evolution, 2022, 6, 1921-1939.	7.8	10
5164	A Pan-Transcriptome Analysis Indicates Efficient Downregulation of the FIB Genes Plays a Critical Role in the Response of Alfalfa to Cold Stress. Plants, 2022, 11, 3148.	3.5	3
5165	Heterotrophic denitrification: An overlooked factor that contributes to nitrogen removal in n-DAMO mixed culture. Environmental Research, 2023, 216, 114802.	7.5	4
5166	Transcriptional profiling reveals a critical role of GmFT2a in soybean staygreen syndrome caused by the pest Riptortus pedestris. New Phytologist, 2023, 237, 1876-1890.	7.3	19
5167	Time-course transcriptome analysis reveals regulation of Arabidopsis seed dormancy by the transcription factors WOX11/12. Journal of Experimental Botany, 2023, 74, 1090-1106.	4.8	5
5168	Endothelial Rap1B mediates T-cell exclusion to promote tumor growth: a novel mechanism underlying vascular immunosuppression. Angiogenesis, 2023, 26, 265-278.	7.2	1
5169	annotate_my_genomes: an easy-to-use pipeline to improve genome annotation and uncover neglected genes by hybrid RNA sequencing. GigaScience, 2022, 11, .	6.4	1
5170	NUDT7 regulates total hepatic CoA levels and the composition of the intestinal bile acid pool in male mice fed a Western diet. Journal of Biological Chemistry, 2023, 299, 102745.	3.4	1
5171	Salt tolerance evolution facilitates antibiotic resistome in soil microbiota: Evidences from dissemination evaluation, hosts identification and co-occurrence exploration. Environmental Pollution, 2023, 317, 120830.	7.5	2
5172	Temporal progress of gene expression analysis with RNA-Seq data: A review on the relationship between computational methods. Computational and Structural Biotechnology Journal, 2023, 21, 86-98.	4.1	8
5173	Recent advances in machine learning applications in metabolic engineering. Biotechnology Advances, 2023, 62, 108069.	11.7	18
5174	Early alveolar epithelial cell necrosis is a potential driver of COVID-19-induced acute respiratory distress syndrome. IScience, 2023, 26, 105748.	4.1	11

#	Article	IF	Citations
5175	Metagenomic insights into the influence of thallium spill on sediment microbial community. Environmental Pollution, 2023, 317, 120660.	7.5	8
5176	Interactions among deep-sea mussels and their epibiotic and endosymbiotic chemoautotrophic bacteria: Insights from multi-omics analysis. Zoological Research, 2023, 44, 106-125.	2.1	4
5177	Industrial effluents boosted antibiotic resistome risk in coastal environments. Environment International, 2023, 171, 107714.	10.0	9
5178	Comparative global gene expression analysis of biofilm forms of Salmonella Typhimurium ATCC 14028 and its seqA mutant. Gene, 2023, 853, 147094.	2.2	1
5179	Aggregated alpha-synuclein transcriptionally activates pro-inflammatory canonical and non-canonical NF-Î°B signaling pathways in peripheral monocytic cells. Molecular Immunology, 2023, 154, 1-10.	2.2	2
5180	Application of mutational profiling: New functional analyses reveal the tRNA recognition mechanism of tRNA m1A22 methyltransferase. Journal of Biological Chemistry, 2023, 299, 102759.	3.4	3
5181	Metal mixtures modeling identifies birth weight-associated gene networks in the placentas of children born extremely preterm. Chemosphere, 2023, 313, 137469.	8.2	3
5182	Identification and characterization of lipocalin-type prostaglandin D2 synthase homologs in the urine of male rockfish. Gene, 2023, 854, 147093.	2.2	1
5183	An evaluation of different detection methods for anaerobic ammonium-oxidizing (anammox) bacteria inhabiting the oil reservoir systems. International Biodeterioration and Biodegradation, 2023, 177, 105536.	3.9	1
5184	Cold-adapted amphipod species upon heat stress: Proteomic responses and their correlation with transcriptomic responses. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2023, 45, 101048.	1.0	0
5185	Antibiotic resistome alteration along a full-scale drinking water supply system deciphered by metagenome assembly: Regulated by seasonality, mobile gene elements and antibiotic resistant gene hosts. Science of the Total Environment, 2023, 862, 160887.	8.0	12
5186	Differential gene expression analysis in the scallop Argopecten purpuratus exposed to altered pH and temperature conditions in an upwelling-influenced farming area. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2023, 45, 101046.	1.0	0
5187	Metagenomics reveals the increased antibiotics resistome through prokaryote rather than virome after overuse of rare earth element compounds. Science of the Total Environment, 2023, 863, 160704.	8.0	2
5188	The transcriptomic analysis of Planorbarius corneus hemocytes (Gastropoda) naturally infected with Bilharziella polonica (Schistosomatidae). Developmental and Comparative Immunology, 2023, 140, 104607.	2.3	0
5189	Genome-wide characterization of the common bean kinome: Catalog and insights into expression patterns and genetic organization. Gene, 2023, 855, 147127.	2.2	3
5190	A transcriptomic study of â€˜Granny Smithâ€™ apple fruit response to x-ray irradiation using RNA-Seq. Scientia Horticulturae, 2023, 311, 111777.	3.6	2
5191	Identification of stress-related characteristics of the <i>WRKY</i> gene family: A case study of <i>Dendrobium catenatum</i>. Ornamental Plant Research, 2022, 2, 1-15.	0.9	7
5192	Time-course RNA-Seq profiling reveals isoform-level gene expression dynamics of the cGAS-STING pathway. Computational and Structural Biotechnology Journal, 2022, 20, 6490-6500.	4.1	0

#	Article	IF	Citations
5193	A convergent malignant phenotype in B-cell acute lymphoblastic leukemia involving the splicing factor SRRM1. NAR Cancer, 2022, 4, .	3.1	1
5194	Genome-wide detection of genotype environment interactions for flowering time in Brassica napus. Frontiers in Plant Science, 0, 13, .	3.6	7
5195	Stemness Activity Underlying Whole Brain Regeneration in a Basal Chordate. Cells, 2022, 11, 3727.	4.1	4
5196	Transcriptome analyses in infertile men reveal germ cellâ€“specific expression and splicing patterns. Life Science Alliance, 2023, 6, e202201633.	2.8	5
5198	pH-Dependent Hydrogenotrophic Denitratation Based on Self-Alkalization. Environmental Science & Technology, 2023, 57, 685-696.	10.0	10
5201	Multi-omics approach to identifying isoform variants as therapeutic targets in cancer patients. Frontiers in Oncology, 0, 12, .	2.8	2
5202	Regional pattern and signatures of gut microbiota in rural residents with coronary heart disease: A metagenomic analysis. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	2
5204	STING Suppresses Mitochondrial VDAC2 to Govern RCC Growth Independent of Innate Immunity. Advanced Science, 2023, 10, .	11.2	8
5207	Mr.Vc v2: An updated version of database with increased data of transcriptome and experimental validated interactions. Frontiers in Microbiology, 0, 13, .	3.5	1
5208	Biofilm formation and inflammatory potential of Staphylococcus saccharolyticus: A possible cause of orthopedic implant-associated infections. Frontiers in Microbiology, 0, 13, .	3.5	1
5209	Plk1 Inhibitors and Abiraterone Synergistically Disrupt Mitosis and Kill Cancer Cells of Disparate Origin Independently of Androgen Receptor Signaling. Cancer Research, 2023, 83, 219-238.	0.9	4
5210	Bacteroides vulgatus attenuates experimental mice colitis through modulating gut microbiota and immune responses. Frontiers in Immunology, 0, 13, .	4.8	12
5211	Genome sequence and silkomics of the spindle ermine moth, Yponomeuta cagnagella, representing the early diverging lineage of the ditrysian Lepidoptera. Communications Biology, 2022, 5, .	4.4	3
5212	Transcriptome-based molecular subtypes and differentiation hierarchies improve the classification framework of acute myeloid leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	12
5213	Transcriptional mapping of the macaque retina and RPE-choroid reveals conserved inter-tissue transcription drivers and signaling pathways. Frontiers in Genetics, 0, 13, .	2.3	0
5214	Genomic Analysis of the Proteasome Subunit Gene Family and Their Response to High Density and Saline-Alkali Stresses in Grass Carp. Fishes, 2022, 7, 350.	1.7	1
5215	Deciphering the community structure and the functional potential of a hypersaline marsh microbial mat community. FEMS Microbiology Ecology, 2022, 98, .	2.7	1
5216	Genomic signature of Fanconi anaemia DNA repair pathway deficiency in cancer. Nature, 2022, 612, 495-502.	27.8	28

#	Article	IF	Citations
5217	m6A modification of U6 snRNA modulates usage of two major classes of pre-mRNA 5â€™ splice site. ELife, 0, 11, .	6.0	14
5218	Global hypo-methylation in a proportion of glioblastoma enriched for an astrocytic signature is associated with increased invasion and altered immune landscape. ELife, 0, 11, .	6.0	3
5220	Integration of single-cell transcriptomes and biological function reveals distinct behavioral patterns in bone marrow endothelium. Nature Communications, 2022, 13, .	12.8	1
5221	Chromatin dynamics associated with seed desiccation tolerance/sensitivity at early germination in Medicago truncatula. Frontiers in Plant Science, 0, 13, .	3.6	2
5222	Radiotherapy in combination with CD47 blockade elicits a macrophage-mediated abscopal effect. Nature Cancer, 2022, 3, 1351-1366.	13.2	36
5223	CD47-SIRPÎ± axis blockade in NASH promotes necroptotic hepatocyte clearance by liver macrophages and decreases hepatic fibrosis. Science Translational Medicine, 2022, 14, .	12.4	24
5224	ADAR1-dependent editing regulates human Î²Âcell transcriptome diversity during inflammation. Frontiers in Endocrinology, 0, 13, .	3.5	5
5225	Strategy for RNA-Seq Experimental Design and Data Analysis. Methods in Molecular Biology, 2023, , 249-278.	0.9	2
5226	A single N6-methyladenosine site regulates lncRNA HOTAIR function in breast cancer cells. PLoS Biology, 2022, 20, e3001885.	5.6	15
5227	Transcriptome analysis of pika heart tissue reveals mechanisms underlying the adaptation of a keystone species on the roof of the world. Frontiers in Genetics, 0, 13, .	2.3	0
5228	Ras drives malignancy through stem cell crosstalk with the microenvironment. Nature, 2022, 612, 555-563.	27.8	17
5230	The ColR/S two-component system is a conserved determinant of host association across Pseudomonas species. ISME Journal, 2023, 17, 286-296.	9.8	4
5233	Creb5 coordinates synovial joint formation with the genesis of articular cartilage. Nature Communications, 2022, 13, .	12.8	4
5234	Pharmacological targeting of glutamatergic neurons within the brainstem for weight reduction. Nature Metabolism, 2022, 4, 1495-1513.	11.9	9
5236	Transcriptome analysis reveals the mechanisms for mycorrhiza-enhanced salt tolerance in rice. Frontiers in Plant Science, 0, 13, .	3.6	4
5237	Cell-type-specific alternative splicing in the Arabidopsis germline. Plant Physiology, 2023, 192, 85-101.	4.8	3
5238	Maternal Undernutrition Induces Cell Signalling and Metabolic Dysfunction in Undifferentiated Mouse Embryonic Stem Cells. Stem Cell Reviews and Reports, 0, , .	3.8	1
5240	Discovering novel reproductive genes in a non-model fly using de novo GridION transcriptomics. Frontiers in Genetics, 0, 13, .	2.3	1

#	Article	IF	Citations
5242	Comparative Penicillium spp. Transcriptomics: Conserved Pathways and Processes Revealed in Ungerminated Conidia and during Postharvest Apple Fruit Decay. Microorganisms, 2022, 10, 2414.	3.6	6
5243	DNA Repair Mechanisms are Activated in Circulating Lymphocytes of Hospitalized Covid-19 Patients. Journal of Inflammation Research, 0, Volume 15, 6629-6644.	3.5	3
5244	Ikaros family proteins redundantly regulate temporal patterning in the developing mouse retina. Development (Cambridge), 2023, 150, .	2.5	9
5245	Genome-Wide Analysis on Transcriptome and Methylome in Prevention of Mammary Tumor Induced by Early Life Combined Botanicals. Cells, 2023, 12, 14.	4.1	3
5246	Genome-Wide Identification and Expression Analysis of m6A Writers, Erasers, and Readers in Litchi (Litchi chinensis Sonn.). Genes, 2022, 13, 2284.	2.4	1
5249	The grape powdery mildew resistance loci Ren2, Ren3, Ren4D, Ren4U, Run1, Run1.2b, Run2.1, and Run2.2 activate different transcriptional responses to Erysiphe necator. Frontiers in Plant Science, 0, 13, .	3.6	3
5250	In the battle of the disease: aÂtranscriptomic analysis of European foulbrood-diseased larvae of the Western honey bee (Apis mellifera). BMC Genomics, 2022, 23, .	2.8	0
5251	Plant microbiomes harbor potential to promote nutrient turnover in impoverished substrates of a Brazilian biodiversity hotspot. ISME Journal, 2023, 17, 354-370.	9.8	14
5252	Integrative Meta-Analysis of Huntingtonâ€™s Disease Transcriptome Landscape. Genes, 2022, 13, 2385.	2.4	3
5253	Lactobacillus reuteri improves the development and maturation of fecal microbiota in piglets through mother-to-infant microbe and metabolite vertical transmission. Microbiome, 2022, 10, .	11.1	14
5254	Comprehensive molecular and morphological resolution of blubber stratification in a deep-diving, fasting-adapted seal. Frontiers in Physiology, 0, 13, .	2.8	1
5260	Suppression of the tonoplast sugar transporter, StTST3.1, affects transitory starch turnover and plant growth in potato. Plant Journal, 2023, 113, 342-356.	5.7	4
5262	The transcription factor c-Jun inhibits RBM39 to reprogram pre-mRNA splicing during genotoxic stress. Nucleic Acids Research, 2022, 50, 12768-12789.	14.5	3
5265	The oriental armyworm genome yields insights into the long-distance migration of noctuid moths. Cell Reports, 2022, 41, 111843.	6.4	10
5267	Genome-level analyses resolve an ancient lineage of symbiotic ascomycetes. Current Biology, 2022, 32, 5209-5218.e5.	3.9	14
5268	Variants in ALDH1A2 reveal an anti-inflammatory role for retinoic acid and a new class of disease-modifying drugs in osteoarthritis. Science Translational Medicine, 2022, 14, .	12.4	9
5270	Branch point strength controls species-specificCAMK2Balternative splicing and regulates LTP. Life Science Alliance, 2023, 6, e202201826.	2.8	1
5273	Altered RNA Editing in Atopic Dermatitis Highlights the Role of Double-Stranded RNA for Immune Surveillance. Journal of Investigative Dermatology, 2023, 143, 933-943.e8.	0.7	2

#	Article	IF	Citations
5274	Integrative Application of Transcriptomics and Metabolomics Provides Insights into Unsynchronized Growth in Sea Cucumber (Stichopus monotuberculatus). International Journal of Molecular Sciences, 2022, 23, 15478.	4.1	3
5275	PPARÎ³ and C/EBPÎ± response to acute cold stress in brown adipose tissue. IScience, 2023, 26, 105848.	4.1	1
5276	Pseudoalignment tools as an efficient alternative to detect repeated transposable elements in scRNAseq data. Bioinformatics, 2023, 39, .	4.1	1
5278	Full-Length Single-Cell RNA-Sequencing with FLASH-seq. Methods in Molecular Biology, 2023, , 123-164.	0.9	6
5279	Gene augmentation prevents retinal degeneration in a CRISPR/Cas9-based mouse model of PRPF31 retinitis pigmentosa. Nature Communications, 2022, 13, .	12.8	9
5280	A critical period of translational control during brain development at codon resolution. Nature Structural and Molecular Biology, 2022, 29, 1277-1290.	8.2	17
5282	Genetic basis of enhanced stress resistance in longâ€lived mutants highlights key role of innate immunity in determining longevity. Aging Cell, 2023, 22, .	6.7	11
5283	Microglial Pten safeguards postnatal integrity of the cortex and sociability. Frontiers in Immunology, 0, 13, .	4.8	1
5284	Sphingolipid subtypes differentially control proinsulin processing and systemic glucose homeostasis. Nature Cell Biology, 2023, 25, 20-29.	10.3	9
5285	Repurposing Tamoxifen as Potential Host-Directed Therapeutic for Tuberculosis. MBio, 2023, 14, .	4.1	7
5287	Glioblastoma stem cells express nonâ€canonical proteins and exclusive mesenchymalâ€like or nonâ€mesenchymalâ€like protein signatures. Molecular Oncology, 0, , .	4.6	3
5288	Phase IIa Study of SurVaxM Plus Adjuvant Temozolomide for Newly Diagnosed Glioblastoma. Journal of Clinical Oncology, 2023, 41, 1453-1465.	1.6	27
5289	A simplified and defined serum-free medium for cultivating fat across species. IScience, 2023, 26, 105822.	4.1	15
5290	Ultrafast prediction of somatic structural variations by filtering out reads matched to pan-genome k-mer sets. Nature Biomedical Engineering, 2023, 7, 853-866.	22.5	4
5291	Alternative splicing and genetic variation of mhc-e: implications for rhesus cytomegalovirus-based vaccines. Communications Biology, 2022, 5, .	4.4	2
5293	Taxonomic, Genomic, and Functional Variation in the Gut Microbiomes of Wild Spotted Hyenas Across 2 Decades of Study. MSystems, 0, , .	3.8	1
5294	Nanobody-tethered transposition enables multifactorial chromatin profiling at single-cell resolution. Nature Biotechnology, 2023, 41, 806-812.	17.5	25
5295	Co-expression of fibrotic genes in inflammatory bowel disease; A localized event?. Frontiers in Immunology, 0, 13, .	4.8	3

#	Article	IF	Citations
5296	Structure-guided isoform identification for the human transcriptome. ELife, 0, 11, .	6.0	14
5297	Ecology, Not Host Phylogeny, Shapes the Oral Microbiome in Closely Related Species. Molecular Biology and Evolution, 2022, 39, .	8.9	8
5300	Comparative transcriptomes of nine tissues for the Heilongjiang brown frog (Rana amurensis). Scientific Reports, 2022, 12, .	3.3	1
5301	Comparative transcriptomics reveals commonalities and differences in the genetic underpinnings of a floral dimorphism. Scientific Reports, 2022, 12, .	3.3	4
5302	Endothelial deletion of the cytochrome P450 reductase leads to cardiac remodelling. Frontiers in Physiology, 0, 13, .	2.8	0
5303	Transcriptome expression profile of compound-K-enriched red ginseng extract (DDK-401) in Korean volunteers and its apoptotic properties. Frontiers in Pharmacology, 0, 13, .	3.5	1
5305	Myeloid cells promote interferon signaling-associated deterioration of the hematopoietic system. Nature Communications, 2022, 13, .	12.8	3
5306	Disentangling the lipid divide: Identification of key enzymes for the biosynthesis of membrane-spanning and ether lipids in Bacteria. Science Advances, 2022, 8, .	10.3	6
5307	Root Physiological Changes and Transcription Analysis of Iris domestica in Response to Persistent Drought. Horticulturae, 2022, 8, 1162.	2.8	1
5308	RNA-Sequencing Muscle Plasticity to Resistance Exercise Training and Disuse in Youth and Older Age. Physiologia, 2022, 2, 164-179.	2.2	0
5310	The Prostate Stromal Transcriptome in Aggressive and Lethal Prostate Cancer. Molecular Cancer Research, 2023, 21, 253-260.	3.4	4
5311	Computationally Efficient Assembly of Pseudomonas aeruginosa Gene Expression Compendia. MSystems, 2023, 8, .	3.8	2
5312	Major histocompatibility complex genomic investigation of endangered Chinese alligator provides insights into the evolution of tetrapod major histocompatibility complex and survival of critically bottlenecked species. Frontiers in Ecology and Evolution, 0, 10, .	2.2	2
5313	Plant Transcriptomics: Data-driven Global Approach to Understand Cellular Processes and Their Regulation in Model and Non-Model Plants. , 2022, , 10-29.		0
5314	ROOT MERISTEM GROWTH FACTOR1 (RGF1)â€“RGF1 INSENSITIVE 1 peptideâ€“receptor pair inhibits lateral root development via the MPK6â€“PUCHI module in Arabidopsis. Journal of Experimental Botany, 2023, 74, 1475-1488.	4.8	3
5315	Achiasmatic meiosis in the unisexual Amazon molly, Poecilia formosa. Chromosome Research, 2022, 30, 443-457.	2.2	10
5316	Benchmarking brain organoid recapitulation of fetal corticogenesis. Translational Psychiatry, 2022, 12, .	4.8	6
5317	Asymmetric gene expression in grain development of reciprocal crosses between tetraploid and hexaploid wheats. Communications Biology, 2022, 5, .	4.4	2

#	Article	IF	Citations
5318	The landscape of therapeutic vulnerabilities in EGFR inhibitor osimertinib drug tolerant persister cells. Npj Precision Oncology, 2022, 6, .	5.4	5
5320	Heterogeneous expression and role of receptor tyrosine kinase-like orphan receptor 2 (ROR2) in small cell lung cancer. Human Cell, 0, , .	2.7	0
5321	MacroH2A impedes metastatic growth by enforcing a discrete dormancy program in disseminated cancer cells. Science Advances, 2022, 8, .	10.3	10
5322	Strobealign: flexible seed size enables ultra-fast and accurate read alignment. Genome Biology, 2022, 23, .	8.8	17
5323	Transgenerational transmission of aspartame-induced anxiety and changes in glutamate-GABA signaling and gene expression in the amygdala. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	21
5325	Reduction of Redox Potential Exerts a Key Role in Modulating Gut Microbial Taxa and Function by Dietary Supplementation of Pectin in a Pig Model. Microbiology Spectrum, 2023, 11, .	3.0	7
5326	The genomic basis of copper tolerance in Drosophila is shaped by a complex interplay of regulatory and environmental factors. BMC Biology, 2022, 20, .	3.8	6
5327	Tip60-mediated H2A.Z acetylation promotes neuronal fate specification and bivalent gene activation. Molecular Cell, 2022, 82, 4627-4646.e14.	9.7	11
5328	Bulk RNA sequencing analysis of developing human induced pluripotent cell-derived retinal organoids. Scientific Data, 2022, 9, .	5.3	5
5329	Cave Thiovulum (Candidatus Thiovulum stygium) differs metabolically and genomically from marine species. ISME Journal, 2023, 17, 340-353.	9.8	3
5330	Gene Expression Profiling of Trematomus bernacchii in Response to Thermal and Stabling Stress. Fishes, 2022, 7, 387.	1.7	1
5334	Molecular signatures in the progression of COVID-19 severity. Scientific Reports, 2022, 12, .	3.3	4
5335	Medium-Chain-Length Fatty Acid Catabolism in Cupriavidus necator H16: Transcriptome Sequencing Reveals Differences from Long-Chain-Length Fatty Acid Î²-Oxidation and Involvement of Several Homologous Genes. Applied and Environmental Microbiology, 2023, 89, .	3.1	2
5336	Piwil2 (Mili) sustains neurogenesis and prevents cellular senescence in the postnatal hippocampus. EMBO Reports, 2023, 24, .	4.5	5
5338	In-depth analysis of alternative splicing landscape in multiple myeloma and potential role of dysregulated splicing factors. Blood Cancer Journal, 2022, 12, .	6.2	4
5339	A Comparative Transcriptomic with UPLC-Q-Exactive MS Reveals Differences in Gene Expression and Components of Iridoid Biosynthesis in Various Parts of Gentiana macrophylla. Genes, 2022, 13, 2372.	2.4	3
5341	A Non-Gradual Development Process of Cicada Eyes at the End of the Fifth-Instar Nymphal Stage to Obtain Visual Ability. Insects, 2022, 13, 1170.	2.2	0
5342	Placental Inflammation Leads to Abnormal Embryonic Heart Development. Circulation, 2023, 147, 956-972.	1.6	13

#	Article	IF	Citations
5343	Slowest possible replicative life at frigid temperatures for yeast. Nature Communications, 2022, 13, .	12.8	1
5345	Embryonic origins of adult pluripotent stem cells. Cell, 2022, 185, 4756-4769.e13.	28.9	16
5347	Loss of linker histone H1 in the maternal genome influences DEMETER-mediated demethylation and affects the endosperm DNA methylation landscape. Frontiers in Plant Science, 0, 13, .	3.6	2
5348	Targeting Nup358/RanBP2 by a viral protein disrupts stress granule formation. PLoS Pathogens, 2022, 18, e1010598.	4.7	2
5349	The transcription factor Zic4 promotes tentacle formation and prevents epithelial transdifferentiation in Hydra. Science Advances, 2022, 8, .	10.3	5
5350	EKLF/Klf1 regulates erythroid transcription by its pioneering activity and selective control of RNA Pol II pause-release. Cell Reports, 2022, 41, 111830.	6.4	6
5351	A genome-wide CRISPR screen identifies WDFY3 as a regulator of macrophage efferocytosis. Nature Communications, 2022, 13, .	12.8	8
5352	Monitoring the 5â€²UTR landscape reveals isoform switches to drive translational efficiencies in cancer. Oncogene, 2023, 42, 638-650.	5.9	16
5354	Comparative Silk Transcriptomics Illuminates Distinctive Impact of Artificial Selection in Silkworm Modern Breeding. Insects, 2022, 13, 1163.	2.2	2
5355	Full-length IL-33 augments pulmonary fibrosis in an ST2- and Th2-independent, non-transcriptomic fashion. Cellular Immunology, 2023, 383, 104657.	3.0	2
5356	Chromosome-scale genome assembly of Eustoma grandiflorum, the first complete genome sequence in the genus Eustoma. G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	2
5357	In vivo PIWI slicing in mouse testes deviates from rules established in vitro. Rna, 2023, 29, 308-316.	3.5	5
5358	scONE-seq: A single-cell multi-omics method enables simultaneous dissection of phenotype and genotype heterogeneity from frozen tumors. Science Advances, 2023, 9, .	10.3	18
5359	Prognostic and Predictive Value of Immune-Related Gene Expression Signatures vs Tumor-Infiltrating Lymphocytes in Early-Stage ERBB2/HER2-Positive Breast Cancer. JAMA Oncology, 2023, 9, 490.	7.1	11
5362	Endogenous IL-1 receptor antagonist restricts healthy and malignant myeloproliferation. Nature Communications, 2023, 14, .	12.8	9
5363	A critical period of prehearing spontaneous Ca²⁺ spiking is required for hairâ€bundle maintenance inÂinner hair cells. EMBO Journal, 2023, 42, .	7.8	8
5366	Inflammatory Cytokine-Induced HIF-1 Activation Promotes Epithelialâ€“Mesenchymal Transition in Endometrial Epithelial Cells. Biomedicines, 2023, 11, 210.	3.2	4
5368	Long-distance control of potato storage organ formation by SELF PRUNING 3D and FLOWERING LOCUS T-like 1. Plant Communications, 2023, 4, 100547.	7.7	5

#	Article	IF	Citations
5369	Altered transcriptome-proteome coupling indicates aberrant proteostasis in Parkinsonâ€™s disease. IScience, 2023, 26, 105925.	4.1	2
5371	Identification and Characterization of mRNA and lncRNA Expression Profiles in Age-Related Hearing Loss. Clinical and Experimental Otorhinolaryngology, 2023, 16, 115-124.	2.1	1
5372	Transcriptomics for Clinical and Experimental Biology Research: Hang on a Seq. Genetics & Genomics Next, 2023, 4, .	1.5	5
5373	Identification of genes involved in chicken follicle selection by ONT sequencing on granulosa cells. Frontiers in Genetics, 0, 13, .	2.3	5
5374	Novel context-specific genome-scale modelling explores the potential of triacylglycerol production by Chlamydomonas reinhardtii. Microbial Cell Factories, 2023, 22, .	4.0	4
5375	Mosquito vector competence for dengue is modulated by insect-specific viruses. Nature Microbiology, 2023, 8, 135-149.	13.3	48
5376	Haplotype-aware pantranscriptome analyses using spliced pangenome graphs. Nature Methods, 2023, 20, 239-247.	19.0	15
5377	From head to rootlet: comparative transcriptomic analysis of a rhizocephalan barnacle Peltogaster reticulata (Crustacea: Rhizocephala). F1000Research, 0, 11, 583.	1.6	0
5378	Knocking-Out OsPDR7 Triggers Up-Regulation of OsZIP9 Expression and Enhances Zinc Accumulation in Rice. Rice Science, 2023, 30, 36-49.	3.9	1
5380	Genomic and Transcriptomic Insights into Salinity Tolerance-Based Niche Differentiation of Synechococcus Clades in Estuarine and Coastal Waters. MSystems, 2023, 8, .	3.8	2
5382	Transcriptomic Signature of the Simulated Microgravity Response in Caenorhabditis elegans and Comparison to Spaceflight Experiments. Cells, 2023, 12, 270.	4.1	2
5383	New Insights into the Role of the Trypanosoma cruzi Aldo-Keto Reductase TcAKR. Pathogens, 2023, 12, 85.	2.8	1
5384	Nanopore long-read RNAseq reveals transcriptional variations in citrus species. Frontiers in Plant Science, 0, 13, .	3.6	1
5387	The Histone Chaperone Network Is Highly Conserved in Physarum polycephalum. International Journal of Molecular Sciences, 2023, 24, 1051.	4.1	0
5389	Airborne bacterial community and antibiotic resistome in the swine farming environment: Metagenomic insights into livestock relevance, pathogen hosts and public risks. Environment International, 2023, 172, 107751.	10.0	11
5390	MetaFunc: Taxonomic and Functional Analyses of High Throughput Sequencing for Microbiomes. Gut Microbiome, 0, , 1-41.	3.2	2
5391	A Bayesian model for unsupervised detection of RNA splicing based subtypes in cancers. Nature Communications, 2023, 14, .	12.8	1
5392	A phase II study of palbociclib plus letrozole plus trastuzumab as neoadjuvant treatment for clinical stages II and III ER+ HER2+ breast cancer (PALTAN). Npj Breast Cancer, 2023, 9, .	5.2	4

#	Article	IF	Citations
5393	Dysregulation of the chromatin environment leads to differential alternative splicing as a mechanism of disease in a human model of autism spectrum disorder. Human Molecular Genetics, 2023, 32, 1634-1646.	2.9	4
5396	A remarkably diverse and well-organized virus community in a filter-feeding oyster. Microbiome, 2023, 11, .	11.1	5
5397	HIV silencing and cell survival signatures in infected T cell reservoirs. Nature, 2023, 614, 318-325.	27.8	35
5398	Physiological and transcriptome analyses of Kluyveromyces marxianus reveal adaptive traits in stress response. Applied Microbiology and Biotechnology, 0, , .	3.6	2
5400	A single silkâ€•and multiple pollenâ€expressed PMEs at the Ga1 locus modulate maize unilateral crossâ€incompatibility. Journal of Integrative Plant Biology, 2023, 65, 1344-1355.	8.5	2
5401	The SPOC domain is a phosphoserine binding module that bridges transcription machinery with co- and post-transcriptional regulators. Nature Communications, 2023, 14, .	12.8	6
5402	A multiplexed inÂvivo approach to identify driver genes in small cell lung cancer. Cell Reports, 2023, 42, 111990.	6.4	8
5403	ACKR3 promotes CXCL12/CXCR4-mediated cell-to-cell-induced lymphoma migration through LTB4 production. Frontiers in Immunology, 0, 13, .	4.8	4
5404	Comparison between the Gametophyte and the Sporophyte Transcriptomes of the Endangered Fern Vandenboschia speciosa. Genes, 2023, 14, 166.	2.4	1
5405	Machine learningâ€driven blood transcriptomeâ€based discovery of SARSâ€CoVâ€2 specific severity biomarkers. Journal of Medical Virology, 2023, 95, .	5.0	3
5406	Whole transcriptomeâ€“based skin virome profiling in typical epidermodysplasia verruciformis reveals Î±-, Î²-, and Î³-HPV infections. JCI Insight, 2023, 8, .	5.0	3
5407	Specific expression of alternatively spliced genes in the turkey (Meleagris gallopavo) reproductive tract revealed their function in spermatogenesis and post-testicular sperm maturation. Poultry Science, 2023, 102, 102484.	3.4	1
5408	Rhizogenic Agrobacterium protein RolB interacts with the TOPLESS repressor proteins to reprogram plant immunity andÂdevelopment. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	6
5409	Transcriptome Dataset of Strawberry (Fragaria Ã— ananassa Duch.) Leaves Using Oxford Nanopore Sequencing under LED Irradiation and Application of Methyl Jasmonate and Methyl Salicylate Hormones Treatment. Data, 2023, 8, 22.	2.3	3
5410	The landscape of differential splicing and transcript alternations in severe <scp>COVID</scp>â€19 infection. FEBS Journal, 2023, 290, 3128-3144.	4.7	3
5411	In-depth analysis of large-scale screening of WRKY members based on genome-wide identification. Frontiers in Genetics, 0, 13, .	2.3	2
5412	MAEL gene contributes to bovine testicular development through the m5C-mediated splicing. IScience, 2023, 26, 105941.	4.1	4
5413	FastViromeExplorer-Novel: Recovering Draft Genomes of Novel Viruses and Phages in Metagenomic Data. Journal of Computational Biology, 0, , .	1.6	0

#	Article	IF	Citations
5414	The venom composition and parthenogenesis mechanism of the parasitoid wasp Microctonus hyperodae, a declining biocontrol agent. Insect Biochemistry and Molecular Biology, 2023, 153, 103897.	2.7	3
5415	Impacts of organic loading rate and hydraulic retention time on organics degradation, interspecies interactions and functional traits in thermophilic anaerobic co-digestion of food waste and sewage sludge. Bioresource Technology, 2023, 370, 128578.	9.6	3
5416	Drought hardening effect on improving transplant stress tolerance in Pinus densiflora. Environmental and Experimental Botany, 2023, 207, 105222.	4.2	7
5417	Ornithine Decarboxylase in Gastric Epithelial Cells Promotes the Immunopathogenesis of Helicobacter pylori Infection. Journal of Immunology, 2022, 209, 796-805.	0.8	2
5421	mRNA transport, translation, and decay in adult mammalian central nervous system axons. Neuron, 2023, 111, 650-668.e4.	8.1	16
5422	Profiling the Spatial Expression Pattern and ceRNA Network of lncRNA, miRNA, and mRNA Associated with the Development of Intermuscular Bones in Zebrafish. Biology, 2023, 12, 75.	2.8	2
5423	The plant peptide hormone phytosulfokine promotes somatic embryogenesis by maintaining redox homeostasis in Cunninghamia lanceolata. Plant Journal, 2023, 113, 716-733.	5.7	9
5424	Progesterone modulates the DSCAM-AS1/miR-130a/ESR1 axis to suppress cell invasion and migration in breast cancer. Breast Cancer Research, 2022, 24, .	5.0	4
5426	Network-based assessment of HDAC6 activity predicts preclinical and clinical responses to the HDAC6 inhibitor ricolinostat in breast cancer. Nature Cancer, 2023, 4, 257-275.	13.2	18
5428	Increased mTOR Signaling and Impaired Autophagic Flux Are Hallmarks of SARS-CoV-2 Infection. Current Issues in Molecular Biology, 2023, 45, 327-336.	2.4	2
5429	Phylotranscriptomic Analyses of Mycoheterotrophic Monocots Show a Continuum of Convergent Evolutionary Changes in Expressed Nuclear Genes From Three Independent Nonphotosynthetic Lineages. Genome Biology and Evolution, 2023, 15, .	2.5	5
5430	Systematic analysis of alternative splicing in time course data using Spycone. Bioinformatics, 2023, 39, .	4.1	3
5432	Cycloâ€glycylproline attenuates hydrogen peroxideâ€induced cellular damage mediated by the MDM2â€p53 pathway in human neural stem cells. Journal of Cellular Physiology, 2023, 238, 434-446.	4.1	2
5433	Safety and effectiveness of neoadjuvant PD-1 inhibitor (toripalimab) plus chemotherapy in stage IIâ€“III NSCLC (LungMate 002): an open-label, single-arm, phase 2 trial. BMC Medicine, 2022, 20, .	5.5	11
5434	The lncRNA LUCAT1 is elevated in inflammatory disease and restrains inflammation by regulating the splicing and stability of NR4A2. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	14
5435	The multilayered hierarchical gene regulatory network reveals interaction of transcription factors in response to cadmium inTamarix hispidaroots. Tree Physiology, 2023, 43, 630-642.	3.1	3
5437	Expression of Markers of Endometrial Receptivity in Obese Infertile PCOS Women before and after the Weight Loss Programâ€”A Preliminary Study. Cells, 2023, 12, 164.	4.1	4
5438	KMCP: accurate metagenomic profiling of both prokaryotic and viral populations by pseudo-mapping. Bioinformatics, 2023, 39, .	4.1	15

#	Article	IF	Citations
5439	496. Using allele-specific expression to uncover cis-regulation in bovine muscle. , 2022, , .		0
5440	Men who inject opioids exhibit altered tRNA-Gly-GCC isoforms in semen. Molecular Human Reproduction, 2023, 29, .	2.8	3
5441	Transcriptome analysis provides StMYBA1 gene that regulates potato anthocyanin biosynthesis by activating structural genes. Frontiers in Plant Science, 0, 14, .	3.6	4
5442	Transcriptomics secondary analysis of severe human infection with SARS-CoV-2 identifies gene expression changes and predicts three transcriptional biomarkers in leukocytes. Computational and Structural Biotechnology Journal, 2023, 21, 1403-1413.	4.1	2
5443	Long Noncoding RNA U90926 Is Induced in Activated Macrophages, Is Protective in Endotoxic Shock, and Encodes a Novel Secreted Protein. Journal of Immunology, 2023, 210, 807-819.	0.8	4
5446	Oncogenic PKA signaling increases c-MYC protein expression through multiple targetable mechanisms. ELife, 0, 12, .	6.0	12
5448	T-REX17 is a transiently expressed non-coding RNA essential for human endoderm formation. ELife, 0, 12, .	6.0	1
5449	Chromosome fusions repatterned recombination rate and facilitated reproductive isolation during Pristionchus nematode speciation. Nature Ecology and Evolution, 0, , .	7.8	11
5450	Exploiting Multi-Omics Profiling and Systems Biology to Investigate Functions of TOMM34. Biology, 2023, 12, 198.	2.8	3
5451	Dietary Walnuts Preserve Aspects of Health Span and Alter the Hippocampal Lipidome in Aged High-Fat Diet-Fed Mice. International Journal of Molecular Sciences, 2023, 24, 2314.	4.1	0
5452	Arbuscular mycorrhizal fungi enhance plant phosphorus uptake through stimulating hyphosphere soil microbiome functional profiles for phosphorus turnover. New Phytologist, 2023, 238, 2578-2593.	7.3	18
5453	<scp>DELLA</scp> proteins regulate spore germination and reproductive development in Physcomitrium patens. New Phytologist, 2023, 238, 654-672.	7.3	3
5454	Integrative analysis of Iso-Seq and RNA-seq reveals dynamic changes of alternative promoter, alternative splicing and alternative polyadenylation during Angiotensin II-induced senescence in rat primary aortic endothelial cells. Frontiers in Genetics, 0, 14, .	2.3	0
5455	Transcriptional Ontogeny Platform of Sex Determination/Sex Differentiation Genes in Almaco Jack Larvae. North American Journal of Aquaculture, 2023, 85, 123-135.	1.4	0
5456	In vitro characterization on the role of <scp>APOE</scp> polymorphism in human hippocampal neurogenesis. Hippocampus, 2023, 33, 322-346.	1.9	3
5457	Progenitor-derived endothelin controls dermal sheath contraction for hair follicle regression. Nature Cell Biology, 0, , .	10.3	2
5458	EGFR Pathway Expression Persists in Recurrent Glioblastoma Independent of Amplification Status. Cancers, 2023, 15, 670.	3.7	2
5459	Alternative RNA Splicing in the Retina: Insights and Perspectives. Cold Spring Harbor Perspectives in Medicine, 2023, 13, a041313.	6.2	3

#	Article	IF	Citations
5460	Proteomics analysis reveals three potential cacao target that interacts with Moniliophthora perniciosa NEP during witches broom disease. Physiological and Molecular Plant Pathology, 2023, 124, 101946.	2.5	2
5462	Understanding Insulin in the Age of Precision Medicine and Big Data: Under-Explored Nature of Genomics. Biomolecules, 2023, 13, 257.	4.0	1
5463	Germline-related molecular phenotype in Metazoa: conservation and innovation highlighted by comparative transcriptomics. EvoDevo, 2023, 14, .	3.2	1
5464	GRAS transcription factors regulate cell division planes in moss overriding the default rule. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	11
5465	In vitro gut microbiome response to carbohydrate supplementation is acutely affected by a sudden change in diet. BMC Microbiology, 2023, 23, .	3.3	1
5466	Adjuvant Temozolomide Chemotherapy With or Without Interferon Alfa Among Patients With Newly Diagnosed High-grade Gliomas. JAMA Network Open, 2023, 6, e2253285.	5.9	9
5467	A multimorphic mutation in IRF4 causes human autosomal dominant combined immunodeficiency. Science Immunology, 2023, 8, .	11.9	10
5469	Molecular Genetic Mechanisms of Heterosis in Sugarcane Cultivars Using a Comparative Transcriptome Analysis of Hybrids and Ancestral Parents. Agronomy, 2023, 13, 348.	3.0	1
5472	Uncovering a miltiradiene biosynthetic gene cluster in the Lamiaceae reveals a dynamic evolutionary trajectory. Nature Communications, 2023, 14, .	12.8	13
5473	Principles of RNA recruitment to viral ribonucleoprotein condensates in a segmented dsRNA virus. ELife, 0, 12, .	6.0	5
5474	Comparison between qPCR and RNA-seq reveals challenges of quantifying HLA expression. Immunogenetics, 2023, 75, 249-262.	2.4	7
5475	YAP1 and WWTR1 expression inversely correlates with neuroendocrine markers in Merkel cell carcinoma. Journal of Clinical Investigation, 2023, 133, .	8.2	3
5477	Characterization and Expression of Holothurian Wnt Signaling Genes during Adult Intestinal Organogenesis. Genes, 2023, 14, 309.	2.4	2
5478	Inhibition of specific signaling pathways rather than epigenetic silencing of effector genes is the leading mechanism of innate tolerance. Frontiers in Immunology, 0, 14, .	4.8	2
5480	Survival-based CRISPR genetic screens across a panel of permissive cell lines identify common and cell-specific SARS-CoV-2 host factors. Heliyon, 2023, 9, e12744.	3.2	5
5481	Killer Knots: Molecular Evolution of Inhibitor Cystine Knot Toxins in Wandering Spiders (Araneae:) Tj ETQq1 1 0.784314 rgBT /Overloc	3.4	4
5482	Microbial Contributions to Iodide Enrichment in Deep Groundwater in the North China Plain. Environmental Science & Technology, 2023, 57, 2625-2635.	10.0	2
5483	Positional cloning identified HvTUBULIN8 as the candidate gene for round lateral spikelet (RLS) in barley (Hordeum vulgare L.). Theoretical and Applied Genetics, 2023, 136, .	3.6	1

#	Article	IF	Citations
5484	Genomic Instability and Protumoral Inflammation Are Associated with Primary Resistance to Antiâ€“PD-1 + Antiangiogenesis in Malignant Pleural Mesothelioma. Cancer Discovery, 2023, 13, 858-879.	9.4	4
5487	Activation of the NLRP1 inflammasome in human keratinocytes by the dsDNA mimetic poly(dA:dT). Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	9
5489	Human zygotic genome activation is initiated from paternal genome. Cell Discovery, 2023, 9, .	6.7	7
5490	Blood and adipose-resident eosinophils are defined by distinct transcriptional profiles. Journal of Leukocyte Biology, 2023, 113, 191-202.	3.3	2
5491	Hematopoietic Cell Autonomous Disruption of Hematopoiesis in a Germline Loss-of-function Mouse Model of RUNX1-FPD. HemaSphere, 2023, 7, e824.	2.7	1
5492	Complex I inhibitor of oxidative phosphorylation in advanced solid tumors and acute myeloid leukemia: phase I trials. Nature Medicine, 2023, 29, 115-126.	30.7	75
5494	The Integration of Data from Different Long-Read Sequencing Platforms Enhances Proteoform Characterization in Arabidopsis. Plants, 2023, 12, 511.	3.5	1
5495	scRNAâ€seq data analysis method to improve analysis performance. IET Nanobiotechnology, 2023, 17, 246-256.	3.8	5
5496	Co-expression network of heat-response transcripts: A glimpse into how splicing factors impact rice basal thermotolerance. Frontiers in Molecular Biosciences, 0, 10, .	3.5	1
5497	SIRT6 is a key regulator of mitochondrial function in the brain. Cell Death and Disease, 2023, 14, .	6.3	12
5498	The Role of Mitotic Slippage in Creating a â€œFemale Pregnancy-like Systemâ€•in a Single Polyploid Giant Cancer Cell. International Journal of Molecular Sciences, 2023, 24, 3237.	4.1	2
5499	Genome-wide identification and characterisation of bHLH transcription factors in Artemisia annua. BMC Plant Biology, 2023, 23, .	3.6	4
5501	Epigenetic Regulation of Corneal Epithelial Differentiation by TET2. International Journal of Molecular Sciences, 2023, 24, 2841.	4.1	1
5502	Transcriptional responses to 2,4-D herbicide treatment of a Eurasian (Myriophyllum spicatum) and a hybrid (M. spicatum Ã— M. sibiricum) genotype of watermilfoil that differ in their sensitivity to 2,4-D. Aquatic Botany, 2023, 186, 103631.	1.6	2
5503	Nanopore Direct RNA Sequencing of Monosome- and Polysome-Bound RNA. Methods in Molecular Biology, 2023, , 281-297.	0.9	2
5504	Transcriptome-based analysis reveals the key genes of sesquiterpene glycosylation in Dendrobium nobile. Food Science and Technology, 0, 43, .	1.7	0
5507	PFOS Induces Lipometabolism Change, Immune Defense, and Endocrine Disorders in Black-Spotted Frogs: Application of Transcriptome Profiling. Diversity, 2023, 15, 196.	1.7	1
5508	Knockout of AMD-associated gene POLDIP2 reduces mitochondrial superoxide in human retinal pigment epithelial cells. Aging, 2023, 15, 1713-1733.	3.1	1

#	Article	IF	Citations
5509	Pyruvate dehydrogenase fuels a critical citrate pool that is essential for Th17 cell effector functions. Cell Reports, 2023, 42, 112153.	6.4	7
5510	Reverse engineering environmental metatranscriptomes clarifies best practices for eukaryotic assembly. BMC Bioinformatics, 2023, 24, .	2.6	2
5511	Effect of Temperature on Microorganisms and Nitrogen Removal in a Multi-Stage Surface Flow Constructed Wetland. Water (Switzerland), 2023, 15, 1256.	2.7	2
5513	DNA virome composition of two sympatric wild felids, bobcat (Lynx rufus) and puma (Puma concolor) in Sonora, Mexico. Frontiers in Ecology and Evolution, 0, 11, .	2.2	0
5514	Increased A-to-I RNA editing in atherosclerosis and cardiomyopathies. PLoS Computational Biology, 2023, 19, e1010923.	3.2	2
5515	Combining time-resolved transcriptomics and proteomics data for Adverse Outcome Pathway refinement in ecotoxicology. Science of the Total Environment, 2023, 869, 161740.	8.0	2
5516	Rewiring of the 3D genome during acquisition of carboplatin resistance in a triple-negative breast cancer patient-derived xenograft. Scientific Reports, 2023, 13, .	3.3	0
5517	Microbial life in 25-m-deep boreholes in ancient permafrost illuminated by metagenomics. Environmental Microbiomes, 2023, 18, .	5.0	1
5518	GTPase splice variants RAC1 and RAC1B display isoform-specific differences in localization, prenylation, and interaction with the chaperone protein SmgGDS. Journal of Biological Chemistry, 2023, 299, 104698.	3.4	2
5519	Rapid evolutionary repair by secondary perturbation of a primary disrupted transcriptional network. EMBO Reports, 2023, 24, .	4.5	0
5520	Interactions between driver genes shape the signaling pathway landscape and direct hepatocellular carcinoma therapy. Cancer Science, 2023, 114, 2386-2399.	3.9	3
5522	Central androgen action reverses hypothalamic astrogliosis and atherogenic risk factors induced by orchiectomy and high-fat diet feeding in male mice. American Journal of Physiology - Endocrinology and Metabolism, 0, , .	3.5	0
5523	Dynamics of the Equine Placental DNA Methylome and Transcriptome from Mid- to Late Gestation. International Journal of Molecular Sciences, 2023, 24, 7084.	4.1	0
5524	Antibodies against endogenous retroviruses promote lung cancer immunotherapy. Nature, 2023, 616, 563-573.	27.8	59
5526	A drug repurposing approach for individualized cancer therapy based on transcriptome sequencing and virtual drug screening. Computers in Biology and Medicine, 2023, 157, 106781.	7.0	1
5527	Host-pathogen interaction involving cytoskeleton changes as well as non-coding regulation as primary mechanisms for SRS resistance in Atlantic salmon. Fish and Shellfish Immunology, 2023, 136, 108711.	3.6	0
5528	Genome-wide identification and expression profiling of the bZIP gene family in Betula platyphylla and the functional characterization of BpChr04G00610 under low-temperature stress. Plant Physiology and Biochemistry, 2023, 198, 107676.	5.8	2
5529	Ontogenesis of the molecular response to sleep loss. Neurobiology of Sleep and Circadian Rhythms, 2023, 14, 100092.	2.8	3

#	Article	IF	Citations
5530	Coal-source acid mine drainage reduced the soil multidrug-dominated antibiotic resistome but increased the heavy metal(loid) resistome and energy production-related metabolism. Science of the Total Environment, 2023, 873, 162330.	8.0	1
5531	QSP: An open sequence database for quorum sensing related gene analysis with an automatic annotation pipeline. Water Research, 2023, 235, 119814.	11.3	6
5532	DIET-like mutualism of Geobacter and methanogens at specific electrode potential boosts production of both methane and hydrogen from propionate. Water Research, 2023, 235, 119911.	11.3	17
5533	Effect and mechanism of nano iron oxide on muskmelon under cadmium stress. South African Journal of Botany, 2023, 157, 82-90.	2.5	2
5534	Physiological and transcriptomic responses of two Artemisia californica populations to drought: implications for restoring drought-resilient native communities. Global Ecology and Conservation, 2023, 43, e02466.	2.1	0
5535	Hydroxylation markedly alters how the polychlorinated biphenyl (PCB) congener, PCB52, affects gene expression in human preadipocytes. Toxicology in Vitro, 2023, 89, 105568.	2.4	7
5536	Arabidopsis transcriptome dataset of the response of imbibed wild-type and glucosinolate-deficient seeds to nitrogen-containing compounds. Data in Brief, 2023, 48, 109047.	1.0	1
5537	Generation of human iPSC-derived neurofibromaspheres for inÂvitro and inÂvivo uses. STAR Protocols, 2023, 4, 102198.	1.2	0
5538	Integrated miRNA-mRNA analysis reveals the molecular mechanism in mandarin fish (Siniperca chuatsi) in response to fresh baits and artificial diets feeding. Aquaculture Reports, 2023, 30, 101554.	1.7	2
5539	The impact of sex and physical activity on the local immune response to muscle pain. Brain, Behavior, and Immunity, 2023, 111, 4-20.	4.1	4
5540	Genome-wide identification and characterization of members of the LEA gene family in Panax notoginseng and their transcriptional responses to dehydration of recalcitrant seeds. BMC Genomics, 2023, 24, .	2.8	5
5541	Microbial community composition and metabolic potential during a succession of algal blooms from Skeletonema sp. to Phaeocystis sp.. Frontiers in Microbiology, 0, 14, .	3.5	2
5542	SOX17 Enhancer Variants Disrupt Transcription Factor Binding And Enhancer Inactivity Drives Pulmonary Hypertension. Circulation, 2023, 147, 1606-1621.	1.6	9
5543	Effect of stimulation intensity of a differential target multiplexed <scp>SCS</scp> program in an animal model of neuropathic pain. Pain Practice, 0, , .	1.9	0
5544	PolyQ length-dependent metabolic alterations and DNA damage drive human astrocyte dysfunction in Huntingtonâ€™s disease. Progress in Neurobiology, 2023, 225, 102448.	5.7	5
5545	River sediment microbial community composition and function impacted by thallium spill. Science of the Total Environment, 2023, 880, 163101.	8.0	3
5552	An Alkali-extracted polysaccharide from Poria cocos activates RAW264.7 macrophages via NF-ÎºB signaling pathway. Arabian Journal of Chemistry, 2023, 16, 104592.	4.9	3
5553	Hidden genetic variation in plasticity provides the potential for rapid adaptation to novel environments. New Phytologist, 2023, 239, 374-387.	7.3	7

#	Article	IF	Citations
5554	Computational approach to evaluate scRNA-seq data quality and gene body coverage with SkewC. STAR Protocols, 2023, 4, 102038.	1.2	0
5555	Sugars and sucrose transporters in pollinia of Phalaenopsis aphrodite (Orchidaceae). Journal of Experimental Botany, 2023, 74, 2556-2571.	4.8	1
5556	Molecular phenotyping of single pancreatic islet leader beta cells by â€œFlash-Seqâ€• Life Sciences, 2023, 316, 121436.	4.3	10
5557	Species interactions, stability, and resilience of the gut microbiota - Helminth assemblage in horses. IScience, 2023, 26, 106044.	4.1	13
5558	A comparative study of COVID-19 transcriptional signatures between clinical samples and preclinical cell models in the search for disease master regulators and drug repositioning candidates. Virus Research, 2023, 326, 199053.	2.2	2
5559	Mechanisms of response and resistance to combined decitabine and ipilimumab for advanced myeloid disease. Blood, 2023, 141, 1817-1830.	1.4	15
5560	Genome Sequencing. , 2021, , 298-317.		0
5562	Does the loss of diadromy imply the loss of salinity tolerance? A gene expression study with replicate nondiadromous populations of Galaxias maculatus. Molecular Ecology, 0, , .	3.9	1
5563	Metagenomic analysis characterizes resistomes of an acidic, multimetal(loid)-enriched coal source mine drainage treatment system. Journal of Hazardous Materials, 2023, 448, 130898.	12.4	2
5564	Airborne antibiotic resistome and human health risk in railway stations during COVID-19 pandemic. Environment International, 2023, 172, 107784.	10.0	3
5566	Contaminants of emerging concern in the Maumee River and their effects on freshwater mussel physiology. PLoS ONE, 2023, 18, e0280382.	2.5	4
5567	Transcriptional reprogramming of skeletal muscle stem cells by the niche environment. Nature Communications, 2023, 14, .	12.8	11
5569	METTL3 regulates breast cancer-associated alternative splicing switches. Oncogene, 2023, 42, 911-925.	5.9	12
5570	Wide distribution of D-xylose dehydrogenase in yeasts reveals a new element in the D-xylose metabolism for bioethanol production. FEMS Yeast Research, 2023, 23, .	2.3	2
5571	Mining Chromodoris quadricolor symbionts for biosynthesis of novel secondary metabolites. Marine Genomics, 2023, 68, 101017.	1.1	1
5572	Cytoprotective Effects of Human Platelet Lysate during the Xeno-Free Culture of Human Donor Corneas. International Journal of Molecular Sciences, 2023, 24, 2882.	4.1	2
5573	Transcriptomic Deconvolution of Neuroendocrine Neoplasms Predicts Clinically Relevant Characteristics. Cancers, 2023, 15, 936.	3.7	0
5574	Toblerone: detecting exon deletion events in cancer using RNA-seq. F1000Research, 0, 12, 130.	1.6	1

#	Article	IF	Citations
5578	The Foundational Data Initiative for Parkinson Disease: Enabling efficient translation from genetic maps to mechanism. Cell Genomics, 2023, 3, 100261.	6.5	12
5579	ESCRT-dependent STING degradation inhibits steady-state and cGAMP-induced signalling. Nature Communications, 2023, 14, .	12.8	25
5582	Two novel, tightly linked, and rapidly evolving genes underlie Aedes aegypti mosquito reproductive resilience during drought. ELife, 0, 12, .	6.0	3
5583	De novo transcriptome assemblies of C3 and C4 non-model grass species reveal key differences in leaf development. BMC Genomics, 2023, 24, .	2.8	4
5584	Functional characterization of interleukin 4 and retinoic acid signaling crosstalk during alternative macrophage activation. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2023, 1868, 159291.	2.4	4
5585	The rubber tree kinome: Genome-wide characterization and insights into coexpression patterns associated with abiotic stress responses. Frontiers in Plant Science, 0, 14, .	3.6	2
5586	PAT1-type GRAS-domain proteins control regeneration by activating DOF3.4 to drive cell proliferation in Arabidopsis roots. Plant Cell, 2023, 35, 1513-1531.	6.6	13
5587	Acute injury to the mouse carotid artery provokes a distinct healing response. Frontiers in Physiology, 0, 14, .	2.8	1
5588	Dissecting and targeting noncanonical functions of EZH2 in multiple myeloma via an EZH2 degrader. Oncogene, 2023, 42, 994-1009.	5.9	6
5589	RNAseq Analysis of FABP4 Knockout Mouse Hippocampal Transcriptome Suggests a Role for WNT/Î²-Catenin in Preventing Obesity-Induced Cognitive Impairment. International Journal of Molecular Sciences, 2023, 24, 3381.	4.1	3
5590	The broad use of the Pm8 resistance gene in wheat resulted in hypermutation of the AvrPm8 gene in the powdery mildew pathogen. BMC Biology, 2023, 21, .	3.8	11
5591	Moesin is an effector of tau-induced actin overstabilization, cell cycle activation, and neurotoxicity in Alzheimerâ€™s disease. IScience, 2023, 26, 106152.	4.1	5
5592	The Combination of Both Heat and Water Stresses May Worsen Botryosphaeria Dieback Symptoms in Grapevine. Plants, 2023, 12, 753.	3.5	7
5593	The catalytic-dead Pcif1 regulates gene expression and fertility inDrosophila. Rna, 2023, 29, 609-619.	3.5	3
5594	Exploring the Anti-Inflammatory Effect of Inulin by Integrating Transcriptomic and Proteomic Analyses in a Murine Macrophage Cell Model. Nutrients, 2023, 15, 859.	4.1	6
5595	Development of a CRISPRi Human Retinal Pigmented Epithelium Model for Functional Study of Age-Related Macular Degeneration Genes. International Journal of Molecular Sciences, 2023, 24, 3417.	4.1	3
5597	Conserved gene signatures shared among MAPT mutations reveal defects in calcium signaling. Frontiers in Molecular Biosciences, 0, 10, .	3.5	4
5598	538. A functional copy number gain at indicine cattle footprint modulates actin-myosin and immune response genes in muscle. , 2022, , .		0

#	Article	IF	Citations
5599	Uncovering a Complex Virome Associated with the Cacao Pathogens Ceratocystis cacaofunesta and Ceratocystis fimbriata. Pathogens, 2023, 12, 287.	2.8	3
5600	Pancreatic microexons regulate islet function and glucose homeostasis. Nature Metabolism, 2023, 5, 219-236.	11.9	4
5601	Transcription factor SOX15 regulates stem cell pluripotency and promotes neural fate during differentiation by activating the neurogenic gene Hes5. Journal of Biological Chemistry, 2023, 299, 102996.	3.4	1
5602	Using single cell atlas data to reconstruct regulatory networks. Nucleic Acids Research, 2023, 51, e38-e38.	14.5	3
5603	REPAC: analysis of alternative polyadenylation from RNA-sequencing data. Genome Biology, 2023, 24, .	8.8	2
5604	Seasonal Changes in the Structure and Function of Gut Microbiota in the Muskrat (Ondatra) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.9	3
5605	The genome of Magnolia hypoleuca provides a new insight into cold tolerance and the evolutionary position of magnoliids. Frontiers in Plant Science, 0, 14, .	3.6	3
5606	Enrichment of tetracycline-degrading bacterial consortia: Microbial community succession and degradation characteristics and mechanism. Journal of Hazardous Materials, 2023, 448, 130984.	12.4	17
5607	FGL2-targeting T cells exhibit antitumor effects on glioblastoma and recruit tumor-specific brain-resident memory T cells. Nature Communications, 2023, 14, .	12.8	3
5608	Intron dynamics reveal principles of gene regulation during the maternal-to-zygotic transition. Rna, 2023, 29, 596-608.	3.5	1
5609	Regulatory dissection of the severe COVID-19 risk locus introgressed by Neanderthals. ELife, 0, 12, .	6.0	7
5611	Identifying RNA Modifications by Direct RNA Sequencing Reveals Complexity of Epitranscriptomic Dynamics in Rice. Genomics, Proteomics and Bioinformatics, 2023, 21, 788-804.	6.9	4
5612	Transcriptome of GH-producing pituitary neuroendocrine tumours and models are significantly affected by somatostatin analogues. Cancer Cell International, 2023, 23, .	4.1	0
5613	Metagenome-Assembled Genomes from Murine Fecal Microbiomes Dominated by Uncharacterized Bacteria. Microbiology Resource Announcements, 2023, 12, .	0.6	0
5614	Amniotes co-opt intrinsic genetic instability to protect germ-line genome integrity. Nature Communications, 2023, 14, .	12.8	4
5616	Transcriptome changes in chlorsulfuron-treated plants are caused by acetolactate synthase inhibition and not induction of a herbicide detoxification system in Marchantia polymorpha. Pesticide Biochemistry and Physiology, 2023, 191, 105370.	3.6	0
5619	Age-differential sexual dimorphisms in CHD8-S62X-mutant mouse synapses and transcriptomes. Frontiers in Molecular Neuroscience, 0, 16, .	2.9	1
5620	Genomic structural variation: A complex but important driver of human evolution. American Journal of Biological Anthropology, 2023, 181, 118-144.	1.1	3

#	Article	IF	Citations
5621	High Sox2 expression predicts taste lineage competency of lingual progenitors in vitro. Development (Cambridge), 2023, 150, .	2.5	3
5622	Transcriptome profiling reveals a global response in harmful dinoflagellate Karlodinium veneficum to naturally-occurring bacterial algicides. Frontiers in Marine Science, 0, 10, .	2.5	1
5623	CD5 expression by dendritic cells directs T cell immunity and sustains immunotherapy responses. Science, 2023, 379, .	12.6	26
5624	Sorting nexin 10 sustains PDGF receptor signaling in glioblastoma stem cells via endosomal protein sorting. JCI Insight, 2023, 8, .	5.0	3
5625	Widespread perturbation of ETS factor binding sites in cancer. Nature Communications, 2023, 14, .	12.8	1
5626	Transcriptomic and Metabolomic Studies Reveal That Toll-like Receptor 2 Has a Role in Glucose-Related Metabolism in Unchallenged Zebrafish Larvae (Danio rerio). Biology, 2023, 12, 323.	2.8	0
5627	BRG1 HSA domain interactions with BCL7 proteins are critical for remodeling and gene expression. Life Science Alliance, 2023, 6, e202201770.	2.8	2
5628	Circulating Interleukin-8 Dynamics Parallels Disease Course and Is Linked to Clinical Outcomes in Severe COVID-19. Viruses, 2023, 15, 549.	3.3	3
5629	Platelet-instructed SPP1+ macrophages drive myofibroblast activation in fibrosis in a CXCL4-dependent manner. Cell Reports, 2023, 42, 112131.	6.4	38
5630	Species-specific dynamics of specialized metabolism in germinating sorghum grain revealed by temporal and tissue-resolved transcriptomics and metabolomics. Plant Physiology and Biochemistry, 2023, 196, 807-820.	5.8	3
5631	The essential roles of FXR in diet and age influenced metabolic changes and liver disease development: a multi-omics study. Biomarker Research, 2023, 11, .	6.8	4
5632	Evolutionary History of thePoecilia pictaSex Chromosomes. Genome Biology and Evolution, 2023, 15, .	2.5	4
5633	Approaches for sRNA Analysis of Human RNA-Seq Data: Comparison, Benchmarking. International Journal of Molecular Sciences, 2023, 24, 4195.	4.1	2
5634	Genome-wide analysis of NBS-LRR genes revealed contribution of disease resistance from Saccharum spontaneum to modern sugarcane cultivar. Frontiers in Plant Science, 0, 14, .	3.6	0
5635	A Natural Glucan from Black Bean Inhibits Cancer Cell Proliferation via PI3K-Akt and MAPK Pathway. Molecules, 2023, 28, 1971.	3.8	3
5636	Variation in microbial CAZyme families across degradation severity in a steppe grassland in northern China. Frontiers in Environmental Science, 0, 11, .	3.3	3
5638	Dynamics of soil microbiome throughout the cultivation life cycle of morel (Morchella sextelata). Frontiers in Microbiology, 0, 14, .	3.5	7
5639	Metagenomic and machine learning-aided identification of biomarkers driving distinctive Cd accumulation features in the root-associated microbiome of two rice cultivars. ISME Communications, 2023, 3, .	4.2	13

#	Article	IF	Citations
5640	Composition and Metabolic Potential of Fe(III)-Reducing Enrichment Cultures of Methanotrophic ANME-2a Archaea and Associated Bacteria. Microorganisms, 2023, 11, 555.	3.6	4
5641	Beyond bacteria: Reconstructing microorganism connections and deciphering the predicted mutualisms in mammalian gut metagenomes. Ecology and Evolution, 2023, 13, .	1.9	1
5642	Skeletal dysplasia-causing TRPV4 mutations suppress the hypertrophic differentiation of human iPSC-derived chondrocytes. ELife, 0, 12, .	6.0	3
5644	Monocytes re-enter the bone marrow during fasting and alter the host response to infection. Immunity, 2023, 56, 783-796.e7.	14.3	33
5645	Transcriptomes of Zebrafish in Early Stages of Multiple Viral Invasions Reveal the Role of Sterols in Innate Immune Switch-On. International Journal of Molecular Sciences, 2023, 24, 4427.	4.1	0
5646	TEFM variants impair mitochondrial transcription causing childhood-onset neurological disease. Nature Communications, 2023, 14, .	12.8	5
5647	Metagenomic analysis reveals patterns and hosts of antibiotic resistance in different pig farms. Environmental Science and Pollution Research, 2023, 30, 52087-52106.	5.3	3
5648	Latitudinal variation and plasticity in response to temperature in Geukensia demissa. Ecology and Evolution, 2023, 13, .	1.9	3
5650	Transposable element and host silencing activity in gigantic genomes. Frontiers in Cell and Developmental Biology, 0, 11, .	3.7	3
5655	Chemical conversion of human conventional <scp>PSCs</scp> to <scp>TSCs</scp> following transient naive gene activation. EMBO Reports, 2023, 24, .	4.5	4
5656	Transcriptomics explores the potential of flavonoid in non-medicinal parts of Saposhnikovia divaricata (Turcz.) Schischk. Frontiers in Plant Science, 0, 14, .	3.6	0
5658	Cross-species predictive modeling reveals conserved drought responses between maize and sorghum. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	1
5659	Specific targeting of inflammatory osteoclastogenesis by the probiotic yeast S. boulardii CNCM I-745 reduces bone loss in osteoporosis. ELife, 0, 12, .	6.0	5
5660	Core cellular and tissueâ€specific mechanisms enable desiccation tolerance in Craterostigma. Plant Journal, 2023, 114, 231-245.	5.7	9
5661	A genomeâ€“wide CRISPR activation screen identifies SCREEM a novel SNAI1 super-enhancer demarcated by eRNAs. Frontiers in Molecular Biosciences, 0, 10, .	3.5	0
5662	Functional Genetics to Understand the Etiology of Autoimmunity. Genes, 2023, 14, 572.	2.4	2
5663	Metabolic Robustness to Growth Temperature of a Cold- Adapted Marine Bacterium. MSystems, 2023, 8, .	3.8	4
5664	Adrenal gene expression dynamics support hibernation in 13-lined ground squirrels. Physiological Genomics, 2023, 55, 155-167.	2.3	0

#	Article	IF	Citations
5665	Diversity and Differential Expression of MicroRNAs in the Human Skeletal Muscle with Distinct Fiber Type Composition. Life, 2023, 13, 659.	2.4	4
5666	Potato tonoplast sugar transporter 1 controls tuber sugar accumulation during postharvest cold storage. Horticulture Research, 2023, 10, .	6.3	2
5667	The RNA binding protein DND1 is elevated in a subpopulation of pro-spermatogonia and targets chromatin modifiers and translational machinery during late gestation. PLoS Genetics, 2023, 19, e1010656.	3.5	0
5669	The majority of microorganisms in gas hydrate-bearing subseafloor sediments ferment macromolecules. Microbiome, 2023, 11, .	11.1	7
5670	Metatranscriptomics Reveals Sequential Expression of Genes Involved in the Production of Melanogenesis Inhibitors by the Defined Microbial Species in Fermented Unpolished Black Rice. Microbiology Spectrum, 2023, 11, .	3.0	1
5671	Functional annotation of the animal genomes: An integrated annotation resource for the horse. PLoS Genetics, 2023, 19, e1010468.	3.5	3
5672	Remodeling oncogenic transcriptomes by small molecules targeting NONO. Nature Chemical Biology, 2023, 19, 825-836.	8.0	15
5673	Comparative phylogenomic insights of KCS and ELO gene families in Brassica species indicate their role in seed development and stress responsiveness. Scientific Reports, 2023, 13, .	3.3	3
5674	USB1 is a miRNA deadenylase that regulates hematopoietic development. Science, 2023, 379, 901-907.	12.6	11
5675	Hot moment of N2O emissions in seasonally frozen peatlands. ISME Journal, 2023, 17, 792-802.	9.8	3
5678	RNA localization mechanisms transcend cell morphology. ELife, 0, 12, .	6.0	10
5679	Mu-opioid receptor-expressing neurons in the paraventricular thalamus modulate chronic morphine-induced wake alterations. Translational Psychiatry, 2023, 13, .	4.8	5
5680	Tumor microenvironment remodeling after neoadjuvant immunotherapy in non-small cell lung cancer revealed by single-cell RNA sequencing. Genome Medicine, 2023, 15, .	8.2	23
5681	Dopamine Inhibits Arabidopsis Growth through Increased Oxidative Stress and Auxin Activity. Stresses, 2023, 3, 351-371.	4.8	0
5682	Omics and imaging combinatorial approach reveals butyrate-induced inflammatory effects in the zebrafish gut. Animal Microbiome, 2023, 5, .	3.8	3
5683	Hippocampal GFAP-positive astrocyte responses to amyloid and tau pathologies. Brain, Behavior, and Immunity, 2023, 110, 175-184.	4.1	16
5685	A complex role of Arabidopsis CDKD;3 in meiotic progression and cytokinesis. Plant Direct, 2023, 7, .	1.9	1
5686	IFNÎ³ is a central node of cancer immune equilibrium. Cell Reports, 2023, 42, 112219.	6.4	6

#	Article	IF	Citations
5687	Identification of the NA+/K+-ATPase Î±-Isoforms in Six Species of Poison Dart Frogs and their Sensitivity to Cardiotonic Steroids. Journal of Chemical Ecology, 2023, 49, 116-132.	1.8	1
5689	Discovering Synergistic Compounds with BYL-719 in PI3K Overactivated Basal-like PDXs. Cancers, 2023, 15, 1582.	3.7	4
5690	CD73-Positive Cell Spheroid Transplantation Attenuates Colonic Atrophy. Pharmaceutics, 2023, 15, 845.	4.5	1
5691	Developmental dynamic transcriptome and systematic analysis reveal the major genes underlying isoflavone accumulation in soybean. Frontiers in Plant Science, 0, 14, .	3.6	4
5693	Microfluidics-free single-cell genomics with templated emulsification. Nature Biotechnology, 2023, 41, 1557-1566.	17.5	34
5695	Improved protocol for single-nucleus RNA-sequencing of frozen human bladder tumor biopsies. Nucleus, 2023, 14, .	2.2	1
5696	Muscle pathology of antisynthetase syndrome according to antibody subtypes. Brain Pathology, 2023, 33, .	4.1	7
5697	Transcriptome Sequencing Reveals the Mechanism behind Chemically Induced Oral Mucositis in a 3D Cell Culture Model. International Journal of Molecular Sciences, 2023, 24, 5058.	4.1	0
5699	Alterations in oligodendrocyte transcriptional networks reveal region-specific vulnerabilities to neurological disease. IScience, 2023, 26, 106358.	4.1	1
5701	Brain injury accelerates the onset of a reversible age-related microglial phenotype associated with inflammatory neurodegeneration. Science Advances, 2023, 9, .	10.3	16
5702	Hologenome analysis reveals independent evolution to chemosymbiosis by deep-sea bivalves. BMC Biology, 2023, 21, .	3.8	2
5703	Overexpression of Parkin in the Neuronal Progenitor Cells from a Patient with Parkinsonâ€™s Disease Shifts the Transcriptome Towards the Normal State. Molecular Neurobiology, 0, , .	4.0	0
5704	Comprehensive transcriptome analysis of different potato cultivars provides insight into early blight disease caused by Alternaria solani. BMC Plant Biology, 2023, 23, .	3.6	4
5708	Epidermal threads reveal the origin of hagfish slime. ELife, 0, 12, .	6.0	2
5709	Multi-omics analysis revealed the brain dysfunction induced by energy metabolism in Pelteobagrus vachelli under hypoxia stress. Ecotoxicology and Environmental Safety, 2023, 254, 114749.	6.0	4
5712	Transcriptome Analysis During Tetrasporogenesis of Gracilariopsis lemaneiformis and Preliminary Study of the Expressions of Its Meiotic Genes. Journal of Ocean University of China, 2023, 22, 541-554.	1.2	0
5713	CRISPR-assisted transcription activation by phase-separation proteins. Protein and Cell, 2023, 14, 874-887.	11.0	4
5714	The temporal transcriptomic signature of cartilage formation. Nucleic Acids Research, 2023, 51, 3590-3617.	14.5	8

#	Article	IF	Citations
5716	RNA-seq data science: From raw data to effective interpretation. Frontiers in Genetics, 0, 14, .	2.3	16
5718	Vitamin B12 attenuates leukocyte inflammatory signature in COVID-19 via methyl-dependent changes in epigenetic markings. Frontiers in Immunology, 0, 14, .	4.8	4
5719	C-Type Natriuretic Peptide Acts as a Microorganism-Activated Regulator of the Skin Commensals Staphylococcus epidermidis and Cutibacterium acnes in Dual-Species Biofilms. Biology, 2023, 12, 436.	2.8	2
5720	Effective root responses to salinity stress include maintained cell expansion and carbon allocation. New Phytologist, 2023, 238, 1942-1956.	7.3	5
5721	P53 Deficiency Accelerate Esophageal Epithelium Intestinal Metaplasia Malignancy. Biomedicines, 2023, 11, 882.	3.2	1
5724	Lymphocytic Choriomeningitis Virus Clone 13 Infection Results in CD8 T Cellâ€“Mediated Host Mortality in Diacylglycerol Kinase Î±â€“Deficient Mice. Journal of Immunology, 2023, 210, 1281-1291.	0.8	0
5726	Low dissolved oxygen supply functions as a global regulator of the growth and metabolism of Aurantiochytrium sp. PKU#Mn16 in the early stages of docosahexaenoic acid fermentation. Microbial Cell Factories, 2023, 22, .	4.0	1
5727	Matrin3 regulates mitotic spindle dynamics by controlling alternative splicing of CDC14B. Cell Reports, 2023, 42, 112260.	6.4	2
5728	Estrogen receptor alpha deficiency in cardiomyocytes reprograms the heart-derived extracellular vesicle proteome and induces obesity in female mice. , 2023, 2, 268-289.		1
5729	The CCR6/CCL20 axis expands RORÎ³t+ Tregs to protect from glomerulonephritis. Kidney International, 2023, 104, 74-89.	5.2	3
5730	Lineage-specific differences and regulatory networks governing human chondrocyte development. ELife, 0, 12, .	6.0	7
5732	Diseased-induced multifaceted variations in community assembly and functions of plant-associated microbiomes. Frontiers in Microbiology, 0, 14, .	3.5	3
5733	Comparative Analysis of the Characteristics, Phylogenetic Relationships of the Complete Chloroplast Genome, and Maternal Origin Track of White Poplar Interspecific Hybrid GM107. Forests, 2023, 14, 587.	2.1	0
5734	NOMe-HiC: joint profiling of genetic variant, DNA methylation, chromatin accessibility, and 3D genome in the same DNA molecule. Genome Biology, 2023, 24, .	8.8	1
5735	RIP140 deficiency enhances cardiac fuel metabolism and protects mice from heart failure. Journal of Clinical Investigation, 2023, 133, .	8.2	2
5738	The <scp>NLRomes</scp> of Zea maysÂ<scp>NAM</scp> founder lines and Zea luxurians display presenceâ€“absence variation, integrated domain diversity, and mobility. Molecular Plant Pathology, 2023, 24, 742-757.	4.2	3
5739	Assembly of novel microbial genomes from gut metagenomes of rhesus macaque (Macaca) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10	9.8	5
5740	A survey of lineageâ€specific genes in Triticeae reveals de novo gene evolution from genomic raw material. Plant Direct, 2023, 7, .	1.9	4

#	Article	IF	Citations
5741	Antipsychotic drug use complicates assessment of gene expression changes associated with schizophrenia. Translational Psychiatry, 2023, 13, .	4.8	3
5747	Transcriptome dataset from Solanum lycopersicum L. cv. Micro-Tom; wild type and two mutants of INDOLE-ACETIC-ACID (SlIAA9) using long-reads sequencing oxford nanopore technologies. BMC Research Notes, 2023, 16, .	1.4	0
5748	Comprehensive analysis of the WRKY gene family in Cucumis metuliferus and their expression profile in response to an early stage of root knot nematode infection. Frontiers in Plant Science, 0, 14, .	3.6	0
5750	A multiâ€omic approach identifies an autism spectrum disorder (<scp>ASD</scp>) regulatory complex of functional epimutations in placentas from children born preterm. Autism Research, 2023, 16, 918-934.	3.8	0
5751	Characterization and simulation of metagenomic nanopore sequencing data with Meta-NanoSim. GigaScience, 2023, 12, .	6.4	5
5752	Ectodermal Wnt signaling, cell fate determination, and polarity of the skate gill arch skeleton. ELife, 0, 12, .	6.0	1
5753	Dynamic transcriptomic responses to divergent acute exercise stimuli in young adults. Physiological Genomics, 2023, 55, 194-212.	2.3	1
5755	Transcriptomic and Metabolomic Profiles Provide Insights into the Red-Stipe Symptom of Morel Fruiting Bodies. Journal of Fungi (Basel, Switzerland), 2023, 9, 373.	3.5	5
5759	Stromal Senescence following Treatment with the CDK4/6 Inhibitor Palbociclib Alters the Lung Metastatic Niche and Increases Metastasis of Drug-Resistant Mammary Cancer Cells. Cancers, 2023, 15, 1908.	3.7	5
5760	Multi-transcriptomics reveals RLMF axis-mediated signaling molecules associated with bovine feed efficiency. Frontiers in Veterinary Science, 0, 10, .	2.2	2
5761	Longitudinal map of transcriptome changes in the Lyme pathogen Borrelia burgdorferi during tick-borne transmission. ELife, 0, 12, .	6.0	3
5762	Gene Coexpression Analysis Identifies Genes Associated with Chlorophyll Content and Relative Water Content in Pearl Millet. Plants, 2023, 12, 1412.	3.5	0
5765	Unexpected phenotypic and molecular changes of combined glucocerebrosidase and acid sphingomyelinase deficiency. DMM Disease Models and Mechanisms, 0, , .	2.4	2
5766	Elucidation of the pathway for biosynthesis of saponin adjuvants from the soapbark tree. Science, 2023, 379, 1252-1264.	12.6	30
5767	Notch activation promotes bone metastasis via <scp>SPARC</scp> inhibition in adenoid cystic carcinoma. Oral Diseases, 0, , .	3.0	1
5768	The DREAM complex functions as conserved master regulator of somatic DNA-repair capacities. Nature Structural and Molecular Biology, 2023, 30, 475-488.	8.2	18
5770	A post-transcriptional regulatory landscape of aging in the female mouse hippocampus. Frontiers in Aging Neuroscience, 0, 15, .	3.4	1
5771	Direct reprogramming of human fibroblasts into insulin-producing cells using transcription factors. Communications Biology, 2023, 6, .	4.4	3

#	Article	IF	Citations
5772	Photobiomodulation Reduces the Cytokine Storm Syndrome Associated with COVID-19 in the Zebrafish Model. International Journal of Molecular Sciences, 2023, 24, 6104.	4.1	2
5774	Torula yeast may improve intestinal health and immune function of weanling pigs. Journal of Animal Science, 2023, 101, .	0.5	0
5776	DNA methyltransferase inhibition induces dynamic gene expression changes in lung CD4+ T cells of neonatal mice with E. coli pneumonia. Scientific Reports, 2023, 13, .	3.3	0
5778	Convergent and complementary selection shaped gains and losses of eusociality in sweat bees. Nature Ecology and Evolution, 2023, 7, 557-569.	7.8	9
5779	DELLA functions evolved by rewiring of associated transcriptional networks. Nature Plants, 2023, 9, 535-543.	9.3	4
5780	Fine mapping and candidate gene analysis of CaFCD1 affecting cuticle biosynthesis in Capsicum annuum L.. Theoretical and Applied Genetics, 2023, 136, .	3.6	1
5781	Setd2 inactivation sensitizes lung adenocarcinoma to inhibitors of oxidative respiration and mTORC1 signaling. Communications Biology, 2023, 6, .	4.4	2
5782	Hidden Genetic Regulation of Human Complex Traits via Brain Isoforms. Phenomics, 0, , .	2.9	0
5784	Discovery and genome-guided mapping of REN12 from Vitis amurensis, conferring strong, rapid resistance to grapevine powdery mildew. Horticulture Research, 2023, 10, .	6.3	5
5785	Single Nucleotide Polymorphism rs9277336 Controls the Nuclear Alpha Actinin 4â€Human Leukocyte Antigenâ€DPA1 Axis and Pulmonary Endothelial Pathophenotypes in Pulmonary Arterial Hypertension. Journal of the American Heart Association, 2023, 12, .	3.7	1
5786	Loss of ancestral function in duckweed roots is accompanied by progressive anatomical reduction and a re-distribution of nutrient transporters. Current Biology, 2023, 33, 1795-1802.e4.	3.9	12
5787	Functional Annotation Routines Used by ABRF Bioinformatics Core Facilities - Observations, Comparisons, and Considerations. Journal of Biomolecular Techniques, 2023, 34, 3fc1f5fe.0b74b9db.	1.5	0
5788	X chromosome dosage and the genetic impact across human tissues. Genome Medicine, 2023, 15, .	8.2	8
5789	Chromosomal dominance in apple after whole genome duplication. Acta Horticulturae, 2023, , 57-64.	0.2	0
5790	Collagen Hydrogel Containing Polyethylenimineâ€Gold Nanoparticles for Drug Release and Enhanced Beating Properties of Engineered Cardiac Tissues. Advanced Healthcare Materials, 2023, 12, .	7.6	14
5791	FAK suppresses antigen processing and presentation to promote immune evasion in pancreatic cancer. Gut, 2024, 73, 131-155.	12.1	7
5792	Metal-Driven Anaerobic Oxidation of Methane as an Important Methane Sink in Methanic Cold Seep Sediments. Microbiology Spectrum, 2023, 11, .	3.0	5
5793	The phenotype of the most common human <scp>ADAR1p150</scp> ZÎ± mutation <scp>P193A</scp> in mice is partially penetrant. EMBO Reports, 2023, 24, .	4.5	8

#	Article	IF	Citations
5794	Evaluation of reference genes for transcript analyses in Komagataella phaffii (Pichia pastoris). Fungal Biology and Biotechnology, 2023, 10, .	5.1	1
5795	A-MYB and BRDT-dependent RNA Polymerase II pause release orchestrates transcriptional regulation in mammalian meiosis. Nature Communications, 2023, 14, .	12.8	8
5796	Cell-autonomous effect of cardiomyocyte branched-chain amino acid catabolism in heart failure in mice. Acta Pharmacologica Sinica, 2023, 44, 1380-1390.	6.1	7
5797	Unexpected genetic and microbial diversity for arsenic cycling in deep sea cold seep sediments. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	3
5800	A novel eukaryotic RdRP-dependent small RNA pathway represses antiviral immunity by controlling an ERK pathway component in the black-legged tick. PLoS ONE, 2023, 18, e0281195.	2.5	1
5801	Transformation of primary murine peritoneal mast cells by constitutive KIT activation is accompanied by loss of Cdkn2a/Arf expression. Frontiers in Immunology, 0, 14, .	4.8	0
5802	Site-1 protease inhibits mitochondrial respiration by controlling the TGF-Î² target gene Mss51. Cell Reports, 2023, 42, 112336.	6.4	1
5803	The effects of circularly polarized light on mating behavior and gene expression in Anomala corpulenta (Coleoptera: Scarabaeidae). Frontiers in Physiology, 0, 14, .	2.8	0
5804	C ₄ gene induction during de-etiolation evolved through changes in cis to allow integration with ancestral C ₃ gene regulatory networks. Science Advances, 2023, 9, .	10.3	4
5805	Glucocorticoid-mediated induction of ZBTB16 affects insulin secretion in human islets and EndoC-Î²H1 Î²-cells. IScience, 2023, 26, 106555.	4.1	0
5806	Spectrum Preserving Tilings Enable Sparse andÂModular Reference Indexing. Lecture Notes in Computer Science, 2023, , 21-40.	1.3	6
5808	Skeletal muscle gene expression dysregulation in long-term spaceflights and aging is clock-dependent. Npj Microgravity, 2023, 9, .	3.7	2
5809	A novel transcriptional signature identifies T-cell infiltration in high-risk paediatric cancer. Genome Medicine, 2023, 15, .	8.2	2
5810	Genome-Wide Analysis of the Odorant Receptor Gene Family in Solenopsis invicta, Ooceraea biroi, and Monomorium pharaonis (Hymenoptera: Formicidae). International Journal of Molecular Sciences, 2023, 24, 6624.	4.1	1
5812	Transcriptomic Changes Predict Metabolic Alterations in LC3 Associated Phagocytosis in Aged Mice. International Journal of Molecular Sciences, 2023, 24, 6716.	4.1	0
5813	A computationally-enhanced hiCLIP atlas reveals Staufen1-RNA binding features and links 3â€² UTR structure to RNA metabolism. Nucleic Acids Research, 2023, 51, 3573-3589.	14.5	2
5815	Hepatic stellate cell activation markers are regulated by the vagus nerve in systemic inflammation. Bioelectronic Medicine, 2023, 9, .	2.3	1
5817	The peptide woods are lovely, dark and deep: Hunting for novel cancer antigens. Seminars in Immunology, 2023, 67, 101758.	5.6	4

#	Article	IF	Citations
5818	Vertically stratified methane, nitrogen and sulphur cycling and coupling mechanisms in mangrove sediment microbiomes. Microbiome, 2023, 11, .	11.1	7
5819	Profiling system-wide variations and similarities between Rheumatic Heart Disease and Acute Rheumatic Feverâ€“A pilot analysis. PLoS Neglected Tropical Diseases, 2023, 17, e0011263.	3.0	0
5821	FHL5 Controls Vascular Diseaseâ€“Associated Gene Programs in Smooth Muscle Cells. Circulation Research, 2023, 132, 1144-1161.	4.5	5
5822	Sampling strategies for sugarcane using either clonal replicates or diverse genotypes can bias the conclusions of RNA-Seq studies. Genetics and Molecular Biology, 2023, 46, .	1.3	0
5823	Lung adenocarcinoma promotion by air pollutants. Nature, 2023, 616, 159-167.	27.8	135
5824	Dual functions of TET1 in germ layer lineage bifurcation distinguished by genomic context and dependence on 5-methylcytosine oxidation. Nucleic Acids Research, 2023, 51, 5469-5498.	14.5	1
5827	Skeletal muscle transcriptomics dissects the pathogenesis of Friedreichâ€™s ataxia. Human Molecular Genetics, 2023, 32, 2241-2250.	2.9	2
5828	Neuroprotective Effects of Genome-Edited Human iPS Cell-Derived Neural Stem/Progenitor Cells on Traumatic Brain Injury. Stem Cells, 2023, 41, 603-616.	3.2	4
5829	High-resolution Nanopore methylome-maps reveal random hyper-methylation at CpG-poor regions as driver of chemoresistance in leukemias. Communications Biology, 2023, 6, .	4.4	2
5833	Functional specialization of short-lived and long-lived macrophage subsets in human tonsils. Journal of Experimental Medicine, 2023, 220, .	8.5	3
5834	Differential Hsp90-dependent gene expression is strain-specific and common among yeast strains. IScience, 2023, 26, 106635.	4.1	0
5835	The transcriptome of Litopenaeus vannamei in zoea larvae and adults infected by Vibrio parahaemolyticus. Frontiers in Marine Science, 0, 10, .	2.5	0
5836	Metagenomic analysis reveals indole signaling effect on microbial community in sequencing batch reactors: Quorum sensing inhibition and antibiotic resistance enrichment. Environmental Research, 2023, 229, 115897.	7.5	1
5837	Differential transcript usage analysis incorporating quantification uncertainty via compositional measurement error regression modeling. Biostatistics, 0, , .	1.5	1
5839	<scp>LncRNA FLAIL</scp> affects alternative splicing and represses flowering in Arabidopsis. EMBO Journal, 2023, 42, .	7.8	5
5842	Increasing cell culture density during a developmental window prevents fated rod precursors derailment toward hybrid rod-glia cells. Scientific Reports, 2023, 13, .	3.3	0
5843	Comparative proteome profile of ungerminated spores and mycelium of the fungus Moniliophthora roreri, causal agent of frosty pod rot disease in cacao. Journal of Phytopathology, 2023, 171, 242-257.	1.0	0
5844	Mosaic results after preimplantation genetic testing for aneuploidy may be accompanied by changes in global gene expression. Frontiers in Molecular Biosciences, 0, 10, .	3.5	4

#	Article	IF	Citations
5845	An Efficient 2D Protocol for Differentiation of iPSCs into Mature Postmitotic Dopaminergic Neurons: Application for Modeling Parkinsonâ€™s Disease. International Journal of Molecular Sciences, 2023, 24, 7297.	4.1	1
5846	Tumor heterogeneity in VHL drives metastasis in clear cell renal cell carcinoma. Signal Transduction and Targeted Therapy, 2023, 8, .	17.1	7
5850	Improved analysis of (e)CLIP data with RCRUNCH yields a compendium of RNA-binding protein binding sites and motifs. Genome Biology, 2023, 24, .	8.8	3
5851	Xanthine Dehydrogenase Is a Modulator of Dopaminergic Neurodegeneration in Response to Bacterial Metabolite Exposure in C. elegans. Cells, 2023, 12, 1170.	4.1	2
5852	Differentiation of astrocytes with characteristics of ventral midbrain from human embryonic stem cells. Stem Cell Reviews and Reports, 0, , .	3.8	1
5855	Definition of the transcriptional units of inherited retinal disease genes by meta-analysis of human retinal transcriptome data. BMC Genomics, 2023, 24, .	2.8	0
5856	Copy number variation in tRNA isodecoder genes impairs mammalian development and balanced translation. Nature Communications, 2023, 14, .	12.8	7
5857	Lamin B1 overexpression alters chromatin organization and gene expression. Nucleus, 2023, 14, .	2.2	4
5858	African American Prostate Cancer Displays Quantitatively Distinct Vitamin D Receptor Cistrome-transcriptome Relationships Regulated by BAZ1A. Cancer Research Communications, 2023, 3, 621-639.	1.7	4
5859	Nutrient-sensing AgRP neurons relay control of liver autophagy during energy deprivation. Cell Metabolism, 2023, 35, 786-806.e13.	16.2	10
5860	Integration of deep learning-based histopathology and transcriptomics reveals key genes associated with fibrogenesis in patients with advanced NASH. Cell Reports Medicine, 2023, 4, 101016.	6.5	2
5861	Vascular Stem Cells and the Role of B-Raf Kinase in Survival, Proliferation, and Apoptosis. International Journal of Molecular Sciences, 2023, 24, 7483.	4.1	0
5862	Bacterial community responses to planktonic and terrestrial substrates in coastal northern Baltic Sea. Frontiers in Marine Science, 0, 10, .	2.5	2
5863	Differential protease content of mast cells and the processing of IL-33 in Alternaria alternata induced allergic airway inflammation in mice. Frontiers in Immunology, 0, 14, .	4.8	1
5864	Microbial functional genes within soil aggregates drive organic carbon mineralization under contrasting tillage practices. Land Degradation and Development, 2023, 34, 3618-3635.	3.9	1
5867	A Genomic and Transcriptomic Analysis of the C-Type Lectin Gene Family Reveals Highly Expanded and Diversified Repertoires in Bivalves. Marine Drugs, 2023, 21, 254.	4.6	5
5868	Metagenome and metabolome insights into the energy compensation and exogenous toxin degradation of gut microbiota in high-altitude rhesus macaques (Macaca mulatta). Npj Biofilms and Microbiomes, 2023, 9, .	6.4	0
5869	Swine farm groundwater is a hidden hotspot for antibiotic-resistant pathogenic Acinetobacter. ISME Communications, 2023, 3, .	4.2	1

#	Article	IF	Citations
5870	Genetics of myocardial interstitial fibrosis in the human heart and association with disease. Nature Genetics, 2023, 55, 777-786.	21.4	13
5871	Acclimation of the Antarctic sea urchin Sterechinus neumayeri to warmer temperatures involves a modulation of cellular machinery. Marine Environmental Research, 2023, 188, 105979.	2.5	1
5873	HSV-2 triggers upregulation of MALAT1 in CD4+ T cells and promotes HIV latency reversal. Journal of Clinical Investigation, 2023, 133, .	8.2	2
5875	Effects of organic and inorganic nitrogen sources on the transcriptome of gellan gum biosynthesis bySphingomonas paucimobilis. Journal of Applied Microbiology, 2023, 134, .	3.1	1
5877	A homology guide for Pacific salmon genus Oncorhynchus resolves patterns of ohnolog retention, resolution and local adaptation following the salmonidâ€specific wholeâ€genome duplication event. Ecology and Evolution, 2023, 13, .	1.9	3
5878	MLX plays a key role in lipid and glucose metabolism in humans: Evidence from in vitro and in vivo studies. Metabolism: Clinical and Experimental, 2023, , 155563.	3.4	1
5880	Oxylipin biosynthetic gene families of Cannabis sativa. PLoS ONE, 2023, 18, e0272893.	2.5	1
5881	Responding to ACL Injury and its Treatments: Comparative Gene Expression between Articular Cartilage and Synovium. Bioengineering, 2023, 10, 527.	3.5	0
5883	Secretory MPP3 reinforce myeloid differentiation trajectory and amplify myeloid cell production. Journal of Experimental Medicine, 2023, 220, .	8.5	6
5884	Progesterone receptor mediates ovulatory transcription through RUNX transcription factor interactions and chromatin remodelling. Nucleic Acids Research, 2023, 51, 5981-5996.	14.5	4
5885	Cloning a profibrotic stem cell variant in idiopathic pulmonary fibrosis. Science Translational Medicine, 2023, 15, .	12.4	4
5886	Myc controls NK cell development, IL-15-driven expansion, and translational machinery. Life Science Alliance, 2023, 6, e202302069.	2.8	4
5889	The power of TOPMed imputation for the discovery of Latino-enriched rare variants associated with type 2 diabetes. Diabetologia, 2023, 66, 1273-1288.	6.3	3
5892	Fertility decline in female mosquitoes is regulated by the orco olfactory co-receptor. IScience, 2023, 26, 106883.	4.1	4
5893	<scp>NONâ€TARGETâ€SITE RESISTANCE DUE TO RAPID PHYSIOLOGICAL RESPONSE IN</scp> 2, <scp>4â€D RESISTANT</scp> Conyza sumatrensis : <scp>REDUCED</scp> 2, <scp>4â€D TRANSLOCATION AND AUXINâ€INDUCED GENE EXPRESSION</scp>. Pest Management Science, 0, , .	3.4	0
5894	Aneuploidy effects on human gene expression across three cell types. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	8
5895	Comparative Transcriptomic Analysis of Three Common Liver Cell Lines. International Journal of Molecular Sciences, 2023, 24, 8791.	4.1	0
5896	Human endogenous retrovirus onco-exaptation counters cancer cell senescence through calbindin. Journal of Clinical Investigation, 2023, 133, .	8.2	5

#	Article	IF	Citations
5897	Integrated microbiome and metabolome analysis reveals the interaction between intestinal flora and serum metabolites as potential biomarkers in hepatocellular carcinoma patients. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	4
5898	Sample Preparation and Differential Gene Expression Analysis of Human Cancer Cell Lines by RNA Sequencing. Methods in Molecular Biology, 2023, , 23-41.	0.9	0
5900	N/S element transformation modulating lithospheric microbial communities by single-species manipulation. Microbiome, 2023, 11, .	11.1	3
5901	Characterizing sediment functional traits and ecological consequences respond to increasing antibiotic pollution. Applied Microbiology and Biotechnology, 0, , .	3.6	0
5902	A draft human pangenome reference. Nature, 2023, 617, 312-324.	27.8	187
5906	A tissue injury sensing and repair pathway distinct from host pathogen defense. Cell, 2023, 186, 2127-2143.e22.	28.9	13
5909	POLG genotype influences degree of mitochondrial dysfunction in iPSC derived neural progenitors, but not the parent iPSC or derived glia. Experimental Neurology, 2023, 365, 114429.	4.1	1
5910	Interleukin 36 receptor-inducible matrix metalloproteinase 13 mediates intestinal fibrosis. Frontiers in Immunology, 0, 14, .	4.8	1
5911	Activation of XBP1 but not ATF6Î± rescues heart failure induced by persistent ER stress in medaka fish. Life Science Alliance, 2023, 6, e202201771.	2.8	0
5912	Seasonal shifts in Feâ€acquisition strategies in Southern Ocean microbial communities revealed by metagenomics and autonomous sampling. Environmental Microbiology, 0, , .	3.8	0
5913	Trichome-Specific Analysis and Weighted Gene Co-Expression Correlation Network Analysis (WGCNA) Reveal Potential Regulation Mechanism of Artemisinin Biosynthesis in Artemisia annua. International Journal of Molecular Sciences, 2023, 24, 8473.	4.1	0
5914	Adipose tissue plasticity in pheochromocytoma patients suggests a role of the splicing machinery in human adipose browning. IScience, 2023, 26, 106847.	4.1	1
5915	Reduction of Paraoxonase Expression Followed by Inactivation across Independent Semiaquatic Mammals Suggests Stepwise Path to Pseudogenization. Molecular Biology and Evolution, 2023, 40, .	8.9	1
5916	Transcriptomic responses in the blood and sputum of cigarette smokers compared to e-cigarette vapers. Respiratory Research, 2023, 24, .	3.6	1
5918	Genome-wide analysis of the CDPK gene family and their important roles response to cold stress in white clover. Plant Signaling and Behavior, 2023, 18, .	2.4	2
5919	Multimodal characterization of murine gastruloid development. Cell Stem Cell, 2023, 30, 867-884.e11.	11.1	15
5920	The large GTPase AtGBPL3 links nuclear envelope formation and morphogenesis to transcriptional repression. Nature Plants, 2023, 9, 766-784.	9.3	2
5921	Interaction of LARP4 to filamin A mechanosensing domain regulates cell migrations. Frontiers in Cell and Developmental Biology, 0, 11, .	3.7	2

#	Article	IF	Citations
5923	Multiâ€omic profiling reveals an <scp>RNA</scp> processing rheostat that predisposes to prostate cancer. EMBO Molecular Medicine, 2023, 15, .	6.9	2
5924	Weaker selection on genes with treatment-specific expression consistent with a limit on plasticity evolution in Arabidopsis thaliana. Genetics, 2023, 224, .	2.9	2
5927	Environmental stress during larval development induces DNA methylation shifts in the migratory painted lady butterfly (Vanessa cardui). Molecular Ecology, 2023, 32, 3513-3523.	3.9	1
5929	Sodium butyrate promotes gastrointestinal development of preweaning bull calves via inhibiting inflammation, balancing nutrient metabolism, and optimizing microbial community functions. Animal Nutrition, 2023, 14, 88-100.	5.1	6
5930	Integrative genetic analysis identifies FLVCR1 as a plasma-membrane choline transporter in mammals. Cell Metabolism, 2023, 35, 1057-1071.e12.	16.2	18
5931	<scp>YAP</scp>/<scp>BRD4</scp>â€controlled <scp>ROR1</scp> promotes tumorâ€initiating cells and hyperproliferation in pancreatic cancer. EMBO Journal, 2023, 42, .	7.8	8
5932	Low-grade glioma risk SNP rs11706832 is associated with type I interferon response pathway genes in cell lines. Scientific Reports, 2023, 13, .	3.3	0
5936	Alpha-Tocopherol Significantly Improved Squalene Production Yield of Aurantiochytrium sp. TWZ-97 through Lowering ROS levels and Up-Regulating Key Genes of Central Carbon Metabolism Pathways. Antioxidants, 2023, 12, 1034.	5.1	3
5937	An observational human study investigating the effect of anabolic androgenic steroid use on the transcriptome of skeletal muscle and whole blood using RNA-Seq. BMC Medical Genomics, 2023, 16, .	1.5	1
5938	Transcriptomic changes in porcine articular cartilage one year following disruption of the anterior cruciate ligament. PLoS ONE, 2023, 18, e0284777.	2.5	1
5940	Mouse nuclear RNAi-defective 2 promotes splicing of weak 5â€² splice sites. Rna, 2023, 29, 1140-1165.	3.5	0
5941	Dual RNA-Seq Profiling Unveils Mycoparasitic Activities of Trichoderma atroviride against Haploid Armillaria ostoyae in Antagonistic Interaction Assays. Microbiology Spectrum, 2023, 11, .	3.0	1
5942	Linking DOM characteristics to microbial community: The potential role of DOM mineralization for arsenic release in shallow groundwater. Journal of Hazardous Materials, 2023, 454, 131566.	12.4	5
5943	Skipper analysis of eCLIP datasets enables sensitive detection of constrained translation factor binding sites. Cell Genomics, 2023, 3, 100317.	6.5	4
5944	miR-22 gene therapy treats HCC by promoting anti-tumor immunity and enhancing metabolism. Molecular Therapy, 2023, 31, 1829-1845.	8.2	7
5945	Transcriptomics of ivermectin response in Caenorhabditis elegans: Integrating abamectin quantitative trait loci and comparison to the Ivermectin-exposed DA1316 strain. PLoS ONE, 2023, 18, e0285262.	2.5	2
5946	HIF prolyl hydroxylase 2/3 deletion disrupts astrocytic integrity and exacerbates neuroinflammation. Glia, 2023, 71, 2024-2044.	4.9	0
5947	Benzo[a]pyrene-induced multigenerational changes in gene expression, behavior, and DNA methylation are primarily influenced by paternal exposure. Toxicology and Applied Pharmacology, 2023, 469, 116545.	2.8	0

#	Article	IF	Citations
5948	Xanthine-induced deficits in hippocampal behavior and abnormal expression of hemoglobin genes. Behavioural Brain Research, 2023, 449, 114476.	2.2	3
5949	Meta-Analysis of Public RNA Sequencing Data Revealed Potential Key Genes Associated with Reproductive Division of Labor in Social Hymenoptera and Termites. International Journal of Molecular Sciences, 2023, 24, 8353.	4.1	2
5953	Formalinâ€fixed paraffinâ€embedded (<scp>FFPE</scp>) samples help to investigate transcriptomic responses in wildlife disease. Molecular Ecology Resources, 0, , .	4.8	0
5956	Transcriptomic changes in liver transplant recipients with non-alcoholic steatohepatitis indicate dysregulation of wound healing. Frontiers in Endocrinology, 0, 14, .	3.5	1
5960	Immunoglobulin E-virus phenotypes of infant bronchiolitis and risk of childhood asthma. Frontiers in Immunology, 0, 14, .	4.8	1
5962	Neurite Outgrowth and Gene Expression Profile Correlate with Efficacy of Human Induced Pluripotent Stem Cell-Derived Dopamine Neuron Grafts. Stem Cells and Development, 2023, 32, 387-397.	2.1	2
5963	A multi-center, prospective cohort study of whole blood gene expression in the tuberculosis-diabetes interaction. Scientific Reports, 2023, 13, .	3.3	3
5964	Circadian transcriptome processing and analysis: a workflow for muscle stem cells. FEBS Open Bio, 0, , .	2.3	0
5965	Molecular profiling of osteoprogenitor cells reveals FOS as a master regulator of bone non-union. Gene, 2023, 874, 147481.	2.2	0
5966	Impact of zero-valent iron on nitrifying granular sludge for 17Î±-ethinylestradiol removal and its mechanism. Chemosphere, 2023, 333, 138904.	8.2	3
5967	ADAR1-mediated RNA editing promotes B cell lymphomagenesis. IScience, 2023, 26, 106864.	4.1	5
5968	Transcriptomic analysis towards identification of defence-responsive genes and pathways upon application of Sargassum seaweed extract on tomato plants infected with Macrophomina phaseolina. 3 Biotech, 2023, 13, .	2.2	3
5970	Identification of two key UDP-glycosyltransferases responsible for the ocotillol-type ginsenoside majonside-R2 biosynthesis in Panax vietnamensis var. fuscidiscus. Planta, 2023, 257, .	3.2	3
5971	Single-cell and spatial transcriptomics: deciphering brain complexity in health and disease. Nature Reviews Neurology, 2023, 19, 346-362.	10.1	33
5972	PRMT1 mediated methylation of cGAS suppresses anti-tumor immunity. Nature Communications, 2023, 14, .	12.8	11
5973	A histone deacetylase 3 and mitochondrial complex I axis regulates toxic formaldehyde production. Science Advances, 2023, 9, .	10.3	8
5975	Chromosome-level genome and high nitrogen stress response of the widespread and ecologically important wetland plant Typha angustifolia. Frontiers in Plant Science, 0, 14, .	3.6	1
5979	iPSC-derived reactive astrocytes from patients with multiple sclerosis protect cocultured neurons in inflammatory conditions. Journal of Clinical Investigation, 2023, 133, .	8.2	5

#	Article	IF	Citations
5980	Integrative profiling of gene expression and chromatin accessibility elucidates specific transcriptional networks in porcine neutrophils. Frontiers in Genetics, 0, 14, .	2.3	2
5981	Transcriptome data analysis of primary cardiomyopathies reveals perturbations in arachidonic acid metabolism. Frontiers in Cardiovascular Medicine, 0, 10, .	2.4	1
5983	TreeTerminus â€"creating transcript trees using inferential replicate counts. IScience, 2023, 26, 106961.	4.1	1
5984	Differential regulation of IL-17A and IL-17F via STAT5 contributes to psoriatic disease. Journal of Allergy and Clinical Immunology, 2023, 152, 783-798.	2.9	6
5985	Mode of action of antifouling compound albofungin in inhibiting barnacle larval settlement. IScience, 2023, 26, 106981.	4.1	0
5986	The transcriptome reveals the molecular regulatory network of primordial follicle depletion in obese mice. Fertility and Sterility, 2023, 120, 899-910.	1.0	4
5988	Single Nematode Transcriptomic Analysis, Using Long-Read Technology, Reveals Two Novel Virulence Gene Candidates in the Soybean Cyst Nematode, Heterodera glycines. International Journal of Molecular Sciences, 2023, 24, 9440.	4.1	2
5990	Cascade capture, oxidization and inactivation for removing multi-species pollutants, antimicrobial resistance and pathogenicity from hospital wastewater. Journal of Hazardous Materials, 2023, 457, 131730.	12.4	1
5991	Mitochondrial pyruvate metabolism and glutaminolysis toggle steady-state and emergency myelopoiesis. Journal of Experimental Medicine, 2023, 220, .	8.5	0
5992	Characteristics of methane emissions from alpine thermokarst lakes on the Tibetan Plateau. Nature Communications, 2023, 14, .	12.8	7
5993	Gut microbiota enhance energy accumulation of black-necked crane to cope with impending migration. Applied Microbiology and Biotechnology, 2023, 107, 4635-4646.	3.6	1
5994	Multigenic resistance to Xylella fastidiosa in wild grapes (Vitis sps.) and its implications within a changing climate. Communications Biology, 2023, 6, .	4.4	6
5995	Selective Concurrence of the Long Non-Coding RNA MALAT1 and the Polycomb Repressive Complex 2 to Promoter Regions of Active Genes in MCF7 Breast Cancer Cells. Current Issues in Molecular Biology, 2023, 45, 4735-4748.	2.4	2
5996	Transcriptome analysis of Euwallacea interjectus reveals differentially expressed unigenes related to developmental stages and egg laying. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2023, 47, 101100.	1.0	0
5997	Reduced trace gas oxidizers as a response to organic carbon availability linked to oligotrophs in desert fertile islands. ISME Journal, 2023, 17, 1257-1266.	9.8	1
5998	Identification of fatty acid amide hydrolase as a metastasis suppressor in breast cancer. Nature Communications, 2023, 14, .	12.8	2
5999	Influences of chronic copper exposure on intestinal histology, antioxidative and immune status, and transcriptomic response in freshwater grouper (Acrossocheilus fasciatus). Fish and Shellfish Immunology, 2023, 139, 108861.	3.6	2
6000	Gut microbiome determines therapeutic effects of OCA on NAFLD by modulating bile acid metabolism. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	7

#	Article	IF	Citations
6001	SeiÃ°r: Efficient calculation of robust ensemble gene networks. Heliyon, 2023, 9, e16811.	3.2	2
6002	Comparative Genomic Analysis of Pancreatic Acinar Cell Carcinoma (PACC) and Pancreatic Ductal Adenocarcinoma (PDAC) Unveils New Actionable Genomic Aberrations in PACC. Clinical Cancer Research, 2023, 29, 3408-3417.	7.0	2
6003	Antimony efflux underpins phosphorus cycling and resistance of phosphate-solubilizing bacteria in mining soils. ISME Journal, 2023, 17, 1278-1289.	9.8	6
6004	Qing-Zhi-Tiao-Gan-Tang (QZTGT) prevents nonalcoholic steatohepatitis (NASH) by expression pattern correction. Journal of Ethnopharmacology, 2023, 317, 116665.	4.1	0
6006	Quantitative trait and transcriptome analysis of genetic complexity underpinning cardiac interatrial septation in mice using an advanced intercross line. ELife, 0, 12, .	6.0	1
6007	Cellular response of Parachlorella kessleri to a solid surface culture environment. Frontiers in Plant Science, 0, 14, .	3.6	0
6010	Metabolic Processes and Biological Macromolecules Defined the Positive Effects of Protein-Rich Biostimulants on Sugar Beet Plant Development. International Journal of Molecular Sciences, 2023, 24, 9720.	4.1	1
6011	Long-read direct RNA sequencing reveals epigenetic regulation of chimeric gene-transposon transcripts in Arabidopsis thaliana. Nature Communications, 2023, 14, .	12.8	5
6012	Integrin-Driven Axon Regeneration in the Spinal Cord Activates a Distinctive CNS Regeneration Program. Journal of Neuroscience, 2023, 43, 4775-4794.	3.6	1
6013	Program and Abstracts. Tissue Engineering - Part A, 2023, 29, 1-1650.	3.1	0
6014	Construction of a de novo assembly pipeline using multiple transcriptome data sets from Cypripedium macranthos (Orchidaceae). PLoS ONE, 2023, 18, e0286804.	2.5	0
6015	The diurnal fluctuation of colonic antibiotic resistome is correlated with nutrient substrates in a pig model. Science of the Total Environment, 2023, 891, 164692.	8.0	2
6016	Gene co-expression in response to Staphylococcus aureus infection reveals networks of genes with specific functions during bovine subclinical mastitis. Journal of Dairy Science, 2023, 106, 5517-5536.	3.4	4
6017	Targeting macrophage Syk enhances responses to immune checkpoint blockade and radiotherapy in high-risk neuroblastoma. Frontiers in Immunology, 0, 14, .	4.8	1
6018	Metastatic Infiltration of Nervous Tissue and Periosteal Nerve Sprouting in Multiple Myeloma-Induced Bone Pain in Mice and Human. Journal of Neuroscience, 2023, 43, 5414-5430.	3.6	2
6019	Coding and noncoding transcriptomes of NODULIN HOMEOBOX (NDX)-deficient Arabidopsis inflorescence. Scientific Data, 2023, 10, .	5.3	2
6020	Not every estimate counts â€“ evaluation of cell composition estimation approaches in brain bulk tissue data. Genome Medicine, 2023, 15, .	8.2	1
6021	Depletion of pyruvate kinase (PK) activity causes glycolytic intermediate imbalances and reveals a PK-TXNIP regulatory axis. Molecular Metabolism, 2023, 74, 101748.	6.5	2

#	Article	IF	Citations
6022	Single-cell transcriptomics combined with proteomics of intrathecal IgG reveal transcriptional heterogeneity of oligoclonal IgG-secreting cells in multiple sclerosis. Frontiers in Cellular Neuroscience, 0, 17, .	3.7	0
6023	A novel computational pipeline for var gene expression augments the discovery of changes in the Plasmodium falciparum transcriptome during transition from in vivo to short-term in vitro culture. ELife, 0, 12, .	6.0	0
6024	Elucidation of the coumarin degradation by Pseudomonas sp. strain NyZ480. Journal of Hazardous Materials, 2023, 457, 131802.	12.4	4
6025	Bivalves Present the Largest and Most Diversified Repertoire of Toll-Like Receptors in the Animal Kingdom, Suggesting Broad-Spectrum Pathogen Recognition in Marine Waters. Molecular Biology and Evolution, 2023, 40, .	8.9	4
6026	Capicua (CIC) mutations in gliomas in association with MAPK activation for exposing a potential therapeutic target. , 2023, 40, .		2
6027	Temperature-dependent RNA editing in octopus extensively recodes the neural proteome. Cell, 2023, 186, 2544-2555.e13.	28.9	13
6028	Rigorous benchmarking of T-cell receptor repertoire profiling methods for cancer RNA sequencing. Briefings in Bioinformatics, 2023, 24, .	6.5	3
6029	Pooled analysis of frontal lobe transcriptomic data identifies key mitophagy gene changes in Alzheimer's disease brain. Frontiers in Aging Neuroscience, 0, 15, .	3.4	2
6030	Pervasive effects of RNA degradation on Nanopore direct RNA sequencing. NAR Genomics and Bioinformatics, 2023, 5, .	3.2	2
6031	Variants in SART3 cause a spliceosomopathy characterised by failure of testis development and neuronal defects. Nature Communications, 2023, 14, .	12.8	3
6032	Vaccine-induced protection against SARS-CoV-2 requires IFN-Î³-driven cellular immune response. Nature Communications, 2023, 14, .	12.8	4
6034	Patient-Induced Pluripotent Stem Cellâ€“Derived Hepatostellate Organoids Establish a Basis for Liver Pathologies in Telomeropathies. Cellular and Molecular Gastroenterology and Hepatology, 2023, , .	4.5	0
6036	Syk Inhibition Reprograms Tumor-Associated Macrophages and Overcomes Gemcitabine-Induced Immunosuppression in Pancreatic Ductal Adenocarcinoma. Cancer Research, 2023, 83, 2675-2689.	0.9	1
6037	Drought and recovery in barley: key gene networks and retrotransposon response. Frontiers in Plant Science, 0, 14, .	3.6	2
6038	Context-aware transcript quantification from long-read RNA-seq data with Bambu. Nature Methods, 2023, 20, 1187-1195.	19.0	20
6040	Metagenomic highlight contrasting elevational pattern of bacteria- and fungi-derived compound decompositions in forest soils. Plant and Soil, 2023, 490, 617-629.	3.7	1
6041	Clinical and molecular correlation defines activity of physiological pathways in life-sustaining kidney xenotransplantation. Nature Communications, 2023, 14, .	12.8	5
6043	Stratification of Tamoxifen Synergistic Combinations for the Treatment of ER+ Breast Cancer. Cancers, 2023, 15, 3179.	3.7	0

#	Article	IF	Citations
6044	Environmental and molecular regulation of asexual reproduction in the sea anemone Nematostella vectensis. Royal Society Open Science, 2023, 10, .	2.4	1
6045	Exogenous interleukin-1 beta stimulation regulates equine tenocyte function and gene expression in three-dimensional culture which can be rescued by pharmacological inhibition of interleukin 1 receptor, but not nuclear factor kappa B, signaling. Molecular and Cellular Biochemistry, 0, , .	3.1	1
6046	Polymorphisms in corticotrophinâ€releasing hormoneâ€“proopiomalanocortin (<scp>CRH</scp>â€“<scp>POMC</scp>) system genes: Neuroimmune contributions to psoriasis disease. Journal of the European Academy of Dermatology and Venereology, 2023, 37, 2028-2040.	2.4	1
6048	Gene expression dynamics of natural assemblages of heterotrophic flagellates during bacterivory. Microbiome, 2023, 11, .	11.1	2
6050	Genetic perturbation of AMP biosynthesis extends lifespan and restores metabolic health in a naturally short-lived vertebrate. Developmental Cell, 2023, 58, 1350-1364.e10.	7.0	3
6051	Nasal airway microRNA profiling of infants with severe bronchiolitis and risk of childhood asthma: a multicentre prospective study. European Respiratory Journal, 2023, 62, 2300502.	6.7	7
6052	Comparative phylotranscriptomics reveals ancestral and derived root nodule symbiosis programmes. Nature Plants, 2023, 9, 1067-1080.	9.3	12
6053	Important functional role of the protein osteopontin in the progression of malignant pleural mesothelioma. Frontiers in Immunology, 0, 14, .	4.8	0
6054	Efficiently quantifying DNA methylation for bulk- and single-cell bisulfite data. Bioinformatics, 2023, 39, .	4.1	0
6055	Denitrification contributes to N2O emission in paddy soils. Frontiers in Microbiology, 0, 14, .	3.5	3
6057	An EZH2-NF-ÎºB regulatory axis drives expression of pro-oncogenic gene signatures in triple negative breast cancer. IScience, 2023, 26, 107115.	4.1	0
6058	Loss of PBAF promotes expansion and effector differentiation of CD8+ TÂcells during chronic viral infection and cancer. Cell Reports, 2023, 42, 112649.	6.4	4
6061	Comparative phylogenetic analysis and transcriptomic profiling of Dengue (DENV-3 genotype I) outbreak in 2021 in Bangladesh. Virology Journal, 2023, 20, .	3.4	3
6063	Altered gut microbiota of obesity subjects promotes colorectal carcinogenesis in mice. EBioMedicine, 2023, 93, 104670.	6.1	4
6065	Transcriptomic approach to uncover dynamic events in the development of mid-season sunburn in apple fruit. G3: Genes, Genomes, Genetics, 0, , .	1.8	0
6066	Tnpo3 controls splicing of the pre-mRNA encoding the canonical TCR Î± chain of iNKT cells. Nature Communications, 2023, 14, .	12.8	0
6067	3D vascularised proximal tubules-on-a-multiplexed chip model for enhanced cell phenotypes. Lab on A Chip, 2023, 23, 3226-3237.	6.0	4
6068	A phase Ib trial of pembrolizumab plus paclitaxel or flat-dose capecitabine in 1st/2nd line metastatic triple-negative breast cancer. Npj Breast Cancer, 2023, 9, .	5.2	0

#	Article	IF	Citations
6069	Absence of TRIC-B from type XIV Osteogenesis Imperfecta osteoblasts alters cell adhesion and mitochondrial function â€“ A multi-omics study. Matrix Biology, 2023, 121, 127-148.	3.6	0
6070	The genome of the reef-building glass spongeAphrocallistes vastusprovides insights into silica biomineralization. Royal Society Open Science, 2023, 10, .	2.4	3
6071	Methylation-related alternative splicing events in H2O2-treated Kyoho grape berries during development. Scientia Horticulturae, 2023, 321, 112255.	3.6	1
6072	Chemical profile and analysis of biosynthetic pathways and genes of volatile terpenes in Pityopsis ruthii, a rare and endangered flowering plant. PLoS ONE, 2023, 18, e0287524.	2.5	0
6074	How do you build a nectar spur? A transcriptomic comparison of nectar spur development in Linaria vulgaris and gibba development in Antirrhinum majus. Frontiers in Plant Science, 0, 14, .	3.6	1
6075	Loss of TJP1 disrupts gastrulation patterning and increases differentiation toward the germ cell lineage in human pluripotent stem cells. Developmental Cell, 2023, 58, 1477-1488.e5.	7.0	4
6080	Transcriptomic and co-expression network analyses on diverse wheat landraces identifies candidate master regulators of the response to early drought. Frontiers in Plant Science, 0, 14, .	3.6	1
6083	Acetylation Targeting Chimera Enables Acetylation of the Tumor Suppressor p53. Journal of the American Chemical Society, 2023, 145, 14932-14944.	13.7	9
6084	Nanopore sequencing unveils the complexity of the cold-activated murine brown adipose tissue transcriptome. IScience, 2023, 26, 107190.	4.1	1
6086	Loss of Growth Differentiation Factor 15 exacerbates lung injury in neonatal mice. American Journal of Physiology - Lung Cellular and Molecular Physiology, 0, , .	2.9	0
6087	Autism-linked UBE3A gain-of-function mutation causes interneuron and behavioral phenotypes when inherited maternally or paternally in mice. Cell Reports, 2023, 42, 112706.	6.4	4
6088	Fortuna Detects Novel Splicing in Drosophila scRNASeq Data. , 2023, , .		0
6089	Meta-analysis of Diurnal Transcriptomics in Mouse Liver Reveals Low Repeatability of Rhythm Analyses. Journal of Biological Rhythms, 2023, 38, 556-570.	2.6	4
6090	The vertically-stratified resistomes in mangrove sediments was driven by the bacterial diversity. Journal of Hazardous Materials, 2023, 458, 131974.	12.4	1
6091	Directed differentiation of human hindbrain neuroepithelial stem cells recapitulates cerebellar granule neurogenesis. Development (Cambridge), 0, , .	2.5	0
6092	Mediator subunit MDT-15 promotes expression of propionic acid breakdown genes to prevent embryonic lethality in Caenorhabditis elegans. G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	1
6093	Prominent epigenetic and transcriptomic changes in CD4+ and CD8+ T cells during and after pregnancy in women with multiple sclerosis and controls. Journal of Neuroinflammation, 2023, 20, .	7.2	1
6094	Maladaptive lymphangiogenesis is associated with synovial iron accumulation and delayed clearance in factor VIIIâ€“deficient mice after induced hemarthrosis. Journal of Thrombosis and Haemostasis, 2023, , .	3.8	1

#	Article	IF	Citations
6095	Microbial biogeochemical cycling reveals the sustainability of the rice-crayfish co-culture model. IScience, 2023, 26, 106769.	4.1	0
6096	Spatial expression patterns of genes encoding sugar sensors in leaves of C4 and C3 grasses. Annals of Botany, 2023, 131, 985-1000.	2.9	0
6097	Defects in lysosomal function and lipid metabolism in human microglia harboring a TREM2 loss of function mutation. Acta Neuropathologica, 2023, 145, 749-772.	7.7	8
6098	A key role for NLRP3 signaling in preterm labor and birth driven by the alarmin S100B. Translational Research, 2023, 259, 46-61.	5.0	8
6099	Comprehensive RNA-Seq Analysis Pipeline for Non-Model Organisms and Its Application in Schmidtea mediterranea. Genes, 2023, 14, 989.	2.4	0
6100	Integrative dissection of gene regulatory elements at base resolution. Cell Genomics, 2023, 3, 100318.	6.5	6
6101	The thymus and T-cell ontogeny in ballan wrasse (Labrus bergylta) is nutritionally modelled. Frontiers in Immunology, 0, 14, .	4.8	1
6102	A novel candidate gene CLN8 regulates fat deposition in avian. Journal of Animal Science and Biotechnology, 2023, 14, .	5.3	3
6104	Relationships between gene expression and behavior in mice in response to systemic modulation of the <scp>Oâ€ClcNAcylation</scp> pathway. Journal of Neurochemistry, 2023, 165, 682-700.	3.9	0
6105	Massively parallel base editing to map variant effects in human hematopoiesis. Cell, 2023, 186, 2456-2474.e24.	28.9	23
6106	Characterization of the cholesterol biosynthetic pathway in Dioscorea transversa. Journal of Biological Chemistry, 2023, 299, 104768.	3.4	1
6107	Eyestalk transcriptome and methyl farnesoate titers provide insight into the physiological changes in the male snow crab, Chionoecetes opilio, after its terminal molt. Scientific Reports, 2023, 13, .	3.3	0
6108	TF-Prioritizer: a Java pipeline to prioritize condition-specific transcription factors. GigaScience, 2022, 12, .	6.4	2
6110	Transcriptome and proteome analysis of dogs with precursor targeted immune-mediated anemia treated with splenectomy. PLoS ONE, 2023, 18, e0285415.	2.5	0
6112	Glycosyltransferases Expression Changes in Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293 Grown on Different Carbon Sources. Foods, 2023, 12, 1893.	4.3	1
6115	Redefining normal breast cell populations using long noncoding RNAs. Nucleic Acids Research, 2023, 51, 6389-6410.	14.5	2
6117	Co-Expression Network Analysis: A Future Approach for Pest Control Target Discovery. Journal of Agricultural and Food Chemistry, 2023, 71, 7201-7209.	5.2	2
6118	The spatiotemporal profile of Dendrobium huoshanense and functional identification of bHLH genes under exogenous MeJA using comparative transcriptomics and genomics. Frontiers in Plant Science, 0, 14, .	3.6	2

#	Article	IF	Citations
6119	The dynamics of touchâ€responsive gene expression in cereals. Plant Journal, 2023, 116, 282-302.	5.7	2
6120	Reciprocal enhancement of SARS-CoV-2 and influenza virus replication in human pluripotent stem cell-derived lung organoids. Emerging Microbes and Infections, 2023, 12, .	6.5	3
6121	Candida expansion in the gut of lung cancer patients associates with an ecological signature that supports growth under dysbiotic conditions. Nature Communications, 2023, 14, .	12.8	7
6125	Cultured Renal Proximal Tubular Epithelial Cells Resemble a Stressed/Damaged Kidney While Supporting BK Virus Infection. Journal of Virology, 2023, 97, .	3.4	0
6126	The mycorrhizal rootâ€shoot axis elicits Coffea arabica growth under low phosphate conditions. New Phytologist, 2023, 239, 271-285.	7.3	2
6127	Respiratory Virusâ€“Specific Nasopharyngeal Lipidome Signatures and Severity in Infants With Bronchiolitis: A Prospective Multicenter Study. Journal of Infectious Diseases, 0, , .	4.0	0
6129	BET inhibition targets ABC-DLBCL constitutive B-cell receptor signaling through PAX5. Blood Advances, 2023, 7, 5108-5121.	5.2	1
6130	Allantoin improves salinity tolerance in Arabidopsis and rice through synergid activation of abscisic acid and brassinosteroid biosynthesis. Plant Molecular Biology, 2023, 112, 143-160.	3.9	3
6132	Mining genes regulating root system architecture in maize based on data integration analysis. Theoretical and Applied Genetics, 2023, 136, .	3.6	1
6133	Multiomics Reveals Symbionts, Pathogens, and Tissue-Specific Microbiome of Blacklegged Ticks (Ixodes) Tj ETQq1 1 0.784314 rgBT /O 2023, 11, .	3.0	2
6134	Application of metagenomic next-generation sequencing in the diagnosis and resistome analysis of community-acquired pneumonia pathogens from bronchoalveolar lavage samples. Journal of Applied Microbiology, 2023, 134, .	3.1	0
6136	A glycan receptor kinase facilitates intracellular accommodation of arbuscular mycorrhiza and symbiotic rhizobia in the legume Lotus japonicus. PLoS Biology, 2023, 21, e3002127.	5.6	6
6137	Methyltransferase-like (METTL) homologues participate in Nicotiana benthamiana antiviral responses. Plant Signaling and Behavior, 2023, 18, .	2.4	2
6138	Stony coral tissue loss disease induces transcriptional signatures of in situ degradation of dysfunctional Symbiodiniaceae. Nature Communications, 2023, 14, .	12.8	12
6140	Selenomonas sputigena acts as a pathobiont mediating spatial structure and biofilm virulence in early childhood caries. Nature Communications, 2023, 14, .	12.8	7
6141	Circular RNA Tmcc1 improves astrocytic glutamate metabolism and spatial memory via NF-Î°B and CREB signaling in a bile duct ligation mouse model: transcriptional and cellular analyses. Journal of Neuroinflammation, 2023, 20, .	7.2	0
6142	Evolutionary Adaptation of Genes Involved in Galactose Derivatives Metabolism in Oil-Tea Specialized Andrena Species. Genes, 2023, 14, 1117.	2.4	0
6143	Dasatinib overcomes glucocorticoid resistance in B-cell acute lymphoblastic leukemia. Nature Communications, 2023, 14, .	12.8	2

#	Article	IF	Citations
6144	Metagenomic analysis reveals gut plasmids as diagnosis markers for colorectal cancer. Frontiers in Microbiology, 0, 14, .	3.5	0
6145	The Rvv two-component regulatory system regulates biofilm formation and colonization in Vibrio cholerae. PLoS Pathogens, 2023, 19, e1011415.	4.7	1
6146	Genomic Insights into Adaptation to Karst Limestone and Incipient Speciation in East Asian Platycarya spp. (Juglandaceae). Molecular Biology and Evolution, 2023, 40, .	8.9	3
6149	Synthetic Epigenetic Reprogramming of Mesenchymal to Epithelial States Using the CRISPR/dCas9 Platform in Triple Negative Breast Cancer. Advanced Science, 2023, 10, .	11.2	5
6150	Integrative transcriptomics and cell systems analyses reveal protective pathways controlled by Igfbpâ€3 in anthracyclineâ€induced cardiotoxicity. FASEB Journal, 2023, 37, .	0.5	0
6152	Peripheral Administration of the Kv1.3-Blocking Peptide HsTX1[R14A] Improves Cognitive Performance in Senescence Accelerated SAMP8 Mice. Neurotherapeutics, 2023, 20, 1198-1214.	4.4	3
6153	The initial ageâ€associated decline in early Tâ€cell progenitors reflects fewer preâ€thymic progenitors and altered signals in the bone marrow and thymus microenvironments. Aging Cell, 2023, 22, .	6.7	1
6155	The Antarctic Scallop Adamussium colbecki Is Unable to Transcriptomically Respond to Captivity and Moderate Thermal Stress. Stresses, 2023, 3, 475-487.	4.8	2
6157	Ex vivo to in vivo model of malignant peripheral nerve sheath tumors for precision oncology. Neuro-Oncology, 0, , .	1.2	1
6159	Association of Antifolate Response Signature Status and Clinical Activity of Pemetrexed-Platinum Chemotherapy in Nonâ€“Small Cell Lung Cancer: The Piedmont Study. Clinical Cancer Research, 2023, 29, 3203-3213.	7.0	0
6161	Over-expression of ADAR1 in mice does not initiate or accelerate cancer formation in vivo. NAR Cancer, 2023, 5, .	3.1	6
6162	Discovery of non-reference processed pseudogenes in the Swedish population. Frontiers in Genetics, 0, 14, .	2.3	0
6163	Phase 1/2a clinical trial in ALS with ropinirole, a drug candidate identified by iPSC drug discovery. Cell Stem Cell, 2023, 30, 766-780.e9.	11.1	8
6164	5-Azacytidine- and retinoic-acid-induced reprogramming of DCCs into dormancy suppresses metastasis via restored TGF-Î²-SMAD4 signaling. Cell Reports, 2023, 42, 112560.	6.4	5
6165	Longitudinal characterization of primary osteosarcoma and derived subcutaneous and orthotopic relapsed patient-derived xenograft models. Frontiers in Oncology, 0, 13, .	2.8	2
6166	Comparative analysis of commonly used bioinformatics software based on omics. Gene Reports, 2023, 32, 101800.	0.8	0
6168	Divergent RNA viruses infecting sea lice, major ectoparasites of fish. PLoS Pathogens, 2023, 19, e1011386.	4.7	0
6169	Theoretical Analysis of Sequencing Bioinformatics Algorithms and Beyond. Communications of the ACM, 2023, 66, 118-125.	4.5	2

#	Article	IF	Citations
6170	Transcriptomic profiling of Parkinson's disease brains reveals disease stage specific gene expression changes. Acta Neuropathologica, 2023, 146, 227-244.	7.7	7
6171	The Viscum album Gene Space database. Frontiers in Plant Science, 0, 14, .	3.6	1
6174	Comparative Transcriptome Profiling Unfolds a Complex Defense and Secondary Metabolite Networks Imparting Corynespora cassiicola Resistance in Soybean (Glycine max (L.) Merrill). International Journal of Molecular Sciences, 2023, 24, 10563.	4.1	1
6175	Small Molecule RBI2 Disrupts Ribosome Biogenesis through Pre-rRNA Depletion. Cancers, 2023, 15, 3303.	3.7	1
6176	A novel ex vivo lung cancer model based on bioengineered rat lungs. Frontiers in Bioengineering and Biotechnology, 0, 11, .	4.1	0
6177	Genomic and transcriptomic analyses illuminate the molecular basis of the unique lifestyle of a tubeworm, Lamellibrachia satsuma. DNA Research, 2023, 30, .	3.4	0
6179	Distinct microbial structure and metabolic potential shaped by significant environmental gradient impacted by ferrous slag weathering. Environment International, 2023, 178, 108067.	10.0	0
6180	A functional link between lariat debranching enzyme and the intron-binding complex is defective in non-photosensitive trichothiodystrophy. Molecular Cell, 2023, 83, 2258-2275.e11.	9.7	2
6182	Peripheral immune system modulates Purkinje cell degeneration in Niemannâ€“Pick disease type C1. Life Science Alliance, 2023, 6, e202201881.	2.8	0
6183	Small molecule inhibition of multiple RNA binding proteins by Ro-08-2750 underlies Musashi-2 independent phenotypes. Rna, 0, , rna.079605.123.	3.5	0
6186	Targeting CCR7-PI3KÎ³ overcomes resistance to tyrosine kinase inhibitors in ALK-rearranged lymphoma. Science Translational Medicine, 2023, 15, .	12.4	2
6187	GDF15 promotes weight loss by enhancing energy expenditure in muscle. Nature, 2023, 619, 143-150.	27.8	31
6188	Bioinformatics and Biostatistics in Precision Medicine. , 2023, , 189-235.		1
6189	The platelet transcriptome and proteome in Alzheimerâ€™s disease and aging: an exploratory cross-sectional study. Frontiers in Molecular Biosciences, 0, 10, .	3.5	1
6190	Design, execution, and interpretation of plant RNA-seq analyses. Frontiers in Plant Science, 0, 14, .	3.6	0
6191	Surface electron-polarized biochar-enhanced anaerobic digestion mechanism revealed by metagenomic binning strategy. Chemical Engineering Journal, 2023, 471, 144474.	12.7	2
6192	Short-Term Supplementation of Pectin Alters Substrate Dynamics and Modulates Microbial Carbohydrate Metabolism in the Gut of a Pig Model. Journal of Agricultural and Food Chemistry, 2023, 71, 10470-10482.	5.2	1
6193	Tutorial: integrative computational analysis of bulk RNA-sequencing data to characterize tumor immunity using RIMA. Nature Protocols, 2023, 18, 2404-2414.	12.0	3

#	Article	IF	Citations
6194	The actions of methotrexate on endothelial cells are dependent on the shear stress-induced regulation of one carbon metabolism. Frontiers in Immunology, 0, 14, .	4.8	0
6195	The Transcriptomic Signature of Cyclical Parthenogenesis. Genome Biology and Evolution, 2023, 15, .	2.5	1
6196	Genome-wide identification of R-SNARE gene family in upland cotton and function analysis of GhVAMP72l response to drought stress. Frontiers in Plant Science, 0, 14, .	3.6	0
6197	Oncogenic K-Ras suppresses global miRNA function. Molecular Cell, 2023, 83, 2509-2523.e13.	9.7	3
6201	Solitary fibrous tumor with IGF-II-induced non-islet cell tumor hypoglycemia: a case report and molecular characterization by next-generation sequencing. Frontiers in Oncology, 0, 13, .	2.8	0
6202	Osmotic stress tolerance and transcriptomic response of Ramazzottius varieornatus (Eutardigrada: Ramazzottiidae) following tun formation. Zoological Journal of the Linnean Society, 0, , .	2.3	2
6203	Evolutionary walks through flower colour space driven by gene expression in Petunia and allies (Petunieae). Proceedings of the Royal Society B: Biological Sciences, 2023, 290, .	2.6	1
6204	Combined CDK4/6 and ERK1/2 Inhibition Enhances Antitumor Activity in NF1-Associated Plexiform Neurofibroma. Clinical Cancer Research, 2023, 29, 3438-3456.	7.0	1
6205	Vaccine-boosted CAR T crosstalk with host immunity to reject tumors with antigen heterogeneity. Cell, 2023, 186, 3148-3165.e20.	28.9	18
6207	Characterization of a barley (Hordeum vulgare L.) mutant with multiple stem nodes and spikes and dwarf (msnsd) and fine-mapping of its causal gene. Frontiers in Plant Science, 0, 14, .	3.6	0
6208	Insights into the Synergistic Antibacterial Activity of Silver Nitrate with Potassium Tellurite against Pseudomonas aeruginosa. Microbiology Spectrum, 2023, 11, .	3.0	2
6209	Galectin-1 Mediates Chronic STING Activation in Tumors to Promote Metastasis through MDSC Recruitment. Cancer Research, 2023, 83, 3205-3219.	0.9	2
6211	de novo PHF5A variants are associated with craniofacial abnormalities, developmental delay, and hypospadias. Genetics in Medicine, 2023, , 100927.	2.4	1
6213	Beyond the reference: gene expression variation and transcriptional response to RNA interference in Caenorhabditis elegans. G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	1
6214	Molecular profiling of aromatase inhibitor sensitive and resistant ER+HER2- postmenopausal breast cancers. Nature Communications, 2023, 14, .	12.8	2
6215	<scp>SETD2</scp> loss in renal epithelial cells drives epithelialâ€toâ€mesenchymal transition in a <scp>TGF</scp>â€²â€independent manner. Molecular Oncology, 0, , .	4.6	0
6216	Dimethyl fumarate-related immune and transcriptional signature is associated with clinical response in multiple sclerosis-treated patients. Frontiers in Immunology, 0, 14, .	4.8	1
6218	Metagenomic Analysis of Intratumoral Microbiome Linking to Response to Neoadjuvant Chemoradiotherapy in Rectal Cancer. International Journal of Radiation Oncology Biology Physics, 2023, 117, 1255-1269.	0.8	1

#	Article	IF	Citations
6221	Genomic virulence features of Beauveria bassiana as a biocontrol agent for the mountain pine beetle population. BMC Genomics, 2023, 24, .	2.8	1
6222	Counting pseudoalignments to novel splicing events. Bioinformatics, 2023, 39, .	4.1	0
6223	Aromatic amino acid biosynthesis impacts root hair development and symbiotic associations in Lotus japonicus. Plant Physiology, 2023, 193, 1508-1526.	4.8	2
6224	Transcriptomic and Proteomic Analysis Reveals the Potential Role of RBMS1 in Adipogenesis and Adipocyte Metabolism. International Journal of Molecular Sciences, 2023, 24, 11300.	4.1	1
6225	Notch signaling regulates a metabolic switch through inhibiting PGC-1Î± and mitochondrial biogenesis in dedifferentiated liposarcoma. Oncogene, 0, , .	5.9	0
6226	Identification of collateral sensitivity and evolutionary landscape of chemotherapy-induced drug resistance using cellular barcoding technology. Frontiers in Pharmacology, 0, 14, .	3.5	2
6227	Genome-wide analysis of the WRKY genes and their important roles during cold stress in white clover. PeerJ, 0, 11, e15610.	2.0	3
6228	Combinatorial targeting of a specific EMT/MET network by macroH2A variants safeguards mesenchymal identity. PLoS ONE, 2023, 18, e0288005.	2.5	0
6229	The Sw-5b NLR immune receptor induces earlier transcriptional changes in response to thrips and mechanical modes of inoculation of Tomato spotted wilt orthotospovirus. Molecular Plant-Microbe Interactions, 0, , .	2.6	1
6230	Identification of Staphylococcus aureus virulence-modulating RNA from transcriptomics data with machine learning. Virulence, 2023, 14, .	4.4	0
6231	Plant <scp>YTHDF</scp> proteins are direct effectors of antiviral immunity against an <scp>N6</scp>â€methyladenosineâ€containing <scp>RNA</scp> virus. EMBO Journal, 2023, 42, .	7.8	4
6232	Antifungal Mechanism of Phenazine-1-Carboxylic Acid against Pestalotiopsis kenyana. International Journal of Molecular Sciences, 2023, 24, 11274.	4.1	3
6233	Metagenomic Evidence for Cobamide Producers Driving Prokaryotic Co-occurrence Associations and Potential Function in Wastewater Treatment Plants. Environmental Science & Technology, 2023, 57, 10640-10651.	10.0	3
6234	Essential roles of RNA cap-proximal ribose methylation in mammalian embryonic development and fertility. Cell Reports, 2023, 42, 112786.	6.4	3
6237	Longitudinal APOE4- and amyloid-dependent changes in the blood transcriptome in cognitively intact older adults. Alzheimer's Research and Therapy, 2023, 15, .	6.2	0
6238	Supplementation of flavonoids and inulin in Totoaba macdonaldi: Microbiota, liver gene expression and growth performance responses. Aquaculture Reports, 2023, 31, 101654.	1.7	0
6239	SEESAW: detecting isoform-level allelic imbalance accounting for inferential uncertainty. Genome Biology, 2023, 24, .	8.8	2
6240	Dual Role of CXCL8 in Maintaining the Mesenchymal State of Glioblastoma Stem Cells and M2-Like Tumor-Associated Macrophages. Clinical Cancer Research, 2023, 29, 3779-3792.	7.0	0

#	Article	IF	Citations
6241	Containers for computational reproducibility. Nature Reviews Methods Primers, 2023, 3, .	21.2	5
6242	Comparison of red raspberry and wild strawberry fruits reveals mechanisms of fruit type specification. Plant Physiology, 2023, 193, 1016-1035.	4.8	1
6243	A newly isolated Bacillus megaterium OQ560352 promotes maize growth in saline soils by altering rhizosphere microbial communities and organic phosphorus utilization. Rhizosphere, 2023, 27, 100746.	3.0	2
6245	Longitudinal map of transcriptome changes in the Lyme pathogen Borrelia burgdorferi during tick-borne transmission. ELife, 0, 12, .	6.0	0
6246	Multiomic Mapping of Acquired Chromosome 1 Copy-Number and Structural Variants to Identify Therapeutic Vulnerabilities in Multiple Myeloma. Clinical Cancer Research, 2023, 29, 3901-3913.	7.0	5
6247	Detecting salivary host and microbiome RNA signature for aiding diagnosis of oral and throat cancer. Oral Oncology, 2023, 145, 106480.	1.5	5
6248	Bioinformatic Analysis of Yeast Two-Hybrid Next-Generation Interaction Screen Data. Methods in Molecular Biology, 2023, , 223-239.	0.9	1
6249	Next-Generation Sequencing Technology: Current Trends and Advancements. Biology, 2023, 12, 997.	2.8	45
6250	Poor Outcome in Postpartum Breast Cancer Patients Is Associated with Distinct Molecular and Immunologic Features. Clinical Cancer Research, 2023, 29, 3729-3743.	7.0	0
6251	Long wavelength-sensing cones of zebrafish retina exhibit multiple layers of transcriptional heterogeneity. Frontiers in Cellular Neuroscience, 0, 17, .	3.7	1
6253	Persistent and transient olfactory deficits in COVID-19 are associated to inflammation and zinc homeostasis. Frontiers in Immunology, 0, 14, .	4.8	2
6255	Furanocoumarins from Heracleum persicum L.: Unveiling their biosynthesis and gene expression. Industrial Crops and Products, 2023, 203, 117160.	5.2	1
6256	Response of the organellar and nuclear (post)transcriptomes of Arabidopsis to drought. Frontiers in Plant Science, 0, 14, .	3.6	3
6257	Predicting transcriptional responses to heat and drought stress from genomic features using a machine learning approach in rice. Frontiers in Plant Science, 0, 14, .	3.6	1
6258	Nicotinamide enhances osteoblast differentiation through activation of the mitochondrial antioxidant defense system. Experimental and Molecular Medicine, 2023, 55, 1531-1543.	7.7	6
6259	Salicylic acid metabolism and signalling coordinate senescence initiation in aspen in nature. Nature Communications, 2023, 14, .	12.8	3
6260	Hippocampal differential expression underlying the neuroprotective effect of delta-9-tetrahydrocannabinol microdose on old mice. Frontiers in Neuroscience, 0, 17, .	2.8	0
6261	Unraveling antibiotic resistomes associated with bacterial and viral communities in intertidal mudflat aquaculture area. Journal of Hazardous Materials, 2023, 459, 132087.	12.4	5

#	Article	IF	Citations
6262	A Genome-Wide Screen for the Exonisation of Reference SINE-VNTR-Alus and Their Expression in CNS Tissues of Individuals with Amyotrophic Lateral Sclerosis. International Journal of Molecular Sciences, 2023, 24, 11548.	4.1	1
6263	Tire-Derived Transformation Product 6PPD-Quinone Induces Mortality and Transcriptionally Disrupts Vascular Permeability Pathways in Developing Coho Salmon. Environmental Science & Technology, 2023, 57, 10940-10950.	10.0	6
6264	SIX1 and EWS/FLI1 co-regulate an anti-metastatic gene network in Ewing Sarcoma. Nature Communications, 2023, 14, .	12.8	2
6265	Sex-specific splicing occurs genome-wide during early Drosophila embryogenesis. ELife, 0, 12, .	6.0	3
6266	Mutant HTT does not affect glial development but impairs myelination in the early disease stage. Frontiers in Neuroscience, 0, 17, .	2.8	0
6268	Gastrointestinal microbiome, resistance genes, and risk assessment of heavy metals in wild giant pandas. Science of the Total Environment, 2023, 899, 165671.	8.0	2
6269	Exome sequencing reveals IFT172 variants in patients with non-syndromic cholestatic liver disease. PLoS ONE, 2023, 18, e0288907.	2.5	0
6270	Major chromosome 5H haplotype switch structures the European two-rowed spring barley germplasm of the past 190Âyears. Theoretical and Applied Genetics, 2023, 136, .	3.6	2
6271	The Impact of Mechanical Cues on the Metabolomic and Transcriptomic Profiles of Human Dermal Fibroblasts Cultured in Ultrashort Self-Assembling Peptide 3D Scaffolds. ACS Nano, 0, , .	14.6	3
6272	Multiomic investigation of Sugarcane mosaic virus resistance in sugarcane. Crop Journal, 2023, 11, 1805-1815.	5.2	0
6274	StHAB1, a negative regulatory factor in abscisic acid signaling, plays crucial roles in potato drought tolerance and shoot branching. Journal of Experimental Botany, 2023, 74, 6708-6721.	4.8	2
6278	A catalog of microbial genes and metagenome-assembled genomes from the quail gut microbiome. Poultry Science, 2023, 102, 102931.	3.4	0
6279	Working with Omics Data: An Interdisciplinary Challenge at the Crossroads of Biology and Computer Science. Neuromethods, 2023, , 313-330.	0.3	0
6280	Histone bivalency regulates the timing of cerebellar granule cell development. Genes and Development, 2023, 37, 570-589.	5.9	3
6282	Common environmental stress responses in a model marine diatom. New Phytologist, 0, , .	7.3	0
6283	The lncRNA HOXA11os regulates mitochondrial function in myeloid cells to maintain intestinal homeostasis. Cell Metabolism, 2023, 35, 1441-1456.e9.	16.2	2
6285	Metagenomic reconstructions of caecal microbiome in Landes, Roman and Zhedong White geese. British Poultry Science, 2023, 64, 565-576.	1.7	0
6286	The transcriptional landscape of endogenous retroelements delineates esophageal adenocarcinoma subtypes. NAR Cancer, 2023, 5, .	3.1	0

#	Article	IF	Citations
6287	Third-Generation Sequencing Reveals the Adaptive Role of the Epigenome in Three Deep-Sea Polychaetes. Molecular Biology and Evolution, 2023, 40, .	8.9	2
6288	RSV replication modifies the XBP1s binding complex on the IRF1 upstream enhancer to potentiate the mucosal anti-viral response. Frontiers in Immunology, 0, 14, .	4.8	0
6289	Co-Expression Networks in Sunflower: Harnessing the Power of Multi-Study Transcriptomic Public Data to Identify and Categorize Candidate Genes for Fungal Resistance. Plants, 2023, 12, 2767.	3.5	1
6290	Spermatogonial fate in mice with increased activin A bioactivity and testicular somatic cell tumours. Frontiers in Cell and Developmental Biology, 0, 11, .	3.7	2
6291	Dosage of the pseudoautosomal gene SLC25A6 is implicated in QTc interval duration. Scientific Reports, 2023, 13, .	3.3	0
6293	Terminal differentiation of villus tip enterocytes is governed by distinct Tgfî² superfamily members. EMBO Reports, 2023, 24, .	4.5	3
6294	Concerning the eXclusion in human genomics: the choice of sex chromosome representation in the human genome drastically affects the number of identified variants. G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	1
6295	The Cardioprotective Effects of Semaglutide Exceed Those of Dietary Weight Loss in Mice With HFpEF. JACC Basic To Translational Science, 2023, 8, 1298-1314.	4.1	3
6296	IPSC derived cardiac fibroblasts of DMD patients show compromised actin microfilaments, metabolic shift and pro-fibrotic phenotype. Biology Direct, 2023, 18, .	4.6	3
6298	The combination of metagenome and metabolome to compare the differential effects and mechanisms of fructose and sucrose on the metabolic disorders and gut microbiota in vitro and in vivo. Food and Function, 2023, 14, 7284-7298.	4.6	2
6299	Differential gene expression in response to fungal pathogen exposure in the aquatic invertebrate, Daphnia dentifera. Ecology and Evolution, 2023, 13, .	1.9	0
6300	Control of protein synthesis through mRNA pseudouridylation by dyskerin. Science Advances, 2023, 9, .	10.3	4
6303	<scp>HISTONE DEACETYLASE</scp> 9 promotes hypocotylâ€specific auxin response under shade. Plant Journal, 2023, 116, 804-822.	5.7	2
6304	The Bacterial Microbiota of Artisanal Cheeses from the Northern Caucasus. Fermentation, 2023, 9, 719.	3.0	3
6305	Development of a knowledge graph framework to ease and empower translational approaches in plant research: a use-case on grain legumes. Frontiers in Artificial Intelligence, 0, 6, .	3.4	0
6306	Occurrence, fate and potential health risks of antibiotic resistomes in a constructed wetlands-reservoir ecosystem for drinking water source improvement. Science of the Total Environment, 2023, 901, 166055.	8.0	0
6307	The cutaneous stress response system in three-spined stickleback and European flounder exposed to oxidative stress: Different mode of action. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2023, 285, 111493.	1.8	0
6308	Cellular and Genomic Features of Muscle Differentiation from Isogenic Fibroblasts and Myoblasts. Cells, 2023, 12, 1995.	4.1	1

#	Article	IF	Citations
6309	Neoadjuvant Afatinib for stage III EGFR-mutant non-small cell lung cancer: a phase II study. Nature Communications, 2023, 14, .	12.8	3
6310	Integration of Meta-Multi-Omics Data Using Probabilistic Graphs and External Knowledge. Cells, 2023, 12, 1998.	4.1	0
6311	When a Calorie Is Not a Calorie: Metabolic and Molecular Effects of Intermittent Fasting in Humans; Exploratory Outcomes of a Randomized Clinical Trial. , 2023, 1, 20230013.		0
6312	A Workflow Guide to RNA-Seq Analysis of Chaperone Function and Beyond. Methods in Molecular Biology, 2023, , 39-60.	0.9	0
6315	metaSpectraST: an unsupervised and database-independent analysis workflow for metaproteomic MS/MS data using spectrum clustering. Microbiome, 2023, 11, .	11.1	0
6316	Targeting STING oligomerization with small-molecule inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	8
6317	Ribosome profiling in the Symbiodiniacean dinoflagellate Fugacium kawagutii shows coordinated protein synthesis of enzymes in different pathways at different times of day. Molecular Microbiology, 2023, 120, 462-471.	2.5	2
6318	An RFX transcription factor regulates ciliogenesis in the closest living relatives of animals. Current Biology, 2023, , .	3.9	1
6319	The Effect of Plastic-Related Compounds on Transcriptome-Wide Gene Expression on CYP2C19-Overexpressing HepG2 Cells. Molecules, 2023, 28, 5952.	3.8	0
6320	Comparative phylogenomics and phylotranscriptomics provide insights into the genetic complexity of nitrogen-fixing root-nodule symbiosis. Plant Communications, 2024, 5, 100671.	7.7	3
6322	Physiological and evolutionary contexts of a new symbiotic species from the nitrogen-recycling gut community of turtle ants. ISME Journal, 2023, 17, 1751-1764.	9.8	0
6324	Unveiling the Protein Components of the Secretory-Venom Gland and Venom of the Scorpion Centruroides possanii (Buthidae) through Omic Technologies. Toxins, 2023, 15, 498.	3.4	1
6325	Distinct molecular profiles of skull bone marrow in health and neurological disorders. Cell, 2023, 186, 3706-3725.e29.	28.9	12
6326	Lactate limits CNS autoimmunity by stabilizing HIF-1Î± in dendritic cells. Nature, 2023, 620, 881-889.	27.8	10
6330	QTL-seq Identifies Pokkali-Derived QTLs and Candidate Genes for Salt Tolerance at Seedling Stage in Rice (Oryza sativa L.). Agriculture (Switzerland), 2023, 13, 1596.	3.1	2
6331	Peeling back the layers of coral holobiont multi-omics data. IScience, 2023, 26, 107623.	4.1	0
6332	Metagenomics-based inference of microbial metabolism towards neuroactive amino acids and the response to antibiotics in piglet colon. Amino Acids, 0, , .	2.7	0
6333	mRNA 3â€™UTR lengthening by alternative polyadenylation attenuates inflammatory responses and correlates with virulence of Influenza A virus. Nature Communications, 2023, 14, .	12.8	1

#	Article	IF	Citations
6338	RNA polymerase II pausing temporally coordinates cell cycle progression and erythroid differentiation. Developmental Cell, 2023, 58, 2112-2127.e4.	7.0	3
6339	The gut microbiota-induced kynurenic acid recruits GPR35-positive macrophages to promote experimental encephalitis. Cell Reports, 2023, 42, 113005.	6.4	5
6342	Pou3f1 orchestrates a gene regulatory network controlling contralateral retinogeniculate projections. Cell Reports, 2023, 42, 112985.	6.4	2
6343	Mapping the T cell repertoire to a complex gut bacterial community. Nature, 2023, 621, 162-170.	27.8	7
6344	Platelet-derived exerkine CXCL4/platelet factor 4 rejuvenates hippocampal neurogenesis and restores cognitive function in aged mice. Nature Communications, 2023, 14, .	12.8	16
6347	A comparative study reveals the relative importance of prokaryotic and eukaryotic proton pump rhodopsins in a subtropical marginal sea. ISME Communications, 2023, 3, .	4.2	1
6350	Gene coâ€option, duplication and divergence of cement proteins underpin the evolution of bioadhesives across barnacle life histories. Molecular Ecology, 2023, 32, 5071-5088.	3.9	0
6353	Biosynthesis of gibberellin-related compounds modulates far-red light responses in the liverwort Marchantia polymorpha. Plant Cell, 2023, 35, 4111-4132.	6.6	3
6354	A fast and globally optimal solution for RNA-seq quantification. Briefings in Bioinformatics, 0, , .	6.5	0
6355	SnakeLines: integrated set of computational pipelines for sequencing reads. Journal of Integrative Bioinformatics, 2023, .	1.5	1
6356	Analysis of subcellular RNA fractions demonstrates significant genetic regulation of gene expression in human brain post-transcriptionally. Scientific Reports, 2023, 13, .	3.3	0
6357	Fiber supplementation protects from antibiotic-induced gut microbiome dysbiosis by modulating gut redox potential. Nature Communications, 2023, 14, .	12.8	5
6359	Chemoautotrophic sulphur oxidizers dominate microbial necromass carbon formation in coastal blue carbon ecosystems. Functional Ecology, 2023, 37, 2634-2651.	3.6	1
6360	Sustained CD28 costimulation is required for self-renewal and differentiation of TCF-1 ⁺ PD-1 ⁺ CD8 T cells. Science Immunology, 2023, 8, .	11.9	4
6361	LZTR1 deficiency exerts high metastatic potential by enhancing sensitivity to EMT induction and controlling KLHL12-mediated collagen secretion. Cell Death and Disease, 2023, 14, .	6.3	1
6363	Endosperm cell death promoted by NAC transcription factors facilitates embryo invasion in Arabidopsis. Current Biology, 2023, 33, 3785-3795.e6.	3.9	3
6366	Cell cycle-linked vacuolar pH dynamics regulate amino acid homeostasis and cell growth. Nature Metabolism, 0, , .	11.9	2
6368	Alternative splicing impacts the rice stripe virus response transcriptome. Virology, 2023, 587, 109870.	2.4	0

#	Article	IF	Citations
6369	Identification of Long Non-Coding RNA Profiles and Potential Therapeutic Agents for Fibrolamellar Carcinoma Based on RNA-Sequencing Data. Genes, 2023, 14, 1709.	2.4	0
6370	MYC disrupts transcriptional and metabolic circadian oscillations in cancer and promotes enhanced biosynthesis. PLoS Genetics, 2023, 19, e1010904.	3.5	1
6372	Patient-derived Enteroids provide a Platform for the Development of Therapeutic Approaches in Microvillus Inclusion Disease. Journal of Clinical Investigation, 0, , .	8.2	1
6373	Early transcriptomic host response signatures in the serum of dengue patients provides insights into clinical pathogenesis and disease severity. Scientific Reports, 2023, 13, .	3.3	1
6375	Knockout of the Cardiac Transcription Factor NKX2-5 Results in Stem Cell-Derived Cardiac Cells with Typical Purkinje Cell-like Signal Transduction and Extracellular Matrix Formation. International Journal of Molecular Sciences, 2023, 24, 13366.	4.1	2
6377	Meta-Analysis of Heat-Stressed Transcriptomes Using the Public Gene Expression Database from Human and Mouse Samples. International Journal of Molecular Sciences, 2023, 24, 13444.	4.1	0
6378	mRNA-Seq and miRNA-Seq Analyses Provide Insights into the Mechanism of Pinellia ternata Bulbil Initiation Induced by Phytohormones. Genes, 2023, 14, 1727.	2.4	1
6379	Revealing metastatic castrationâ€resistant prostate cancer master regulator through <scp>lncRNAs</scp>â€centered regulatory network. Cancer Medicine, 2023, 12, 19279-19290.	2.8	0
6383	Thermophilic methane oxidation is widespread in Aotearoa-New Zealand geothermal fields. Frontiers in Microbiology, 0, 14, .	3.5	0
6385	Mining Public Data to Investigate the Virome of Neglected Pollinators and Other Floral Visitors. Viruses, 2023, 15, 1850.	3.3	0
6386	Targeting nucleic acid sensors in tumor cells to reprogram biogenesis and RNA cargo of extracellular vesicles for TÂcell-mediated cancer immunotherapy. Cell Reports Medicine, 2023, 4, 101171.	6.5	2
6388	Synaptic and transcriptomic features of cortical and amygdala pyramidal neurons predict inefficient fear extinction. Cell Reports, 2023, 42, 113066.	6.4	2
6389	Profiling of repetitive RNA sequences in the blood plasma of patients with cancer. Nature Biomedical Engineering, 2023, 7, 1627-1635.	22.5	5
6390	Young SINEs in pig genomes impact gene regulation, genetic diversity, and complex traits. Communications Biology, 2023, 6, .	4.4	2
6393	Transposable elements as tissue-specific enhancers in cancers of endodermal lineage. Nature Communications, 2023, 14, .	12.8	9
6394	The Soybean Expression Atlas v2: A comprehensive database of over 5000 RNAâ€seq samples. Plant Journal, 2023, 116, 1041-1051.	5.7	1
6395	A comparative fullâ€length transcriptomic resource provides insight into the perennial monocarpic mass flowering. Plant Journal, 2023, 116, 1842-1855.	5.7	0
6396	Long non-coding RNA SNHG8 drives stress granule formation in tauopathies. Molecular Psychiatry, 2023, 28, 4889-4901.	7.9	0

#	Article	IF	Citations
6397	Promiscuous CYP87A enzyme activity initiates cardenolide biosynthesis in plants. Nature Plants, 2023, 9, 1607-1617.	9.3	6
6398	Bacterial lipopolysaccharide modulates immune response in the colorectal tumor microenvironment. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	2
6399	Cross-species analysis of SHH medulloblastoma models reveals significant inhibitory effects of trametinib on tumor progression. Cell Death Discovery, 2023, 9, .	4.7	1
6400	Dysregulation of the Wnt/Î²-catenin signaling pathway via Rnf146 upregulation in a VPA-induced mouse model of autism spectrum disorder. Experimental and Molecular Medicine, 2023, 55, 1783-1794.	7.7	2
6401	Precision Medicine in a Community Cancer Center: Pan-Cancer DNA/RNA Sequencing of Tumors Reveals Clinically Relevant Gene Fusions. Biologics, 2023, 3, 198-208.	4.1	0
6402	On a path toward a broad-spectrum anti-viral: inhibition of HIV-1 and coronavirus replication by SR kinase inhibitor harmine. Journal of Virology, 0, , .	3.4	1
6403	SARS-CoV-2 infection severity and mortality is modulated by repeat-mediated regulation of alternative splicing. Microbiology Spectrum, 2023, 11, .	3.0	1
6404	Understanding the internal differences behind unsynchronized growth in sea cucumber Holothuria leucospilota by integration of transcriptomic and metabolomic data. Aquaculture Reports, 2023, 32, 101688.	1.7	0
6405	Activation of the transcription factor NFAT5 in the tumor microenvironment enforces CD8+ T cell exhaustion. Nature Immunology, 2023, 24, 1645-1653.	14.5	1
6406	Comparative analysis of gonadal transcriptomes between turtle and alligator identifies common molecular cues activated during the temperature-sensitive period for sex determination. Gene, 2023, 888, 147763.	2.2	1
6407	Comprehensive physiological, cytological, and transcriptional regulatory analyses reveal the coloration mechanism of culm yellow-slot mutation in moso bamboo (Phyllostachys edulis). Industrial Crops and Products, 2023, 204, 117328.	5.2	0
6408	De novo transcriptome analysis of Dysoxylum binectariferum to unravel the biosynthesis of pharmaceutically relevant specialized metabolites. Frontiers in Plant Science, 0, 14, .	3.6	0
6409	Increased hyaluronan by naked mole-rat Has2 improves healthspan in mice. Nature, 2023, 621, 196-205.	27.8	19
6410	Endothelial Cell Response in Kawasaki Disease and Multisystem Inflammatory Syndrome in Children. International Journal of Molecular Sciences, 2023, 24, 12318.	4.1	2
6411	Analysis of cnidarian Gcm suggests a neuronal origin of glial EAAT1 function. Scientific Reports, 2023, 13, .	3.3	0
6412	Acute and Long-Term Consequences of Co-opted doublesex on the Development of Mimetic Butterfly Color Patterns. Molecular Biology and Evolution, 2023, 40, .	8.9	2
6413	Investigating Neuron Degeneration in Huntingtonâ€™s Disease Using RNA-Seq Based Transcriptome Study. Genes, 2023, 14, 1801.	2.4	1
6414	Growth dynamics and molecular bases of evolutionary novel jaw extensions in halfbeaks and needlefishes (Beloniformes). Molecular Ecology, 2023, 32, 5798-5811.	3.9	1

#	Article	IF	Citations
6415	Glioma Stem Cells Are Sensitized to BCL-2 Family Inhibition by Compromising Histone Deacetylases. International Journal of Molecular Sciences, 2023, 24, 13688.	4.1	0
6416	Integrative Transcriptomic Profiling of the Wilms Tumor. Cancers, 2023, 15, 3846.	3.7	0
6417	Transcriptome Profile Analyses of Head Kidney in Roach (Rutilus rutilus), Common Bream (Abramis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Differences in Fish Vigour among Parental Species and Their Hybrids?. Biology, 2023, 12, 1199.	2.8	0
6418	MacroH2A restricts inflammatory gene expression in melanoma cancer-associated fibroblasts by coordinating chromatin looping. Nature Cell Biology, 2023, 25, 1332-1345.	10.3	4
6419	Human cardiovascular disease model predicts xanthine oxidase inhibitor cardiovascular risk. PLoS ONE, 2023, 18, e0291330.	2.5	0
6420	Investigation of lncRNA in Bos taurus Mammary Tissue during Dry and Lactation Periods. Genes, 2023, 14, 1789.	2.4	1
6421	BSFbase: The comprehensive genomic resource for a natural recycler, the black soldier fly (Hermetia illucens L.). Insect Science, 2023, 30, 1011-1016.	3.0	1
6422	Identification of Unique microRNA Profiles in Different Types of Idiopathic Inflammatory Myopathy. Cells, 2023, 12, 2198.	4.1	2
6423	Long-read sequencing reveals the landscape of aberrant alternative splicing and novel therapeutic target in colorectal cancer. Genome Medicine, 2023, 15, .	8.2	2
6424	In silico analysis of Hsp70 genes in Ctenopharyngodon idella and their expression profiles in response to environmental stresses. Biotechnology and Biotechnological Equipment, 2023, 37, .	1.3	0
6425	Gene signature discovery and systematic validation across diverse clinical cohorts for TB prognosis and response to treatment. PLoS Computational Biology, 2023, 19, e1010770.	3.2	0
6426	Transcriptomic analyses during development reveal mechanisms of integument structuring and color production. Evolutionary Ecology, 0, , .	1.2	0
6427	Identifying novel mechanisms of biallelic TP53 loss refines poor outcome for patients with multiple myeloma. Blood Cancer Journal, 2023, 13, .	6.2	0
6428	C. elegans germ granules sculpt both germline and somatic RNAome. Nature Communications, 2023, 14, .	12.8	2
6429	Activation-induced deaminase expression defines mature B cell lymphoma in the mouse. Frontiers in Immunology, 0, 14, .	4.8	0
6430	Comprehensive modular analyses of scar subtypes illuminate underlying molecular mechanisms and potential therapeutic targets. International Wound Journal, 2024, 21, .	2.9	0
6431	Transcriptomic sequencing data illuminate insecticide-induced physiological stress mechanisms in aquatic non-target invertebrates. Environmental Pollution, 2023, 335, 122306.	7.5	1
6432	Analyzing alternative splicing in Alzheimerâ€™s disease postmortem brain: a cell-level perspective. Frontiers in Molecular Neuroscience, 0, 16, .	2.9	0

#	Article	IF	Citations
6433	Metagenomic analysis reveals microbial metabolic potentials alterations under antibiotic stress during sludge anaerobic digestion. Journal of Environmental Chemical Engineering, 2023, 11, 110746.	6.7	10
6434	Tumor-intrinsic expression of the autophagy gene Atg16l1 suppresses anti-tumor immunity in colorectal cancer. Nature Communications, 2023, 14, .	12.8	2
6435	Seasonality Determines the Variations of Biofilm Microbiome and Antibiotic Resistome in a Pilot-Scale Chlorinated Drinking Water Distribution System Deciphered by Metagenome Assembly. Environmental Science & Technology, 2023, 57, 11430-11441.	10.0	3
6436	Exportin 1 inhibition prevents neuroendocrine transformation through SOX2 down-regulation in lung and prostate cancers. Science Translational Medicine, 2023, 15, .	12.4	1
6437	Microbial gene expression in Guaymas Basin subsurface sediments responds to hydrothermal stress and energy limitation. ISME Journal, 2023, 17, 1907-1919.	9.8	4
6438	Preexisting tumor-resident T cells with cytotoxic potential associate with response to neoadjuvant antiâ€“PD-1 in head and neck cancer. Science Immunology, 2023, 8, .	11.9	9
6439	Starvation responses impact interaction dynamics of human gut bacteria Bacteroides thetaiotaomicron and Roseburia intestinalis. ISME Journal, 2023, 17, 1940-1952.	9.8	0
6440	BAP1 promotes osteoclast function by metabolic reprogramming. Nature Communications, 2023, 14, .	12.8	1
6441	BASIDIN as a New Protein Effector of the Phytopathogen Causing Witcheâ€™s Broom Disease in Cocoa. International Journal of Molecular Sciences, 2023, 24, 11714.	4.1	0
6442	APOBEC3B regulates R-loops and promotes transcription-associated mutagenesis in cancer. Nature Genetics, 2023, 55, 1721-1734.	21.4	6
6443	Molecular Changes in the Brain of the Wintering Calidris pusilla in the Mangroves of the Amazon River Estuary. International Journal of Molecular Sciences, 2023, 24, 12712.	4.1	0
6444	The archaeal Lsm protein from Pyrococcus furiosus binds co-transcriptionally to poly(U)-rich target RNAs. Biological Chemistry, 2023, .	2.5	0
6445	GÎ±s is dispensable for Î²-arrestin coupling but dictates GRK selectivity and is predominant for gene expression regulation by Î²2-adrenergic receptor. Journal of Biological Chemistry, 2023, , 105293.	3.4	0
6446	Identification of Splice Variants and Isoforms in Transcriptomics and Proteomics. Annual Review of Biomedical Data Science, 2023, 6, 357-376.	6.5	5
6447	Epigenetic inheritance is unfaithful at intermediately methylated CpG sites. Nature Communications, 2023, 14, .	12.8	1
6448	Syntrophic entanglements for propionate and acetate oxidation under thermophilic and high-ammonia conditions. ISME Journal, 2023, 17, 1966-1978.	9.8	2
6449	Comprehensive Transcriptome Analysis in the Testis of the Silkworm, Bombyx mori. Insects, 2023, 14, 684.	2.2	0
6450	Assessing the Effects of Dietary Cadmium Exposure on the Gastrointestinal Tract of Beef Cattle via Microbiota and Transcriptome Profile. Animals, 2023, 13, 3104.	2.3	0

#	Article	IF	Citations
6451	An extended catalog of integrated prophages in the infant and adult fecal microbiome shows high prevalence of lysogeny. Frontiers in Microbiology, 0, 14, .	3.5	3
6452	An integrated systems biology approach reveals differences in formate metabolism in the genus Methanothermobacter. IScience, 2023, 26, 108016.	4.1	1
6453	Expanded olfactory system in ray-finned fishes capable of terrestrial exploration. BMC Biology, 2023, 21, .	3.8	2
6454	cfOmics: a cell-free multi-Omics database for diseases. Nucleic Acids Research, 0, , .	14.5	0
6455	Transcriptomics of mussel transmissible cancer MtrBTN2 suggests accumulation of multiple cancer traits and oncogenic pathways shared among bilaterians. Open Biology, 2023, 13, .	3.6	0
6456	Investigation of evolutionary dynamics for drug resistance in 3D spheroid model system using cellular barcoding technology. PLoS ONE, 2023, 18, e0291942.	2.5	0
6457	A clinically useful and biologically informative genomic classifier for papillary thyroid cancer. Frontiers in Endocrinology, 0, 14, .	3.5	0
6458	Sexual dimorphic gene expression profile of perirenal adipose tissue in ovine fetuses with growth restriction. Frontiers in Physiology, 0, 14, .	2.8	1
6460	Microbes from mature compost to promote bacterial chemotactic motility via tricarboxylic acid cycle-regulated biochemical metabolisms for enhanced composting performance. Bioresource Technology, 2023, 387, 129633.	9.6	2
6461	Comparative analysis of nascent RNA sequencing methods and their applications in studies of cotranscriptional splicing dynamics. Plant Cell, 0, , .	6.6	1
6462	Lgr5-expressing secretory cells form a Wnt inhibitory niche in cartilage critical for chondrocyte identity. Cell Stem Cell, 2023, 30, 1179-1198.e7.	11.1	2
6463	A comprehensive genomic catalog from global cold seeps. Scientific Data, 2023, 10, .	5.3	2
6464	<tt>simpleaf</tt>: a simple, flexible, and scalable framework for single-cell data processing using alevin-fry. Bioinformatics, 2023, 39, .	4.1	1
6465	Spliceosome mutations are associated with clinical response in a phase 1b/2 study of the PLK1 inhibitor onvansertib in combination with decitabine in relapsed or refractory acute myeloid leukemia. Annals of Hematology, 2023, 102, 3049-3059.	1.8	0
6466	Gene expression signatures associated with chronic endometritis revealed by RNA sequencing. Frontiers in Medicine, 0, 10, .	2.6	1
6467	A Single-Cell Taxonomy Predicts Inflammatory Niche Remodeling to Drive Tissue Failure and Outcome in Human AML. Blood Cancer Discovery, 2023, 4, 394-417.	5.0	4
6468	Differential outcomes and immune checkpoint inhibitor response among endometrial cancer patients with MLH1 hypermethylation versus MLH1 â€œLynch-likeâ€•mismatch repair gene mutation. Gynecologic Oncology, 2023, 177, 132-141.	1.4	2
6469	Occurrence and fate of antibiotic-resistance genes and their potential hosts in high-moisture alfalfa silage treated with or without formic acid bactericide. Journal of Environmental Management, 2023, 347, 119235.	7.8	0

#	Article	IF	Citations
6470	Phenotypic and genomic characterization of Bathyarchaeum tardum gen. nov., sp. nov., a cultivated representative of the archaeal class Bathyarchaeia. Frontiers in Microbiology, 0, 14, .	3.5	3
6471	Transcriptional Response to Standard AML Drugs Identifies Synergistic Combinations. International Journal of Molecular Sciences, 2023, 24, 12926.	4.1	0
6472	Neuronal mTORC1 inhibition promotes longevity without suppressing anabolic growth and reproduction in C. elegans. PLoS Genetics, 2023, 19, e1010938.	3.5	3
6473	Crosstalk between small-cell lung cancer cells and astrocytes mimics brain development to promote brain metastasis. Nature Cell Biology, 2023, 25, 1506-1519.	10.3	2
6474	The unique gut microbiome of giant pandas involved in protein metabolism contributes to the hostâ€™s dietary adaption to bamboo. Microbiome, 2023, 11, .	11.1	9
6475	The multi-kingdom microbiome of the goat gastrointestinal tract. Microbiome, 2023, 11, .	11.1	3
6476	Impact of the Physical Cellular Microenvironment on the Structure and Function of a Model Hepatocyte Cell Line for Drug Toxicity Applications. Cells, 2023, 12, 2408.	4.1	0
6477	Role of natural transformation in the evolution of small cryptic plasmids in Synechocystis sp. <scp>PCC</scp> 6803. Environmental Microbiology Reports, 2023, 15, 656-668.	2.4	1
6478	NanopoReaTA: a user-friendly tool for nanopore-seq real-time transcriptional analysis. Bioinformatics, 2023, 39, .	4.1	0
6479	TET2 lesions enhance the aggressiveness of CEBPA-mutant acute myeloid leukemia by rebalancing GATA2 expression. Nature Communications, 2023, 14, .	12.8	1
6481	Genes possibly related to symbiosis in early life stages of Acropora tenuis inoculated with Symbiodinium microadriaticum. Communications Biology, 2023, 6, .	4.4	1
6482	A repertoire of candidate effector proteins of the fungus Ceratocystis cacaofunesta. Scientific Reports, 2023, 13, .	3.3	0
6483	Molecular landscape and functional characterization of centrosome amplification in ovarian cancer. Nature Communications, 2023, 14, .	12.8	1
6484	Globally distributed Myxococcota with photosynthesis gene clusters illuminate the origin and evolution of a potentially chimeric lifestyle. Nature Communications, 2023, 14, .	12.8	5
6486	Long- and short-read RNA sequencing from five reproductive organs of boar. Scientific Data, 2023, 10, .	5.3	1
6487	cgMSI: pathogen detection within species from nanopore metagenomic sequencing data. BMC Bioinformatics, 2023, 24, .	2.6	0
6489	Peptides from conserved tandem direct repeats of SHORT-LEAF regulate gametophore development in moss P. patens. Plant Physiology, 2023, 194, 434-455.	4.8	1
6490	Successional action of Bacteroidota and Firmicutes in decomposing straw polymers in a paddy soil. Environmental Microbiomes, 2023, 18, .	5.0	0

#	Article	IF	Citations
6491	Transcriptomic analysis implicates ABA signaling and carbon supply in the differential outgrowth of petunia axillary buds. BMC Plant Biology, 2023, 23, .	3.6	0
6492	Splicing regulation of GFPT1 muscle-specific isoform and its roles in glucose metabolisms and neuromuscular junction. IScience, 2023, 26, 107746.	4.1	0
6493	A glossy mutant in onion (Allium cepa L.) shows decreased expression of wax biosynthesis genes. Frontiers in Plant Science, 0, 14, .	3.6	0
6494	Benchmarking long-read RNA-sequencing analysis tools using in silico mixtures. Nature Methods, 2023, 20, 1810-1821.	19.0	10
6495	Microbial Gene Ontology informed deep neural network for microbe functionality discovery in human diseases. PLoS ONE, 2023, 18, e0290307.	2.5	1
6496	Invasive plant species interact with drought to shift key functions and families in the native rhizosphere. Plant and Soil, 0, , .	3.7	0
6497	A spatial sequencing atlas of age-induced changes in the lung during influenza infection. Nature Communications, 2023, 14, .	12.8	3
6498	Facing lethal temperatures: Heatâ€shock response in desert and temperate ants. Ecology and Evolution, 2023, 13, .	1.9	1
6499	Clonal cooperation through soluble metabolite exchange facilitates metastatic outgrowth by modulating Allee effect. Science Advances, 2023, 9, .	10.3	1
6500	Imprinting at the KBTBD6 locus involves species-specific maternal methylation and monoallelic expression in livestock animals. Journal of Animal Science and Biotechnology, 2023, 14, .	5.3	1
6501	Antibiotic resistome and associated bacterial communities in agricultural soil following the amendments of swine manureâ€“derived fermentation bed waste. Environmental Science and Pollution Research, 2023, 30, 104520-104531.	5.3	0
6502	Comparison of antiviral responses in two bat species reveals conserved and divergent innate immune pathways. IScience, 2023, 26, 107435.	4.1	2
6503	Epigenomic response to albuterol treatment in asthma-relevant airway epithelial cells. Clinical Epigenetics, 2023, 15, .	4.1	2
6504	Systematic identification of gene combinations to target in innate immune cells to enhance T cell activation. Nature Communications, 2023, 14, .	12.8	0
6505	Radiation impacts gene redundancy and biofilm regulation of cryoconite microbiomes in Northern Hemisphere glaciers. Microbiome, 2023, 11, .	11.1	0
6507	Interaction between phenylpropane metabolism and oil accumulation in the developing seed of Brassica napus revealed by high temporal-resolution transcriptomes. BMC Biology, 2023, 21, .	3.8	2
6508	Capsaicin indirectly regulates TRPA1 via the arachidonic acid cascade, resulting in TJ opening. Bioscience, Biotechnology and Biochemistry, 0, , .	1.3	0
6509	Chromatin loop dynamics during cellular differentiation are associated with changes to both anchor and internal regulatory features. Genome Research, 2023, 33, 1258-1268.	5.5	1

#	Article	IF	Citations
6510	Genomic and transcriptomic analyses reveal polygenic architecture for ecologically important traits in aspen (PopulusÂtremuloides Michx.). Ecology and Evolution, 2023, 13, .	1.9	0
6512	Metagenomics reveals the abundance and accumulation trend of antibiotic resistance gene profile under long-term no tillage in a rainfed agroecosystem. Frontiers in Microbiology, 0, 14, .	3.5	1
6513	Hypoxia-inducible factor 1 signaling drives placental aging and can provoke preterm labor. ELife, 0, 12, .	6.0	0
6515	Nasopharyngeal fungal subtypes of infant bronchiolitis and disease severity risk. EBioMedicine, 2023, 95, 104742.	6.1	0
6516	bettercallsal: better calling of Salmonella serotypes from enrichment cultures using shotgun metagenomic profiling and its application in an outbreak setting. Frontiers in Microbiology, 0, 14, .	3.5	0
6517	Lysyl oxidase-like 1-antisense 1 (LOXL1-AS1) lncRNA differentially regulates gene and protein expression, signaling and morphology of human ocular cells. Human Molecular Genetics, 2023, 32, 3053-3062.	2.9	1
6519	Transcriptome analysis reveals insights into adaptive responses of two marine microalgae species to Nordic seasons. Algal Research, 2023, 74, 103222.	4.6	0
6521	Sexual dimorphic eyestalk transcriptome of kuruma prawn Marsupenaeus japonicus. Gene, 2023, 885, 147700.	2.2	0
6523	Development of Nanopore sequencing-based full-length transcriptome database toward functional genome annotation of the Pacific oyster, Crassostrea gigas. Genomics, 2023, 115, 110697.	2.9	0
6526	Concurrent predictors of an immune responsive tumor microenvironment within tumor mutational burden-high breast cancer. Frontiers in Oncology, 0, 13, .	2.8	0
6527	Differential involvement of WRKY genes in abiotic stress tolerance of Dendrobium huoshanense. Industrial Crops and Products, 2023, 204, 117295.	5.2	3
6528	Host nutrient sensing is mediated by mTOR signaling in cnidarian-dinoflagellate symbiosis. Current Biology, 2023, 33, 3634-3647.e5.	3.9	1
6529	A pan-cancer clinical platform to predict immunotherapy outcomes and prioritize immuno-oncology combinations in early-phase trials. Med, 2023, 4, 710-727.e5.	4.4	0
6530	Transcriptomic network analysis reveals key drivers of response to anti-TNF biologics in patients with rheumatoid arthritis. Rheumatology, 0, , .	1.9	0
6533	Using transcriptomics to examine the physiological status of wild-caught walleye (Sander) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	2.4	3
6534	Skin-type-dependent development of murine mechanosensory neurons. Developmental Cell, 2023, 58, 2032-2047.e6.	7.0	4
6537	A MYCN-independent mechanism mediating secretome reprogramming and metastasis in MYCN -amplified neuroblastoma. Science Advances, 2023, 9, .	10.3	0
6538	Interpretation of SNP combination effects on schizophrenia etiology based on stepwise deep learning with multi-precision data. Briefings in Functional Genomics, 0, , .	2.7	0

#	Article	IF	Citations
6539	Multi-omic profiling and real time ex vivo modelling of imatinib-resistant dermatofibrosarcoma protuberans with fibrosarcomatous transformation. Human Cell, 2023, 36, 2228-2236.	2.7	1
6541	Predicting gene expression changes upon epigenomic drug treatment. F1000Research, 0, 12, 1089.	1.6	0
6542	Interspecies comparison of the early transcriptomic changes associated with hepatitis B virus exposure in human and macaque immune cell populations. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	0
6546	Desiccation induces varied responses within a soil bacterial genus. Environmental Microbiology, 2023, 25, 3075-3086.	3.8	2
6547	The <scp>polyA</scp> tail facilitates splicing of last introns with weak 3â€² splice sites via <scp>PABPN1</scp>. EMBO Reports, 2023, 24, .	4.5	1
6548	Cocoa Apoplastome Contains Defense Proteins Against Pathogens. Phytopathology, 2024, 114, 427-440.	2.2	0
6549	Gene presence/absence variation in Mytilus galloprovincialis and its implications in gene expression and adaptation. IScience, 2023, 26, 107827.	4.1	0
6550	Mouse models of SYNGAP1 -related intellectual disability. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.1	4
6553	Pleiotropy with sex-specific traits reveals genetic aspects of sex differences in Parkinsonâ€™s disease. Brain, 2024, 147, 858-870.	7.6	0
6554	Identification of early gene expression profiles associated with long-lasting antibody responses to the Ebola vaccine Ad26.ZEBOV/MVA-BN-Filo. Cell Reports, 2023, 42, 113101.	6.4	1
6555	Salinity-triggered homogeneous selection constrains the microbial function and stability in lakes. Applied Microbiology and Biotechnology, 2023, 107, 6591-6605.	3.6	1
6556	Risk assessment of parabens in a transcriptomics-based in vitro test. Chemico-Biological Interactions, 2023, 384, 110699.	4.0	0
6558	Chromosome-level Dinobdella ferox genome provided a molecular model for its specific parasitism. Parasites and Vectors, 2023, 16, .	2.5	0
6560	Increasing temperature-driven changes in life history traits and gene expression of an Antarctic tardigrade species. Frontiers in Physiology, 0, 14, .	2.8	1
6562	Calorie restriction outperforms bariatric surgery in a murine model of obesity and triple-negative breast cancer. JCI Insight, 2023, 8, .	5.0	2
6563	FLIBase: a comprehensive repository of full-length isoforms across human cancers and tissues. Nucleic Acids Research, 0, , .	14.5	2
6567	Neoadjuvant Durvalumab Alone or Combined with Novel Immuno-Oncology Agents in Resectable Lung Cancer: The Phase II NeoCOAST Platform Trial. Cancer Discovery, 2023, 13, 2394-2411.	9.4	8
6568	The distribution variation of pathogens and virulence factors in different geographical populations of giant pandas. Frontiers in Microbiology, 0, 14, .	3.5	0

#	Article	IF	Citations
6569	Transcriptome analysis revealed the existence of family-specific regulation of growth traits in grass carp. Genomics, 2023, 115, 110706.	2.9	0
6579	eQTL Catalogue 2023: New datasets, X chromosome QTLs, and improved detection and visualisation of transcript-level QTLs. PLoS Genetics, 2023, 19, e1010932.	3.5	3
6580	Advanced Age in Humans and Mouse Models of Glioblastoma Show Decreased Survival from Extratumoral Influence. Clinical Cancer Research, 2023, 29, 4973-4989.	7.0	2
6581	FSHR-mTOR-HIF1 signaling alleviates mouse follicles from AMPK-induced atresia. Cell Reports, 2023, 42, 113158.	6.4	0
6582	The senescent secretome drives PLVAP expression in cultured human hepatic endothelial cells to promote monocyte transmigration. IScience, 2023, 26, 107966.	4.1	0
6585	The Next-Generation Oral Selective Estrogen Receptor Degrader Camizestrant (AZD9833) Suppresses ER+ Breast Cancer Growth and Overcomes Endocrine and CDK4/6 Inhibitor Resistance. Cancer Research, 2023, 83, 3989-4004.	0.9	3
6587	EDIL3 as an Angiogenic Target of Immune Exclusion Following Checkpoint Blockade. Cancer Immunology Research, 2023, 11, 1493-1507.	3.4	0
6588	NCOA5 Haploinsufficiency in Myeloid-Lineage Cells Sufficiently Causes Nonalcoholic Steatohepatitis and Hepatocellular Carcinoma. Cellular and Molecular Gastroenterology and Hepatology, 2023, , .	4.5	1
6591	Spenito-dependent metabolic sexual dimorphism intrinsic to fat storage cells. Genetics, 0, , .	2.9	0
6592	Microscopic and transcriptomic changes in porcine synovium one year following disruption of the anterior cruciate ligament. Osteoarthritis and Cartilage, 2023, , .	1.3	2
6593	Parallel tuning of semiâ€dwarfism via differential splicing of Brachytic1 in commercial maize and smallholder sorghum. New Phytologist, 2023, 240, 1930-1943.	7.3	0
6596	The BAF chromatin remodeling complex licenses planarian stem cells access to ectodermal and mesodermal cell fates. BMC Biology, 2023, 21, .	3.8	1
6598	The Abundant and Unique Transcripts and Alternative Splicing of the Artificially Autododecaploid London Plane (Platanus Ã— acerifolia). International Journal of Molecular Sciences, 2023, 24, 14486.	4.1	0
6599	Contract-Driven Design of Scientific Data Analysis Workflows. , 2023, , .		0
6600	Gallic acid acts as an anti-inflammatory agent via PPARÎ³-mediated immunomodulation and antioxidation in fish gut-liver axis. Aquaculture, 2024, 578, 740142.	3.5	1
6601	Longitudinal dysregulation of long non-coding RNAs in Parkinsonâ€™s disease. Experimental Biology and Medicine, 0, , .	2.4	0
6606	Artificial switches induce the bespoke production of functional compounds in marine microalgae Chlorella by neutralizing CO2. , 2023, 16, .		2
6607	Polysome propensity and tunable thresholds in coding sequence length enable differential mRNA stability. Science Advances, 2023, 9, .	10.3	1

#	Article	IF	Citations
6608	Deciphering the genetic architecture of resistance to Corynespora cassiicola in soybean (Glycine max) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 14, .	3.6	0
6609	The VBNC state: a fundamental survival strategy of Acinetobacter baumannii. MBio, 2023, 14, .	4.1	3
6610	Selective reduction of visceral adipose tissue with injectable ice slurry. Scientific Reports, 2023, 13, .	3.3	0
6611	Molecular subtypes of epilepsy associated with post-surgical seizure recurrence. Brain Communications, 2023, 5, .	3.3	1
6614	Folic acid supplementation in a mouse model of diabetes in pregnancy alters insulin sensitivity in female mice and beta cell mass in offspring. FASEB Journal, 2023, 37, .	0.5	1
6615	Pathway2Targets: an open-source pathway-based approach to repurpose therapeutic drugs and prioritize human targets. PeerJ, 0, 11, e16088.	2.0	0
6619	Defective monocyte plasticity and altered <scp>cAMP</scp> pathway characterize <scp>USB1</scp>â€mutated poikiloderma with neutropenia Clericuzio type. British Journal of Haematology, 2024, 204, 683-693.	2.5	1
6621	A resource of singleâ€cell gene expression profiles in a planarian <scp>Dugesia japonica</scp>. Development Growth and Differentiation, 0, , .	1.5	0
6623	Circulating Tumor DNA Analysis in Advanced Urothelial Carcinoma: Insights from Biological Analysis and Extended Clinical Follow-up. Clinical Cancer Research, 2023, 29, 4797-4807.	7.0	2
6624	Transposons contribute to the functional diversification of the head, gut, and ovary transcriptomes acrossDrosophilanatural strains. Genome Research, 2023, 33, 1541-1553.	5.5	0
6625	Multi-omics analysis reveals the molecular basis of flavonoid accumulation in fructus of Gardenia (Gardenia jasminoides Ellis). BMC Genomics, 2023, 24, .	2.8	0
6626	Interspecies coâ€expression analysis of lateral root development using inducible systems in rice, Medicago, and Arabidopsis. Plant Journal, 2023, 116, 1052-1063.	5.7	1
6627	On de novo Bridging Paired-end RNA-seq Data. , 2023, , .		1
6628	Comprehensive isoform-level analysis reveals the contribution of alternative isoforms to venom evolution and repertoire diversity. Genome Research, 2023, 33, 1554-1567.	5.5	3
6630	Comparative Transcriptome Analysis Reveals Genes Associated with Alkaloid Diversity in Javanese Long Pepper (Piper retrofractum) Fruits. International Journal of Plant Biology, 2023, 14, 896-909.	2.6	0
6631	Chromatin analysis of adult pluripotent stem cells reveals a unique stemness maintenance strategy. Science Advances, 2023, 9, .	10.3	1
6632	Ethanologenesis from glycerol by the gut acetogen Blautia schinkii. Environmental Microbiology, 0, , .	3.8	0
6635	Multivalent insulin receptor activation using insulinâ€“DNA origami nanostructures. Nature Nanotechnology, 2024, 19, 237-245.	31.5	1

#	Article	IF	Citations
6638	Photosynthesis regulation, cell membrane stabilization and methylglyoxal detoxification seems major altered pathways under cold stress as revealed by integrated multi-omics meta-analysis. Physiology and Molecular Biology of Plants, 0, , .	3.1	0
6643	Candida auris â€"macrophage cellular interactions and transcriptional response. Infection and Immunity, 0, , .	2.2	3
6644	Evolution and development of fruits of Erycina pusilla and other orchid species. PLoS ONE, 2023, 18, e0286846.	2.5	1
6646	PHINDaccess Hackathons for COVID-19 and Host-Pathogen Interaction: Lessons Learned and Recommendations for Low- and Middle-Income Countries. BioMed Research International, 2023, 2023, 1-12.	1.9	0
6647	Where the minor things are: a pan-eukaryotic survey suggests neutral processes may explain much of minor intron evolution. Nucleic Acids Research, 2023, 51, 10884-10908.	14.5	4
6650	RNA-binding deficient TDP-43 drives cognitive decline in a mouse model of TDP-43 proteinopathy. ELife, 0, 12, .	6.0	4
6652	Phenotypic and genomic characterization of the first alkaliphilic aceticlastic methanogens and proposal of a novel genus Methanocrinis gen.nov. within the family Methanotrichaceae. Frontiers in Microbiology, 0, 14, .	3.5	1
6653	RNA sequencing of peripheral blood in amyotrophic lateral sclerosis reveals distinct molecular subtypes: Considerations for biomarker discovery. Neuropathology and Applied Neurobiology, 2023, 49, .	3.2	2
6656	Genome-wide chromatin interaction map for Trypanosoma cruzi. Nature Microbiology, 2023, 8, 2103-2114.	13.3	2
6658	Gibberellin and miRNA156-targeted SlSBP genes synergistically regulate tomato floral meristem determinacy and ovary patterning. Development (Cambridge), 2023, 150, .	2.5	2
6659	Stromal netrin-1 coordinates renal arteriogenesis and mural cell differentiation. Development (Cambridge), 0, , .	2.5	2
6660	Molecular insights into nitrogen constraint for niche partitioning and physiological adaptation of coastal Synechococcus assemblages. Environmental Research, 2023, 239, 117383.	7.5	0
6661	Gut Bacteroides act in a microbial consortium to cause susceptibility to severe malaria. Nature Communications, 2023, 14, .	12.8	0
6662	Next-Generation sequencing transforming clinical practice and precision medicine. Clinica Chimica Acta, 2023, 551, 117568.	1.1	1
6664	Reducing chlorophyll levels in seedâ€filling stages results in higher seed nitrogen without impacting canopy carbon assimilation. Plant, Cell and Environment, 2024, 47, 278-293.	5.7	0
6665	Citronellol biosynthesis in pelargonium is a multistep pathway involving progesterone 5Î²-reductase and/or iridoid synthase-like enzymes. Plant Physiology, 2024, 194, 1006-1023.	4.8	0
6668	Regulation of dermal fibroblasts by human neutrophil peptides. Scientific Reports, 2023, 13, .	3.3	0
6671	Metatranscriptomics reveals diversity of symbiotic interaction and mechanisms of carbon exchange in the marine cyanolichen Lichina pygmaea. New Phytologist, 2024, 241, 2243-2257.	7.3	3

#	Article	IF	Citations
6673	Insights into the Evolution of Ohnologous Sequences and Their Epigenetic Marks Post-WGD in Malus Domestica. Genome Biology and Evolution, 2023, 15, .	2.5	0
6674	Integrative CUT&Tag-RNA-Seq analysis of histone variant macroH2A1-dependent orchestration of human induced pluripotent stem cellÂreprogramming. Epigenomics, 2023, 15, 863-877.	2.1	0
6675	A novel zinc finger transcription factor, BcMsn2, is involved in growth, development, and virulence in Botrytis cinerea. Frontiers in Microbiology, 0, 14, .	3.5	0
6676	BPIFB1 loss alters airway mucus properties and diminishes mucociliary clearance. American Journal of Physiology - Lung Cellular and Molecular Physiology, 0, , .	2.9	0
6677	T3SS chaperone of the CesT family is required for secretion of the anti-sigma factor BtrA in Bordetella pertussis. Emerging Microbes and Infections, 2023, 12, .	6.5	0
6678	Spontaneous metastasis xenograft models link <scp>CD44</scp> isoform 4 to angiogenesis, hypoxia, <scp>EMT</scp> and mitochondriaâ€related pathways in colorectal cancer. Molecular Oncology, 0, , .	4.6	1
6680	Optimized method for differential gene expression analysis in non-model species: Case of Cedrela odorata L.. MethodsX, 2023, 11, 102449.	1.6	0
6682	Elevated A-to-I RNA editing in COVID-19 infected individuals. NAR Genomics and Bioinformatics, 2023, 5, .	3.2	3
6683	The Effect of Bifidobacterium animalis subsp. lactis Bl-04 on Influenza A Virus Infection in Mice. Microorganisms, 2023, 11, 2582.	3.6	0
6684	Vesicular Stomatitis Virus Elicits Early Transcriptome Response in Culicoides sonorensis Cells. Viruses, 2023, 15, 2108.	3.3	0
6685	Contrasting genes conferring short- and long-term biofilm adaptation in Listeria. Microbial Genomics, 2023, 9, .	2.0	1
6686	Seasonal variations of biofilm C, N and S cycling genes in a pilot-scale chlorinated drinking water distribution system. Water Research, 2023, 247, 120759.	11.3	1
6687	Regulation of gene expression downstream of a novel Fgf/Erk pathway during Xenopus development. PLoS ONE, 2023, 18, e0286040.	2.5	0
6688	FSHD muscle shows perturbation in fibroadipogenic progenitor cells, mitochondrial function and alternative splicing independently of inflammation. Human Molecular Genetics, 0, , .	2.9	0
6689	Genome- and transcriptome-wide characterization of ZIP gene family reveals their potential role in radish (Raphanus sativus) response to heavy metal stresses. Scientia Horticulturae, 2024, 324, 112564.	3.6	0
6690	Macrophage AMPK Î²1 activation by PF-06409577 reduces the inflammatory response, cholesterol synthesis, and atherosclerosis in mice. IScience, 2023, 26, 108269.	4.1	0
6692	RBFOX2 regulated EYA3 isoforms partner with SIX4 or ZBTB1 to control transcription during myogenesis. IScience, 2023, 26, 108258.	4.1	0
6693	Performance of computational algorithms to deconvolve heterogeneous bulk ovarian tumor tissue depends on experimental factors. Genome Biology, 2023, 24, .	8.8	1

#	Article	IF	Citations
6695	Spatiotemporal Deposition of Cell Wall Polysaccharides in Oat Endosperm during Grain Development. Plant Physiology, 0, , .	4.8	2
6696	Diversification of small RNA pathways underlies germline RNAi incompetence in wild C. elegans strains. Genetics, 0, , .	2.9	2
6698	Pet cats may shape the antibiotic resistome of their ownerâ€™s gut and living environment. Microbiome, 2023, 11, .	11.1	3
6699	IMP: bridging the gap for medicinal plant genomics. Nucleic Acids Research, 0, , .	14.5	0
6700	Breast cancer therapies reduce risk of Alzheimerâ€™s disease and promote estrogenic pathways and action in brain. IScience, 2023, 26, 108316.	4.1	1
6701	Principal Component Analysis of Alternative Splicing Profiles Revealed by Long-Read ONT Sequencing in Human Liver Tissue and Hepatocyte-Derived HepG2 and Huh7 Cell Lines. International Journal of Molecular Sciences, 2023, 24, 15502.	4.1	1
6702	Assembly and annotation of the black spruce genome provide insights on spruce phylogeny and evolution of stress response. G3: Genes, Genomes, Genetics, 2023, 14, .	1.8	1
6703	Genomic and transcriptomic characterization of delta SARS-CoV-2 infection in free-ranging white-tailed deer (Odocoileus virginianus). IScience, 2023, 26, 108319.	4.1	1
6704	Genomic and transcriptomic insights into complex virusâ€“prokaryote interactions in marine biofilms. ISME Journal, 2023, 17, 2303-2312.	9.8	0
6705	Clinical data warehouses for disease diagnosis: A focus on exosomal MicroRNA biomarkers. Informatics in Medicine Unlocked, 2023, , 101390.	3.4	0
6706	Downregulation of Ubiquitin-Specific Protease 15 (USP15) Does Not Provide Therapeutic Benefit in Experimental Mesial Temporal Lobe Epilepsy. Molecular Neurobiology, 0, , .	4.0	0
6708	PSI Photoinhibition and Changing CO2 Levels Initiate Retrograde Signals to Modify Nuclear Gene Expression. Antioxidants, 2023, 12, 1902.	5.1	0
6709	Genetic vulnerability to Crohnâ€™s disease reveals a spatially resolved epithelial restitution program. Science Translational Medicine, 2023, 15, .	12.4	0
6710	Phylogenetic and ecophysiological novelty of subsurface mercury methylators in mangrove sediments. ISME Journal, 2023, 17, 2313-2325.	9.8	0
6711	Loss of Cardiac Splicing Regulator RBM20 Is Associated With Early-OnsetÂAtrial Fibrillation. JACC Basic To Translational Science, 2024, 9, 163-180.	4.1	1
6712	Arbuscular mycorrhizal fungi heterokaryons have two nuclear populations with distinct roles in hostâ€“plant interactions. Nature Microbiology, 2023, 8, 2142-2153.	13.3	4
6713	Integrative genome-scale analyses reveal post-transcriptional signatures of early human small intestinal development in a directed differentiation organoid model. BMC Genomics, 2023, 24, .	2.8	1
6714	Genome-wide transcriptional responses of osteoblasts to different titanium surface topographies. Materials Today Bio, 2023, 23, 100852.	5.5	0

#	Article	IF	Citations
6715	Multiomics analysis reveals the genetic and metabolic characteristics associated with the low prevalence of dental caries. Journal of Oral Microbiology, 2023, 15, .	2.7	0
6716	Unraveling the occasional occurrence of berry astringency in table grape cv. Scarlet Royal: a physiological and transcriptomic analysis. Frontiers in Plant Science, 0, 14, .	3.6	0
6717	Immunological and clinicopathological features predict HER2-positive breast cancer prognosis in the neoadjuvant NeoALTTO and CALGB 40601 randomized trials. Nature Communications, 2023, 14, .	12.8	1
6718	Modulatory role of RNA helicases in MBNL-dependent alternative splicing regulation. Cellular and Molecular Life Sciences, 2023, 80, .	5.4	0
6719	Mitochondrial subtype MB-G3 contains potential novel biomarkers and therapeutic targets associated with prognosis of medulloblastoma. Biomarkers, 2023, 28, 643-651.	1.9	0
6720	Deciphering triterpenoid saponin biosynthesis by leveraging transcriptome response to methyl jasmonate elicitation in Saponaria vaccaria. Nature Communications, 2023, 14, .	12.8	2
6721	TNRC18 engages H3K9me3 to mediate silencing of endogenous retrotransposons. Nature, 2023, 623, 633-642.	27.8	3
6722	Virally encoded interleukin-6 facilitates KSHV replication in monocytes and induction of dysfunctional macrophages. PLoS Pathogens, 2023, 19, e1011703.	4.7	2
6723	3D sheep rumen epithelial structures driven from single cells in vitro. Veterinary Research, 2023, 54, .	3.0	1
6724	NAD+ regulates nucleotide metabolism and genomic DNA replication. Nature Cell Biology, 2023, 25, 1774-1786.	10.3	0
6725	Domestication shapes the pig gut microbiome and immune traits from the scale of lineage to population. Journal of Evolutionary Biology, 2023, 36, 1695-1711.	1.7	1
6726	Integration of FUNDC1-associated mitochondrial protein import and mitochondrial quality control contributes to TDP-43 degradation. Cell Death and Disease, 2023, 14, .	6.3	2
6727	Association of Cutibacterium acnes with human thyroid cancer. Frontiers in Endocrinology, 0, 14, .	3.5	1
6728	The CRTC-1 transcriptional domain is required for COMPASS complex-mediated longevity in C. elegans. Nature Aging, 2023, 3, 1358-1371.	11.6	0
6729	Bacterial genome size and gene functional diversity negatively correlate with taxonomic diversity along a pH gradient. Nature Communications, 2023, 14, .	12.8	3
6730	Genome-Wide Extrachromosomal Circular DNA Profiling of Paired Hepatocellular Carcinoma and Adjacent Liver Tissues. Cancers, 2023, 15, 5309.	3.7	0
6731	Functional Consequences of Shifting Transcript Boundaries in Glucose Starvation. Molecular and Cellular Biology, 2023, 43, 611-628.	2.3	0
6732	Characterization of the microbiome and volatile compounds in anal gland secretions from domestic cats (Felis catus) using metagenomics and metabolomics. Scientific Reports, 2023, 13, .	3.3	0

#	Article	IF	Citations
6734	Functional players involved in the distinct nitrogen metabolism in two geographically different paddy soils. Biology and Fertility of Soils, 0, , .	4.3	1
6735	Light-dark fluctuated metabolic features of diazotrophic and non-diazotrophic cyanobacteria and their coexisting bacteria. Science of the Total Environment, 2024, 910, 168702.	8.0	0
6736	Toxic effects on ciliates under nano-/micro-plastics coexist with silver nanoparticles. Journal of Hazardous Materials, 2024, 465, 133058.	12.4	1
6737	The Rauvolfia tetraphylla genome suggests multiple distinct biosynthetic routes for yohimbane monoterpene indole alkaloids. Communications Biology, 2023, 6, .	4.4	2
6738	A dual role of RBM42 in modulating splicing and translation of CDKN1A/p21 during DNA damage response. Nature Communications, 2023, 14, .	12.8	0
6739	Molecular signatures of alternative reproductive strategies in a facultatively social hover wasp. Molecular Ecology, 0, , .	3.9	0
6740	Metabolic Rewiring in Tea Plants in Response to Gray Blight Disease Unveiled by Multi-Omics Analysis. Metabolites, 2023, 13, 1122.	2.9	1
6741	Lactate receptor GPR81 drives breast cancer growth and invasiveness through regulation of ECM properties and Notch ligand DLL4. BMC Cancer, 2023, 23, .	2.6	1
6742	Exploring the genetic landscape of nitrogen uptake in durum wheat: genome-wide characterization and expression profiling of NPF and NRT2 gene families. Frontiers in Plant Science, 0, 14, .	3.6	0
6743	Experimental mining plumes and ocean warming trigger stress in a deep pelagic jellyfish. Nature Communications, 2023, 14, .	12.8	2
6744	Daily fluctuation of colonic microbiome in response to nutrient substrates in a pig model. Npj Biofilms and Microbiomes, 2023, 9, .	6.4	0
6745	Comparison of genomic diversity between single and pooled Staphylococcus aureus colonies isolated from human colonization cultures. Microbial Genomics, 2023, 9, .	2.0	2
6746	Comparative Physiological and Transcriptome Analysis of Crossostephium chinense Reveals Its Molecular Mechanisms of Salt Tolerance. International Journal of Molecular Sciences, 2023, 24, 16812.	4.1	0
6747	RNA-seq RNAaccess identified as the preferred method for gene expression analysis of low quality FFPE samples. PLoS ONE, 2023, 18, e0293400.	2.5	0
6748	Transcriptional reprogramming by mutated IRF4 in lymphoma. Nature Communications, 2023, 14, .	12.8	1
6749	Characterization of a partially saturated and glycosylated apocarotenoid from wheat that is depleted upon leaf rust infection. Gene, 2024, 893, 147927.	2.2	0
6750	Dehydration yields distinct transcriptional shifts associated with glycogen metabolism and increases feeding in the western flower thrips, Frankliniella occidentalis. Entomologia Experimentalis Et Applicata, 2024, 172, 154-167.	1.4	0
6751	De novo genome assembly of the invasive mosquito species Aedes japonicus and Aedes koreicus. Parasites and Vectors, 2023, 16, .	2.5	0

#	Article	IF	Citations
6752	Rosaceae Fruit Transcriptome Database (ROFT) â€“ a useful genomic resource for comparing fruits of apple, peach, strawberry, and raspberry. Horticulture Research, 0, , .	6.3	0
6753	Metagenomic analysis reveals distinct changes in the gut microbiome of obese Chinese children. BMC Genomics, 2023, 24, .	2.8	1
6754	Diversity at single nucleotide to pangenome scales among sulfur cycling bacteria in salt marshes. Applied and Environmental Microbiology, 2023, 89, .	3.1	0
6755	Rewiring Saccharomyces cerevisiae metabolism for optimised TaxolÂ® precursors production. Metabolic Engineering Communications, 2024, 18, e00229.	3.6	0
6757	Gene interaction network analysis in multiple myeloma detects complex immune dysregulation associated with shorter survival. Blood Cancer Journal, 2023, 13, .	6.2	0
6758	Isoform-level transcriptome-wide association uncovers genetic risk mechanisms for neuropsychiatric disorders in the human brain. Nature Genetics, 2023, 55, 2117-2128.	21.4	3
6759	Multiple light signaling pathways control solar tracking in sunflowers. PLoS Biology, 2023, 21, e3002344.	5.6	1
6760	Revealing the tumor suppressive sequence within KL1 domain of the hormone Klotho. Oncogene, 2024, 43, 354-362.	5.9	1
6761	Design, construction, and functional characterization of a tRNA neochromosome in yeast. Cell, 2023, 186, 5237-5253.e22.	28.9	13
6762	Debugging and consolidating multiple synthetic chromosomes reveals combinatorial genetic interactions. Cell, 2023, 186, 5220-5236.e16.	28.9	12
6763	Characterization of wooden breast myopathy: a focus on syndecans and ECM remodeling. Frontiers in Physiology, 0, 14, .	2.8	0
6764	The DNA repair enzyme, aprataxin, plays a role in innate immune signaling. Frontiers in Aging Neuroscience, 0, 15, .	3.4	0
6765	Systematic transcriptome-wide meta-analysis across endocrine disrupting chemicals reveals shared and unique liver pathways, gene networks, and disease associations. Environment International, 2024, 183, 108339.	10.0	0
6766	Pathogenic Bacteria Are the Primary Determinants Shaping PM_{2.5}-Borne Resistomes in the Municipal Food Waste Treatment System. Environmental Science & Technology, 2023, 57, 19965-19978.	10.0	0
6767	Association of SLC12A1 and GLUR4 Ion Transporters with Neoadjuvant Chemoresistance in Luminal Locally Advanced Breast Cancer. International Journal of Molecular Sciences, 2023, 24, 16104.	4.1	0
6768	Osmolar Modulation Drives Reversible Cell Cycle Exit and Human Pluripotent Cell Differentiation via NFâ€Î²Ð' and WNT Signaling. Advanced Science, 2024, 11, .	11.2	0
6769	Sequential host-bacteria and bacteria-bacteria interactions determine the microbiome establishment of Nematostella vectensis. Microbiome, 2023, 11, .	11.1	0
6770	Sperm chromatin accessibilityâ€™s involvement in the intergenerational effects of stress hormone receptor activation. Translational Psychiatry, 2023, 13, .	4.8	0

#	Article	IF	Citations
6771	REVEILLE2 thermosensitive splicing: a molecular basis for the integration of nocturnal temperature information by the Arabidopsis circadian clock. New Phytologist, 2024, 241, 283-297.	7.3	0
6772	The SPOC proteins DIDO3 and PHF3 co-regulate gene expression and neuronal differentiation. Nature Communications, 2023, 14, .	12.8	1
6773	Sirtuin3 ensures the metabolic plasticity of neurotransmission during glucose deprivation. Journal of Cell Biology, 2024, 223, .	5.2	2
6774	Comparison of Alternative Splicing Landscapes Revealed by Long-Read Sequencing in Hepatocyte-Derived HepG2 and Huh7 Cultured Cells and Human Liver Tissue. Biology, 2023, 12, 1494.	2.8	0
6775	Forces driving transposable element load variation during Arabidopsis range expansion. Plant Cell, 0, , .	6.6	0
6776	System-wide analysis of RNA and protein subcellular localization dynamics. Nature Methods, 2024, 21, 60-71.	19.0	4
6777	Regulation of expression quantitative trait loci by SVA retrotransposons within the major histocompatibility complex. Experimental Biology and Medicine, 0, , .	2.4	1
6778	Stuttering associated with a pathogenic variant in the chaperone protein cyclophilin 40. Brain, 2023, 146, 5086-5097.	7.6	1
6779	The influence of Acetobacter pomorum bacteria on the developmental progression of Drosophila suzukii via gluconic acid secretion. Molecular Ecology, 2024, 33, .	3.9	1
6782	The ubiquitin-proteasome pathway inhibitor TAK-243 has major effects on calcium handling in mammalian cells. Biochimica Et Biophysica Acta - Molecular Cell Research, 2024, 1871, 119618.	4.1	0
6787	Suppressed transcript diversity and immune response in COVID-19 ICU patients: a longitudinal study. Life Science Alliance, 2024, 7, e202302305.	2.8	0
6788	Nociceptive and Transcriptomic Responses in a Swine Diabetic Wound Model Treated With a Topical Angiotensin 1 Receptor Antagonist. Nursing Research, 2024, 73, 118-125.	1.7	0
6790	The role of midbody-associated mRNAs in regulating abscission. Journal of Cell Biology, 2023, 222, .	5.2	4
6791	A gene network-driven approach to infer novel pathogenicity-associated genes: application to Pseudomonas aeruginosa PAO1. MSystems, 0, , .	3.8	0
6794	The AIRN lncRNA is imprinted and paternally expressed in pigs. Journal of Animal Science, 2023, 101, .	0.5	0
6797	Transcriptome analysis of genes involved in flower and leaf color of Oncidium by RNA-seq. Acta Scientiarum Polonorum, Hortorum Cultus, 2023, 22, 3-17.	0.6	0
6798	Complexation of histone deacetylase inhibitor belinostat to Cu(II) prevents premature metabolic inactivation in vitro and demonstrates potent anti-cancer activity in vitro and ex vivo in colon cancer. Cellular Oncology (Dordrecht), 0, , .	4.4	0
6800	KSHV vIL-6 enhances inflammatory responses by epigenetic reprogramming. PLoS Pathogens, 2023, 19, e1011771.	4.7	0

#	Article	IF	Citations
6801	TEAD Inhibition Overcomes YAP1/TAZ-Driven Primary and Acquired Resistance to KRASG12C Inhibitors. Cancer Research, 2023, 83, 4112-4129.	0.9	4
6802	Peripheral Blood IL5RA Gene Expression as a Diagnostic Biomarker for Eosinophilic Esophagitis. Clinical Gastroenterology and Hepatology, 2023, , .	4.4	0
6806	Dominant negative variants in KIF5B cause osteogenesis imperfecta via down regulation of mTOR signaling. PLoS Genetics, 2023, 19, e1011005.	3.5	0
6809	Single-cell RNA-seq reveals novel immune-associated biomarkers for predicting prognosis in AML patients with RUNX1::RUNX1T1. International Immunopharmacology, 2023, 125, 111178.	3.8	0
6810	Assessing inorganic nitrogen transport in marine phytoplankton assemblages through the 15N-tracer technique and metatranscriptomics. Marine Ecology - Progress Series, 0, , .	1.9	0
6811	Rat deconvolution as knowledge miner for immune cell trafficking from toxicogenomics databases. Toxicological Sciences, 0, , .	3.1	1
6812	Opportunities and tradeoffs in single-cell transcriptomic technologies. Trends in Genetics, 2023, , .	6.7	0
6815	MAJIQlopedia: an encyclopedia of RNA splicing variations in human tissues and cancer. Nucleic Acids Research, 0, , .	14.5	0
6817	Fiber-deficient diet inhibits colitis through the regulation of the niche and metabolism of a gut pathobiont. Cell Host and Microbe, 2023, 31, 2007-2022.e12.	11.0	3
6818	Small Cell Lung Cancer Plasticity Enables NFIB-Independent Metastasis. Cancer Research, 2024, 84, 226-240.	0.9	1
6819	Fitness and transcriptomic analysis of pathogenic Vibrio parahaemolyticus in seawater at different shellfish harvesting temperatures. Microbiology Spectrum, 2023, 11, .	3.0	0
6820	Testosterone Replacement Therapy in Klinefelter Syndromeâ€"Follow-up Study Associating Hemostasis and RNA Expression. Journal of Clinical Endocrinology and Metabolism, 0, , .	3.6	0
6821	SINGLE-CELL TRANSCRIPTOME ANALYSIS IN HEALTH AND DISEASE. Shock, 0, , .	2.1	0
6822	Identification of QTL associated with resistance to Phytophthora fruit rot in cucumber (Cucumis) Tj ETQq1 1 0.784314 rgBT /Overlock	3.6	0
6823	A transcriptional atlas identifies key regulators and networks for the development of spike tissues in barley. Cell Reports, 2023, 42, 113441.	6.4	0
6824	Seq2science: an end-to-end workflow for functional genomics analysis. PeerJ, 0, 11, e16380.	2.0	1
6826	R-Loop Accumulation in Spliceosome Mutant Leukemias Confers Sensitivity to PARP1 Inhibition by Triggering Transcriptionâ€"Replication Conflicts. Cancer Research, 2024, 84, 577-597.	0.9	0
6828	Transcriptome Analysis of Macrophytesâ€™ Myriophyllum spicatum Response to Ammonium Nitrogen Stress Using the Whole Plant Individual. Plants, 2023, 12, 3875.	3.5	0

#	Article	IF	Citations
6829	Two modes of gene regulation by TFL1 mediate its dual function in flowering time and shoot determinacy of Arabidopsis. Development (Cambridge), 2023, 150, .	2.5	1
6834	SARS-CoV-2 activates the TLR4/MyD88 pathway in human macrophages: A possible correlation with strong pro-inflammatory responses in severe COVID-19. Heliyon, 2023, 9, e21893.	3.2	1
6835	Shotgun metagenomes from productive lakes in an urban region of Sweden. Scientific Data, 2023, 10, .	5.3	0
6836	Transcriptome-wide association analyses reveal the impact of regulatory variants on rice panicle architecture and causal gene regulatory networks. Nature Communications, 2023, 14, .	12.8	1
6837	Identifying N6-Methyladenosine Sites in HepG2 Cell Lines Using Oxford Nanopore Technology. International Journal of Molecular Sciences, 2023, 24, 16477.	4.1	0
6839	Temporary Knockdown of p53 During Focal Limb Irradiation Increases the Development of Sarcomas. Cancer Research Communications, 2023, 3, 2455-2467.	1.7	0
6840	Key processes required for the different stages of fungal carnivory by a nematode-trapping fungus. PLoS Biology, 2023, 21, e3002400.	5.6	1
6841	Cell-free multi-omics analysis reveals potential biomarkers in gastrointestinal cancer patientsâ€™ blood. Cell Reports Medicine, 2023, 4, 101281.	6.5	2
6842	Temporal dynamics of microbial composition and antibiotic resistome in fermentation bed culture pig farms across various ages. Science of the Total Environment, 2024, 912, 168728.	8.0	1
6843	Differences in syncytia formation by SARS-CoV-2 variants modify host chromatin accessibility and cellular senescence via TP53. Cell Reports, 2023, 42, 113478.	6.4	0
6849	Allelopathic potential of Haloxylon ammodendron against Syntrichia caninervis and comparative analysis of soil microbial differences between inside and outside of the bare patches under its canopies. Applied Soil Ecology, 2024, 194, 105205.	4.3	0
6852	Fine mapping and identification of CaTTG1, a candidate gene that regulates the hypocotyl anthocyanin accumulation in Capsicum annuum L. Horticultural Plant Journal, 2023, , .	5.0	0
6853	Transcriptome Analysis Reveals Cross-Tissue Metabolic Pathway Changes in Female Rana dybowskii during Emergence from Hibernation. Fishes, 2023, 8, 569.	1.7	0
6854	Amelioration of Tau and ApoE4-linked glial lipid accumulation and neurodegeneration with an LXR agonist. Neuron, 2024, 112, 384-403.e8.	8.1	5
6857	ATM deficiency confers specific therapeutic vulnerabilities in bladder cancer. Science Advances, 2023, 9, .	10.3	0
6858	Alternative Splicing under Cold Stress in Paper Mulberry. Plants, 2023, 12, 3950.	3.5	2
6859	Multiomics analysis of metabolic heterogeneity in cervical cancer cell lines with or without HPV. Frontiers in Oncology, 0, 13, .	2.8	0
6860	Cell-free RNA signatures predict Alzheimerâ€™s disease. IScience, 2023, 26, 108534.	4.1	0

#	Article	IF	Citations
6861	Nod1-dependent NF-kB activation initiates hematopoietic stem cell specification in response to small Rho GTPases. Nature Communications, 2023, 14, .	12.8	1
6863	Effect of nano-hydroxyapatite and phosphate on thorium toxicity â€“ Arabidopsis transcriptomic study. Environmental and Experimental Botany, 2024, 217, 105573.	4.2	0
6864	Sex and Age Impact CD4+ T Cell Susceptibility to HIV In Vitro through Cell Activation Dynamics. Cells, 2023, 12, 2689.	4.1	0
6865	CDK4/6 inhibition enhances SHP2 inhibitor efficacy and is dependent upon RB function in malignant peripheral nerve sheath tumors. Science Advances, 2023, 9, .	10.3	2
6867	Swine farming shifted the gut antibiotic resistome of local people. Journal of Hazardous Materials, 2024, 465, 133082.	12.4	2
6868	An intrusion and environmental effects of man-made silver nanoparticles in cold seeps. Science of the Total Environment, 2024, 912, 168890.	8.0	0
6869	MESIA: multi-epigenome sample integration approach for precise peak calling. Scientific Reports, 2023, 13, .	3.3	0
6872	Metagenomic insight into the acidophilic functional communities driving elemental geochemical cycles in an acid mine drainage lake. Journal of Hazardous Materials, 2024, 466, 133070.	12.4	0
6873	A mouse model of Weaver syndrome displays overgrowth and excess osteogenesis reversible with KDM6A/6B inhibition. JCI Insight, 0, , .	5.0	0
6874	SlMYB7, an AtMYB4-Like R2R3-MYB Transcription Factor, Inhibits Anthocyanin Accumulation in Solanum lycopersicum Fruits. Journal of Agricultural and Food Chemistry, 2023, 71, 18758-18768.	5.2	1
6876	Physiology governing diatom vs. dinoflagellate bloom and decline in coastal Santa Monica Bay. Frontiers in Microbiology, 0, 14, .	3.5	0
6880	Effects of disinfectant type and dosage on biofilm's activity, viability, microbiome and antibiotic resistome in bench-scale drinking water distribution systems. Water Research, 2024, 249, 120958.	11.3	0
6881	An accurate aging clock developed from large-scale gut microbiome and human gene expression data. IScience, 2024, 27, 108538.	4.1	1
6884	Altered splicing machinery in lung carcinoids unveils NOVA1, PRPF8 and SRSF10 as novel candidates to understand tumor biology and expand biomarker discovery. Journal of Translational Medicine, 2023, 21, .	4.4	0
6885	The genomes of Scedosporium between environmental challenges and opportunism. IMA Fungus, 2023, 14, .	3.8	0
6886	Noctiluca scintillans bloom alters the composition and carbohydrate utilization of associated bacterial community and enriches potential pathogenic bacterium Vibrio anguillarum. Water Research, 2024, 249, 120974.	11.3	0
6887	The influence of maternal high fat diet during lactation on offspring hematopoietic priming. Endocrinology, 0, , .	2.8	0
6888	A Comparative Kidney Transcriptome Analysis of Bicarbonate-Loaded insrr-Null Mice. Current Issues in Molecular Biology, 2023, 45, 9709-9722.	2.4	0

#	Article	IF	Citations
6889	Early mucosal events promote distinct mucosal and systemic antibody responses to live attenuated influenza vaccine. Nature Communications, 2023, 14, .	12.8	2
6890	Altered CELF4 splicing factor enhances pancreatic neuroendocrine tumors aggressiveness influencing mTOR and everolimus response. Molecular Therapy - Nucleic Acids, 2024, 35, 102090.	5.1	0
6891	Phase I/II Study of the WEE1 Inhibitor Adavosertib (AZD1775) in Combination with Carboplatin in Children with Advanced Malignancies: Arm C of the AcSÃ©-ESMART Trial. Clinical Cancer Research, 2024, 30, 741-753.	7.0	0
6892	Topological data analysis reveals a core gene expression backbone that defines form and function across flowering plants. PLoS Biology, 2023, 21, e3002397.	5.6	1
6893	Bone marrow adipocytes fuel emergency hematopoiesis after myocardial infarction. , 2023, 2, 1277-1290.		1
6894	Leukemia-intrinsic determinants of CAR-T response revealed by iterative in vivo genome-wide CRISPR screening. Nature Communications, 2023, 14, .	12.8	0
6895	Multiâ€omics analyses reveal the interaction between colonic microbiota and host in Min and Yorkshire pigs. , 0, , .		0
6898	Transcriptomic Insights into Archaeal Nitrification in the Amundsen Sea Polynya, Antarctica. Journal of Microbiology, 0, , .	2.8	0
6899	Evaluation of long acting GLP1R/GCGR agonist in a DIO and biopsy-confirmed mouse model of NASH suggest a beneficial role of GLP-1/glucagon agonism in NASH patients. Molecular Metabolism, 2024, 79, 101850.	6.5	0
6900	Dividing out quantification uncertainty allows efficient assessment of differential transcript expression with edgeR. Nucleic Acids Research, 2024, 52, e13-e13.	14.5	1
6901	Metagenomic Analyses of Viruses in the Orchid Mycorrhizal Interaction Using Improved Assemble Tools. Methods in Molecular Biology, 2024, , 67-81.	0.9	0
6902	Systematic analysis of alternative exon-dependent interactome remodeling reveals multitasking functions of gene regulatory factors. Molecular Cell, 2023, 83, 4222-4238.e10.	9.7	2
6903	FTY720 requires vitamin B12-TCN2-CD320 signaling in astrocytes to reduce disease in an animal model of multiple sclerosis. Cell Reports, 2023, 42, 113545.	6.4	0
6904	Cross-species comparative hippocampal transcriptomics in Alzheimerâ€™s disease. IScience, 2024, 27, 108671.	4.1	0
6905	Looking for a needle in a haystack: de novo phenotypic target identification reveals Hippo pathway-mediated miR-202 regulation of egg production. Nucleic Acids Research, 0, , .	14.5	0
6907	Transcriptional changes are tightly coupled to chromatin reorganization during cellular aging. Aging Cell, 0, , .	6.7	0
6908	Using long-read CAGE sequencing to profile cryptic-promoter-derived transcripts and their contribution to the immunopeptidome. Genome Research, 2023, 33, 2143-2155.	5.5	1
6909	Genome-Wide Characterization of Berberine Bridge Enzyme Gene Family in Wheat (<i>Triticum) Tj ETQq1 1 0.784314 rgBT /Overlock 1 of Agricultural and Food Chemistry, 0, , .	5.2	0

#	Article	IF	Citations
6910	AA2P-mediated DNA demethylation synergizes with stem cell agonists to promote expansion of hematopoietic stem cells. Cell Reports Methods, 2023, 3, 100663.	2.9	1
6911	Human and mouse neutrophils share core transcriptional programs in both homeostatic and inflamed contexts. Nature Communications, 2023, 14, .	12.8	1
6912	Characterization of nucleolar SUMO isopeptidases unveils a general p53-independent checkpoint of impaired ribosome biogenesis. Nature Communications, 2023, 14, .	12.8	1
6914	Bifidobacterium infantis associates with T cell immunity in human infants and is sufficient to enhance antigen-specific T cells in mice. Science Advances, 2023, 9, .	10.3	0
6915	Environmental regulation of male fertility is mediated through Arabidopsis bHLH89, 91 and 10. Journal of Experimental Botany, 0, , .	4.8	0
6916	Bradysia (Sciara) coprophila larvae up-regulate DNA repair pathways and down-regulate developmental regulators in response to ionizing radiation. Genetics, 2024, 226, .	2.9	0
6917	Harnessing PROTAC technology to combat stress hormone receptor activation. Nature Communications, 2023, 14, .	12.8	0
6918	OBMeta: a comprehensive web server to analyze and validate gut microbial features and biomarkers for obesity-associated metabolic diseases. Bioinformatics, 0, , .	4.1	0
6919	The ontogeny of lymphoid organs and IgM+ B-cells in ballan wrasse (Labrus bergylta) reveals a potential site for extrarenal B-cell lymphopoiesis: The pancreas. Fish and Shellfish Immunology, 2024, 144, 109273.	3.6	0
6921	Physiological and transcriptomic analysis reveals the toxic and protective mechanisms of marine microalga Chlorella pyrenoidosa in response to TiO2 nanoparticles and UV-B radiation. Science of the Total Environment, 2024, 912, 169174.	8.0	0
6923	RedRibbon: A new rankâ€“rank hypergeometric overlap for gene and transcript expression signatures. Life Science Alliance, 2024, 7, e202302203.	2.8	1
6927	Effects of polystyrene microplastics on Euglena gracilis: Intracellular distribution and the protozoan transcriptional responses. Aquatic Toxicology, 2024, 266, 106802.	4.0	0
6928	Protistan community composition and metabolism in the North Pacific Subtropical Gyre: Influences of mesoscale eddies and depth. Environmental Microbiology, 2024, 26, .	3.8	0
6929	PD-L1 overexpression induces STAT signaling and promotes the secretion of pro-angiogenic cytokines in non-small cell lung cancer (NSCLC). Lung Cancer, 2024, 187, 107438.	2.0	2
6930	Identification of the transcriptome signatures and immune-inflammatory responses in postmenopausal osteoporosis. Heliyon, 2024, 10, e23675.	3.2	0
6931	Genes with epigenetic alterations in human pancreatic islets impact mitochondrial function, insulin secretion, and type 2 diabetes. Nature Communications, 2023, 14, .	12.8	2
6932	Genome-wide family prediction unveils molecular mechanisms underlying the regulation of agronomic traits in Urochloa ruziziensis. Frontiers in Plant Science, 0, 14, .	3.6	0
6933	Synonymous codon usage regulates translation initiation. Cell Reports, 2023, 42, 113413.	6.4	0

#	Article	IF	Citations
6934	Gut Microbiome Analysis and Screening of Lactic Acid Bacteria with Probiotic Potential in Anhui Swine. Animals, 2023, 13, 3812.	2.3	0
6935	Single-cell transcriptome and metagenome profiling reveals the genetic basis of rumen functions and convergent developmental patterns in ruminants. Genome Research, 2023, 33, 1690-1707.	5.5	0
6936	Proteomic profiling of interferonâ€responsive reactive astrocytes in rodent and human. Glia, 2024, 72, 625-642.	4.9	0
6937	Multivariate investigation of aging in mouse models expressing the Alzheimerâ€™s protective APOE2 allele: integrating cognitive metrics, brain imaging, and blood transcriptomics. Brain Structure and Function, 0, , .	2.3	1
6938	The effect of intercropping leguminous green manure on theanine accumulation in the tea plant: A metagenomic analysis. Plant, Cell and Environment, 2024, 47, 1141-1159.	5.7	0
6939	Chemical and Genetic Modulation of Complex I of the Electron Transport Chain Enhances the Biotherapeutic Protein Production Capacity of CHO Cells. Cells, 2023, 12, 2661.	4.1	0
6940	A super-pangenome of the North American wild grape species. Genome Biology, 2023, 24, .	8.8	3
6941	Genome-resolved metatranscriptomics reveals conserved root colonization determinants in a synthetic microbiota. Nature Communications, 2023, 14, .	12.8	1
6942	Single-cell transcriptomics reveals the heterogeneity of the immune landscape of IDH-wildtype high-grade gliomas. Cancer Immunology Research, 0, , .	3.4	0
6943	LimoRhyde2: Genomic analysis of biological rhythms based on effect sizes. PLoS ONE, 2023, 18, e0292089.	2.5	1
6944	Sensory neurons promote immune homeostasis in the lung. Cell, 2024, 187, 44-61.e17.	28.9	3
6945	A histone deacetylase network regulates epigenetic reprogramming and viral silencing in HIV-infected cells. Cell Chemical Biology, 2023, 30, 1617-1633.e9.	5.2	1
6946	Implications of tRNA abundance on translation elongation across bovine tissues. Frontiers in Genetics, 0, 14, .	2.3	0
6947	Proteomic Approach to Investigating Expression, Localization, and Functions of the SOWAHD Gene Protein Product during Granulocytic Differentiation. Biochemistry (Moscow), 2023, 88, 1668-1682.	1.5	0
6949	GRD-1/PTR-11, the C. elegans hedgehog/patched-like morphogen-receptor pair, modulates developmental rate. Development (Cambridge), 2023, 150, .	2.5	1
6951	A multi-omics dataset for the analysis of frontotemporal dementia genetic subtypes. Scientific Data, 2023, 10, .	5.3	0
6952	Comparative transcriptomic effects of Harpephyllum caffrum extracts and sodium metabisulphite on hydrogen peroxide stressed Saccharomyces cerevisiae cells using RNA-seq. Food Bioscience, 2024, 57, 103464.	4.4	0
6953	Generation of somatic de novo structural variation as a hallmark of cellular senescence in human lung fibroblasts. Frontiers in Cell and Developmental Biology, 0, 11, .	3.7	0

#	Article	IF	Citations
6954	Differential Effects of PTH (1-34), PTHrP (1-36), and Abaloparatide on the Murine Osteoblast Transcriptome. Journal of the Endocrine Society, 2023, 8, .	0.2	0
6955	ChREBP is activated by reductive stress and mediates GCKR-associated metabolic traits. Cell Metabolism, 2024, 36, 144-158.e7.	16.2	0
6957	ApoA-I Protects Pancreatic Î²-Cells From Cholesterol-Induced Mitochondrial Damage and Restores Their Ability to Secrete Insulin. Arteriosclerosis, Thrombosis, and Vascular Biology, 2024, 44, .	2.4	1
6959	<scp>MpTGA</scp>, together with <scp>MpNPR</scp>, regulates sexual reproduction and independently affects oil body formation in Marchantia polymorpha. New Phytologist, 0, , .	7.3	0
6961	baz-2 enhances systemic proteostasis inÂvivo by regulating acetylcholine metabolism. Cell Reports, 2023, 42, 113577.	6.4	0
6962	Nitrate reduction coupling with As(III) oxidation in neutral As-contaminated paddy soil preserves nitrogen, reduces N2O emissions and alleviates As toxicity. Science of the Total Environment, 2024, 912, 169360.	8.0	0
6965	Comparative analysis of cysteine proteases reveals gene family evolution of the group 1 allergens in astigmatic mites. Clinical and Translational Allergy, 2023, 13, .	3.2	0
6966	Elucidating The Lignocellulose Digestion Mechanism Coptotermes curvignathus Based on Carbohydrate-Active Enzymes Profle Using The Meta-Transcriptomic Approach. , 2023, 52, 177-186.		0
6969	The response of LncRNAs associated with photosynthesis-and pigment synthesis-related genes to green light in Chlamydomonas reinhardtii. Photosynthesis Research, 0, , .	2.9	0
6970	CRISPRi-Mediated Treatment of Dominant Rhodopsin-Associated Retinitis Pigmentosa. CRISPR Journal, 2023, 6, 502-513.	2.9	0
6971	Targeting gut microbial nitrogen recycling and cellular uptake of ammonium to improve bortezomib resistance in multiple myeloma. Cell Metabolism, 2024, 36, 159-175.e8.	16.2	1
6972	Downregulation of the expression of subgenomic chromosome A7 genes promotes plant height in resynthesized allopolyploid Brassica napus. Theoretical and Applied Genetics, 2024, 137, .	3.6	1
6973	Drying without dying: A genome database for desiccation-tolerant plants and evolution of desiccation tolerance. Plant Physiology, 2024, 194, 2249-2262.	4.8	0
6974	Combined absence of TRP53 target genes ZMAT3, PUMA and p21 cause a high incidence of cancer in mice. Cell Death and Differentiation, 2024, 31, 159-169.	11.2	0
6975	The Viromes of Six Ecosystem Service Provider Parasitoid Wasps. Viruses, 2023, 15, 2448.	3.3	1
6977	Predicting gene expression changes upon epigenomic drug treatment. F1000Research, 0, 12, 1089.	1.6	0
6979	Establishment of the Myeloid TBX-Code Reveals Aberrant Expression of T-Box Gene TBX1 in Chronic Myeloid Leukemia. International Journal of Molecular Sciences, 2024, 25, 32.	4.1	0
6980	ISGF3 and STAT2/IRF9 Control Basal and IFN-Induced Transcription through Genome-Wide Binding of Phosphorylated and Unphosphorylated Complexes to Common ISRE-Containing ISGs. International Journal of Molecular Sciences, 2023, 24, 17635.	4.1	0

#	Article	IF	Citations
6983	USP7/Maged1-mediated H2AÂmonoubiquitination in the paraventricular thalamus: an epigenetic mechanism involved in cocaine use disorder. Nature Communications, 2023, 14, .	12.8	0
6985	Transcription factor 12â€mediated selfâ€feedback regulatory mechanism is required in DUX4 fusion leukaemia. Clinical and Translational Medicine, 2023, 13, .	4.0	0
6986	Hiding from heat: The transcriptomic response of two clam species is modulated by behaviour and habitat. Journal of Thermal Biology, 2024, 119, 103776.	2.5	0
6987	Gastrulationâ€stage alcohol exposure induces similar rates of craniofacial malformations in male and female C57BL/6J mice. Birth Defects Research, 0, , .	1.5	0
6988	Quantitative subcellular reconstruction reveals a lipid mediated inter-organelle biogenesis network. Nature Cell Biology, 0, , .	10.3	3
6990	Effects of temperature on viral load, inclusion body formation, and host response in Pacific Herring with viral erythrocytic necrosis (VEN). Journal of Aquatic Animal Health, 2024, 36, 45-56.	1.4	0
6991	Social isolation-induced transcriptomic changes in mouse hippocampus impact the synapse and show convergence with human genetic risk for neurodevelopmental phenotypes. PLoS ONE, 2023, 18, e0295855.	2.5	0
6993	Unsupervised machine learning identifies distinct ALS molecular subtypes in post-mortem motor cortex and blood expression data. Acta Neuropathologica Communications, 2023, 11, .	5.2	1
6994	Small RNA signatures of the anterior cruciate ligament from patients with knee joint osteoarthritis. Frontiers in Molecular Biosciences, 0, 10, .	3.5	0
6995	Immune determinants of CAR-T cell expansion in solid tumor patients receiving GD2 CAR-T cell therapy. Cancer Cell, 2024, 42, 35-51.e8.	16.8	2
6996	Arabidopsis thaliana GLYCINE RICH RNAâ€BINDING PROTEIN 7 interaction with its iCLIP target LHCB1.1 correlates with changes in RNA stability and circadian oscillation. Plant Journal, 0, , .	5.7	0
6997	Transcript assembly and annotations: Bias and adjustment. PLoS Computational Biology, 2023, 19, e1011734.	3.2	0
6998	De novo transcriptome assembly of mouse male germ cells reveals novel genes, stage-specific bidirectional promoter activity, and noncoding RNA expression. Genome Research, 2023, 33, 2060-2078.	5.5	1
6999	Protein kinase C delta regulates mononuclear phagocytes and hinders response to immunotherapy in cancer. Science Advances, 2023, 9, .	10.3	0
7000	Venomous gland transcriptome and venom proteomic analysis of the scorpion Androctonus amoreuxi reveal new peptides with anti-SARS-CoV-2 activity. Peptides, 2024, 173, 171139.	2.4	0
7003	Inferring secretory and metabolic pathway activity from omic data with secCellFie. Metabolic Engineering, 2023, , .	7.0	0
7004	Molecular Characteristics of SUN5 in Banna Mini-Pig Inbred Line (BMI) and Its Expression Regulation in Testis. Russian Journal of Genetics, 2023, 59, 1345-1357.	0.6	0
7009	Root branching under high salinity requires auxin-independent modulation of LATERAL ORGAN BOUNDARY DOMAIN 16 function. Plant Cell, 0, , .	6.6	1

#	Article	IF	Citations
7010	Comparative Physiological and Transcriptome Analyses of Tolerant and Susceptible Cultivars Reveal the Molecular Mechanism of Cold Tolerance in Anthurium andraeanum. International Journal of Molecular Sciences, 2024, 25, 250.	4.1	0
7011	Multiomics analysis reveals metabolic subtypes and identifies diacylglycerol kinase Î± (DGKA) as a potential therapeutic target for intrahepatic cholangiocarcinoma. Cancer Communications, 2024, 44, 226-250.	9.2	0
7012	KrÃ¼ppel-like factor 4 in transcriptional control of the three unique isoforms of Agouti-related peptide in mice. Physiological Genomics, 2024, 56, 265-275.	2.3	0
7015	Investigating iRHOM2-Associated Transcriptional Changes in Tylosis With Esophageal Cancer. , 2024, 3, 385-395.		0
7016	Rapamycin-sensitive mechanisms confine the growth of fission yeast below the temperatures detrimental to cell physiology. IScience, 2024, 27, 108777.	4.1	0
7017	FSHÎ² links photoperiodic signaling to seasonal reproduction in Japanese quail. ELife, 0, 12, .	6.0	0
7018	Molecular and Metabolic Analysis of Arsenic-Exposed Humanized AS3MT Mice. Environmental Health Perspectives, 2023, 131, .	6.0	1
7019	Response of Bacillus velezensis 83 to interaction with Colletotrichum gloeosporioides resembles a Greek phalanx-style formation: A stress resistant phenotype with antibiosis capacity. Microbiological Research, 2024, 280, 127592.	5.3	0
7020	EGFR-activated myofibroblasts promote metastasis of pancreatic cancer. Cancer Cell, 2024, 42, 101-118.e11.	16.8	2
7023	Stabilization of Epithelial Î²-Catenin Compromises Mammary Cell Fate Acquisition and Branching Morphogenesis. Journal of Investigative Dermatology, 2023, , .	0.7	1
7024	An exhausted-like microglial population accumulates in aged and APOE4 genotype Alzheimerâ€™s brains. Immunity, 2023, , .	14.3	0
7025	Sex-limited experimental evolution drives transcriptomic divergence in a hermaphrodite. Genome Biology and Evolution, 0, , .	2.5	0
7026	Renal macrophages monitor and remove particles from urine to prevent tubule obstruction. Immunity, 2024, 57, 106-123.e7.	14.3	2
7027	Metatranscriptomics Reveals the RNA Virome of Ixodes Persulcatus in the Chinaâ€“North Korea Border, 2017. Viruses, 2024, 16, 62.	3.3	0
7028	Genome-wide kinetic profiling of pre-mRNA 3â€² end cleavage. Rna, 2024, 30, 256-270.	3.5	0
7029	Root transcriptomic provides insights on molecular mechanisms involved in the tolerance to water deficit in Pisum sativum inoculated with Pseudomonas sp.. Planta, 2024, 259, .	3.2	0
7030	Impact of plastic-related compounds on the gene expression signature of HepG2 cells transfected with CYP3A4. Archives of Toxicology, 0, , .	4.2	0
7031	Dynamics of rhizosphere microbial structure and function associated with the biennial bearing of moso bamboo. Journal of Environmental Management, 2024, 351, 119977.	7.8	0

#	Article	IF	Citations
7032	Combination therapy with oral antiviral and anti-inflammatory drugs improves the efficacy of delayed treatment in a COVID-19 hamster model. EBioMedicine, 2024, 99, 104950.	6.1	0
7033	Reference gene catalog and metagenome-assembled genomes from the gut microbiome reveal the microbial composition, antibiotic resistome, and adaptability of a lignocellulose diet in the giant panda. Environmental Research, 2024, 245, 118090.	7.5	0
7034	Enhancing immune responses of ESC-based TAA cancer vaccines with a novel OMV delivery system. Journal of Nanobiotechnology, 2024, 22, .	9.1	0
7035	RNA sequencing unravels novel L cell constituents and mechanisms of GLP-1 secretion in human gastric bypass-operated intestine. Diabetologia, 2024, 67, 356-370.	6.3	0
7036	Longevity interventions modulate mechanotransduction and extracellular matrix homeostasis in C. elegans. Nature Communications, 2024, 15, .	12.8	1
7037	Proteogenomic characterization of small cell lung cancer identifies biological insights and subtype-specific therapeutic strategies. Cell, 2024, 187, 184-203.e28.	28.9	4
7038	Lymphatic endothelial-like cells promote glioblastoma stem cell growth through cytokine-driven cholesterol metabolism. Nature Cancer, 2024, 5, 147-166.	13.2	3
7039	N ⁶ -methyladenosine (M ⁶ A) in fetal offspring modifies mitochondrial gene expression following gestational nano-TiO ₂ inhalation exposure. Nanotoxicology, 2023, 17, 651-668.	3.0	0
7040	Critical contribution of mitochondria in the development of cardiomyopathy linked to desmin mutation. Stem Cell Research and Therapy, 2024, 15, .	5.5	1
7041	The microbial metabolite urolithin A reduces Clostridioides difficile toxin expression and toxin-induced epithelial damage. MSystems, 2024, 9, .	3.8	0
7042	Single molecule real-time sequencing data sets of Hypericum perforatum L. plantlets and cell suspension cultures. Scientific Data, 2024, 11, .	5.3	0
7043	Translation of non-canonical open reading frames as a cancer cell survival mechanism in childhood medulloblastoma. Molecular Cell, 2024, 84, 261-276.e18.	9.7	0
7044	Ehf and Fezf2 regulate late medullary thymic epithelial cell and thymic tuft cell development. Frontiers in Immunology, 0, 14, .	4.8	1
7045	Integration of multi-omics technologies for molecular diagnosis in ataxia patients. Frontiers in Genetics, 0, 14, .	2.3	0
7046	Blood DNA methylation profiling identifies cathepsin Z dysregulation in pulmonary arterial hypertension. Nature Communications, 2024, 15, .	12.8	0
7047	Comprehensive Identification of the Î²-Amylase (BAM) Gene Family in Response to Cold Stress in White Clover. Plants, 2024, 13, 154.	3.5	0
7048	Clostridium butyricum and carbohydrate active enzymes contribute to the reduced fat deposition in pigs. , 2024, 3, .		3
7049	Long-read transcriptome landscapes of primary and metastatic liver cancers at transcript resolution. Biomarker Research, 2024, 12, .	6.8	0

#	Article	IF	Citations
7050	A major endogenous glycoside hydrolase mediating quercetin uptake in Bombyx mori. PLoS Genetics, 2024, 20, e1011118.	3.5	0
7051	Functional host-specific adaptation of the intestinal microbiome in hominids. Nature Communications, 2024, 15, .	12.8	0
7052	Combined small-molecule treatment accelerates maturation of human pluripotent stem cell-derived neurons. Nature Biotechnology, 0, , .	17.5	1
7053	Early-stage idiopathic Parkinsonâ€™s disease is associated with reduced circular RNA expression. Npj Parkinson's Disease, 2024, 10, .	5.3	0
7054	Diurnal retinal and choroidal gene expression patterns support a role for circadian biology in myopia pathogenesis. Scientific Reports, 2024, 14, .	3.3	0
7055	Insights into the differences related to the resistance mechanisms to the highly toxic fruit Hippomane mancinella (Malpighiales: Euphorbiaceae) between the larvae of the sister species Anastrepha acris and Anastrepha ludens (Diptera: Tephritidae) through comparative transcriptomics. Frontiers in Physiology, 0, 15, .	2.8	0
7056	SpliceProt 2.0: A Sequence Repository of Human, Mouse, and Rat Proteoforms. International Journal of Molecular Sciences, 2024, 25, 1183.	4.1	0
7057	Ribosomal profiling of human endogenous retroviruses in healthy tissues. BMC Genomics, 2024, 25, .	2.8	0
7058	Selective vulnerability of layer 5a corticostriatal neurons in Huntingtonâ€™s disease. Neuron, 2024, 112, 924-941.e10.	8.1	1
7059	IKKÎ² deletion from CNS macrophages increases neuronal excitability and accelerates the onset of EAE, while from peripheral macrophages reduces disease severity. Journal of Neuroinflammation, 2024, 21, .	7.2	0
7060	Dementia with Lewy Bodies: Genomics, Transcriptomics, and Its Future with Data Science. Cells, 2024, 13, 223.	4.1	0
7061	Transcriptomic profiling of early synucleinopathy in rats induced with preformed fibrils. Npj Parkinson's Disease, 2024, 10, .	5.3	2
7062	Comparative Analysis of Chloroplast Pan-Genomes and Transcriptomics Reveals Cold Adaptation in Medicago sativa. International Journal of Molecular Sciences, 2024, 25, 1776.	4.1	0
7063	A GPCR-neuropeptide axis dampens hyperactive neutrophils by promoting an alternative-like polarization during bacterial infection. Immunity, 2024, 57, 333-348.e6.	14.3	2
7064	LipidSIM: Inferring mechanistic lipid biosynthesis perturbations from lipidomics with a flexible, low-parameter, Markov modeling framework. Metabolic Engineering, 2024, 82, 110-122.	7.0	0
7065	Investigation of the usefulness of liver-specific deconvolution method by establishing a liver benchmark dataset. NAR Genomics and Bioinformatics, 2024, 6, .	3.2	1
7066	Multi-omics integration identifies cell-state-specific repression by PBRM1-PIAS1 cooperation. Cell Genomics, 2024, 4, 100471.	6.5	0
7067	Small-molecule agonist AdipoRon alleviates diabetic retinopathy through the AdipoR1/AMPK/EGR4 pathway. Journal of Translational Medicine, 2024, 22, .	4.4	0

#	Article	IF	Citations
7068	Single-cell transcriptome landscape of circulating CD4+ TÂcell populations in autoimmune diseases. Cell Genomics, 2024, 4, 100473.	6.5	1
7069	Microbiota modulation by dietary oat beta-glucan prevents steatotic liver disease progression. JHEP Reports, 2024, 6, 100987.	4.9	0
7070	Identification of candidate regulators of the response to early heat stress in climate-adapted wheat landraces via transcriptomic and co-expression network analyses. Frontiers in Plant Science, 0, 14, .	3.6	0
7071	Inactivation of lmo0946 (sif) induces the SOS response and MGEs mobilization and silences the general stress response and virulence program in Listeria monocytogenes. Frontiers in Microbiology, 0, 14, .	3.5	0
7072	Gene architecture is a determinant of the transcriptional response to bulky DNA damages. Life Science Alliance, 2024, 7, e202302328.	2.8	1
7073	Phylogenomic analyses and chromosome ploidy identification reveal multiple cryptic species in Allium sikkimense complex (Amaryllidaceae). Frontiers in Plant Science, 0, 14, .	3.6	0
7074	Transcriptome data from silica-preserved leaf tissue reveal gene flow patterns in a Caribbean bromeliad. Annals of Botany, 2024, 133, 459-472.	2.9	0
7075	RNA structure profiling at single-cell resolution reveals new determinants of cell identity. Nature Methods, 0, , .	19.0	2
7076	Altered gene expression linked to germline dysfunction following exposure of Caenorhabditis elegans to DEET. IScience, 2024, 27, 108699.	4.1	0
7081	Systematic identification of genotype-dependent enhancer variants in eosinophilic esophagitis. American Journal of Human Genetics, 2024, 111, 280-294.	6.2	0
7086	Yeast strains isolated from fermented beverage produce extracellular vesicles with anti-inflammatory effects. Scientific Reports, 2024, 14, .	3.3	0
7087	Formulated hydroxy fatty acids from fruit pomaces reduce apple scab development caused by Venturia inaequalis through a dual mode of action. Frontiers in Plant Science, 0, 14, .	3.6	0
7088	Neutrophil activation and clonal CAR-T re-expansion underpinning cytokine release syndrome during ciltacabtagene autoleucel therapy in multiple myeloma. Nature Communications, 2024, 15, .	12.8	0
7091	Transcriptional signals of transformation in human cancer. Genome Medicine, 2024, 16, .	8.2	0
7092	Polysaccharide preferred minority-dominant community assembly and exoenzyme enrichment in transparent exopolymer particles: Implication for global carbon cycle in water. Science of the Total Environment, 2024, 914, 169976.	8.0	0
7093	Transcriptome analysis of primary adult <scp>B</scp>â€cell lineage acute lymphoblastic leukemia identifies pathogenic variants and gene fusions, and predicts subtypes for in depth molecular diagnosis. European Journal of Haematology, 2024, 112, 731-742.	2.2	0
7094	Neural extracellular matrix regulates visual sensory motor integration. IScience, 2024, 27, 108846.	4.1	0
7095	Low-level resource partitioning supports coexistence among functionally redundant bacteria during successional dynamics. ISME Journal, 2024, 18, .	9.8	0

#	Article	IF	Citations
7096	Associations of TACSTD2/<scp>TROP2</scp> and NECTINâ€4/<scp>NECTIN</scp>â€4 with molecular subtypes, <scp>PDâ€L1</scp> expression, and FGFR3 mutational status in two advanced urothelial bladder cancer cohorts. Histopathology, 2024, 84, 863-876.	2.9	0
7097	Effect of clodronate on gene expression in the peripheral blood of horses. Journal of Veterinary Pharmacology and Therapeutics, 2024, 47, 187-192.	1.3	0
7100	IKZF3/Aiolos H195Y mutation identified in a mouse model of B cell leukemia results in altered DNA binding and altered STAT5-dependent gene expression. Gene, 2024, 900, 148131.	2.2	0
7101	Voltage-gated ion channels are expressed in the Malpighian tubules and anal papillae of the yellow fever mosquito (Aedes aegypti), and may regulate ion transport during salt and water imbalance. Journal of Experimental Biology, 2024, 227, .	1.7	1
7104	Deciphering maternal-fetal cross-talk in the human placenta during parturition using single-cell RNA sequencing. Science Translational Medicine, 2024, 16, .	12.4	0
7105	Gut microbiota reflect adaptation of cave-dwelling tadpoles to resource scarcity. ISME Journal, 2024, 18, .	9.8	0
7106	Metagenomics reveals the influence of small microplastics on microbial communities in coastal sediments. Science of the Total Environment, 2024, 914, 169982.	8.0	0
7107	Ecological niches and assembly dynamics of diverse microbial consortia in the gastrointestine of goat kids. ISME Journal, 2024, 18, .	9.8	0
7108	Development of an epigenetic clock to predict visual age progression of human skin. Frontiers in Aging, 0, 4, .	2.6	0
7109	Differential Gene Expression in Human Fibroblasts Simultaneously Exposed to Ionizing Radiation and Simulated Microgravity. Biomolecules, 2024, 14, 88.	4.0	0
7110	Fecal and oral microbiome analysis of snakes from China reveals a novel natural emerging disease reservoir. Frontiers in Microbiology, 0, 14, .	3.5	0
7111	Development of a mouse model expressing a bifunctional glutathione-synthesizing enzyme to study glutathione limitation inÂvivo. Journal of Biological Chemistry, 2024, 300, 105645.	3.4	0
7115	shinyDeepDR: A user-friendly R Shiny app for predicting anti-cancer drug response using deep learning. Patterns, 2024, 5, 100894.	5.9	0
7116	Genomic resources for a historical collection of cultivated two-row European spring barley genotypes. Scientific Data, 2024, 11, .	5.3	2
7124	Pancreatic cancer acquires resistance to MAPK pathway inhibition by clonal expansion and adaptive DNA hypermethylation. Clinical Epigenetics, 2024, 16, .	4.1	0
7126	SperMD: the expression atlas of sperm maturation. BMC Bioinformatics, 2024, 25, .	2.6	1
7127	An in situ digital synthesis strategy for the discovery and description of ocean life. Science Advances, 2024, 10, .	10.3	0
7128	Field survey of the phase and sex ratios of the brown alga <scp>Dictyota dichotoma</scp> (Dictyotales, Phaeophyceae) using sexâ€specific molecular markers. Phycological Research, 2024, 72, 123-132.	1.6	0

#	Article	IF	Citations
7129	Consolidation of a Molecular Signature of Healing in Cutaneous Leishmaniasis Is Achieved during the First 10 Days of Treatment. Journal of Immunology, 2024, 212, 894-903.	0.8	0
7130	Selective induction of human renal interstitial progenitor-like cell lineages from iPSCs reveals development of mesangial and EPO-producing cells. Cell Reports, 2024, 43, 113602.	6.4	0
7131	Plantar Skin Exhibits Altered Physiology, Constitutive Activation of Wound-Associated Phenotypes, and Inherently Delayed Healing. Journal of Investigative Dermatology, 2024, , .	0.7	0
7132	Myofibroblastic cancerâ€associated fibroblast subtype heterogeneity in pancreatic cancer. Journal of Surgical Oncology, 2024, 129, 860-868.	1.7	0
7133	Guidelines and important considerations for â€˜omics-level studies. , 2024, , 189-209.		0
7134	Rigor and reproducibility of RNA sequencing analyses. , 2024, , 211-245.		0
7135	Soluble and multivalent Jag1 DNA origami nanopatterns activate Notch without pulling force. Nature Communications, 2024, 15, .	12.8	2
7137	Maternal dietary choline levels cause transcriptome shift due to genotype-by-diet interactions in rainbow trout (Oncorhynchus mykiss). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2024, 49, 101193.	1.0	0
7140	Global biogeography and ecological implications of cobamide-producing prokaryotes. ISME Journal, 2024, 18, .	9.8	2
7141	Thermotolerance capabilities, blood metabolomics and mammary gland hemodynamics and transcriptomic profiles of slick-haired Holstein cattle during mid-lactation in Puerto Rico. Journal of Dairy Science, 2024, , .	3.4	0
7142	Review of gene expression using microarray and RNA-seq. , 2024, , 159-187.		0
7143	Deciphering the Role of ERBB3 Isoforms in Renal Cell Carcinoma: A Comprehensive Genomic and Transcriptomic Analysis. Medicina (Lithuania), 2024, 60, 181.	2.0	0
7145	DNA-guided transcription factor cooperativity shapes face and limb mesenchyme. Cell, 2024, 187, 692-711.e26.	28.9	2
7148	Nasopharyngeal airway long noncoding RNAs of infants with bronchiolitis and subsequent risk of developing childhood asthma. Journal of Allergy and Clinical Immunology, 2024, , .	2.9	0
7149	Interferon induced circRNAs escape herpesvirus host shutoff and suppress lytic infection. EMBO Reports, 2024, 25, 1541-1569.	4.5	0
7150	Aromatic amino acid metabolites alter interferon signaling and influenza pathogenesis. Frontiers in Molecular Biosciences, 0, 10, .	3.5	0
7152	The hagfish genome and the evolution of vertebrates. Nature, 2024, 627, 811-820.	27.8	3
7155	Multilevel analysis between Physcomitrium patens and Mortierellaceae endophytes explores potential longâ€standing interaction among land plants and fungi. Plant Journal, 2024, 118, 304-323.	5.7	0

#	Article	IF	Citations
7161	Tumor- and circulating-free DNA methylation identifies clinically relevant small cell lung cancer subtypes. Cancer Cell, 2024, 42, 225-237.e5.	16.8	0
7162	Significant Variations in Double-Stranded RNA Levels in Cultured Skin Cells. Cells, 2024, 13, 226.	4.1	0
7163	A novel computational pipeline for var gene expression augments the discovery of changes in the Plasmodium falciparum transcriptome during transition from in vivo to short-term in vitro culture. ELife, 0, 12, .	6.0	0
7164	The unfolded protein response of the endoplasmic reticulum protects Caenorhabditis elegans against DNA damage caused by stalled replication forks. G3: Genes, Genomes, Genetics, 2024, 14, .	1.8	0
7165	Transcriptional profiling identifies the early responses to Puccinia triticina infection in the adult plant leaf rust resistant wheat variety Toropi. Plant Pathology, 2024, 73, 832-845.	2.4	0
7166	Diurnal Rhythms in the Red Seaweed Gracilariopsis chorda are Characterized by Unique Regulatory Networks of Carbon Metabolism. Molecular Biology and Evolution, 2024, 41, .	8.9	0
7167	Neofunctionalization driven by positive selection led to the retention of the loqs2 gene encoding an Aedes specific dsRNA binding protein. BMC Biology, 2024, 22, .	3.8	0
7168	Secretory leukocyte protease inhibitor protects against severe urinary tract infection in mice. MBio, 2024, 15, .	4.1	0
7170	Phylogenomic curation of Ovate Family Proteins (OFPs) in the Uâ€™s Triangle of Brassica L. indicates stress-induced growth modulation. PLoS ONE, 2024, 19, e0297473.	2.5	0
7171	A Chromosome-Level Genome Assembly of the Non-Hematophagous Leech Whitmania pigra (Whitman) Tj ETQq1 1 0.784314 rgBT /Ove	2.4	0
7172	Multiomic analysis implicates nuclear hormone receptor signalling in clustering epilepsy. Translational Psychiatry, 2024, 14, .	4.8	1
7175	The helicase domain of human Dicer prevents RNAi-independent activation of antiviral and inflammatory pathways. EMBO Journal, 2024, 43, 806-835.	7.8	0
7176	Loss of Pip4k2c confers liver-metastatic organotropism through insulin-dependent PI3K-AKT pathway activation. Nature Cancer, 2024, 5, 433-447.	13.2	0
7177	Functional characterization of genes related to triterpene and flavonoid biosynthesis in Cyclocarya paliurus. Planta, 2024, 259, .	3.2	1
7179	TcSERPIN, an inhibitor that interacts with cocoa defense proteins and has biotechnological potential against human pathogens. Frontiers in Plant Science, 0, 15, .	3.6	0
7181	DNMT3B PWWP mutations cause hypermethylation of heterochromatin. EMBO Reports, 2024, 25, 1130-1155.	4.5	0
7182	Nanopore Direct RNA Sequencing Reveals the Short-Term Salt Stress Response in Maize Roots. Plants, 2024, 13, 405.	3.5	0
7184	Long-term effects of myo-inositol on traumatic brain injury: Epigenomic and transcriptomic studies. IBRO Neuroscience Reports, 2024, 16, 291-299.	1.6	0

#	Article	IF	Citations
7185	Convergent evolution of water-conducting cells in Marchantia recruited the ZHOUPI gene promoting cell wall reinforcement and programmed cell death. Current Biology, 2024, 34, 793-807.e7.	3.9	0
7186	Fatty acid production and associated gene pathways are altered by increased salinity and dimethyl sulfoxide treatments during cryopreservation of Symbiodinium pilosum (Symbiodiniaceae). Cryobiology, 2024, 114, 104855.	0.7	0
7187	Removal of antibiotic resistance genes during swine manure composting is strongly impaired by high levels of doxycycline residues. Waste Management, 2024, 177, 76-85.	7.4	0
7188	Conserved CKI1-mediated signaling is required for female germline specification in Marchantia polymorpha. Current Biology, 2024, 34, 1324-1332.e6.	3.9	1
7189	Heat Shock Protein Genes Affect the Rapid Cold Hardening Ability of Two Invasive Tephritids. Insects, 2024, 15, 90.	2.2	0
7190	Molecular Insights into the Accelerated Sprouting of and Apical Dominance Release in Potato Tubers Subjected to Post-Harvest Heat Stress. International Journal of Molecular Sciences, 2024, 25, 1699.	4.1	0
7191	Systems immunology of transcriptional responses to viral infection identifies conserved antiviral pathways across macaques and humans. Cell Reports, 2024, 43, 113706.	6.4	0
7193	Integrated Transcriptomics and Metabolomics Analysis Reveals the Effects of Cutting on the Synthesis of Flavonoids and Saponins in Chinese Herbal Medicine Astragalus mongholious. Metabolites, 2024, 14, 97.	2.9	0
7195	BCL7A and BCL7B potentiate SWI/SNF-complex-mediated chromatin accessibility to regulate gene expression and vegetative phase transition in plants. Nature Communications, 2024, 15, .	12.8	0
7197	Forensically relevant anatomical brain regions cannot be sub-differentiated by RNA expression analysis. Forensic Science, Medicine, and Pathology, 0, , .	1.4	0
7199	Linking gene expression to clinical outcomes in pediatric Crohnâ€™s disease using machine learning. Scientific Reports, 2024, 14, .	3.3	0
7200	Unveiling CRESS DNA Virus Diversity in Oysters by Virome. Viruses, 2024, 16, 228.	3.3	0
7201	An extended wave of global mRNA deadenylation sets up a switch in translation regulation across the mammalian oocyte-to-embryo transition. Cell Reports, 2024, 43, 113710.	6.4	1
7202	The functional decline of tomato plants infected by Candidatus Liberbacter solanacearum: an RNA-seq transcriptomic analysis. Frontiers in Plant Science, 0, 15, .	3.6	0
7203	Transcriptome-Wide Identification and Expression Analysis of bHLH Family Genes in Iris domestica under Drought and Cu Stress. International Journal of Molecular Sciences, 2024, 25, 1773.	4.1	0
7204	Blood transcriptomics analysis offers insights into variant-specific immune response to SARS-CoV-2. Scientific Reports, 2024, 14, .	3.3	0
7205	Lung endothelium exploits susceptible tumor cell states to instruct metastatic latency. Nature Cancer, 0, , .	13.2	1
7206	Dysfunction of duplicated pair rice histone acetyltransferases causes segregation distortion and an interspecific reproductive barrier. Nature Communications, 2024, 15, .	12.8	0

#	Article	IF	Citations
7207	Nkx2.3 transcription factor is a key regulator of mucous cell identity in salivary glands. Developmental Biology, 2024, 509, 1-10.	2.0	0
7208	Genome-wide identification and analysis of WD40 proteins reveal that NtTTG1 enhances drought tolerance in tobacco (Nicotiana tabacum). BMC Genomics, 2024, 25, .	2.8	0
7209	State-transition modeling of blood transcriptome predicts disease evolution and treatment response in chronic myeloid leukemia. Leukemia, 2024, 38, 769-780.	7.2	0
7210	BCG as an Innovative Option for HCC Treatment: Repurposing and Mechanistic Insights. Advanced Science, 2024, 11, .	11.2	0
7211	Reference transcriptome assembly of a protogynous sex change fish, harlequin sandsmelt (Parapercis) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.1	0
7212	Auxin coâ€receptor <scp>IAA17</scp>/<scp>AXR3</scp> controls cell elongation in Arabidopsis thaliana root solely by modulation of nuclear auxin pathway. New Phytologist, 2024, 241, 2448-2463.	7.3	1
7213	Molecular and mineral responses of corals grown under artificial Calcite Sea conditions. Geobiology, 2024, 22, .	2.4	0
7216	Role of Transcriptomics in Precision Oncology. Reports of Radiotherapy & Oncology, 2024, 11, .	0.1	0
7222	SLE serum induces altered goblet cell differentiation and leakiness in human intestinal organoids. EMBO Molecular Medicine, 2024, 16, 547-574.	6.9	0
7223	Nigral transcriptomic profiles in Engrailed-1 hemizygous mouse models of Parkinsonâ€™s disease reveal upregulation of oxidative phosphorylation-related genes associated with delayed dopaminergic neurodegeneration. Frontiers in Aging Neuroscience, 0, 16, .	3.4	0
7224	Transcriptional signature of host shift in the seed beetle Zabrotes subfasciatus. Genetics and Molecular Biology, 2024, 47, .	1.3	0
7225	Regulatory Pathways in Growth Plate Chondrocytes that Are Impacted by Matrix Vesicle microRNA Identified by Targeted RISC Pulldown and Sequencing of the Resulting Transcriptome. Calcified Tissue International, 2024, 114, 409-418.	3.1	0
7227	Spatio-temporal transcriptome and storage compound profiles of developing faba bean (Vicia faba) seed tissues. Frontiers in Plant Science, 0, 15, .	3.6	0
7228	Proteotransciptomics of the Most Popular Host Sea Anemone Entacmaea quadricolor Reveals Not All Toxin Genes Expressed by Tentacles Are Recruited into Its Venom Arsenal. Toxins, 2024, 16, 85.	3.4	0
7229	Multiomics analyses reveal the central role of the nucleolus and its machinery during heat stress acclimation in Pinus radiata. Journal of Experimental Botany, 2024, 75, 2558-2573.	4.8	0
7230	Identification of candidate genes associated with host-seeking behavior in the parasitoid wasp Diachasmimorpha longicaudata. BMC Genomics, 2024, 25, .	2.8	0
7231	In situ community transcriptomics illuminates CO ₂ -fixation potentials and supporting roles of phagotrophy and proton pump in plankton in a subtropical marginal sea. Microbiology Spectrum, 2024, 12, .	3.0	0
7232	Ultrahigh frequencies of peripherally matured LGI1- and CASPR2-reactive B cells characterize the cerebrospinal fluid in autoimmune encephalitis. Proceedings of the National Academy of Sciences of the United States of America, 2024, 121, .	7.1	1

#	Article	IF	Citations
7236	Diverging cell wall strategies for drought adaptation in two maize inbreds with contrasting lodging resistance. Plant, Cell and Environment, 2024, 47, 1747-1768.	5.7	0
7237	Gut resistome profiling reveals high diversity and fluctuations in pancreatic cancer cohorts. Frontiers in Cellular and Infection Microbiology, 0, 14, .	3.9	0
7238	PpSCARECROW1 (PpSCR1) regulates leaf blade and mid-vein development in Physcomitrium patens. Plant Molecular Biology, 2024, 114, .	3.9	0
7239	First neurotranscriptome of adults Tambaquis (Colossoma macropomum) with characterization and differential expression between males and females. Scientific Reports, 2024, 14, .	3.3	0
7240	Daily fluctuation of Lactobacillus species and their antibiotic resistome in the colon of growing pigs. Science of the Total Environment, 2024, 918, 170821.	8.0	0
7243	Changes in Soil Chemistry and Microbial Communities in Rhizospheres of Planted Gastrodia elata on a Barren Slope and under a Forest. Forests, 2024, 15, 331.	2.1	0
7244	Compromised transcription-mRNA export factor THOC2 causes R-loop accumulation, DNA damage and adverse neurodevelopment. Nature Communications, 2024, 15, .	12.8	0
7245	Transcriptome Sequencing of Rectretohalophyte Aeluropus lagopoides Revealed Molecular Insight of Salt Stress Adaptation. Journal of Plant Growth Regulation, 0, , .	5.1	0
7246	A paternal signal induces endosperm proliferation upon fertilization in Arabidopsis. Science, 2024, 383, 646-653.	12.6	0
7247	Influence of TP53 Comutation on the Tumor Immune Microenvironment and Clinical Outcomes With Immune Checkpoint Inhibitors in STK11-Mutant Nonâ€“Small-Cell Lung Cancer. JCO Precision Oncology, 2024, , .	3.0	0
7248	Global repair is the primary nucleotide excision repair subpathway for the removal of pyrimidine-pyrimidone (6-4) damage from the Arabidopsis genome. Scientific Reports, 2024, 14, .	3.3	0
7249	The adaptation of bumblebees to extremely high elevation associated with their gut microbiota. MSystems, 2024, 9, .	3.8	0
7250	Persistence of backtracking by human RNA polymerase II. Molecular Cell, 2024, 84, 897-909.e4.	9.7	0
7251	A Potential Prognostic Gene Signature Associated with p53-Dependent NTRK1 Activation and Increased Survival of Neuroblastoma Patients. Cancers, 2024, 16, 722.	3.7	0
7252	Tumoral and stromal hMENA isoforms impact tertiary lymphoid structure localization in lung cancer and predict immune checkpoint blockade response in patients with cancer. EBioMedicine, 2024, 101, 105003.	6.1	0
7253	Exploring the Functions of Mutant p53 through TP53 Knockout in HaCaT Keratinocytes. Current Issues in Molecular Biology, 2024, 46, 1451-1466.	2.4	0
7255	Modulation of the wheat transcriptome by TaZFP13D under well-watered and drought conditions. Plant Molecular Biology, 2024, 114, .	3.9	0
7256	Oligogalacturonide application increases resistance to Fusarium head blight in durum wheat. Journal of Experimental Botany, 0, , .	4.8	0

#	Article	IF	Citations
7258	MGMT activated by Wnt pathway promotes cisplatin tolerance through inducing slow-cycling cells and nonhomologous end joining in colorectal cancer. Journal of Pharmaceutical Analysis, 2024, , .	5.3	0
7259	Semen promotes oocyte development in Sebastes schlegelii elucidating ovarian development dynamics in live-bearing fish. IScience, 2024, 27, 109193.	4.1	0
7260	The short-term effect of simulated acid rain and nitrogen deposition on the soil microbial functional profile targeting C, N, and P cycling. Applied Soil Ecology, 2024, 197, 105327.	4.3	0
7261	Agarose amplification based sequencing characterization cell-free RNA in preimplantation spent embryo medium. Analytica Chimica Acta, 2024, 1296, 342331.	5.4	0
7262	Distribution patterns and functional diversity of DNA viruses determined by ecological niches in huge river ecosystems. Virology, 2024, 593, 110015.	2.4	0
7266	Exploiting epigenetic targets to overcome taxane resistance in prostate cancer. Cell Death and Disease, 2024, 15, .	6.3	0
7267	Pan-transcriptomic analysis reveals alternative splicing control of cold tolerance in rice. Plant Cell, 0, , .	6.6	0
7268	The transcriptional regulatory network modulating human trophoblast stem cells to extravillous trophoblast differentiation. Nature Communications, 2024, 15, .	12.8	0
7270	Accounting for isoform expression increases power to identify genetic regulation of gene expression. PLoS Computational Biology, 2024, 20, e1011857.	3.2	0
7271	Deciphering soil resistance and virulence gene risks in conventional and organic farming systems. Journal of Hazardous Materials, 2024, 468, 133788.	12.4	0
7272	Effective AAV-mediated gene replacement therapy in retinal organoids modeling AIPL1-associated LCA4. Molecular Therapy - Nucleic Acids, 2024, 35, 102148.	5.1	0
7273	The dopamine transporter antagonist vanoxerine inhibits G9a and suppresses cancer stem cell functions in colon tumors. Nature Cancer, 0, , .	13.2	1
7274	The IL6/JAK/STAT3 signaling axis is a therapeutic vulnerability in SMARCB1-deficient bladder cancer. Nature Communications, 2024, 15, .	12.8	0
7275	RNA-Seq and RNA Expression Profiling. Molecular Pathology Library, 2023, , 113-123.	0.1	0
7276	Cognitive and immunological effects of yoga compared to memory training in older women at risk for alzheimerâ€™s disease. Translational Psychiatry, 2024, 14, .	4.8	0
7277	Molecular profiling of the hippocampus of children with autism spectrum disorder. Molecular Psychiatry, 0, , .	7.9	0
7278	Tissue-location-specific transcription programs drive tumor dependencies in colon cancer. Nature Communications, 2024, 15, .	12.8	0
7279	A retroviral link to vertebrate myelination through retrotransposon-RNA-mediated control of myelin gene expression. Cell, 2024, 187, 814-830.e23.	28.9	0

#	Article	IF	Citations
7280	Inhibition of Aurora Kinase Induces Endogenous Retroelements to Induce a Type I/III IFN Response via RIG-I. Cancer Research Communications, 2024, 4, 540-555.	1.7	0
7281	RNA-sequencing predicts a role of androgen receptor and aldehyde dehydrogenase 1A1 in osteosarcoma lung metastases. Oncogene, 2024, 43, 1007-1018.	5.9	0
7282	Ranking the risk of antibiotic resistance genes by metagenomic and multifactorial analysis in hospital wastewater systems. Journal of Hazardous Materials, 2024, 468, 133790.	12.4	0
7283	Feedingâ€structure morphogenesis in â€œrhabditidâ€•and diplogastrid nematodes is not controlled by a conserved genetic module. Evolution & Development, 2024, 26, .	2.0	1
7284	Differential responses of selectively bred mussels (Perna canaliculus) to heat stressâ€”survival, immunology, gene expression and microbiome diversity. Frontiers in Physiology, 0, 14, .	2.8	0
7285	Transcriptional profiling of peripheral blood mononuclear cells identifies inflammatory phenotypes in Ataxia Telangiectasia. Orphanet Journal of Rare Diseases, 2024, 19, .	2.7	0
7287	Transcriptome profile of pecan scab resistant and susceptible trees from a pecan provenance collection. BMC Genomics, 2024, 25, .	2.8	0
7288	Gene co-expression network analysis reveal core responsive genes in Parascaris univalens tissues following ivermectin exposure. PLoS ONE, 2024, 19, e0298039.	2.5	0
7290	T- and L-Type Calcium Channels Maintain Calcium Oscillations in the Murine Zona Glomerulosa. Hypertension, 2024, 81, 811-822.	2.7	0
7291	Genome-wide identification, stress- and hormone-responsive expression characteristics, and regulatory pattern analysis of Scutellaria baicalensis SbSPLs. Plant Molecular Biology, 2024, 114, .	3.9	0
7294	Linking genomic prediction of fillet fat content in Atlantic salmon to underlying changes in lipid metabolism regulation. Aquaculture, 2024, 584, 740678.	3.5	0
7297	Activation of gp130 signaling in T cells drives T _H 17-mediated multi-organ autoimmunity. Science Signaling, 2024, 17, .	3.6	0
7299	Biochemical, molecular, and physiological assessments of crude oil dietary exposure in sub-adult red drum (Sciaenops ocellatus). Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2024, 278, 109864.	2.6	0
7300	Transcriptomic evaluation of tau and TDP-43 synergism shows tauopathy predominance and reveals potential modulating targets. Neurobiology of Disease, 2024, 193, 106441.	4.4	0
7301	Large-scale analysis reveals splicing biomarkers for tuberculosis progression and prognosis. Computers in Biology and Medicine, 2024, 171, 108187.	7.0	0
7302	A single cell atlas of frozen shoulder capsule identifies features associated with inflammatory fibrosis resolution. Nature Communications, 2024, 15, .	12.8	0
7303	Inter-species interactions between two bacterial flower commensals and a floral pathogen reduce disease incidence and alter pathogen activity. MBio, 2024, 15, .	4.1	0
7304	Promotion of cold stress tolerance in transplanted Pinus densiflora seedlings after long-term moderate drought hardening. Forest Ecology and Management, 2024, 557, 121773.	3.2	0

#	Article	IF	Citations
7305	Retinal dysfunction in Huntingtonâ€™s disease mouse models concurs with local gliosis and microglia activation. Scientific Reports, 2024, 14, .	3.3	0
7306	Stress-induced stenotic vascular remodeling via reduction of plasma omega-3 fatty acid metabolite 4-oxoDHA by noradrenaline. Scientific Reports, 2024, 14, .	3.3	0
7307	Integrated fullâ€length transcriptome and metabolome analysis reveals the defence response of melon to gummy stem blight. Plant, Cell and Environment, 2024, 47, 1997-2010.	5.7	0
7308	Transcriptomic Insights and Cytochrome P450 Gene Analysis in Kadsura coccinea for Lignan Biosynthesis. Genes, 2024, 15, 270.	2.4	0
7309	Aberrant miR-29 is a predictive feature of severe phenotypes in pediatric Crohnâ€™s disease. JCI Insight, 2024, 9, .	5.0	0
7310	Single-cell spatial transcriptomic and translatomic profiling of dopaminergic neurons in health, aging, and disease. Cell Reports, 2024, 43, 113784.	6.4	0
7311	Metagenomic analysis of the microbial communities and associated network of nitrogen metabolism genes in the Ryukyu limestone aquifer. Scientific Reports, 2024, 14, .	3.3	0
7312	An iron rheostat controls hematopoietic stem cell fate. Cell Stem Cell, 2024, 31, 378-397.e12.	11.1	0
7313	The symbiont Wolbachia alleviates pesticide susceptibility in the twoâ€spotted spider mite Tetranychus urticae through enhanced host detoxification pathways. Insect Science, 0, , .	3.0	0
7314	First-in-Class Humanized Antibody against Alternatively Spliced Tissue Factor Augments Anti-Metastatic Efficacy of Chemotherapy in a Preclinical Model of Pancreatic Ductal Adenocarcinoma. International Journal of Molecular Sciences, 2024, 25, 2580.	4.1	0
7315	Downregulation of Ribosomal Protein Genes Is Revealed in a Model of Rat Hippocampal Neuronal Culture Activation with GABA(A)R/GlyRa2 Antagonist Picrotoxin. Cells, 2024, 13, 383.	4.1	0
7316	Dynamic root microbiome sustains soybean productivity under unbalanced fertilization. Nature Communications, 2024, 15, .	12.8	0
7317	Host-pathogen interactions: databases and approaches for data generation. , 2024, , 15-51.		0
7318	Dynamic and distinct histone modifications facilitate human trophoblast lineage differentiation. Scientific Reports, 2024, 14, .	3.3	0
7319	Targeting HDAC6 to treat heart failure with preserved ejection fraction in mice. Nature Communications, 2024, 15, .	12.8	0
7320	Ultrafast sound production mechanism in one of the smallest vertebrates. Proceedings of the National Academy of Sciences of the United States of America, 2024, 121, .	7.1	0
7321	Genome-scale pan-cancer interrogation of lncRNA dependencies using CasRx. Nature Methods, 2024, 21, 584-596.	19.0	0
7322	Gene-edited Mtsoc1 triple mutant Medicago plants do not flower. Frontiers in Plant Science, 0, 15, .	3.6	0

#	Article	IF	Citations
7323	Pooled effector library screening in protoplasts rapidly identifies novel Avr genes. Nature Plants, 2024, 10, 572-580.	9.3	0
7324	Genome-wide identification of the N6-methyladenosine regulatory genes reveals NtFIP37B increases drought resistance of tobacco (Nicotiana tabacum L.). BMC Plant Biology, 2024, 24, .	3.6	0
7325	Cellular reprogramming in vivo initiated by SOX4 pioneer factor activity. Nature Communications, 2024, 15, .	12.8	0
7326	Waterlogging Hardening Effect on Transplant Stress Tolerance in Pinus densiflora. Forests, 2024, 15, 445.	2.1	0
7327	Sexual dimorphism during integrative endocrine and immune responses to ionizing radiation in mice. Scientific Reports, 2024, 14, .	3.3	0
7328	Cellâ€typeâ€specific transcriptomics uncovers spatial regulatory networks in bioenergy sorghum stems. Plant Journal, 0, , .	5.7	0
7330	Cross-evaluation of E.Âcoliâ€™s operon structures via a whole-cell model suggests alternative cellular benefits for low- versus high-expressing operons. Cell Systems, 2024, , .	6.2	0
7338	Histone butyrylation in the mouse intestine is mediated by the microbiota and associated with regulation of gene expression. Nature Metabolism, 2024, 6, 697-707.	11.9	0
7339	Circulating tumor cell clustering modulates RNA splicing and polyadenylation to facilitate metastasis. Cancer Letters, 2024, 588, 216757.	7.2	0
7342	Transcriptomics and metabolomics analysis reveal the dietary copper deficiency and supplementation effects of liver gene expression and metabolite change in grazing sheep. BMC Genomics, 2024, 25, .	2.8	0
7345	SOX17 enables immune evasion of early colorectal adenomas and cancers. Nature, 2024, 627, 636-645.	27.8	0
7346	Ror homolog nhr-23 is essential for both developmental clock and circadian clock in C. elegans. Communications Biology, 2024, 7, .	4.4	0
7347	Differential regulation of miRNAs involved in the susceptible and resistance responses of wheat cultivars to wheat streak mosaic virus and Triticum mosaic virus. BMC Genomics, 2024, 25, .	2.8	0
7348	Transcriptome Responses to Different Salinity Conditions in Litoditis marina, Revealed by Long-Read Sequencing. Genes, 2024, 15, 317.	2.4	0
7349	Chemical modification patterns for microRNA therapeutic mimics: a structure-activity relationship (SAR) case-study on miR-200c. Nucleic Acids Research, 2024, 52, 2792-2807.	14.5	0
7350	Investigating the overlap of machine learning algorithms in the final results of RNA-seq analysis on gene expression estimation. Health Information Science and Systems, 2024, 12, .	5.2	0
7351	Red pandas with different diets and environments exhibit different gut microbial functional composition and capacity. Integrative Zoology, 0, , .	2.6	0
7352	Maternal inflammation regulates fetal emergency myelopoiesis. Cell, 2024, 187, 1402-1421.e21.	28.9	0

#	Article	IF	Citations
7353	On the Way to Translatomic Mapping, a State-of-the-Art. Russian Journal of Plant Physiology, 2023, 70, .	1.1	0
7354	BRG1 establishes the neuroectodermal chromatin landscape to restrict dorsal cell fates. Science Advances, 2024, 10, .	10.3	0
7355	Sarcoma microenvironment cell states and ecosystems are associated with prognosis and predict response to immunotherapy. Nature Cancer, 2024, 5, 642-658.	13.2	0
7356	Transcriptomic Profiling of Pleural Effusions: Differences in Malignant and Infectious Fluids. Medicina (Lithuania), 2024, 60, 424.	2.0	0
7357	Metabolomic and transcriptomic analysis of bitter compounds in Dendrocalamopsis oldhamii shoots. Journal of Food Composition and Analysis, 2024, 130, 106140.	3.9	0
7358	Pseudomonas aeruginosa transcriptome analysis of metal restriction in ex vivo cystic fibrosis sputum. Microbiology Spectrum, 2024, 12, .	3.0	0
7359	A human lymphoma organoid model for evaluating and targeting the follicular lymphoma tumor immune microenvironment. Cell Stem Cell, 2024, 31, 410-420.e4.	11.1	0
7360	Complete genome assembly provides a highâ€quality skeleton for <scp>panâ€NLRome</scp> construction in melon. Plant Journal, 0, , .	5.7	0
7361	Dual role of <scp>GRHL3</scp> in bladder carcinogenesis depending on histological subtypes. Molecular Oncology, 0, , .	4.6	0
7362	Decoding the leaf apical meristem of Guarea glabra Vahl (Meliaceae): insight into the evolution of indeterminate pinnate leaves. Scientific Reports, 2024, 14, .	3.3	0
7363	The effect of gonadal hormones on the gene expression of brain-pituitary in protandrous black porgy, Acanthopagrus schlegelii. General and Comparative Endocrinology, 2024, 351, 114482.	1.8	0
7364	Widespread stable noncanonical peptides identified by integrated analyses of ribosome profiling and ORF features. Nature Communications, 2024, 15, .	12.8	0
7365	How tool combinations in different pipeline versions affect the outcome in RNA-seq analysis. NAR Genomics and Bioinformatics, 2024, 6, .	3.2	0
7366	Study on somatic embryogenesis of cinnamomum camphora based on transcriptome sequencing. Revista Brasileira De Botanica, 0, , .	1.3	0
7367	Human cortical neurogenesis is altered via glucocorticoid-mediated regulation of ZBTB16 expression. Neuron, 2024, 112, 1426-1443.e11.	8.1	0
7369	Clinical and genomic characterization of chemoradiation-resistant HPV-positive oropharyngeal squamous cell carcinoma. Frontiers in Oncology, 0, 14, .	2.8	0
7370	Metagenomic analysis of the intestinal microbiome reveals the potential mechanism involved in Bacillus amyloliquefaciens in treating schistosomiasis japonica in mice. Microbiology Spectrum, 2024, 12, .	3.0	0
7371	Eubacterium rectale is a potential marker of altered gut microbiota in psoriasis and psoriatic arthritis. Microbiology Spectrum, 2024, 12, .	3.0	0

#	Article	IF	Citations
7372	Human otic progenitor cell models of congenital hearing loss reveal potential pathophysiologic mechanisms of Zika virus and cytomegalovirus infections. MBio, 2024, 15, .	4.1	0
7373	Genetic and transcriptomic landscape of colonic diverticulosis. Gut, 0, , gutjnl-2023-331267.	12.1	0
7374	Transcriptomic analysis delineates preterm prelabor rupture of membranes from preterm labor in preterm fetal membranes. BMC Medical Genomics, 2024, 17, .	1.5	0
7375	Zeolitic imidazolate frameworks activate endosomal Toll-like receptors and potentiate immunogenicity of SARS-CoV-2 spike protein trimer. Science Advances, 2024, 10, .	10.3	0
7376	CASZ1 Is Essential for Skin Epidermal Terminal Differentiation. Journal of Investigative Dermatology, 2024, , .	0.7	0
7378	Cell-cycle inhibition and immune microenvironment in breast cancer treated with ribociclib and letrozole or chemotherapy. Npj Breast Cancer, 2024, 10, .	5.2	0
7379	Transcriptomic, Proteomic, and Genomic Mutational Fraction Differences Based on HPV Status Observed in Patient-Derived Xenograft Models of Penile Squamous Cell Carcinoma. Cancers, 2024, 16, 1066.	3.7	0
7380	Constructing the metabolic network of wheat kernels based on structure-guided chemical modification and multi-omics data. Journal of Genetics and Genomics, 2024, , .	3.9	0
7382	Proteomic analysis of the developing mammalian brain links PCDH19 to the Wnt/Î²-catenin signalling pathway. Molecular Psychiatry, 0, , .	7.9	0
7383	Introgressions lead to reference bias in wheat RNA-seq analysis. BMC Biology, 2024, 22, .	3.8	0
7384	Differential involvement of PEBP genes in early flowering of Peucedanum praeruptorum Dunn. Postharvest Biology and Technology, 2024, 212, 112860.	6.0	0
7385	Forward genetic screen using a gene-breaking trap approach identifies a novel role of grin2bb-associated RNA transcript (grin2bbART) in zebrafish heart function. Frontiers in Cell and Developmental Biology, 0, 12, .	3.7	0
7386	Transcriptomics: illuminating the molecular landscape of vegetable crops: a review. Journal of Plant Biochemistry and Biotechnology, 0, , .	1.7	0
7387	Regulation of nonâ€canonical proteins from diverse origins through the nonsenseâ€mediated mRNA decay pathway. Proteomics, 0, , .	2.2	0
7388	Field application of de novo transcriptomic analysis to evaluate the effects of sublethal freshwater salinization on Gasterosteus aculeatus in urban streams. PLoS ONE, 2024, 19, e0298213.	2.5	0
7389	Clobetasol propionate, a Nrf-2 inhibitor, sensitizes human lung cancer cells to radiation-induced killing via mitochondrial ROS-dependent ferroptosis. Acta Pharmacologica Sinica, 0, , .	6.1	0
7391	Starvation resistance in the nematode Pristionchus pacificus requires a conserved supplementary nuclear receptor. Zoological Letters, 2024, 10, .	1.3	0
7392	MLL1 regulates cytokine-driven cell migration and metastasis. Science Advances, 2024, 10, .	10.3	0

#	Article	IF	Citations
7393	Multimodal stimulation screens reveal unique and shared genes limiting TÂcell fitness. Cancer Cell, 2024, 42, 623-645.e10.	16.8	0
7395	Transcriptome Profiling of a Salt Excluder Hybrid Grapevine Rootstock â€˜Ruggeriâ€™ throughout Salinity. Plants, 2024, 13, 837.	3.5	0
7396	Landscape of global urban environmental resistome and its association with local socioeconomic and medical status. Science China Life Sciences, 0, , .	4.9	0
7397	Computational identification of natural senotherapeutic compounds that mimic dasatinib based on gene expression data. Scientific Reports, 2024, 14, .	3.3	0
7398	Integrated metabolomic and transcriptomic analysis reveals the mechanism of high polysaccharide content in tetraploid Dendrobium catenatum Lindl. Industrial Crops and Products, 2024, 212, 118391.	5.2	0
7399	Molecular adaptations underlying high-frequency hearing in the brain of CF bats species. BMC Genomics, 2024, 25, .	2.8	0
7402	DeTox: a pipeline for the detection of toxins in venomous organisms. Briefings in Bioinformatics, 2024, 25, .	6.5	0
7403	Opsin expression varies across larval development and taxa in pteriomorphian bivalves. Frontiers in Neuroscience, 0, 18, .	2.8	0
7404	Transcriptome Data Analysis Applied to Grapevine Growth Stage Identification. Agronomy, 2024, 14, 613.	3.0	0
7406	Microbiota-derived indoles alleviate intestinal inflammation and modulate microbiome by microbial cross-feeding. Microbiome, 2024, 12, .	11.1	0
7407	Magnesium oxide nanoparticles reduce clubroot by regulating plant defense response and rhizosphere microbial community of tumorous stem mustard (Brassica juncea var. tumida). Frontiers in Microbiology, 0, 15, .	3.5	0
7409	Transcriptional chronology reveals conserved genes involved in pennate diatom sexual reproduction. Molecular Ecology, 2024, 33, .	3.9	0
7411	Microbial communities, functional, and flavor differences among three different-colored high-temperature Daqu: A comprehensive metagenomic, physicochemical, and electronic sensory analysis. Food Research International, 2024, 184, 114257.	6.2	0
7412	SKA2 regulated hyperactive secretory autophagy drives neuroinflammation-induced neurodegeneration. Nature Communications, 2024, 15, .	12.8	0
7413	Tailored midgut gene expression in Spodoptera litura (Lepidoptera: Noctuidae) feeding on Zea mays indicates a tug of war. Arthropod-Plant Interactions, 0, , .	1.1	0
7414	Pervasive environmental chemicals impair oligodendrocyte development. Nature Neuroscience, 0, , .	14.8	0
7415	N-Acetylcysteine Alters Disease Progression and Increases Janus Kinase Mutation Frequency in a Mouse Model of Precursor B-Cell Acute Lymphoblastic Leukemia. Journal of Pharmacology and Experimental Therapeutics, 2024, 389, 40-50.	2.5	0
7416	ATRX guards against aberrant differentiation in mesenchymal progenitor cells. Nucleic Acids Research, 0, , .	14.5	0

#	Article	IF	Citations
7417	Genome-scale requirements for dynein-based transport revealed by a high-content arrayed CRISPR screen. Journal of Cell Biology, 2024, 223, .	5.2	0
7418	Non-coding autoimmune risk variant defines role for ICOS in T peripheral helper cell development. Nature Communications, 2024, 15, .	12.8	0
7419	Unraveling athletic performance: Transcriptomics and external load monitoring in handball competition. PLoS ONE, 2024, 19, e0299556.	2.5	0
7420	A vaccine targeting antigen-presenting cells through CD40 induces protective immunity against Nipah disease. Cell Reports Medicine, 2024, 5, 101467.	6.5	0
7421	Protocol for identifying differentially expressed genes using the RumBall RNA-seq analysis platform. STAR Protocols, 2024, 5, 102926.	1.2	0
7422	Identification of gene regulatory networks affected across drug-resistant epilepsies. Nature Communications, 2024, 15, .	12.8	0
7423	Longitudinal Mapping of Personal Biotic and Abiotic Exposomes and Transcriptome in Underwater Confined Space Using Wearable Passive Samplers. Environmental Science & Technology, 2024, 58, 5229-5243.	10.0	0
7424	T cells with increased responsiveness cause obesity in mice without diet intervention. IScience, 2024, 27, 109471.	4.1	0
7425	Machine learning on alignment features for parent-of-origin classification of simulated hybrid RNA-seq. BMC Bioinformatics, 2024, 25, .	2.6	0
7427	The Madagascar palm genome provides new insights on the evolution of Apocynaceae specialized metabolism. Heliyon, 2024, 10, e28078.	3.2	0
7428	Analyzes of mealybug (Pseudococcus longispinus) virome reveal grapevine viruses diversity. Tropical Plant Pathology, 0, , .	1.5	0
7429	Gut bacteriaâ€“derived serotonin promotes immune tolerance in early life. Science Immunology, 2024, 9, .	11.9	0
7430	metaProbiotics: a tool for mining probiotic from metagenomic binning data based on a language model. Briefings in Bioinformatics, 2024, 25, .	6.5	0
7431	Transcriptomics of Hostâ€“Pathogen Interaction. , 2024, , 377-397.		0
7432	Lose-lose consequences of bacterial community-driven invasions in soil. Microbiome, 2024, 12, .	11.1	0
7434	Physiological and molecular mechanisms of radicle development of somatic embryos in Schisandra chinensis cultured in the dark. Plant Cell, Tissue and Organ Culture, 2024, 157, .	2.3	0
7435	Module-based regularization improves Gaussian graphical models when observing noisy data. Applied Network Science, 2024, 9, .	1.5	0
7436	PvGeneExpDB: An integrative gene expression database for in-depth understanding on the Pacific white shrimp (Litopenaeus vannamei). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2024, 50, 101227.	1.0	0

#	Article	IF	Citations
7437	Detecting differential transcript usage in complex diseases with SPIT. Cell Reports Methods, 2024, 4, 100736.	2.9	0
7438	Microbial species pool-mediated diazotrophic community assembly in crop microbiomes during plant development. MSystems, 2024, 9, .	3.8	0
7439	Uncovering the molecular mechanisms of russet skin formation in Niagara grapevine (Vitis vinifera Ã—) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.3	0
7440	The Use of Nanopore Sequencing to Analyze the Chloroplast Transcriptome Part II: Bioinformatic Analyzes and Virtual RNA Blots. Methods in Molecular Biology, 2024, , 259-267.	0.9	0
7442	Comparative transcriptomic and epigenomic analyses to identify the cold resistance-associated genes and disclose the regulatory mechanisms in tilapias. Aquaculture, 2024, 587, 740858.	3.5	0
7443	The solute carrier SLC7A1 may act as a protein transporter at the blood-brain barrier. European Journal of Cell Biology, 2024, 103, 151406.	3.6	0
7444	Meta-analysis of public RNA sequencing data of abscisic acid-related abiotic stresses in Arabidopsis thaliana. Frontiers in Plant Science, 0, 15, .	3.6	0
7445	Acute Administration of HIV-1 Tat Protein Drives Glutamatergic Alterations in a Rodent Model of HIV-Associated Neurocognitive Disorders. Molecular Neurobiology, 0, , .	4.0	0
7446	Interaction of tetracycline and copper co-intake in inducing antibiotic resistance genes and potential pathogens in mouse gut. Environment International, 2024, 186, 108594.	10.0	0
7447	InPACT: a computational method for accurate characterization of intronic polyadenylation from RNA sequencing data. Nature Communications, 2024, 15, .	12.8	0
7448	Vine tea total flavonoids activate the AMPK/mTOR pathway to amelioration hepatic steatosis in mice fed a highâ€fat diet. Journal of Food Science, 0, , .	3.1	0
7449	The WIP6 transcription factor TOO MANY LATERALS specifies vein type in C4 and C3 grass leaves. Current Biology, 2024, 34, 1670-1686.e10.	3.9	0
7453	Assessing the complementary information from an increased number of biologically relevant features in liquid biopsy-derived RNA-Seq data. Heliyon, 2024, 10, e27360.	3.2	0
7455	Comparison of SARS-CoV-2 variants of concern in primary human nasal cultures demonstrates Delta as most cytopathic and Omicron as fastest replicating. MBio, 2024, 15, .	4.1	0
7457	The impact of genetically controlled splicing on exon inclusion and protein structure. PLoS ONE, 2024, 19, e0291960.	2.5	0
7458	Comprehensive transcriptome analysis reveals altered mRNA splicing and post-transcriptional changes in the aged mouse brain. Nucleic Acids Research, 2024, 52, 2865-2885.	14.5	0